Analisi e Modificazioni di Sequenze di DNA o di RNA con la

TEORIA TRICROMATICA DELL'EQUILIBRIO DEI SISTEMI

I MISTERI DEL DNA

(Parte Seconda)

Relazioni tra SARS-CoV-2 e il Codice Sorgente del Vaccino mRNA SARS-CoV-2 BioNTech/Pfizer

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RIASSUNTO

Questo lavoro rappresenta il coerente proseguimento di quanto è stato già pubblicato nel documento "*I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis*". In questa "Parte Seconda", avvalendoci della Teoria Tricromatica dell'Equilibrio dei Sistemi (e del suo programma computerizzato) e usando sempre la stessa sequenza di 22 basi di *RNA* del *Gene RdRp* del *SARS-CoV-2* (una delle sequenze di RNA utilizzate come controllo positivo del tampone rinofaringeo), sono state indagate alcune relazioni tra il SARS-CoV-2 e il Codice Sorgente del Vaccino mRNA SARS-CoV-2 BioNTech/Pfizer. Attraverso l'analisi comparata tra la sequenza sopracitata e il 3'-UTR del Vaccino sono stati identificati nel 3'-UTR piccoli segmenti di sequenza significativi non contigui. Essendo stato accertato che la sintesi dell'mRNA del Coronavirus può comportare la fusione di sequenze non contigue, per mezzo di un successivo laborioso lavoro, simulando una **trascrizione "saltante" dell'RNA (Jumping RNA Transcription)**, questi segmenti sono stati scrupolosamente collegati tra loro. Le **sequenze** ottenute da questi assemblaggi sono state oggetto di ricerca nella banca dati del DNA e dell'Rna (ricerche BLAST). Le ricerche BLAST hanno evidenziato diversi allineamenti significativi tra particolari "organismi", sequenze (in certi casi numerosi aminoacidi) e/o prodotti e parte del 3'-UTR del Vaccino. In particolare, tra gli altri, sono stati identificati i seguenti organismi: ***Pipistrello***, **Pangolino**, ***Virus dell'Immunodeficienza Umana*** (***HIV-1***) e i **Bacilli del Parantrace *(Bacillus Paranthracis)*** e dell'***Antrace (Bacillus Anthracis)***. Questi risultati, che ben si armonizzano con quelli ottenuti nel documento "I Misteri del Dna (Parte Prima)", meritano un urgente e approfondito dibattito internazionale. Per rendere possibile la replicazione dei risultati ottenuti, una parte di questo documento è stata dedicata all'insegnamento della procedura per l'identificazione e l'unione di segmenti di sequenza significativi non contigui del 3'-UTR del Vaccino mRNA SARS-CoV-2 Biontech/Pfizer. La metodologia proposta in questo documento apre prospettive nuove e promettenti per avviare studi finalizzati all'identificazione di sequenze ignote di DNA (o RNA) a partire da altre sequenze note.

GUIDA ALLA LETTURA

INTRODUZIONE

Nell'introduzione sono riassunte alcune considerazioni discusse in "*Misteri del DNA (Parte Prima)*", anticipati dei concetti che saranno sviluppati nel corso della trattazione di questo documento e mostrati alcuni abstract di articoli che trattano il ***"Jumping"** (il **"salto"**) **dell'RNA durante la replicazione e la trascrizione virale***.

CAPITOLO I

In questo capitolo è riportata la composizione del Codice Sorgente integrale del Vaccino mRNA Sars-Cov-2 BioNTech/Pfizer. Questo Codice Sorgente codifica per la glicoproteina spike SARS-CoV-2. Del Codice Sorgente è mostrata una breve descrizione delle 6 parti costituenti e una tabella che sintetizza tutte le sue caratteristiche. Per consentire le ricerche di specifici segmenti della sequenza nella banca dati del Dna e dell'Rna (Ricerche BLAST), la sequenza originaria del Codice Sorgente è stata modificata sostituendo la lettera "**Ψ**" (Ψ = 1-metil-3'-pseudouridile) con la lettera "**T**" (Timina)].

CAPITOLO II

In questo capitolo sono spiegate le caratteristiche generali delle **3'-UTR** (3'-Regioni Non Tradotte), sezioni di *RNA messaggero* (mRNA) dalle molteplici caratteristiche e funzioni, molte delle quali ancora non comprese. Successivamente, sono approfondite le caratteristiche del 3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer.

CAPITOLO III

In questo capitolo sono mostrati i risultati delle ricerche BLAST effettuate su due sequenze: 1) la **Sequenza "HIV-1"** (**ACGCAATGCCCGTCCTGGT**), la **prima sequenza** ottenuta dalla fusione di **TRE** segmenti di sequenza non contigui del *3'-UTR*; 2) la **Sequenza "AES (1)"** (**ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGGT**), l'***Amino-terminal Enhancer of Split*** *o potenziatore ammino-terminale dell'mRNA diviso*, uno dei componenti principali del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*.

CAPITOLO IV

In questo capitolo sono mostrati i risultati delle ricerche BLAST effettuate su due sequenze: 1) la **Sequenza "ANTHRAX"** (**CCGTCCTGGAGACACCTCCC**), la **seconda**

sequenza ottenuta dalla fusione di **DUE** segmenti di sequenza non contigui del *3'-UTR*; 2) la **Sequenza "AES (2)"** (**CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCACCTGCCCCACTCACCACCTCTGCTAGTTCCAGACACCTCC**), l'***Amino-terminal Enhancer of Split*** *o potenziatore ammino-terminale dell'mRNA diviso*, uno dei componenti principali del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*.

CAPITOLO V

In questo capitolo sono mostrati i risultati delle ricerche BLAST effettuate su due sequenze: 1) la **Sequenza "BAT CORONAVIRUS"** (**AAAACGCGCTAACACC**), la **seconda sequenza** ottenuta dalla fusione di **QUATTRO** segmenti di sequenza non contigui del *3'-UTR*; 2) la **Sequenza "12S"** (**AAAACGCTTAGCCTAGCCACACC**), ***Mitochondrial encoded 12S ribosomal RNA***, uno dei componenti principali del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*.

CAPITOLO VI

In questo capitolo sono mostrati i risultati delle ricerche BLAST effettuate su due sequenze: 1) la **Sequenza "ZINC FINGER"** (**CCGTCCTGGACTCACCACC**), la **seconda sequenza** ottenuta dalla fusione di **DUE** segmenti di sequenza non contigui del *3'-UTR*; 2) la **Sequenza "AES (3)"** (**CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCACCTGCCCCACTCACCACC**), l'***Amino-terminal Enhancer of Split*** *o potenziatore ammino-terminale dell'mRNA diviso*, uno dei componenti principali del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*.

CAPITOLO VII

In questo capitolo è spiegato il motivo per cui è stata utilizzata la **sequenza di RNA "GTGAAATGGTCATGTGTGGCGG"** per l'analisi del ***3'-UTR del Vaccino mRNA SARS-CoV-2 Biontech/Pfizer***.

CAPITOLO VIII

In questo capitolo è spiegata sinteticamente la procedura utilizzata per identificare e unire tra loro i piccoli segmenti di sequenza significativi non contigui del ***3'-UTR del Vaccino mRNA SARS-CoV-2 Biontech/Pfizer***.

INTRODUZIONE

In un precedente lavoro (si veda "I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis"), avvalendoci della **TEORIA TRICROMATICA DELL'EQUILIBRIO DEI SISTEMI** (**T.T.E.S.**), una teoria dei sistemi con la quale è possibile osservare, analizzare, controllare e modificare lo stato di qualsiasi sistema (http://www.ttesystems.eu/; http://www.ttesystems.eu/applicazioni.php), e del suo programma computerizzato, ***è stata* modificata una sequenza di 22 basi di *RNA* del *Gene RdRp* del *SARS-CoV-2***. Questa sequenza è una delle sequenze di RNA utilizzate come controllo positivo del tampone rinofaringeo, insieme ad altre sequenze dei geni del *SARS-CoV-2*. Sono stati individuati in parte e chiariti meglio i legami tra l'**RNA** del ***SARS-CoV-2*** e il genoma del ***Pipistrello*** e del ***Pangolino***, entrambi considerati implicati nell'infezione da *Covid-19*. Dalle ricerche BLAST (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC146917/) sono emersi però anche inaspettati allineamenti significativi corrispondenti rispettivamente ad una sequenza dalle caratteristiche nuove (*misc_feature*) del ***Virus dell'Immunodeficienza Umana*** (***HIV-1***), a diverse sequenze dell'***Influenzavirus A*** e, soprattutto, a numerose sequenze dei ***Bacilli del Parantrace (Bacillus Paranthracis)*** e dell'***Antrace (Bacillus Anthracis)***, quest'ultimo un batterio gram-positivo infettivo, agente eziologico del ***carbonchio ematico*** nell'animale e dell'***antrace*** nell'uomo (batterio quest'ultimo considerato nella categoria di massima priorità degli agenti infettivi associati a rischio potenziale d'uso come arma biologica).

In questa "**Parte Seconda**", avvalendoci sempre della **T.T.E.S.** (e del suo programma computerizzato) e usando **la stessa sequenza di 22 basi di *RNA* del *Gene RdRp* del *SARS-CoV-2***, sono state indagate alcune relazioni tra il *SARS-CoV-2* e il *Codice Sorgente del Vaccino mRNA SARS-CoV-2 BioNTech/Pfizer*. In particolare, la nostra attenzione si è concentrata sul **3'-UTR** (3'-Untranslated Region = 3'-Regione Non Tradotta), note *regioni di RNA messaggero* (mRNA) con molteplici caratteristiche e funzioni, molte delle quali non sono ancora comprese. Per evidenziare eventuali "**affinità**" tra la **sequenza di *RNA* del *Gene RdRp* del *SARS-CoV-2* (GTGAAATGGTCATGTGTGGCGG)** sopra citata e il **3'-UTR del vaccino**, abbiamo utilizzato i ***"trend non manifesti"*** generati da questa sequenza e con essi analizzato il **3'-UTR** [I *"trend non manifesti" sono andamenti, non chiaramente identificabili, presenti in tutte le sequenze di DNA e di RNA (per i necessari approfondimenti si consultino i capitoli VII e VIII in "I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis"*)]. L'analisi del **3'-UTR** ha permesso di **identificare** piccoli segmenti di sequenza significativi, ma dislocati a distanza gli uni dagli altri (***segmenti di sequenza non contigui***). Dopo aver identificato questi piccoli segmenti, essendo stato accertato che la *sintesi dell'mRNA del Coronavirus* può comportare la **fusione di sequenze non contigue**, per mezzo di un successivo laborioso lavoro, simulando **una trascrizione "saltante" dell'RNA** (per approfondimenti si veda la pagina successiva), questi segmenti sono stati scrupolosamente collegati tra loro. Essi sono stati **opportunamente uniti insieme** attraverso una ***procedura innovativa*** pubblicata nel Capitolo di questo documento.

Le **quattro sequenze** (solo alcune tra quelle possibili) ottenute da questi assemblaggi sono state oggetto di ricerca nella banca dati del DNA e dell'Rna (ricerche BLAST). Le ricerche BLAST hanno evidenziato diversi stupefacenti allineamenti significativi di "organismi" e "prodotti", i quali saranno discussi nei capitoli successivi.

Prima di passare al Capitolo I, qui di seguito riporto gli abstract di una serie di articoli che discutono del **"Jumping" (il "salto") dell'RNA durante la replicazione e la trascrizione virale**.

Nell'articolo intitolato *"Coronavirus: A Jumping RNA Transcription"* (https://pubmed.ncbi.nlm.nih.gov/3454265/), gli autori (Lai et al. **1987**) sottolineano che *"*Le **RNA polimerasi DNA e RNA-dipendenti** (***DNA- and RNA-dependent RNA polymerases***) di solito riconoscono sequenze specifiche del promotore e avviano la **trascrizione dell'RNA** ad alcune distanze a valle del promotore. L'inizio della trascrizione richiede solo *nucleosidi trifosfati complementari*, sebbene gli *oligonucleotidi* possano, in alcune condizioni, agire come primer per la trascrizione (Niyogi e Stevens 1965; Minkley e Pribnow 1973). Un'eccezione a questa regola generale è l'**RNA polimerasi RNA-dipendente del virus dell'influenza**, **che utilizza *mRNA chiusi* derivati dalle cellule ospiti come primer per la trascrizione** (Plotch et al. 1981). I **trascritti di RNA completati** nelle cellule di mammifero sono frequentemente elaborati da un **meccanismo di splicing dell'RNA**, mediante il quale un RNA leader dall'estremità 5' viene fuso con sequenze di RNA a valle (Padgett et al. 1986). In questo processo, **vengono rimossi segmenti di sequenze di introni**. Questo ***splicing dell'RNA*** può essere mediato sia da *specifici componenti nucleari* (Padgett et al. 1986) sia dalle *stesse molecole di RNA*,….." (https://pubmed.ncbi.nlm.nih.gov/3454265/).

Wu, Hung-Yi, in "*Factors directing the RNA-dependent RNA polymerase jump during discontinuous transcription in coronaviruses*" [PhD diss., University of Tennessee, **2003**. (https://trace.tennessee.edu/utk_graddiss/5210/)] spiega che "….gli **RNA messaggeri subgenomici del coronavirus** sono insoliti tra gli RNA messaggeri del virus in quanto sono 5' e 3' co-terminali con il genoma virale dell'RNA a più filamenti. Sebbene sia generalmente accettato che la **struttura co-terminale sia il risultato di un processo di trascrizione discontinuo per cui la RNA polimerasi RNA-dipendente (RdRP) salta in modo simile ad alta frequenza (sequenza) (simile alla ricombinazione per scelta di copia) da un donatore di un filamento di RNA accettore**, non è noto quali meccanismi dirigano il RdRp a saltare……..Questi risultati mostrano che **specifici elementi strutturali dell'RNA dirigono il salto di RdRp durante gli eventi di ricombinazione intermolecolare richiesti** (cioè **trascrizione discontinua**) **nel processo di replicazione del coronavirus**. I progetti di farmaci razionali per interrompere questi elementi possono portare a molecole terapeutiche per il trattamento dell'infezione da coronavirus, compresa l'infezione da coronavirus SARS che ad oggi sembra essere un membro del gruppo 2." (https://trace.tennessee.edu/utk_graddiss/5210/).

Recentemente, X Zhou et al., in "*Era-like GTP protein gene expression in rice*" [Braz J Biol. **2021 Jul 9**; 82:e250700. (https://www.scielo.br/j/bjb/a/F9VbZ5ymsY7mVFtwhTRwF5f/?lang=en) eCollection 2021.] scrivono che "…*Le **mutazioni** (cambiamenti genetici nelle sequenze del genoma) sono le alterazioni del DNA che possono essere naturali o spontanee e indotte a causa di reazioni biochimiche o radiazioni che danneggiano il DNA cellulare*. C'è un'altra causa di mutazioni che è nota come **trasposoni o geni di salto** che possono **cambiare la loro posizione nel genoma** durante la meiosi o la replicazione del DNA….L'**uso di mutazioni indotte** per studiare la mutagenesi nelle piante coltivate è molto comune, nonché un metodo promettente per lo screening delle piante coltivate con tratti nuovi e migliorati per il miglioramento della resa e della produzione. L'utilizzo di **mutazioni inserzionali** attraverso **trasposoni o geni di salto** di solito genera **alleli mutanti stabili** che sono per lo più etichettati per la *presenza o l'assenza di geni di salto o elementi trasponibili*. Gli *elementi trasponibili* possono essere utilizzati per l'*identificazione di geni mutati* in piante coltivate e anche per l'*inserimento stabile di elementi trasponibili in piante coltivate mutate*. Le ***proteine che legano il nucleotide guanina*** **(GTP)** hanno un ruolo importante nell'indurre la tolleranza nelle piante di riso per combattere le condizioni di stress abiotico." (https://pubmed.ncbi.nlm.nih.gov/34259718/).

Ancora più recentemente, Thomas W Christy et al., in "*Direct Mapping of Higher-Order RNA Interactions by SHAPE-JuMP*" [Biochemistry. 2021 Jun 29;60(25):1971-1982. doi: https://doi.org/10.1021/acs.biochem.1c00270. Epub **2021 Jun 14**] spiegano che "***La struttura di ordine superiore governa la funzione per molti RNA***. Tuttavia, discernere questa struttura per grandi molecole di RNA in soluzione è una sfida irrisolta. Qui, presentiamo **SHAPE-JuMP** (*acilazione selettiva 2'-idrossile analizzata dall'estensione del primer e coppie unite giustapposte*) ***per interrogare le interazioni terziarie dell'RNA attraverso lo spazio***. Una piccola molecola bifunzionale viene utilizzata per *collegare chimicamente i nucleotidi prossimali* in una struttura a RNA. Il *sito di reticolazione dell'RNA* viene quindi **codificato in DNA complementare** (**cDNA**) in un unico passaggio diretto utilizzando una **trascrittasi inversa ingegnerizzata che "salta" attraverso i nucleotidi reticolati**. *I* ***cDNA*** *risultanti contengono una* ***delezione*** *relativa alla sequenza di RNA nativa*, che può essere rilevata mediante sequenziamento, *che indica i siti dei nucleotidi reticolati*. **SHAPE-JuMP** misura la prossimità della struttura terziaria dell'RNA in modo conciso attraverso grandi molecole di RNA con una **risoluzione nanometrica**. SHAPE-JuMP è particolarmente efficace nella misurazione delle interazioni nelle giunzioni multielica e nell'impaccamento loop-to-helix, consente la modellazione della piega globale per RNA fino a diverse centinaia di nucleotidi di lunghezza, facilita la classificazione dei modelli strutturali in base alla coerenza con i vincoli attraverso lo spazio e è pronto per consentire l'interrogazione strutturale in fase di soluzione e la **modellazione di RNA complessi**." (https://pubmed.ncbi.nlm.nih.gov/34121404/).

Infine, alcuni giorni fa, Yan Zhao et. al., in "*The strand-biased transcription of SARS-CoV-2 and unbalanced inhibition by remdesivir*" [VOLUME 24, ISSUE 8, 102857, AUGUST 20, 2021, Published: **July 13, 2021** https://www.cell.com/iscience/issue?pii=S2589-0042(21)X0008-9] nel riassunto dell'articolo riportano che "La **sindrome respiratoria acuta grave coronavirus 2 (SARS-CoV-2)**, un virus a RNA a filamento singolo positivo, causa la pandemia della ***malattia da coronavirus 19***. **Durante la replicazione e la trascrizione virale, l'RNA polimerasi RNA-dipendente "salta" lungo lo stampo del genoma, determinando trascrizioni discontinue a filamento negativo**. Sebbene siano state segnalate le architetture dell'mRNA di senso di SARS-CoV-2, il suo filamento negativo era inesplorato. Qui, abbiamo sequenziato in profondità entrambi i filamenti di RNA e abbiamo scoperto che *la trascrizione SARS-CoV-2 è fortemente distorta per formare il filamento di senso con efficienza di trascrizione variabile per diversi geni*. **Durante la sintesi del filamento negativo, si formano anche numerosi trascritti di fusione non canonici**, guidati dall'omologia di sequenza di 3-15 nt sparsi lungo il genoma ma più ***inclini ad essere inibiti dall'inibitore della RNA polimerasi SARS-CoV-2 remdesivir***. Il farmaco reprime anche più sintesi del filamento negativo rispetto a quella positiva, come supportato da un modello di simulazione matematica e quantificazioni sperimentali. Nel complesso, questo studio apre nuove prospettive sulla biogenesi di SARS-CoV-2 e può facilitare lo sviluppo di ***vaccini antivirali*** e la ***progettazione di farmaci***." (https://pubmed.ncbi.nlm.nih.gov/34278249/).

CAPITOLO I

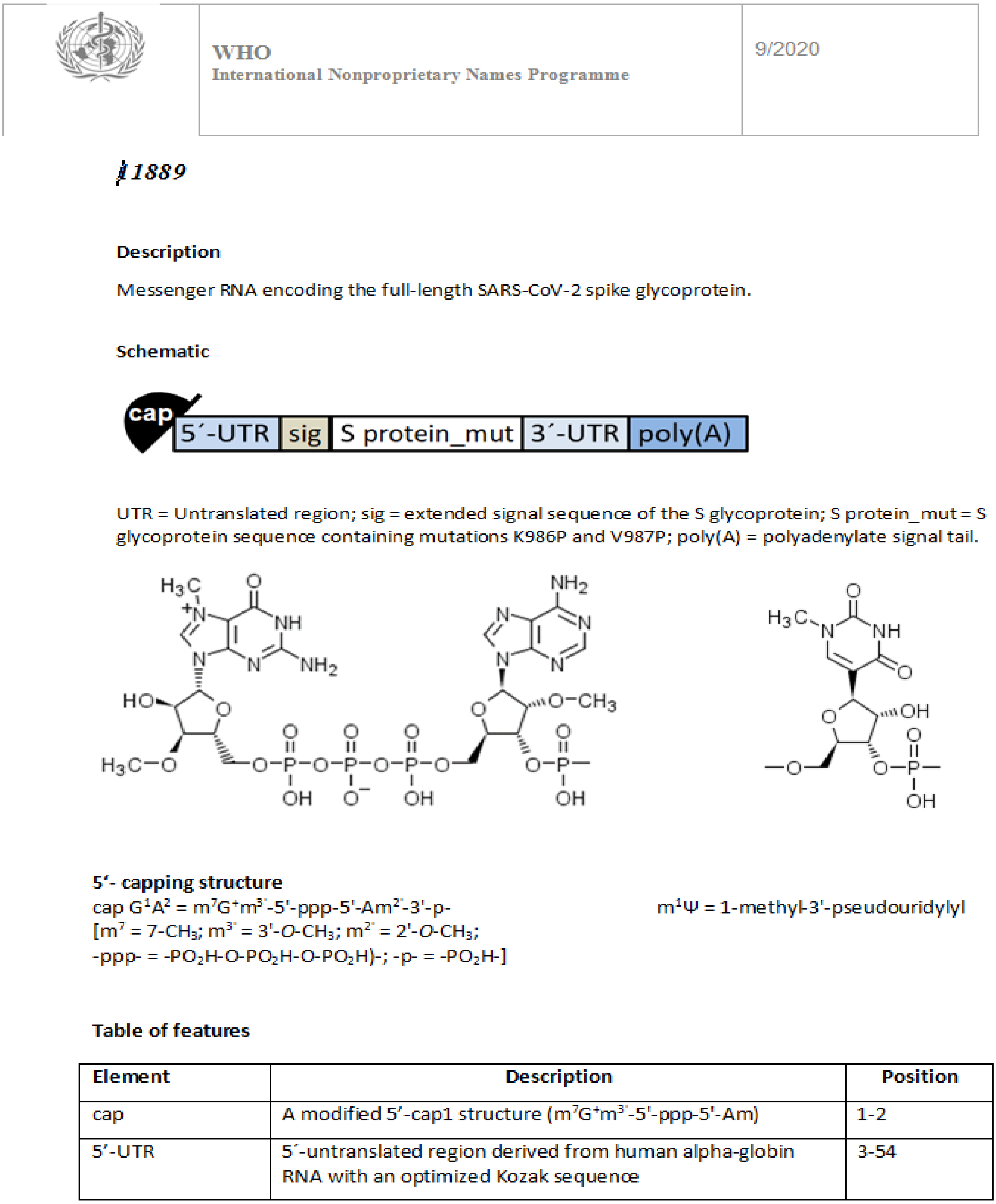
IL CODICE
SORGENTE INTEGRALE
DEL VACCINO mRNA
SARS-COV-2
BIONTECH/PFIZER

OBIETTIVI DEL CAPITOLO I

In questo capitolo è riportata la composizione del Codice Sorgente integrale del Vaccino mRNA Sars-Cov-2 BioNTech/Pfizer. Questo Codice Sorgente codifica per la glicoproteina spike SARS-CoV-2. Del Codice Sorgente è mostrata una breve descrizione delle 6 parti costituenti e una tabella che sintetizza tutte le sue caratteristiche. Nel paragrafo 1.2, la sequenza originaria del Codice Sorgente è stata modificata sostituendo la lettera "**Ψ**" (Ψ = 1-metil-3'-pseudouridile) con la lettera "**T**" (Timina). Questa sostituzione è stata effettuata per consentire le ricerche di specifici segmenti della sequenza nella banca dati del Dna e dell'Rna (Ricerche BLAST).

1.1 LO “SCREENSHOT” DEL CODICE SORGENTE INTEGRALE DEL VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER

Quello che segue è lo “SCREENSHOT” del codice sorgente integrale del Vaccino mRNA Sars-Cov-2 BioNTech/Pfizer (BNT162b2) (https://berthub.eu/articles/11889.doc):



WHO
International Nonproprietary Names Programme

9/2020

11889

Description

Messenger RNA encoding the full-length SARS-CoV-2 spike glycoprotein.

Schematic

UTR = Untranslated region; sig = extended signal sequence of the S glycoprotein; S protein_mut = S glycoprotein sequence containing mutations K986P and V987P; poly(A) = polyadenylate signal tail.

5'- capping structure
cap G^1A^2 = $m^7G^+m^{3'}$-5'-ppp-5'-$Am^{2'}$-3'-p-
[m^7 = 7-CH_3; $m^{3'}$ = 3'-*O*-CH_3; $m^{2'}$ = 2'-*O*-CH_3;
-ppp- = -PO_2H-O-PO_2H-O-PO_2H)-; -p- = -PO_2H-]

$m^1\Psi$ = 1-methyl-3'-pseudouridylyl

Table of features

Element	Description	Position
cap	A modified 5′-cap1 structure ($m^7G^+m^{3'}$-5'-ppp-5'-Am)	1-2
5′-UTR	5´-untranslated region derived from human alpha-globin RNA with an optimized Kozak sequence	3-54

sig	S glycoprotein signal peptide (extended leader sequence), which guides translocation of the nascent polypeptide chain into the endoplasmic reticulum.	55-102
S protein_mut	Codon-optimized sequence encoding full-length SARS-CoV-2 spike (S) glycoprotein containing mutations K986P and V987P to ensure the S glycoprotein remains in an antigenically optimal pre-fusion conformation; stop codons: 3874-3879 (underlined)	103-3879
3'-UTR	The 3´ untranslated region comprises two sequence elements derived from the amino-terminal enhancer of split (AES) mRNA and the mitochondrial encoded 12S ribosomal RNA to confer RNA stability and high total protein expression.	3880-4174
poly(A)	A 110-nucleotide poly(A)-tail consisting of a stretch of 30 adenosine residues, followed by a 10-nucleotide linker sequence and another 70 adenosine residues.	4175-4284

Sequence / Séquence / Secuencia

```
GAGAAΨAAAC ΨAGΨAΨΨCΨΨ CΨGGΨCCCCA CAGACΨCAGA GAGAACCCGC   50
CACCAΨGΨΨC GΨGΨΨCCΨGG ΨGCΨGCΨGCC ΨCΨGGΨGΨCC AGCCAGΨGΨG  100
ΨGAACCΨGAC CACCAGAACA CAGCΨGCCΨC CAGCCΨACAC CAACAGCΨΨΨ  150
ACCAGAGGCG ΨGΨACΨACCC CGACAAGGΨG ΨΨCAGAΨCCA GCGΨGCΨGCA  200
CΨCΨACCCAG GACCΨGΨΨCC ΨGCCΨΨΨCΨΨ CAGCAACGΨG ACCΨGGΨΨCC  250
ACGCCAΨCCA CGΨGΨCCGGC ACCAAΨGGCA CCAAGAGAΨΨ CGACAACCCC  300
GΨGCΨGCCCΨ ΨCAACGACGG GGΨGΨACΨΨΨ GCCAGCACCG AGAAGΨCCAA  350
CAΨCAΨCAGA GGCΨGGAΨCΨ ΨCGGCACCAC ACΨGGACAGC AAGACCCAGA  400
GCCΨGCΨGAΨ CGΨGAACAAC GCCACCAACG ΨGGΨCAΨCAA AGΨGΨGCGAG  450
ΨΨCCAGΨΨCΨ GCAACGACCC CΨΨCCΨGGGC GΨCΨACΨACC ACAAGAACAA  500
CAAGAGCΨGG AΨGGAAAGCG AGΨΨCCGGGΨ GΨACAGCAGC GCCAACAACΨ  550
GCACCΨΨCGA GΨACGΨGΨCC CAGCCΨΨΨCC ΨGAΨGGACCΨ GGAAGGCAAG  600
CAGGGCAACΨ ΨCAAGAACCΨ GCGCGAGΨΨC GΨGΨΨΨAAGA ACAΨCGACGG  650
CΨACΨΨCAAG AΨCΨACAGCA AGCACACCCC ΨAΨCAACCΨC GΨGCGGGAΨC  700
ΨGCCΨCAGGG CΨΨCΨCΨGCΨ CΨGGAACCCC ΨGGΨGGAΨCΨ GCCCAΨCGGC  750
AΨCAACAΨCA CCCGGΨΨΨCA GACACΨGCΨG GCCCΨGCACA GAAGCΨACCΨ  800
GACACCΨGGC GAΨAGCAGCA GCGGAΨGGAC AGCΨGGΨGCC GCCGCΨΨACΨ  850
AΨGΨGGGCΨA CCΨGCAGCCΨ AGAACCΨΨCC ΨGCΨGAAGΨA CAACGAGAAC  900
GGCACCAΨCA CCGACGCCGΨ GGAΨΨGΨGCΨ CΨGGAΨCCΨC ΨGAGCGAGAC  950
AAAGΨGCACC CΨGAAGΨCCΨ ΨCACCGΨGGA AAAGGGCAΨC ΨACCAGACCA 1000
GCAACΨΨCCG GGΨGCAGCCC ACCGAAΨCCA ΨCGΨGCGGΨΨ CCCCAAΨAΨC 1050
ACCAAΨCΨGΨ GCCCCΨΨCGG CGAGGΨGΨΨC AAΨGCCACCA GAΨΨCGCCΨC 1100
ΨGΨGΨACGCC ΨGGAACCGGA AGCGGAΨCAG CAAΨΨGCGΨG GCCGACΨACΨ 1150
CCGΨGCΨGΨA CAACΨCCGCC AGCΨΨCAGCA CCΨΨCAAGΨG CΨACGGCGΨG 1200
ΨCCCCΨACCA AGCΨGAACGA CCΨGΨGCΨΨC ACAAACGΨGΨ ACGCCGACAG 1250
CΨΨCGΨGAΨC CGGGGAGAΨG AAGΨGCGGCA GAΨΨGCCCCΨ GGACAGACAG 1300
GCAAGAΨCGC CGACΨACAAC ΨACAAGCΨGC CCGACGACΨΨ CACCGGCΨGΨ 1350
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GΨGAΨΨGCCΨ GGAACAGCAA CAACCΨGGAC ΨCCAAAGΨCG GCGGCAACΨA 1400
CAAΨΨACCΨG ΨACCGGCΨGΨ ΨCCGGAAGΨC CAAΨCΨGAAG CCCΨΨCGAGC 1450
GGGACAΨCΨC CACCGAGAΨC ΨAΨCAGGCCG GCAGCACCCC ΨΨGΨAACGGC 1500
GΨGGAAGGCΨ ΨCAACΨGCΨA CΨΨCCCACΨG CAGΨCCΨACG GCΨΨΨCAGCC 1550
CACAAAΨGGC GΨGGGCΨAΨC AGCCCΨACAG AGΨGGΨGGΨG CΨGAGCΨΨCG 1600
AACΨGCΨGCA ΨGCCCCΨGCC ACAGΨGΨGCG GCCCΨAAGAA AAGCACCAAΨ 1650
CΨCGΨGAAGA ACAAAΨGCGΨ GAACΨΨCAAC ΨΨCAACGGCC ΨGACCGGCAC 1700
CGGCGΨGCΨG ACAGAGAGCA ACAAGAAGΨΨ CCΨGCCAΨΨC CAGCAGΨΨΨG 1750
GCCGGGAΨAΨ CGCCGAΨACC ACAGACGCCG ΨΨAGAGAΨCC CCAGACACΨG 1800
GAAAΨCCΨGG ACAΨCACCCC ΨΨGCAGCΨΨC GGCGGAGΨGΨ CΨGΨGAΨCAC 1850
CCCΨGGCACC AACACCAGCA AΨCAGGΨGGC AGΨGCΨGΨAC CAGGACGΨGA 1900
ACΨGΨACCGA AGΨGCCCGΨG GCCAΨΨCACG CCGAΨCAGCΨ GACACCΨACA 1950
ΨGGCGGGΨGΨ ACΨCCACCGG CAGCAAΨGΨG ΨΨΨCAGACCA GAGCCGGCΨG 2000
ΨCΨGAΨCGGA GCCGAGCACG ΨGAACAAΨAG CΨACGAGΨGC GACAΨCCCCA 2050
ΨCGGCGCΨGG AAΨCΨGCGCC AGCΨACCAGA CACAGACAAA CAGCCCΨCGG 2100
AGAGCCAGAA GCGΨGGCCAG CCAGAGCAΨC AΨΨGCCΨACA CAAΨGΨCΨCΨ 2150
GGGCGCCGAG AACAGCGΨGG CCΨACΨCCAA CAACΨCΨAΨC GCΨAΨCCCCA 2200
CCAACΨΨCAC CAΨCAGCGΨG ACCACAGAGA ΨCCΨGCCΨGΨ GΨCCAΨGACC 2250
AAGACCAGCG ΨGGACΨGCAC CAΨGΨACAΨC ΨGCGGCGAΨΨ CCACCGAGΨG 2300
CΨCCAACCΨG CΨGCΨGCAGΨ ACGGCAGCΨΨ CΨGCACCCAG CΨGAAΨAGAG 2350
CCCΨGACAGG GAΨCGCCGΨG GAACAGGACA AGAACACCCA AGAGGΨGΨΨC 2400
GCCCAAGΨGA AGCAGAΨCΨA CAAGACCCCΨ CCΨAΨCAAGG ACΨΨCGGCGG 2450
CΨΨCAAΨΨΨC AGCCAGAΨΨC ΨGCCCGAΨCC ΨAGCAAGCCC AGCAAGCGGA 2500
GCΨΨCAΨCGA GGACCΨGCΨG ΨΨCAACAAAG ΨGACACΨGGC CGACGCCGGC 2550
ΨΨCAΨCAAGC AGΨAΨGGCGA ΨΨGΨCΨGGGC GACAΨΨGCCG CCAGGGAΨCΨ 2600
GAΨΨΨGCGCC CAGAAGΨΨΨA ACGGACΨGAC AGΨGCΨGCCΨ CCΨCΨGCΨGA 2650
CCGAΨGAGAΨ GAΨCGCCCAG ΨACACAΨCΨG CCCΨGCΨGGC CGGCACAAΨC 2700
ACAAGCGGCΨ GGACAΨΨΨGG AGCAGGCGCC GCΨCΨGCAGA ΨCCCCΨΨΨGC 2750
ΨAΨGCAGAΨG GCCΨACCGGΨ ΨCAACGGCAΨ CGGAGΨGACC CAGAAΨGΨGC 2800
ΨGΨACGAGAA CCAGAAGCΨG AΨCGCCAACC AGΨΨCAACAG CGCCAΨCGGC 2850
AAGAΨCCAGG ACAGCCΨGAG CAGCACAGCA AGCGCCCΨGG GAAAGCΨGCA 2900
GGACGΨGGΨC AACCAGAAΨG CCCAGGCACΨ GAACACCCΨG GΨCAAGCAGC 2950
ΨGΨCCΨCCAA CΨΨCGGCGCC AΨCAGCΨCΨG ΨGCΨGAACGA ΨAΨCCΨGAGC 3000
AGACΨGGACC CΨCCΨGAGGC CGAGGΨGCAG AΨCGACAGAC ΨGAΨCACAGG 3050
CAGACΨGCAG AGCCΨCCAGA CAΨACGΨGAC CCAGCAGCΨG AΨCAGAGCCG 3100
CCGAGAΨΨAG AGCCΨCΨGCC AAΨCΨGGCCG CCACCAAGAΨ GΨCΨGAGΨGΨ 3150
GΨGCΨGGGCC AGAGCAAGAG AGΨGGACΨΨΨ ΨGCGGCAAGG GCΨACCACCΨ 3200
GAΨGAGCΨΨC CCΨCAGΨCΨG CCCCΨCACGG CGΨGGΨGΨΨΨ CΨGCACGΨGA 3250
CAΨAΨGΨGCC CGCΨCAAGAG AAGAAΨΨΨCA CCACCGCΨCC AGCCAΨCΨGC 3300
CACGACGGCA AAGCCCACΨΨ ΨCCΨAGAGAA GGCGΨGΨΨCG ΨGΨCCAACGG 3350
CACCCAΨΨGG ΨΨCGΨGACAC AGCGGAACΨΨ CΨACGAGCCC CAGAΨCAΨCA 3400
CCACCGACAA CACCΨΨCGΨG ΨCΨGGCAACΨ GCGACGΨCGΨ GAΨCGGCAΨΨ 3450
GΨGAACAAΨA CCGΨGΨACGA CCCΨCΨGCAG CCCGAGCΨGG ACAGCΨΨCAA 3500
AGAGGAACΨG GACAAGΨACΨ ΨΨAAGAACCA CACAAGCCCC GACGΨGGACC 3550
ΨGGGCGAΨAΨ CAGCGGAAΨC AAΨGCCAGCG ΨCGΨGAACAΨ CCAGAAAGAG 3600
AΨCGACCGGC ΨGAACGAGGΨ GGCCAAGAAΨ CΨGAACGAGA GCCΨGAΨCGA 3650
CCΨGCAAGAA CΨGGGGAAGΨ ACGAGCAGΨA CAΨCAAGΨGG CCCΨGGΨACA 3700
ΨCΨGGCΨGGG CΨΨΨAΨCGCC GGACΨGAΨΨG CCAΨCGΨGAΨ GGΨCACAAΨC 3750
AΨGCΨGΨGΨΨ GCAΨGACCAG CΨGCΨGΨAGC ΨGCCΨGAAGG GCΨGΨΨGΨAG 3800
CΨGΨGGCAGC ΨGCΨGCAAGΨ ΨCGACGAGGA CGAΨΨCΨGAG CCCGΨGCΨGA 3850
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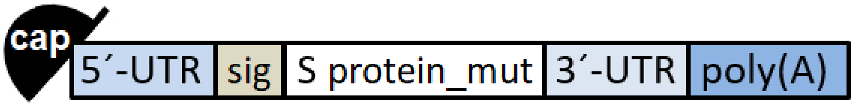
AGGGCGΨGAA ACΨGCACΨAC ACAΨGAΨGAC ΨCGAGCΨGGΨ ACΨGCAΨGCA 3900
CGCAAΨGCΨA GCΨGCCCCΨΨ ΨCCCGΨCCΨG GGΨACCCCGA GΨCΨCCCCCG 3950
ACCΨCGGGΨC CCAGGΨAΨGC ΨCCCACCΨCC ACCΨGCCCCA CΨCACCACCΨ 4000
CΨGCΨAGΨΨC CAGACACCΨC CCAAGCACGC AGCAAΨGCAG CΨCAAAACGC 4050
ΨΨAGCCΨAGC CACACCCCCA CGGGAAACAG CAGΨGAΨΨAA CCΨΨΨAGCAA 4100
ΨAAACGAAAG ΨΨΨAACΨAAG CΨAΨACΨAAC CCCAGGGΨΨG GΨCAAΨΨΨCG 4150
ΨGCCAGCCAC ACCCΨGGAGC ΨAGCAAAAAA AAAAAAAAAA AAAAAAAAAA 4200
AAAAGCAΨAΨ GACΨAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 4250
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 4284

Ψ = 1-methyl-3'-pseudouridylyl

1.2 LA COMPOSIZIONE DEL CODICE SORGENTE INTEGRALE DEL VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER

Il codice sorgente RNA messaggero che codifica per la glicoproteina spike SARS-CoV-2 a lunghezza intera è lungo 4284 caratteri (o nucleotidi) ed è costituito da 6 parti (https://berthub.eu/articles/11889.doc; https://berthub.eu/articles/posts/reverse-engineering-source-code-of-the-biontech-pfizer-vaccine/; https://www.who.int/publications/i/item/mrna-vaccines-against-covid-19-pfizer-biontech-covid-19-vaccinebnt162b2 https://www.dday.it/redazione/38006/il-vaccino-pfizer-e-stato-sviluppato-come-un-software-il-codice-sorgente-ci-racconta-come-e-perche-funziona).

Esso è rappresentato schematicamente come segue:



cap = “cappuccio” GA; **5’-UTR** = regione non tradotta; **sig** = sequenza segnale estesa della glicoproteina S; **S protein_mut** = sequenza della glicoproteina S contenente le mutazioni K986P e V987P; **3’-UTR** = regione non tradotta; **poly(A)** = coda del segnale di poliadenilato.

Qui di seguito una breve descrizione delle 6 parti costituenti e nella pagina successiva la tabella che sintetizza tutte le caratteristiche:

cap: raffigurato come un cappellino, si riferisce alla sequenza **GA** (*posizione 1 e 2*) necessaria per iniziare la lettura e la traduzione della sequenza successiva;

5’-UTR: questa sequenza (*dalla posizione 3 alla 54*) è letta dalla cellula ma non viene tradotta. Essa assicura la direzione della traduzione successiva. In essa, **la lettera “Ψ” sostituisce la lettera “U” (Uracile)** per evitare che il sistema immunitario dell’organismo identifichi l’RNA messaggero del vaccino e lo distrugga;

sig: è la sequenza (*dalla posizione 55 alla 102*) del peptide di segnalazione della glicoproteina S e serve a guidare la glicoproteina S attraverso il reticolo endoplasmatico fino all’uscita dalla cellula;

S protein_mut: questa è la sequenza (*dalla posizione 103 alla 3879*) costitutiva della proteina Spike modificata (mutazioni K986P e V987P) che entrando in circolo nell’organismo stimolerà il suo sistema immunitario;

3’-UTR: la funzione di questa sequenza (*dalla posizione 3880 alla 4174*) non è chiara, ma assicura certamente la direzione corretta della lettura delle informazioni. **L’approfondimento di alcune caratteristiche della sequenza 3’-UTR è l’oggetto del lavoro che presento in questo documento**;

poly(A): questa sequenza (*dalla posizione 4175 alla 4284*) ha la funzione di proteggere l’mRNA dalla degradazione. In questa sequenza, le lettere “A” alla fine del codice permettono che l’mRNA venga utilizzato molte volte, fino al totale completamento di tali lettere.

Tabella delle caratteristiche

Elementi	**Descrizione**	**Posizione**
cap	**Una struttura 5’-cap1 modificata ($m^7G^+m^{3'}$-5’-ppp-5’-Am)**	**1-2**
5’-UTR	5’- regione non tradotta derivata da RNA di alfa-globina umana con una sequenza Kozak ottimizzata.	3-54
sig	**Peptide segnale della glicoproteina S (sequenza direttrice estesa), la quale guida la traslocazione della catena polipeptidica nascente nel reticolo endoplasmatico.**	**55-102**
S protein_mut	**Sequenza ottimizzata del codone che codifica la glicoproteina Spike SARS-CoV-2 a lunghezza intera (S) contenente le mutazioni K986P e V987P per garantire che la glicoproteina S rimanga in una conformazione di prefusione antigenicamente ottimale; codoni di stop: 3874-3879 (sottolineato).**	**103-3879**
3’-UTR	**La regione non tradotta 3’ comprende due elementi di sequenza derivati dal potenziatore ammino-terminale dell’mRNA diviso (AES) e l’RNA ribosomiale 12S codificato mitocondriale per conferire stabilità all’RNA e un’elevata espressione proteica totale.**	**3880-4174**
poli(A)	Una coda di poli(A) da 110 nucleotidi costituita da un tratto di 30 residui di adenosina, seguita da una sequenza di collegamento di 10 nucleotidi e da altri 70 residui di adenosina.	4175-4284

1.3 LA SEQUENZA DEL VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER

Quello che segue è il “codice sorgente” integrale del Vaccino mRNA
Sars-Cov-2 BioNTech/Pfizer (BNT162b2) (https://berthub.eu/articles/11889.doc):

Ψ = 1-metil-3’-pseudouridile

Sequenza

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GAGAAΨAAAC ΨAGΨAΨΨCΨΨ CΨGGΨCCCCA CAGACΨCAGA GAGAACCCGC   50
CACCAΨGΨΨC GΨGΨΨCCΨGG ΨGCΨGCΨGCC ΨCΨGGΨGΨCC AGCCAGΨGΨG  100
ΨGAACCΨGAC CACCAGAACA CAGCΨGCCΨC CAGCCΨACAC CAACAGCΨΨΨ  150
ACCAGAGGCG ΨGΨACΨACCC CGACAAGGΨG ΨΨCAGAΨCCA GCGΨGCΨGCA  200
CΨCΨACCCAG GACCΨGΨΨCC ΨGCCΨΨΨCΨΨ CAGCAACGΨG ACCΨGGΨΨCC  250
ACGCCAΨCCA CGΨGΨCCGGC ACCAAΨGGCA CCAAGAGAΨΨ CGACAACCCC  300
GΨGCΨGCCCΨ ΨCAACGACGG GGΨGΨACΨΨΨ GCCAGCACCG AGAAGΨCCAA  350
CAΨCAΨCAGA GGCΨGGAΨCΨ ΨCGGCACCAC ACΨGGACAGC AAGACCCAGA  400
GCCΨGCΨGAΨ CGΨGAACAAC GCCACCAACG ΨGGΨCAΨCAA AGΨGΨGCGAG  450
ΨΨCCAGΨΨCΨ GCAACGACCC CΨΨCCΨGGGC GΨCΨACΨACC ACAAGAACAA  500
CAAGAGCΨGG AΨGGAAAGCG AGΨΨCCGGGΨ GΨACAGCAGC GCCAACAACΨ  550
GCACCΨΨCGA GΨACGΨGΨCC CAGCCΨΨΨCC ΨGAΨGGACCΨ GGAAGGCAAG  600
CAGGGCAACΨ ΨCAAGAACCΨ GCGCGAGΨΨC GΨGΨΨΨAAGA ACAΨCGACGG  650
CΨACΨΨCAAG AΨCΨACAGCA AGCACACCCC ΨAΨCAACCΨC GΨGCGGGAΨC  700
ΨGCCΨCAGGG CΨΨCΨCΨGCΨ CΨGGAACCCC ΨGGΨGGAΨCΨ GCCCAΨCGGC  750
AΨCAACAΨCA CCCGGΨΨΨCA GACACΨGCΨG GCCCΨGCACA GAAGCΨACCΨ  800
GACACCΨGGC GAΨAGCAGCA GCGGAΨGGAC AGCΨGGΨGCC GCCGCΨΨACΨ  850
AΨGΨGGGCΨA CCΨGCAGCCΨ AGAACCΨΨCC ΨGCΨGAAGΨA CAACGAGAAC  900
GGCACCAΨCA CCGACGCCGΨ GGAΨΨGΨGCΨ CΨGGAΨCCΨC ΨGAGCGAGAC  950
AAAGΨGCACC CΨGAAGΨCCΨ ΨCACCGΨGGA AAAGGGCAΨC ΨACCAGACCA 1000
GCAACΨΨCCG GGΨGCAGCCC ACCGAAΨCCA ΨCGΨGCGGΨΨ CCCCAAΨAΨC 1050
ACCAAΨCΨGΨ GCCCCΨΨCGG CGAGGΨGΨΨC AAΨGCCACCA GAΨΨCGCCΨC 1100
ΨGΨGΨACGCC ΨGGAACCGGA AGCGGAΨCAG CAAΨΨGCGΨG GCCGACΨACΨ 1150
CCGΨGCΨGΨA CAACΨCCGCC AGCΨΨCAGCA CCΨΨCAAGΨG CΨACGGCGΨG 1200
ΨCCCCΨACCA AGCΨGAACGA CCΨGΨGCΨΨC ACAAACGΨGΨ ACGCCGACAG 1250
CΨΨCGΨGAΨC CGGGGAGAΨG AAGΨGCGGCA GAΨΨGCCCCΨ GGACAGACAG 1300
GCAAGAΨCGC CGACΨACAAC ΨACAAGCΨGC CCGACGACΨΨ CACCGGCΨGΨ 1350
GΨGAΨΨGCCΨ GGAACAGCAA CAACCΨGGAC ΨCCAAAGΨCG GCGGCAACΨA 1400
CAAΨΨACCΨG ΨACCGGCΨGΨ ΨCCGGAAGΨC CAAΨCΨGAAG CCCΨΨCGAGC 1450
GGGACAΨCΨC CACCGAGAΨC ΨAΨCAGGCCG GCAGCACCCC ΨΨGΨAACGGC 1500
GΨGGAAGGCΨ ΨCAACΨGCΨA CΨΨCCCACΨG CAGΨCCΨACG GCΨΨΨCAGCC 1550
CACAAAΨGGC GΨGGGCΨAΨC AGCCCΨACAG AGΨGGΨGGΨG CΨGAGCΨΨCG 1600
AACΨGCΨGCA ΨGCCCCΨGCC ACAGΨGΨGCG GCCCΨAAGAA AAGCACCAAΨ 1650
CΨCGΨGAAGA ACAAAΨGCGΨ GAACΨΨCAAC ΨΨCAACGGCC ΨGACCGGCAC 1700
CGGCGΨGCΨG ACAGAGAGCA ACAAGAAGΨΨ CCΨGCCAΨΨC CAGCAGΨΨΨG 1750
GCCGGGAΨAΨ CGCCGAΨACC ACAGACGCCG ΨΨAGAGAΨCC CCAGACACΨG 1800
GAAAΨCCΨGG ACAΨCACCCC ΨΨGCAGCΨΨC GGCGGAGΨGΨ CΨGΨGAΨCAC 1850
CCCΨGGCACC AACACCAGCA AΨCAGGΨGGC AGΨGCΨGΨAC CAGGACGΨGA 1900
ACΨGΨACCGA AGΨGCCCGΨG GCCAΨΨCACG CCGAΨCAGCΨ GACACCΨACA 1950
ΨGGCGGGΨGΨ ACΨCCACCGG CAGCAAΨGΨG ΨΨΨCAGACCA GAGCCGGCΨG 2000
ΨCΨGAΨCGGA GCCGAGCACG ΨGAACAAΨAG CΨACGAGΨGC GACAΨCCCCA 2050
ΨCGGCGCΨGG AAΨCΨGCGCC AGCΨACCAGA CACAGACAAA CAGCCCΨCGG 2100
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AGAGCCAGAA GCGΨGGCCAG CCAGAGCAΨC AΨΨGCCΨACA CAAΨGΨCΨCΨ 2150
GGGCGCCGAG AACAGCGΨGG CCΨACΨCCAA CAACΨCΨAΨC GCΨAΨCCCCA 2200
CCAACΨΨCAC CAΨCAGCGΨG ACCACAGAGA ΨCCΨGCCΨGΨ GΨCCAΨGACC 2250
AAGACCAGCG ΨGGACΨGCAC CAΨGΨACAΨC ΨGCGGCGAΨΨ CCACCGAGΨG 2300
CΨCCAACCΨG CΨGCΨGCAGΨ ACGGCAGCΨΨ CΨGCACCCAG CΨGAAΨAGAG 2350
CCCΨGACAGG GAΨCGCCGΨG GAACAGGACA AGAACACCCA AGAGGΨGΨΨC 2400
GCCCAAGΨGA AGCAGAΨCΨA CAAGACCCCΨ CCΨAΨCAAGG ACΨΨCGGCGG 2450
CΨΨCAAΨΨΨC AGCCAGAΨΨC ΨGCCCGAΨCC ΨAGCAAGCCC AGCAAGCGGA 2500
GCΨΨCAΨCGA GGACCΨGCΨG ΨΨCAACAAAG ΨGACACΨGGC CGACGCCGGC 2550
ΨΨCAΨCAAGC AGΨAΨGGCGA ΨΨGΨCΨGGGC GACAΨΨGCCG CCAGGGAΨCΨ 2600
GAΨΨΨGCGCC CAGAAGΨΨΨA ACGGACΨGAC AGΨGCΨGCCΨ CCΨCΨGCΨGA 2650
CCGAΨGAGAΨ GAΨCGCCCAG ΨACACAΨCΨG CCCΨGCΨGGC CGGCACAAΨC 2700
ACAAGCGGCΨ GGACAΨΨΨGG AGCAGGCGCC GCΨCΨGCAGA ΨCCCCΨΨΨGC 2750
ΨAΨGCAGAΨG GCCΨACCGGΨ ΨCAACGGCAΨ CGGAGΨGACC CAGAAΨGΨGC 2800
ΨGΨACGAGAA CCAGAAGCΨG AΨCGCCAACC AGΨΨCAACAG CGCCAΨCGGC 2850
AAGAΨCCAGG ACAGCCΨGAG CAGCACAGCA AGCGCCCΨGG GAAAGCΨGCA 2900
GGACGΨGGΨC AACCAGAAΨG CCCAGGCACΨ GAACACCCΨG GΨCAAGCAGC 2950
ΨGΨCCΨCCAA CΨΨCGGCGCC AΨCAGCΨCΨG ΨGCΨGAACGA ΨAΨCCΨGAGC 3000
AGACΨGGACC CΨCCΨGAGGC CGAGGΨGCAG AΨCGACAGAC ΨGAΨCACAGG 3050
CAGACΨGCAG AGCCΨCCAGA CAΨACGΨGAC CCAGCAGCΨG AΨCAGAGCCG 3100
CCGAGAΨΨAG AGCCΨCΨGCC AAΨCΨGGCCG CCACCAAGAΨ GΨCΨGAGΨGΨ 3150
GΨGCΨGGGCC AGAGCAAGAG AGΨGGACΨΨΨ ΨGCGGCAAGG GCΨACCACCΨ 3200
GAΨGAGCΨΨC CCΨCAGΨCΨG CCCCΨCACGG CGΨGGΨGΨΨΨ CΨGCACGΨGA 3250
CAΨAΨGΨGCC CGCΨCAAGAG AAGAAΨΨΨCA CCACCGCΨCC AGCCAΨCΨGC 3300
CACGACGGCA AAGCCCACΨΨ ΨCCΨAGAGAA GGCGΨGΨΨCG ΨGΨCCAACGG 3350
CACCCAΨΨGG ΨΨCGΨGACAC AGCGGAACΨΨ CΨACGAGCCC CAGAΨCAΨCA 3400
CCACCGACAA CACCΨΨCGΨG ΨCΨGGCAACΨ GCGACGΨCGΨ GAΨCGGCAΨΨ 3450
GΨGAACAAΨA CCGΨGΨACGA CCCΨCΨGCAG CCCGAGCΨGG ACAGCΨΨCAA 3500
AGAGGAACΨG GACAAGΨACΨ ΨΨAAGAACCA CACAAGCCCC GACGΨGGACC 3550
ΨGGGCGAΨAΨ CAGCGGAAΨC AAΨGCCAGCG ΨCGΨGAACAΨ CCAGAAAGAG 3600
AΨCGACCGGC ΨGAACGAGGΨ GGCCAAGAAΨ CΨGAACGAGA GCCΨGAΨCGA 3650
CCΨGCAAGAA CΨGGGGAAGΨ ACGAGCAGΨA CAΨCAAGΨGG CCCΨGGΨACA 3700
ΨCΨGGCΨGGG CΨΨΨAΨCGCC GGACΨGAΨΨG CCAΨCGΨGAΨ GGΨCACAAΨC 3750
AΨGCΨGΨGΨΨ GCAΨGACCAG CΨGCΨGΨAGC ΨGCCΨGAAGG GCΨGΨΨGΨAG 3800
CΨGΨGGCAGC ΨGCΨGCAAGΨ ΨCGACGAGGA CGAΨΨCΨGAG CCCGΨGCΨGA 3850
AGGGCGΨGAA ACΨGCACΨAC ACAΨGAΨGAC ΨCGAGCΨGGΨ ACΨGCAΨGCA 3900
CGCAAΨGCΨA GCΨGCCCCΨΨ ΨCCCGΨCCΨG GGΨACCCCGA GΨCΨCCCCCG 3950
ACCΨCGGGΨC CCAGGΨAΨGC ΨCCCACCΨCC ACCΨGCCCCA CΨCACCACCΨ 4000
CΨGCΨAGΨΨC CAGACACCΨC CCAAGCACGC AGCAAΨGCAG CΨCAAAACGC 4050
ΨΨAGCCΨAGC CACACCCCCA CGGGAAACAG CAGΨGAΨΨAA CCΨΨΨAGCAA 4100
ΨAAACGAAAG ΨΨΨAACΨAAG CΨAΨACΨAAC CCCAGGGΨΨG GΨCAAΨΨΨCG 4150
ΨGCCAGCCAC ACCCΨGGAGC ΨAGCAAAAAA AAAAAAAAAA AAAAAAAAAA 4200
AAAAGCAΨAΨ GACΨAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 4250
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA                  4284
```

SEQUENZA MODIFICATA

[la lettera “Ψ” è stata sostituita con la lettera “T” (Timina)].

Questa sostituzione è stata effettuata per consentire le ricerche di specifici segmenti della sequenza nella banca dati del Dna e dell’Rna (Ricerche BLAST). Nella banca dati la lettera T (Timina) si riferisce indistintamente sia all’Uracile (U), sia alla Timina (T).

```
GAGAATAAAC TAGTATTCTT CTGGTCCCCA CAGACTCAGA GAGAACCCGC   50
CACCATGTTC GTGTTCCTGG TGCTGCTGCC TCTGGTGTCC AGCCAGTGTG  100
TGAACCTGAC CACCAGAACA CAGCTGCCTC CAGCCTACAC CAACAGCTTT  150
ACCAGAGGCG TGTACTACCC CGACAAGGTG TTCAGATCCA GCGTGCTGCA  200
CTCTACCCAG GACCTGTTCC TGCCTTTCTT CAGCAACGTG ACCTGGTTCC  250
ACGCCATCCA CGTGTCCGGC ACCAATGGCA CCAAGAGATT CGACAACCCC  300
GTGCTGCCCT TCAACGACGG GGTGTACTTT GCCAGCACCG AGAAGTCCAA  350
CATCATCAGA GGCTGGATCT TCGGCACCAC ACTGGACAGC AAGACCCAGA  400
GCCTGCTGAT CGTGAACAAC GCCACCAACG TGGTCATCAA AGTGTGCGAG  450
TTCCAGTTCT GCAACGACCC CTTCCTGGGC GTCTACTACC ACAAGAACAA  500
CAAGAGCTGG ATGGAAAGCG AGTTCCGGGT GTACAGCAGC GCCAACAACT  550
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CAGGGCAACT TCAAGAACCT GCGCGAGTTC GTGTTTAAGA ACATCGACGG  650
CTACTTCAAG ATCTACAGCA AGCACACCCC TATCAACCTC GTGCGGGATC  700
TGCCTCAGGG CTTCTCTGCT CTGGAACCCC TGGTGGATCT GCCCATCGGC  750
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CCGTGCTGTA CAACTCCGCC AGCTTCAGCA CCTTCAAGTG CTACGGCGTG 1200
TCCCCTACCA AGCTGAACGA CCTGTGCTTC ACAAACGTGT ACGCCGACAG 1250
CTTCGTGATC CGGGGAGATG AAGTGCGGCA GATTGCCCCT GGACAGACAG 1300
GCAAGATCGC CGACTACAAC TACAAGCTGC CCGACGACTT CACCGGCTGT 1350
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CAATTACCTG TACCGGCTGT TCCGGAAGTC CAATCTGAAG CCCTTCGAGC 1450
GGGACATCTC CACCGAGATC TATCAGGCCG GCAGCACCCC TTGTAACGGC 1500
GTGGAAGGCT TCAACTGCTA CTTCCCACTG CAGTCCTACG GCTTTCAGCC 1550
CACAAATGGC GTGGGCTATC AGCCCTACAG AGTGGTGGTG CTGAGCTTCG 1600
AACTGCTGCA TGCCCCTGCC ACAGTGTGCG GCCCTAAGAA AAGCACCAAT 1650
CTCGTGAAGA ACAAATGCGT GAACTTCAAC TTCAACGGCC TGACCGGCAC 1700
CGGCGTGCTG ACAGAGAGCA ACAAGAAGTT CCTGCCATTC CAGCAGTTTG 1750
GCCGGGATAT CGCCGATACC ACAGACGCCG TTAGAGATCC CCAGACACTG 1800
GAAATCCTGG ACATCACCCC TTGCAGCTTC GGCGGAGTGT CTGTGATCAC 1850
CCCTGGCACC AACACCAGCA ATCAGGTGGC AGTGCTGTAC CAGGACGTGA 1900
ACTGTACCGA AGTGCCCGTG GCCATTCACG CCGATCAGCT GACACCTACA 1950
TGGCGGGTGT ACTCCACCGG CAGCAATGTG TTTCAGACCA GAGCCGGCTG 2000
TCTGATCGGA GCCGAGCACG TGAACAATAG CTACGAGTGC GACATCCCCA 2050
TCGGCGCTGG AATCTGCGCC AGCTACCAGA CACAGACAAA CAGCCCTCGG 2100
AGAGCCAGAA GCGTGGCCAG CCAGAGCATC ATTGCCTACA CAATGTCTCT 2150
GGGCGCCGAG AACAGCGTGG CCTACTCCAA CAACTCTATC GCTATCCCCA 2200
```

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CCAACTTCAC CATCAGCGTG ACCACAGAGA TCCTGCCTGT GTCCATGACC 2250
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CTCCAACCTG CTGCTGCAGT ACGGCAGCTT CTGCACCCAG CTGAATAGAG 2350
CCCTGACAGG GATCGCCGTG GAACAGGACA AGAACACCCA AGAGGTGTTC 2400
GCCCAAGTGA AGCAGATCTA CAAGACCCCT CCTATCAAGG ACTTCGGCGG 2450
CTTCAATTTC AGCCAGATTC TGCCCGATCC TAGCAAGCCC AGCAAGCGGA 2500
GCTTCATCGA GGACCTGCTG TTCAACAAAG TGACACTGGC CGACGCCGGC 2550
TTCATCAAGC AGTATGGCGA TTGTCTGGGC GACATTGCCG CCAGGGATCT 2600
GATTTGCGCC CAGAAGTTTA ACGGACTGAC AGTGCTGCCT CCTCTGCTGA 2650
CCGATGAGAT GATCGCCCAG TACACATCTG CCCTGCTGGC CGGCACAATC 2700
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TGTACGAGAA CCAGAAGCTG ATCGCCAACC AGTTCAACAG CGCCATCGGC 2850
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TGTCCTCCAA CTTCGGCGCC ATCAGCTCTG TGCTGAACGA TATCCTGAGC 3000
AGACTGGACC CTCCTGAGGC CGAGGTGCAG ATCGACAGAC TGATCACAGG 3050
CAGACTGCAG AGCCTCCAGA CATACGTGAC CCAGCAGCTG ATCAGAGCCG 3100
CCGAGATTAG AGCCTCTGCC AATCTGGCCG CCACCAAGAT GTCTGAGTGT 3150
GTGCTGGGCC AGAGCAAGAG AGTGGACTTT TGCGGCAAGG GCTACCACCT 3200
GATGAGCTTC CCTCAGTCTG CCCCTCACGG CGTGGTGTTT CTGCACGTGA 3250
CATATGTGCC CGCTCAAGAG AAGAATTTCA CCACCGCTCC AGCCATCTGC 3300
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CACCCATTGG TTCGTGACAC AGCGGAACTT CTACGAGCCC CAGATCATCA 3400
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GTGAACAATA CCGTGTACGA CCCTCTGCAG CCCGAGCTGG ACAGCTTCAA 3500
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TGGGCGATAT CAGCGGAATC AATGCCAGCG TCGTGAACAT CCAGAAAGAG 3600
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CCTGCAAGAA CTGGGGAAGT ACGAGCAGTA CATCAAGTGG CCCTGGTACA 3700
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ATGCTGTGTT GCATGACCAG CTGCTGTAGC TGCCTGAAGG GCTGTTGTAG 3800
CTGTGGCAGC TGCTGCAAGT TCGACGAGGA CGATTCTGAG CCCGTGCTGA 3850
AGGGCGTGAA ACTGCACTAC ACATGATGAC TCGAGCTGGT ACTGCATGCA 3900
CGCAATGCTA GCTGCCCCTT TCCCGTCCTG GGTACCCCGA GTCTCCCCCG 3950
ACCTCGGGTC CCAGGTATGC TCCCACCTCC ACCTGCCCCA CTCACCACCT 4000
CTGCTAGTTC CAGACACCTC CCAAGCACGC AGCAATGCAG CTCAAAACGC 4050
TTAGCCTAGC CACACCCCCA CGGGAAACAG CAGTGATTAA CCTTTAGCAA 4100
TAAACGAAAG TTTAACTAAG CTATACTAAC CCCAGGGTTG GTCAATTTCG 4150
TGCCAGCCAC ACCCTGGAGC TAGCAAAAAA AAAAAAAAAA AAAAAAAAAA 4200
AAAAGCATAT GACTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 4250
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA                  4284
```

CAPITOLO II

LA REGIONE NON TRADOTTA TRE PRIMO (3’-UTR) DEL VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER

OBIETTIVI DEL CAPITOLO II

All’inizio del capitolo sono spiegate le caratteristiche generali delle **3’-UTR** (3’-Regioni Non Tradotte), sezioni di *RNA messaggero* (mRNA) che seguono immediatamente la traduzione del Codone di Terminazione (o Codone di Arresto). Successivamente sono approfondite le caratteristiche del 3’-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer: due elementi di sequenza derivati dal **potenziatore ammino-terminale dell’mRNA diviso (AES)** e l’**RNA ribosomiale 12S codificato mitocondriale** per conferire stabilità all’RNA e un’elevata espressione proteica totale.

2.1 LE REGIONI NON TRADOTTE TRE PRIMO (3’-UTR)

3’-UTR (**3’-U**ntrlaslated region) sono le sezioni di ***RNA messaggero*** (**mRNA**) che seguono immediatamente la **traduzione del Codone di Terminazione** (o **Codone di Arresto**). Il 3’-UTR contiene spesso *regioni regolatorie che influenzano in modo post-trascrizionale l’espressione genica* (https://en.wikipedia.org/wiki/Three_prime_untranslated_region).
Le *regioni di regolamentazione* all’interno del 3’-UTR possono influenzare la **poliadenilazione** [l’aggiunta di una **coda di poli(A)** a un trascritto di RNA (in genere mRNA); https://en.wikipedia.org/wiki/Polyadenylation], l’efficienza di traduzione, la localizzazione e stabilità dell’mRNA. Il 3’-UTR contiene sia siti di legame per *proteine regolatrici* che ***microRNA*** (**miRNA**). Legandosi a siti specifici all’interno del 3’-UTR, i *miRNA* possono ridurre l’espressione genica di vari *mRNA* inibendo la traduzione o causando direttamente la degradazione del trascritto. Il 3’-UTR ha anche *regioni silenziatori* che si legano alle proteine repressive e inibiscono l’espressione dell’mRNA (https://en.wikipedia.org/wiki/Three_prime_untranslated_region).
Molti 3’-UTR contengono anche **Elementi ricchi di AU** o **Adenilato-Uridilato** (**ARE**) (https://en.wikipedia.org/wiki/AU-rich_element). Le **proteine leganti le ARE** (**ARE-BP**) si legano agli *elementi ricchi di AU* in un modo che dipende dal tipo di tessuto, dal tipo di cellula, dalla tempistica, dalla localizzazione cellulare e dall’ambiente. In risposta a diversi segnali intracellulari ed extracellulari, gli *ARE-BP* possono promuovere il decadimento dell’mRNA, influenzare la stabilità dell’mRNA o attivare la traduzione. Questo meccanismo di regolazione genica è coinvolto nella *crescita cellulare, nella differenziazione cellulare e nell’adattamento agli stimoli esterni. Agisce quindi sui trascritti codificanti per citochine, fattori di crescita, oncosoppressori, proto-oncogeni, cicline, enzimi, fattori di trascrizione, recettori e proteine di membrana* (https://en.wikipedia.org/wiki/Three_prime_untranslated_region). Gli ARE sembra svolgano un ruolo critico anche nella risposta immunitaria (https://en.wikipedia.org/wiki/AU-rich_element). Il 3’-UTR contiene anche la **sequenza AAUAAA** che dirige l’aggiunta di diverse centinaia di *residui di Adenina* [**coda di Poli (A)**] alla fine della trascrizione dell’mRNA. La **Proteina legante Poli (A)** [*Poly (A) binding protein* (**PABP**)] (https://en.wikipedia.org/wiki/Poly(A)-binding_protein) si lega a questa coda, contribuendo alla regolazione della traduzione, stabilità ed esportazione dell’mRNA. Ad esempio, il **PABP** legato alla **coda di Poli (A)** interagisce con le proteine associate all’estremità 5’ del trascritto, *provocando una circolarizzazione dell’mRNA che promuove la traduzione* (https://en.wikipedia.org/wiki/Three_prime_untranslated_region).
Il 3’-UTR può anche contenere sequenze che attraggono proteine per associare l’mRNA con il citoscheletro, *trasportalo da o verso il nucleo cellulare o eseguire altri tipi di localizzazione*. Oltre alle sequenze all’interno del 3’-UTR, le caratteristiche fisiche della regione, inclusa la sua *lunghezza e struttura secondaria*, contribuiscono alla regolamentazione della traduzione. La *lunghezza del 3’-UTR* è significativa poiché **3’-UTR più lunghi sono associati a livelli inferiori di espressione genica**. Una possibile spiegazione per questo fenomeno è che *le regioni più lunghe hanno una maggiore probabilità di possedere più siti di legame dei miRNA che hanno la capacità di inibire la traduzione*.

Il 3’-UTR contiene anche sequenze che segnalano *aggiunte da fare*, sia alla trascrizione stessa che al prodotto della traduzione. **Questi diversi meccanismi di regolazione genica assicurano che i geni corretti siano espressi nelle cellule corrette al momento opportuno** (https://en.wikipedia.org/wiki/Three_prime_untranslated_region).
Le **mutazioni 3’-UTR** possono essere molto consequenziali perché un’alterazione può essere responsabile dell’espressione alterata di molti geni. Trascrizionalmente, una mutazione può influenzare solo l’allele e i geni che sono fisicamente collegati. Tuttavia, poiché le **proteine leganti 3’-UTR** funzionano anche nell’elaborazione e nell’esportazione nucleare dell’mRNA, una mutazione può anche influenzare altri geni non correlati. La **disregolazione delle proteine leganti l’ARE (AUBP)** a causa di *mutazioni nelle regioni ricche di AU* può portare a malattie tra cui *tumorigenesi (cancro), neoplasie ematopoietiche, leucemogenesi e disturbi dello spettro autistico/ritardo dello sviluppo*. Elementi nel 3’-UTR sono stati anche collegati a *leucemia mieloide acuta umana, alfa-talassemia, neuroblastoma, cheratinopatia, aniridia, sindrome IPEX e difetti cardiaci congeniti* (https://en.wikipedia.org/wiki/Three_prime_untranslated_region). **Le poche malattie mediate da UTR identificate suggeriscono solo gli innumerevoli collegamenti ancora da scoprire**. Infatti, nonostante la nostra attuale comprensione dei 3’-UTR, **ci sono ancora molti misteri da svelare**. Poiché gli mRNA di solito contengono diversi *elementi di controllo sovrapposti*, è spesso difficile specificare l’identità e la funzione di ciascun elemento 3’-UTR, per non parlare dei fattori regolatori che possono legarsi a questi siti. Inoltre, ogni 3’-UTR contiene molti elementi alternativi ricchi di AU e segnali di poliadenilazione. Questi elementi ad azione cis e trans, insieme ai miRNA, offrono una gamma virtualmente illimitata di possibilità di controllo all’interno di un singolo mRNA. Infine, il destino ultimo di una trascrizione risiede nella via di trasduzione del segnale in cui è coinvolto (https://en.wikipedia.org/wiki/Three_prime_untranslated_region).

2.2 LA REGIONE NON TRADOTTA TRE PRIMO (3’-UTR) DEL VACCINO SARS-COV-2 mRNA BIONTECH/PFIZER

Nella sequenza del “codice sorgente” del vaccino (si veda il Capitolo I°), il **3’-UTR** segue il *doppio* **Codone di Terminazione “**TGATGA”, il quale segnala la fine della traduzione della *glicoproteina Spike modificata* (si veda la sequenza sotto riportata. Le lettere del **3’-UTR** sono colorate di rosso).

```
                                       TGATGAC TCGAGCTGGT ACTGCATGCA 3900
CGCAATGCTA GCTGCCCCTT TCCCGTCCTG GGTACCCCGA GTCTCCCCCG 3950
ACCTCGGGTC CCAGGTATGC TCCCACCTCC ACCTGCCCCA CTCACCACCT 4000
CTGCTAGTTC CAGACACCTC CCAAGCACGC AGCAATGCAG CTCAAAACGC 4050
TTAGCCTAGC CACACCCCCA CGGGAAACAG CAGTGATTAA CCTTTAGCAA 4100
TAAACGAAAG TTTAACTAAG CTATACTAAC CCCAGGGTTG GTCAATTTCG 4150
TGCCAGCCAC ACCCTGGAGC TAGCAAAAAA AAAAAAAAAA AAAAAAAAAA 4200
AAAAGCATAT GACTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 4250
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA                  4284
```

Nel documento dell’**Organizzazione Mondiale della Sanità** (World Health Organization; https://berthub.eu/articles/11889.doc) è riportato che il 3’-UTR del vaccino Sars-Cov-2 mRNA BioNTech/Pfizer “comprende due elementi di sequenza derivati dal **potenziatore ammino-terminale dell’mRNA diviso (AES)** e l’**RNA ribosomiale 12S codificato mitocondriale** per conferire stabilità all’RNA e un’elevata espressione proteica totale”.

Il **Ponteziatore Ammino-terminale di Split (AES)** o di divisione è un regolatore trascrizionale della *famiglia dei potenziatori simile alla transducina/Groucho* (https://pubmed.ncbi.nlm.nih.gov/21937451/). “..I **Groucho/Transducina-Like Enhancer of Split (TLE)** sono una famiglia conservata di proteine “*corepressor*” (i corepressori sono proteine che non possono legare direttamente il DNA ma reprimono la trascrizione interagendo con le proteine partner) presenti in animali ……e esseri umani. Le **proteine Groucho/TLE** svolgono importanti funzioni per tutta la durata della vita degli animali, interagendo con diversi percorsi e regolando processi fondamentali come il metabolismo. Tuttavia, queste proteine hanno funzioni particolarmente cruciali nello sviluppo animale, dove sono richieste in più tessuti in modo temporalmente regolato.” (https://pubmed.ncbi.nlm.nih.gov/26172616/).

In uno studio, gli autori hanno appurato che l’**AES interagisce con l’oncoproteina NUP98-HOXA9 e ne migliora la capacità di trasformazione**. In particolare, “***NUP98-HOXA9 è il prototipo delle oncoproteine di fusione NUP98 che causano la leucemia mieloide acuta***. *Consiste in una porzione N-terminale ricca di FG della nucleoporina NUP98 fusa alla regione dell’omeodominio della proteina homeobox HOXA9 e* ***agisce come un fattore di trascrizione aberrante****…..* ***L’AES si localizza principalmente all’interno del nucleo****. AES ha anche mostrato una forte interazione con NUP98 wild-type. AES ha aumentato l’attività trascrizionale di NUP98-HOXA9. In presenza di NUP98-HOXA9, l’AES ha causato un aumento della proliferazione a lungo termine delle cellule CD34+ umane primarie con un marcato aumento del numero di cellule primitive.* ***Questi effetti di AES non sono stati osservati in assenza di NUP98-HOXA9. Il knockdown di***

AES ha diminuito gli effetti trascrizionali e proliferativi di NUP98-HOXA9*. L'AES ha causato un allontanamento dal lignaggio eritroide nelle cellule che esprimono NUP98-HOXA9.* ***Questi dati stabiliscono AES come partner di interazione di NUP98-HOXA9 e mostrano che coopera con NUP98-HOXA9 nella regolazione trascrizionale e nella trasformazione cellulare.***" (https://pubmed.ncbi.nlm.nih.gov/21937451/).
In un altro studio, l'**AES** è stato identificato come **un soppressore di tumori e metastasi in alcuni tipi di cancro**, incluso il **cancro del colon-retto (CRC)**, ma si sa molto poco sulla regolazione dell'espressione di AES. I risultati hanno rivelato che l'***asse CK1δ/ε-AES*** è importante per la *tumorigenesi e la metastasi del CRC* e l'inibizione mirata di questo asse può essere una potenziale strategia terapeutica per il CRC (https://pubmed.ncbi.nlm.nih.gov/33754069/).
Allo stesso modo (https://pubmed.ncbi.nlm.nih.gov/28178391/), *i livelli di espressione di AES* erano inversamente correlati con gli stadi clinici del **Carcinoma Prostatico a (PCa) umano**. I risultati suggeriscono che l'AES svolge un ruolo importante nel controllo della crescita tumorale e della metastasi del PCa regolando le vie di segnalazione sia AR che Notch.

L'**RNA ribosomiale 12S codificato mitocondriale** (spesso abbreviato come **rRNA 12S** o **12S**), noto anche come *peptide derivato dai mitocondri MOTS-c* o *open reading frame mitocondriale del 12S rRNA-c* è l'***SSU rRNA*** del ribosoma mitocondriale (l'*SSU rRNA, l'acido ribonucleico ribosomiale a piccola sub unità*, è il più piccolo dei due principali componenti di RNA del ribosoma) (https://en.wikipedia.org/wiki/MT-RNR1). Associato a un certo numero di proteine ribosomiali, l'rRNA SSU forma la piccola subunità del ribosoma. È codificato da *SSU- rDNA* (https://en.wikipedia.org/wiki/SSU_rRNA). Negli esseri umani, **12S** è codificata dal gene **MT-RNR1** ed è lungo 959 nucleotidi. **L'*rRNA 12S*** *è l'omologo mitocondriale* degli *RNA ribosomiali procariotici* ***16S*** ed *eucariotici nucleari* ***18S***. Il gene **MT-RNR1** codifica per una proteina responsabile della **regolazione della sensibilità all'insulina e dell'omeostasi metabolica**. La proteina agisce come un inibitore del ciclo dei folati e protegge anche dall'*insulino- resistenza dipendente dall'età* e dalla *dieta*, nonché dall'*obesità indotta dalla dieta* (https://en.wikipedia.org/wiki/MT-RNR1). Le *mutazioni nel gene MT-RNR1* possono essere associate alla **perdita dell'udito** e al **deficit del complesso IV** della **catena respiratoria mitocondriale**, noto anche come **deficit della citocromo c ossidasi**. La *carenza di citocromo c ossidasi* è una rara condizione genetica che può colpire più parti del corpo, inclusi i *muscoli scheletrici*, il *cuore*, il *cervello* o il *fegato*. Le manifestazioni cliniche comuni comprendono *miopatia*, *ipotonia*, ed *encefalo miopatia*, *acidosi lattica* e *cardiomiopatia ipertrofica*. Una mutazione 9952G>A è stata trovata in un paziente con la carenza di citocromo c ossidasi (https://en.wikipedia.org/wiki/MT-RNR1).

CAPITOLO III

LA SEQUENZA “HIV-1”, “AES (1)” E I RISULTATI DELLE RICERCHE BLAST

OBIETTIVI DEL CAPITOLO III

Come anticipato nell'Introduzione, a partire da questo capitolo, sono presentate delle sequenze ottenute dalla fusione di segmenti non contigui del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*. Tutte le sequenze ottenute da questi assemblaggi sono state oggetto di ricerca nella banca dati del DNA e dell'RNA (ricerche BLAST).
In particolare, in questo capitolo sono mostrati i risultati delle ricerche BLAST effettuate su **due sequenze**:

1) la **Sequenza "HIV-1"** (**ACGCAATGCCCGTCCTGGT**), la **prima sequenza** ottenuta dalla fusione di **TRE segmenti di sequenza non contigui del *3'-UTR***;

2) la **Sequenza "AES (1)"** (**ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGGT**), ***A*mino-terminal *E*nhancer of *S*plit** *o potenziatore ammino-terminale dell'mRNA diviso*, uno dei componenti principali del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer* (Per il significato di **AES** si rimanda allo studio del Capitolo II di questo documento).

La **Sequenza "HIV-1"** è così chiamata perché il **Virus dell'Immunodeficienza Umana** (**HIV**) è uno degli allineamenti significativi più sconcertanti identificati dalla ricerca BLAST. Sono state riscontrate ben **28** sequenze di questo virus. Il "prodotto" corrispondente a questi 28 allineamenti significativi è la ***Glicoproteina dell'involucro*** (***Envelope glycoprotein***) del **gene Env** (un *gene virale* che codifica per la proteina che forma l'**involucro virale**. Per approfondimenti si vedano le pagina 122, 131 e 138). Desidero far notare che la ***Glicoproteina dell'involucro*** (***Envelope glycoprotein***) del **gene Env** dell'**HIV-1** è lo stesso prodotto identificato dalla ricerca BLAST eseguita sulla *sequenza di RNA del Gene RdRp (RdRp_SARSr-F)* oggetto di studio del documento intitolato "I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis" (si veda la pagina 176 e le pagine seguenti nel documento appena citato).

Un altro sconcertante quanto inaspettato allineamento significativo della **Sequenza "HIV-1"** si riferisce a parte del "**dominio correlato alla nucleasi (NERD)**". Questo dominio si trova in una serie di proteine batteriche (*Halomonas*), archeali e vegetali. In una ricerca (per approfondimenti si veda pagina 105), **NERD** è considerato un dominio correlato all'elaborazione del DNA presente nel **plasmide di virulenza dell'ANTRACE, pXO1** (e in molti altri agenti patogeni). La *nucleasi* (**NERD**) è così chiamata a causa della sua lontana somiglianza con le **endonucleasi** (*enzimi idrolitici* che dividono in due una catena polinucleotidica). Per inciso, si noti che in "I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis" [si vedano i Capitoli IX, X, XI del documento appena citato) sono state riportate numerose sequenze di **Bacillus Anthracis** identificate dalle ricerche BLAST eseguite sulla *sequenza di RNA del Gene RdRp (RdRp_SARSr-F)*].

Parte del "**Leukocyte immunoglobulin-like receptor subfamily A member 6 (LILRA6)"** è invece l'importante "prodotto" riscontrato da un altro allineamento significativo della **Sequenza "HIV-1"**. Questo allineamento si riferisce alla tartaruga più grande del mondo (***Dermochelys coriacea*** *o Tartaruga liuto*). Le malattie associate al gene **LILRA6** includono il **fenomeno di Shwartzman**, una rara reazione di un corpo a particolari tipi di tossine, chiamate **endotossine**, che causano **trombosi nel tessuto colpito**. L'eliminazione della trombosi determina un **blocco reticoloendoteliale**, che impedisce la ripulitura della trombosi causata da un'introduzione ripetuta della tossina. Ciò causerà la *necrosi dei tessuti*. Il **fenomeno Shwartzman** è anche correlato alla *granulocitopenia* e all'*orticaria tipo Arthus*, quest' ultima una malattia da reazione di ipersensibilità di tipo III caratterizzata da ***vasculiti locali***, accompagnate da *sintomi dolorosi, edema, emorragia o necrosi* e ha una base fisica nella deposizione di *complessi immuni antigene-anticorpo nelle pareti vascolari o sierose* (per approfondimenti si veda pagina 101).

Un segmento di sequenza della "**Transglutaminase-like cysteine peptidase**" **(Superfamiglia simile alla transglutaminasi)**, un prodotto del batterio **Rhizobium grahamii**, è anch'esso il risultato di un allineamento significativo della **Sequenza "HIV-1"** correlato con la **coagulazione del sangue**. Questa famiglia comprende le transglutaminasi animali e altre proteine batteriche di funzione sconosciuta. La conservazione della sequenza in questa superfamiglia coinvolge principalmente **tre motivi** che ruotano attorno ai residui conservati di *cisteina*, *istidina* e *aspartato* che formano la **triade catalitica nella transglutaminasi strutturalmente caratterizzata**, il *fattore XIIIa della coagulazione del sangue umano* (per approfondimenti si veda pagina 113).

La **proteina simile ad ADAMTS 4**, che nell'uomo è codificata dal gene **ADAMTSL4** (membro della **famiglia di geni simili ad ADAMTS**), è *una disintegrina e metalloproteinasi con motivi di trombospondina* che codifica per una proteina con sette ripetizioni di **trombospondina di tipo 1**. Essa è il risultato di un allineamento significativo della **Sequenza "HIV-1"** identificato nel **Rospo comune** (Bufo Bufo). Il dominio ripetuto della trombospondina di tipo 1 si trova in molte proteine con diverse funzioni biologiche tra cui l'***adesione cellulare*** , l'***angiogenesi*** e il ***patterning del sistema nervoso in via di sviluppo***. *La proteina simile ad ADAMTS 4* è coinvolta nella ***regolazione positiva dell'apoptosi*** e ***può facilitare la biogenesi delle microfibrille FBN1***. Diverse proteine ADAMTS sono pesantemente implicate nei disordini genetici e acquisiti, umani e animali (per approfondimenti si veda pagina 120).

Un segmento di sequenza di un prodotto di **Drosophila subobscura** (una specie di moscerino della frutta), "**prolow-density lipoprotein receptor-related protein 1**" [***proteina 1 correlata al recettore delle lipoproteine a bassa densità*** (**LRP1**) o *recettore alfa-2-macroglobulina* (**A2MR**), *recettore dell'apolipoproteina E* (**APOER**) o cluster di *differenziazione 91* (**CD91**)], è il risultato di un altro allineamento significativo della **Sequenza "HIV-1"**. **LRP1** è una proteina che forma un recettore presente nel membrana plasmatica di cellule coinvolte nell'endocitosi mediata da recettori. Nell'uomo, la proteina LRP1 è codificata dal gene LRP1 ed è coinvolta nel metabolismo delle lipoproteine, nella motilità cellulare e nelle **malattie neurodegenerative, l'aterosclerosi e il cancro** (per approfondimenti si veda pagina 108).

Altri importanti allineamenti significativi della **Sequenza "HIV-1"** hanno riguardato i seguenti prodotti:

1) **Type IV secretory system conjugative DNA transfer family protein**. **I sistemi di secrezione di tipo IV (T4SS)** sono grandi complessi proteici che attraversano l'involucro cellulare di molti batteri. ***Il sistema T4S è impiegato dai batteri patogeni per esportare DNA di virulenza e/o proteine direttamente dal citoplasma batterico nella cellula ospite*** (per approfondimenti si veda pagina 118);

2) **DNA mismatch repair protein MutS**. **MutS** (**Mutator S**) è una ***proteina di riparazione del DNA di mismatch*** e implica la ***correzione di coppie di basi non corrispondenti*** che sono state perse dall'elemento di correzione (frammento di Klenow) del complesso della DNA polimerasi. Il Mismatch Repair System post-replicativo (**MMRS**) agisce per correggere mutazioni puntiformi o piccoli loop di inserimento/delezione prodotti durante la replicazione del DNA (per approfondimenti si veda pagina 124);

3) **Class I SAM-dependent methyltransferase**. Le **metiltransferasi dipendenti dalla S-adenosil-L-metionina (SAM)** svolgono ruoli importanti nella **metilazione** delle biomolecole. La **metilazione**, così come altre *modificazioni epigenetiche*, può modulare la *trascrizione genica*, o addirittura **silenziare o attivare completamente i geni**, **senza mutazioni nel gene stesso**. **L'ipo e l'ipermetilazione del DNA sono implicate in molte malattie**. Le cellule cancerose in genere mostrano una **minore attività di metilazione del DNA in generale**, sebbene spesso ipermetilazione in siti che non sono metilati nelle cellule normali; questa sovrametilazione spesso funziona come un modo per inattivare i **geni oncosoppressori** (per approfondimenti si veda pagina 127);

4) **Mitochondrial antiviral-signaling protein**. La **proteina di segnalazione antivirale mitocondriale (MAVS)** è una proteina essenziale per l'**immunità innata antivirale**. MAVS si trova nella membrana esterna dei mitocondri, dei perossisomi e del reticolo endoplasmatico (ER). La proteina MAVS induce l'**apoptosi nelle cellule ospiti infettate da virus** interagendo con una proteasi chiamata caspasi 8 (per approfondimenti si veda pagina 133);

5) **Plakophilin-1**. Nell'uomo questa proteina è codificata dal ***gene PKP1***, il quale codifica per un **membro delle famiglie di geni arm-repeat** (armadillo) e **placofilina**. **PKP1** ha dimostrato di interagire con la **Desmoplachina**. La **Desmoplachina** è una proteina nell'uomo codificata dal **gene DSP**. È stata riscontrata una diminuzione dell'espressione della desmoplachina in pazienti con cancro orofaringeo e cancro al seno, che può alterare le proprietà di adesione cellula-cellula e propagare metastasi (per approfondimenti si veda pagina 135).

Prima di concludere l’esposizione dei risultati della **Sequenza “HIV-1”**, desidero sottolineare la presenza due suoi allineamenti significativi con il **Pipistrellus Pipistrellus**, di altri numerosi allineamenti con gli organismi **Klebsiella pneumoniae** (la cui infezione implica sintomi **febbrili** e **polmonari**) e **Pseudomonas** (un batterio notevolmente implicato in **patologie polmonari**) e l’allineamento con il prodotto “**dCMP deaminase family protein**”, un’enzima che lega **Zn++** (**ione Zinco**). In passato, **Pseudomonas** è stato oggetto di un nostro studio specifico [Analisi e modificazioni di Sequenze di DNA o di RNA con la T T E S (Capitolo I° - Parte Prima) e Analisi e modificazioni di Sequenze di DNA o di RNA con la T T E S (Capitolo I - Parte Seconda)], mentre **Klebsiella pneumoniae** e il ruolo dello **ione Zinco** sono stati ampiamente discussi in “I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis”. Come vedremo nel Capitolo VI, lo **ione Zinco** continua ad avere un’importanza fondamentale per il nostro attuale studio.

Riguardo i risultati della ricerca BLAST sulla **Sequenza “AES (1)”** (si veda il paragrafo 3.2), essi hanno confermato che l’***Amino-terminal Enhancer of Split*** è il “prodotto” principale, così come **dichiarato nel documento scaricato dalla WHO** (https://berthub.eu/articles/11889.doc), documento relativo al “codice sorgente” integrale del *Vaccino mRNA Sars-Cov-2 BioNTech/Pfizer (BNT162b2)*. Pur se coerente con il documento sopracitato, **questo risultato è invece fortemente in contraddizione** con quanto accertato con i risultati della ricerca BLAST eseguiti sulla **SEQUENZA “HIV-1”**.

3.1 LA SEQUENZA “HIV-1” E I RISULTATI DELLA RICERCA BLAST

Quella mostrata qui di seguito è la sequenza totale del *3’-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*. Le lettere colorate sono i **TRE segmenti di sequenza non contigui** che sono stati identificati in questa ricerca. Essi, uniti insieme, formano la **Sequenza “HIV-1”**. Questa sequenza è stata sottoposta ad una ricerca BLAST e nelle pagine seguenti sono mostrati gli *allineamenti significativi* ottenuti e gli “**organismi**” e i **prodotti** a cui tali allineamenti si riferiscono.

```
                                                 C TCGAGCTGGT ACTGCATGCA 3900
CGCAATGCTA GCTGCCCCTT TCCCGTCCTG GGTACCCCGA GTCTCCCCCG 3950
ACCTCGGGTC CCAGGTATGC TCCCACCTCC ACCTGCCCCA CTCACCACCT 4000
CTGCTAGTTC CAGACACCTC CCAAGCACGC AGCAATGCAG CTCAAAACGC 4050
TTAGCCTAGC CACACCCCCA CGGGAAACAG CAGTGATTAA CCTTTAGCAA 4100
TAAACGAAAG TTTAACTAAG CTATACTAAC CCCAGGGTTG GTCAATTTCG 4150
TGCCAGCCAC ACCCTGGAGC TAGC
```

QUERY: **ACGCAATGCCCGTCCTGGT**

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	**5000**
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F

SEQUENZE SELEZIONATE: 1547

Description	Name	Taxid	Score	Score	cover	Value	Ident	Len	Accession
Oricola thermophila strain MEBiC13590 chromosome, complete genome	NA	2742145	36.2	66.4	94%	12	100.00	3998539	CP054836.1
Flavobacterium haoranii strain KCTC 23008 chromosome, complete...	NA	683124	36.2	36.2	94%	12	100.00	2871082	CP045292.1
Citrobacter freundii isolate MGYG-HGUT-02495 genome assembly,...	NA	546	36.2	66.4	100%	12	100.00	5258449	LR699006.1
Salmo trutta genome assembly, chromosome: 4	river trout	8032	36.2	36.2	94%	12	100.00	73168960	LR584420.1
Citrobacter freundii strain FDAARGOS_61 chromosome, complete...	NA	546	36.2	66.4	100%	12	100.00	5258481	**CP026045.1**
Citrobacter freundii strain CRCB-101 chromosome,	NA	546	36.2	66.4	100%	12	100.00	5311319	CP024819.1

complete genome									
Citrobacter freundii strain BD genome	NA	546	36.2	66.4	100%	12	100.00	5098116	CP018810.1
Pseudomonas xanthomarina strain LMG 23572 genome assembly,...	NA	271420	36.2	36.2	94%	12	100.00	4332289	LT629970.1
Dermochelys coriacea leukocyte immunoglobulin-like receptor...	leatherback ...	27794	36.2	36.2	94%	12	100.00	2216	XM_038382257.1
Citrobacter freundii strain RHBSTW-00011 chromosome, complete...	NA	546	36.2	66.4	100%	12	100.00	5384013	CP056907.1
Citrobacter freundii strain RHBSTW-00200 chromosome, complete...	NA	546	36.2	36.2	94%	12	100.00	5266015	CP055551.1
Shigella sonnei strain SE6-1 chromosome, complete genome	NA	624	34.2	34.2	89%	47	100.00	4762774	CP055292.1
Citrobacter freundii strain ZY198 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4997964	CP055247.1
Salmonella enterica strain FDAARGOS_718 chromosome	NA	28901	34.2	68.4	89%	47	100.00	4667369	CP054901.1
Salmonella enterica strain FDAARGOS_717 chromosome	NA	28901	34.2	34.2	89%	47	100.00	4822365	CP054897.1
Escherichia coli strain CFS3273 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	5123217	CP026932.2
Citrobacter sp. TSA-1 chromosome, complete genome	NA	184912	34.2	64.4	94%	47	100.00	4919713	CP053573.1
Salmonella enterica subsp. salamae serovar 6,8:a:z52 strain...	NA	2577915	34.2	34.2	89%	47	100.00	4605416	CP053318.1
Citrobacter freundii strain CitB chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4827866	CP048416.1
Citrobacter koseri strain SCAID URN1-2019 chromosome	NA	545	34.2	34.2	89%	47	100.00	4650688	CP052059.1
Citrobacter freundii strain SCAID PHRX1-2019 chromosome	NA	546	34.2	64.4	94%	47	100.00	4664379	CP052058.1
Escherichia coli strain 52148 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4859628	CP050382.1
Xanthomonas oryzae pv. oryzae strain K2 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	4984295	CP050113.1
Xanthomonas oryzae pv. oryzae strain K3 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	4945802	CP050114.1
Xanthomonas oryzae pv. oryzae strain K3a chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	4880106	CP050115.1
Coregonus sp. 'balchen' genome assembly, chromosome: 18	NA	861768	34.2	34.2	89%	47	100.00	51949489	LR778270.1
Citrobacter freundii ATCC 8090 = MTCC 1658 = NBRC 12681 strain...	NA	1006003	34.2	64.4	94%	47	100.00	4957773	CP049015.1
Escherichia coli strain CM IVRI KOL-1 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4945239	CP033158.1
Xanthomonas oryzae pv. oryzae strain K1 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	4981423	CP049205.1
Escherichia coli 2018.02.02CC DNA, complete genome	NA	562	34.2	34.2	89%	47	100.00	4574715	AP021896.1

Escherichia coli 2017.15.01CC DNA, complete genome	NA	562	34.2	34.2	89%	47	100.00	4869407	AP021890.1
Citrobacter freundii strain 62 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4695344	CP048382.1
Escherichia coli strain 164 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4892242	CP048367.1
Escherichia coli strain 32-4 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4853092	CP048310.1
Escherichia coli strain 163 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4819649	CP048371.1
Escherichia coli strain 2407 a chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4941120	CP025967.1
Citrobacter sp. LUTT5 chromosome, complete genome	NA	2697370	34.2	64.4	94%	47	100.00	5034577	CP047606.1
Klebsiella pneumoniae strain YML0508 chromosome, complete genome	NA	573	34.2	34.2	89%	47	100.00	5352780	CP045193.1
Citrobacter freundii strain L75 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5125834	CP047307.1
Xanthomonas oryzae pv. oryzae strain ITCCBB0002 chromosome,...	NA	64187	34.2	34.2	89%	47	100.00	4731568	CP046148.1
Citrobacter freundii strain 680 chromosome, complete genome	NA	546	34.2	98.6	94%	47	100.00	5167642	CP038658.1
Citrobacter freundii strain 565 chromosome, complete genome	NA	546	34.2	98.6	94%	47	100.00	5207876	CP038656.1
Citrobacter freundii strain 154 chromosome, complete genome	NA	546	34.2	98.6	94%	47	100.00	5143118	CP038653.1
Xanthomonas oryzae pv. oryzae strain LN18 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	5024861	CP045238.1
Citrobacter braakii strain MiY-A chromosome, complete genome	NA	57706	34.2	64.4	94%	47	100.00	4917491	CP045771.1
Citrobacter sp. S39 chromosome, complete genome	NA	2660638	34.2	64.4	94%	47	100.00	4806164	CP045555.1
Salmonella enterica subsp. enterica serovar Schwarzengrund...	NA	340190	34.2	34.2	89%	47	100.00	4630202	CP045447.1
Salmonella enterica subsp. enterica serovar Schwarzengrund...	NA	340190	34.2	34.2	89%	47	100.00	4631209	CP045444.1
Citrobacter freundii strain E51 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5070767	CP042534.1
Citrobacter freundii strain E11 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5088693	CP042524.1
Citrobacter freundii strain E33 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5022915	CP042517.1
Citrobacter freundii strain C50 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5095110	CP042478.1
Enterobacter hormaechei strain E5 chromosome, complete genome	NA	158836	34.2	34.2	89%	47	100.00	4841070	CP042571.1
Salmonella enterica subsp. enterica serovar Corvallis strain...	NA	593905	34.2	34.2	89%	47	100.00	4799356	CP044200.1
Citrobacter koseri strain FDAARGOS_646 chromosome, complete...	NA	545	34.2	34.2	89%	47	100.00	4581018	CP044097.1
Citrobacter werkmanii strain FDAARGOS_616 chromosome, complete...	NA	67827	34.2	34.2	89%	47	100.00	4932938	CP044101.1
Citrobacter portucalensis strain FDAARGOS_617	NA	1639133	34.2	64.4	94%	47	100.00	4926736	CP044098.1

chromosome,...									
Escherichia coli strain CVM N56639 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4891172	CP043752.1
Enterobacter chengduensis strain WCHECl-C4 = WCHECh050004...	NA	2494701	34.2	68.4	89%	47	100.00	5111427	CP043318.1
Xanthomonas oryzae pv. oryzae strain BXO1 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	4991257	CP033201.1
Escherichia coli strain WCHEC005237 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4832939	CP026580.3
Stieleria maiorica strain Mal15 chromosome	NA	2795974	34.2	34.2	89%	47	100.00	9894293	CP036264.1
Escherichia coli strain SCEC020023 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4883746	CP025950.4
Salmonella enterica strain CFSAN079107 chromosome, complete...	NA	28901	34.2	34.2	89%	47	100.00	4872954	CP042440.1
Salmonella enterica strain CFSAN079094 chromosome, complete...	NA	28901	34.2	34.2	89%	47	100.00	4918293	CP042438.1
Xanthomonas oryzae pv. oryzae strain JW11089 chromosome,...	NA	64187	34.2	34.2	89%	47	100.00	5010511	CP033193.2
Escherichia coli strain ECOL-18-VL-LA-PA-Ryan-0026 chromosome,...	NA	562	34.2	34.2	89%	47	100.00	4857938	CP041392.1
Salmonella enterica strain MAC15 chromosome, complete genome	NA	28901	34.2	34.2	89%	47	100.00	5052222	CP030749.1
Citrobacter sp. CF971 chromosome, complete genome	NA	2566012	34.2	64.4	94%	47	100.00	4955441	CP041051.1
Citrobacter freundii strain R47 chromosome R47, complete sequence	NA	546	34.2	64.4	94%	47	100.00	4952107	CP040698.1
Salmonella enterica subsp. enterica serovar Weltevreden strain...	NA	57743	34.2	34.2	89%	47	100.00	4994320	CP040701.1
Salmonella enterica subsp. enterica serovar Senftenberg SL1800...	NA	28150	34.2	34.2	89%	47	100.00	4980580	AP019692.1
Xanthomonas oryzae pv. oryzae strain PXO61 chromosome, complet...	NA	64187	34.2	34.2	89%	47	100.00	4968141	CP033187.3
Citrobacter sp. TBCP-5362 chromosome, complete genome	NA	2576406	34.2	34.2	89%	47	100.00	4569707	CP040234.1
Escherichia coli strain EC-129 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4820005	CP038453.1
Enterobacter soli strain LF7a, complete genome	NA	885040	34.2	34.2	89%	47	100.00	4812833	CP003026.1
Citrobacter sp. SL156 chromosome, complete genome	NA	2079228	34.2	98.6	94%	47	100.00	4985174	CP026550.1
Escherichia coli strain 219 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	5003410	CP020514.1
Thermaerobacter sp. FW80 chromosome, complete genome	NA	2546351	34.2	34.2	89%	47	100.00	2953026	CP037895.1
Xanthomonas oryzae pv. oryzae strain PXO513 chromosome, comple...	NA	64187	34.2	34.2	89%	47	100.00	4915674	CP033188.1
Xanthomonas oryzae pv. oryzae strain PXO421 chromosome, comple...	NA	64187	34.2	34.2	89%	47	100.00	4909962	CP033189.1

Xanthomonas oryzae pv. oryzae strain PXO404 chromosome, comple...	NA	64187	34.2	34.2	89%	47	100.00	4914700	CP033190.1
Xanthomonas oryzae pv. oryzae strain PXO364 chromosome, comple...	NA	64187	34.2	34.2	89%	47	100.00	4904940	CP033191.1
Xanthomonas oryzae pv. oryzae strain KXO85 chromosome, complet...	NA	64187	34.2	34.2	89%	47	100.00	4975259	CP033197.1
Xanthomonas oryzae pv. oryzae strain AUST2013 chromosome,...	NA	64187	34.2	34.2	89%	47	100.00	4958184	CP033196.1
Citrobacter sp. LY-1 chromosome, complete genome	NA	2546350	34.2	34.2	89%	47	100.00	5211009	CP037864.1
Citrobacter freundii strain CAV1857 chromosome, complete genome	NA	546	34.2	98.6	94%	47	100.00	4947788	CP037734.1
Citrobacter freundii complex strain ABFQG, complete genome	NA	2529121	34.2	64.4	94%	47	100.00	4883650	CP036435.1
Escherichia coli strain WCHEC025970 chromosome, complete genome	NA	562	34.2	68.4	89%	47	100.00	4794992	CP036177.1
Citrobacter koseri strain NCTC11075 genome assembly, chromosom...	NA	545	34.2	34.2	89%	47	100.00	4785757	LR134204.1
Salmonella enterica subsp. houtenae strain NCTC7318 genome...	NA	59205	34.2	34.2	89%	47	100.00	4867363	LR134159.1
Citrobacter freundii strain NCTC9750 genome assembly,...	NA	546	34.2	64.4	94%	47	100.00	4960737	LR134118.1
Xanthomonas oryzae pv. oryzae strain YN24 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	5028971	CP018089.1
Xanthomonas oryzae pv. oryzae strain ScYc-b chromosome, comple...	NA	64187	34.2	34.2	89%	47	100.00	4865653	CP018087.1
Salmonella enterica subsp. enterica serovar Senftenberg strain...	NA	28150	34.2	34.2	89%	47	100.00	4818442	CP034233.1
Citrobacter koseri strain FDAARGOS_530 chromosome, complete...	NA	545	34.2	34.2	89%	47	100.00	4581001	CP033780.1
Citrobacter freundii strain FDAARGOS_549 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	4974986	CP033744.1
Citrobacter freundii strain FDAARGOS_550 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	4969137	CP033742.1
Escherichia coli M217 DNA, complete genome	NA	562	34.2	34.2	89%	47	100.00	4825589	AP019189.1
Citrobacter freundii strain HM38 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4899014	CP024672.1
Citrobacter freundii strain UMH19 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4996291	CP024673.1
Citrobacter werkmanii strain UMH18 chromosome, complete genome	NA	67827	34.2	34.2	89%	47	100.00	5062051	CP024675.1
Citrobacter freundii strain UMH16 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5195086	CP024677.1

Citrobacter freundii strain UMH15 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5343952	CP024679.1
Citrobacter freundii strain UMH14 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4859315	CP024680.1
Citrobacter freundii strain AR_0116 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5121015	CP032184.1
Xanthomonas oryzae pv. oryzae strain XM9 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	4920509	CP020334.1
Cronobacter sakazakii strain CS-09 chromosome, complete genome	NA	28141	34.2	68.4	89%	47	100.00	4496886	CP027109.1
Xanthomonas oryzae pv. oryzae strain SK2-3 chromosome, complet...	NA	64187	34.2	34.2	89%	47	100.00	4934446	CP019515.1
Xanthomonas oryzae pv. oryzae strain IX-280 chromosome, comple...	NA	64187	34.2	34.2	89%	47	100.00	4963594	CP019226.1
Xanthomonas oryzae pv. oryzae strain PXO142 chromosome, comple...	NA	64187	34.2	34.2	89%	47	100.00	4982118	CP031698.1
Escherichia coli isolate **Escherichia** coli str. 3426 genome...	NA	562	34.2	34.2	89%	47	100.00	4922897	LS992185.1
Citrobacter freundii isolate Citrobacter freundii str. U2785...	NA	546	34.2	64.4	94%	47	100.00	5009078	LS992183.1
Citrobacter freundii isolate Citrobacter freundii str. E2614...	NA	546	34.2	98.6	94%	47	100.00	5172644	LS992175.1
Escherichia coli strain BR32-DEC chromosome	NA	562	34.2	34.2	89%	47	100.00	4838618	CP035350.1
Citrobacter freundii strain R17 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5124258	CP035276.1
Escherichia coli strain NCTC11121 genome assembly, chromosome: 1	NA	562	34.2	34.2	89%	47	100.00	4635216	LR134220.1
Xanthomonas oryzae pv. oryzae strain ScYc-b chromosome, comple...	NA	64187	34.2	34.2	89%	47	100.00	4865660	CP031469.1
Xanthomonas oryzae pv. oryzae strain JL25 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	4900521	CP031457.1
Xanthomonas oryzae pv. oryzae strain PX086 chromosome, complet...	NA	64187	34.2	34.2	89%	47	100.00	5015823	CP031463.1
Xanthomonas oryzae pv. oryzae strain YC11 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	4867200	CP031464.1
Xanthomonas oryzae pv. oryzae strain JL33 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	4898917	CP031459.1
Xanthomonas oryzae pv. oryzae strain JP01 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	4948537	CP031460.1
Xanthomonas oryzae pv. oryzae strain HuN37 chromosome, complet...	NA	64187	34.2	34.2	89%	47	100.00	4915452	CP031456.1
Xanthomonas oryzae pv. oryzae strain PXO61 chromosome, complet...	NA	64187	34.2	34.2	89%	47	100.00	4994045	CP021789.1

Xanthomonas oryzae pv. oryzae strain PXO61 chromosome, complet...	NA	64187	34.2	34.2	89%	47	100.00	4980838	CP021788.1
Salmonella enterica subsp. enterica serovar Gaminara str....	NA	1242094	34.2	34.2	89%	47	100.00	4834965	CP030288.1
Escherichia coli strain WCHEC005784 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4812358	CP028578.2
Escherichia coli strain NCTC11023 genome assembly, chromosome: 1	NA	562	34.2	68.4	89%	47	100.00	4705041	LS483297.1
Escherichia coli strain NCTC9966 genome assembly, chromosome: 1	NA	562	34.2	34.2	89%	47	100.00	4705297	LS483296.1
Salmonella enterica subsp. enterica serovar Senftenberg strain...	NA	28150	34.2	34.2	89%	47	100.00	5029670	LS483465.1
Escherichia coli strain HS30-1 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4423666	CP029492.1
Citrobacter sp. CRE-46 strain AR_0157 chromosome, complete genome	NA	1703250	34.2	34.2	89%	47	100.00	5262516	CP029727.1
Xanthomonas oryzae pv. oryzae strain PXO61 chromosome, complet...	NA	64187	34.2	34.2	89%	47	100.00	4999360	CP020942.1
Salmonella enterica subsp. enterica serovar Newport str....	NA	1454620	34.2	34.2	89%	47	100.00	4695514	CP007216.2
Escherichia coli strain AR435 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4831922	CP029115.1
Salmonella enterica subsp. enterica serovar Corvallis strain...	NA	593905	34.2	34.2	89%	47	100.00	4887378	CP027677.1
Escherichia coli strain 675SK2 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4889200	CP027701.1
Escherichia coli strain APEC 01 chromosome	NA	562	34.2	34.2	89%	47	100.00	4609982	CP028310.1
Linum usitatissimum chromosome Lu1	flax	4006	34.2	34.2	89%	47	100.00	29425369	CP027619.1
Citrobacter freundii strain B9-C2 chromosome	NA	546	34.2	64.4	94%	47	100.00	5028563	CP027849.1
Citrobacter koseri strain FDAARGOS_287 chromosome, complete...	NA	545	34.2	34.2	89%	47	100.00	4925369	CP022073.2
Citrobacter braakii strain FDAARGOS_290 chromosome, complete...	NA	57706	34.2	64.4	94%	47	100.00	4834774	CP022049.2
Citrobacter koseri strain AR_0025 chromosome, complete genome	NA	545	34.2	34.2	89%	47	100.00	4798293	CP026697.1
Citrobacter koseri strain AR_0024 chromosome, complete genome	NA	545	34.2	34.2	89%	47	100.00	4919580	CP026709.1
Salmonella enterica subsp. enterica serovar Derby isolate...	NA	28144	34.2	34.2	89%	47	100.00	4846817	CP026609.1
Citrobacter freundii complex sp. CFNIH4 chromosome, complete...	NA	2077148	34.2	64.4	94%	47	100.00	5079781	CP026231.1
Citrobacter freundii complex sp. CFNIH3 chromosome, complete...	NA	2077147	34.2	64.4	94%	47	100.00	5334524	CP026235.1
Escherichia coli strain ECONIH6 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4869246	CP026199.1
Escherichia coli strain	NA	562	34.2	34.2	89%	47	100.00	4800548	CP025627.1

SCEC020007 chromosome, complete genome									
Escherichia coli strain CRE1493 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4877335	CP019071.1
Escherichia coli strain AR_0014, complete genome	NA	562	34.2	34.2	89%	47	100.00	4839565	CP024859.1
Escherichia coli strain AR_0011, complete genome	NA	562	34.2	34.2	89%	47	100.00	4856773	CP024855.1
Escherichia coli strain CREC-532 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4837992	CP024830.1
Escherichia coli strain CREC-629 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4938993	CP024815.1
Escherichia coli strain FDAARGOS_434 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4897877	CP023870.1
Citrobacter koseri strain FDAARGOS_393 chromosome, complete...	NA	545	34.2	34.2	89%	47	100.00	4875257	CP023527.1
Escherichia coli strain 1190 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4900891	CP023386.1
Escherichia coli strain 360/16 chromosome	NA	562	34.2	34.2	89%	47	100.00	4748376	CP023201.1
Halomonas sp. hl-4 genome assembly, chromosome: I	NA	1761789	34.2	34.2	89%	47	100.00	4238682	LT907845.1
Salmonella enterica subsp. enterica serovar Derby strain...	NA	28144	34.2	34.2	89%	47	100.00	4850334	CP022494.1
Citrobacter freundii strain 18-1, complete genome	NA	546	34.2	64.4	94%	47	100.00	5215381	CP022273.1
Escherichia coli strain AR_0137, complete genome	NA	562	34.2	34.2	89%	47	100.00	4746578	CP021879.1
Escherichia coli strain EC1515, complete genome	NA	562	34.2	34.2	89%	47	100.00	5167363	CP021844.1
Escherichia coli strain EC974, complete genome	NA	562	34.2	34.2	89%	47	100.00	5167701	CP021840.1
Escherichia coli strain AR_0150, complete genome	NA	562	34.2	34.2	89%	47	100.00	4864149	CP021736.1
Escherichia coli strain AR_0114, complete genome	NA	562	34.2	34.2	89%	47	100.00	4786118	CP021732.1
Escherichia coli strain AR_0151, complete genome	NA	562	34.2	34.2	89%	47	100.00	4862952	CP021691.1
Escherichia coli strain AR_0162, complete genome	NA	562	34.2	34.2	89%	47	100.00	4810234	CP021683.1
Escherichia coli strain AR_0149, complete genome	NA	562	34.2	34.2	89%	47	100.00	4830167	CP021532.1
Escherichia coli strain 5CRE51, complete genome	NA	562	34.2	34.2	89%	47	100.00	5041366	CP021175.1
Pantoea stewartii subsp. stewartii DC283, complete genome	NA	660596	34.2	34.2	89%	47	100.00	4528215	CP017581.1
Citrobacter werkmanii strain BF-6, complete genome	NA	67827	34.2	34.2	89%	47	100.00	4929789	CP019986.1
Xanthomonas oryzae pv. oryzae strain XF89b, complete genome	NA	64187	34.2	34.2	89%	47	100.00	4966744	CP011532.1
Salmonella enterica subsp. enterica serovar Apapa str....	NA	1242088	34.2	34.2	89%	47	100.00	4801658	CP019403.1
Citrobacter koseri isolate 0123A_53_520, complete genome	NA	545	34.2	34.2	89%	47	100.00	4752495	CP017665.1
Escherichia coli strain S50, complete genome	NA	562	34.2	34.2	89%	47	100.00	4797106	CP010238.1
Pseudomonas putida strain PP112420, complete genome	NA	303	34.2	34.2	89%	47	100.00	6031212	CP017073.1
Escherichia coli strain	NA	562	34.2	34.2	89%	47	100.00	4794148	CP018121.1

MRSN346355, complete genome									
Escherichia coli strain MRSN346638, complete genome	NA	562	34.2	34.2	89%	47	100.00	4798436	CP018115.1
Escherichia coli strain MRSN346595, complete genome	NA	562	34.2	34.2	89%	47	100.00	4796421	CP018109.1
Escherichia coli strain MRSN352231, complete genome	NA	562	34.2	34.2	89%	47	100.00	4794148	CP018103.1
Escherichia coli strain Y5, complete genome	NA	562	34.2	34.2	89%	47	100.00	4839266	CP013483.1
Xanthomonas oryzae pv. oryzae strain PXO602, complete genome	NA	64187	34.2	34.2	89%	47	100.00	4951791	CP013679.1
Xanthomonas oryzae pv. oryzae strain PXO563, complete genome	NA	64187	34.2	34.2	89%	47	100.00	4936308	CP013678.1
Xanthomonas oryzae pv. oryzae strain PXO524, complete genome	NA	64187	34.2	34.2	89%	47	100.00	4954304	CP013677.1
Xanthomonas oryzae pv. oryzae strain PXO282, complete genome	NA	64187	34.2	34.2	89%	47	100.00	4961996	CP013676.1
Xanthomonas oryzae pv. oryzae strain PXO236, complete genome	NA	64187	34.2	34.2	89%	47	100.00	4968717	CP013675.1
Xanthomonas oryzae pv. oryzae strain PXO211, complete genome	NA	64187	34.2	34.2	89%	47	100.00	5033346	CP013674.1
Xanthomonas oryzae pv. oryzae strain PXO145, complete genome	NA	64187	34.2	34.2	89%	47	100.00	5039763	CP013961.1
Xanthomonas oryzae pv. oryzae strain PXO71, complete genome	NA	64187	34.2	34.2	89%	47	100.00	4906999	CP013670.1
Citrobacter freundii strain SL151, complete genome	NA	546	34.2	98.6	94%	47	100.00	5096586	CP016952.1
Citrobacter freundii strain B38, complete genome	NA	546	34.2	64.4	94%	47	100.00	5134500	CP016762.1
Halomonas sp. HL-93 genome assembly, chromosome: I	NA	1666906	34.2	34.2	89%	47	100.00	4144542	LT593974.1
Salmonella enterica subsp. enterica serovar Weltevreden str....	NA	1173939	34.2	34.2	89%	47	100.00	5047093	CP014996.1
Escherichia coli str. Sanji, complete genome	NA	1441627	34.2	34.2	89%	47	100.00	4891769	CP011061.1
Xanthomonas oryzae pv. oryzae strain PXO83, complete genome	NA	64187	34.2	34.2	89%	47	100.00	5025428	CP012947.1
Salmonella enterica subsp. enterica serovar Weltevreden genome...	NA	57743	34.2	34.2	89%	47	100.00	4966880	LN890524.1
Salmonella enterica subsp. enterica serovar Weltevreden genome...	NA	57743	34.2	34.2	89%	47	100.00	4875411	LN890522.1
Salmonella enterica subsp. enterica serovar Weltevreden genome...	NA	57743	34.2	34.2	89%	47	100.00	5129845	LN890520.1
Salmonella enterica subsp. enterica serovar Weltevreden genome...	NA	57743	34.2	34.2	89%	47	100.00	5062936	LN890518.1
Citrobacter portucalensis strain P10159, complete genome	NA	1639133	34.2	34.2	89%	47	100.00	5080321	CP012554.1
Oblitimonas alkaliphila strain E5571 chromosome	NA	1697053	34.2	34.2	89%	47	100.00	2397029	CP012365.1
Oblitimonas alkaliphila strain E1148 chromosome, complete genome	NA	1697053	34.2	34.2	89%	47	100.00	2377259	CP012364.1
Oblitimonas alkaliphila strain D3318 chromosome, complete genome	NA	1697053	34.2	34.2	89%	47	100.00	2294397	CP012362.1
Oblitimonas alkaliphila strain D2441 chromosome, complete	NA	1697053	34.2	34.2	89%	47	100.00	2400551	CP012361.1

genome									
Oblitimonas alkaliphila strain C6918 chromosome, complete genome	NA	1697053	34.2	34.2	89%	47	100.00	2312033	CP012360.1
Oblitimonas alkaliphila strain C6819 chromosome, complete genome	NA	1697053	34.2	34.2	89%	47	100.00	2272143	CP012359.1
Oblitimonas alkaliphila strain B4199 chromosome, complete genome	NA	1697053	34.2	34.2	89%	47	100.00	2494031	CP012358.1
Citrobacter freundii strain CAV1741, complete genome	NA	546	34.2	98.6	94%	47	100.00	5029496	CP011657.1
Citrobacter freundii strain CAV1321, complete genome	NA	546	34.2	98.6	94%	47	100.00	4976908	CP011612.1
Xanthomonas oryzae pv. oryzae PXO86, complete genome	NA	1458476	34.2	34.2	89%	47	100.00	5016623	CP007166.1
Pseudomonas sp. MRSN12121, complete genome	NA	1611770	34.2	64.4	94%	47	100.00	6929263	CP010892.1
Escherichia coli genome assembly FHI29, scaffold...	NA	562	34.2	34.2	89%	47	100.00	197697	LM995855.1
Citrobacter koseri genome assembly PRJEB6512_assembly_1,...	NA	545	34.2	34.2	89%	47	100.00	4763704	LK931336.1
Citrobacter freundii CFNIH1, complete genome	NA	1333848	34.2	34.2	89%	47	100.00	5099034	CP007557.1
Escherichia coli strain XJW9B277 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4845658	CP068041.1
Leclercia sp. 4-9-1-25 chromosome, complete genome	NA	2815358	34.2	34.2	89%	47	100.00	4392327	CP076838.1
Escherichia coli strain Survcare045 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4829544	CP076318.1
Salmonella enterica subsp. enterica serovar Corvallis strain...	NA	593905	34.2	34.2	89%	47	100.00	4796034	CP075112.1
Salmonella enterica strain CFSAN060807 chromosome, complete...	NA	28901	34.2	34.2	89%	47	100.00	4753965	CP075109.1
Salmonella enterica strain CFSAN073554 chromosome, complete...	NA	28901	34.2	34.2	89%	47	100.00	4721400	CP075102.1
Salmonella enterica subsp. enterica serovar Derby strain...	NA	28144	34.2	34.2	89%	47	100.00	4733388	CP075036.1
Salmonella enterica subsp. enterica serovar Newport strain...	NA	108619	34.2	34.2	89%	47	100.00	4770886	CP075034.1
Salmonella enterica subsp. enterica serovar Newport strain...	NA	108619	34.2	34.2	89%	47	100.00	4781894	CP075033.1
Salmonella enterica subsp. enterica strain CFSAN001999...	NA	59201	34.2	68.4	89%	47	100.00	4631017	CP074675.1
Sodalis sp. dw_23 chromosome, complete genome	NA	2697027	34.2	34.2	89%	47	100.00	6443694	CP075169.1
Citrobacter koseri strain Colony389 chromosome	NA	545	34.2	34.2	89%	47	100.00	4925469	CP075491.1
Salmonella enterica subsp. enterica serovar Weltevreden strain...	NA	57743	34.2	34.2	89%	47	100.00	4920208	CP074657.1
Salmonella enterica subsp. enterica serovar Newport strain...	NA	108619	34.2	34.2	89%	47	100.00	4777375	CP074333.1
Salmonella enterica subsp. enterica serovar Weltevreden strain...	NA	57743	34.2	34.2	89%	47	100.00	4939325	CP074328.1
Salmonella enterica subsp. enterica serovar Newport strain...	NA	108619	34.2	34.2	89%	47	100.00	4682982	CP074337.1

Salmonella enterica subsp. enterica serovar Javiana strain...	NA	363569	34.2	34.2	89%	47	100.00	4737692	CP074281.1
Salmonella enterica subsp. enterica serovar Javiana strain...	NA	363569	34.2	34.2	89%	47	100.00	4663258	CP074276.1
Salmonella enterica subsp. enterica serovar Braenderup strain...	NA	149391	34.2	34.2	89%	47	100.00	4756723	CP074290.1
Salmonella enterica subsp. enterica serovar Derby str....	NA	1299223	34.2	34.2	89%	47	100.00	4833413	CP074219.1
Salmonella enterica subsp. enterica serovar Javiana strain...	NA	363569	34.2	34.2	89%	47	100.00	4567788	CP074205.1
Escherichia coli strain EC16 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4844032	CP074120.1
Xanthomonas oryzae strain AH28 chromosome, complete genome	NA	347	34.2	34.2	89%	47	100.00	4923022	CP074076.1
Citrobacter sp. MGH105 chromosome, complete genome	NA	1686380	34.2	64.4	94%	47	100.00	5093209	CP073048.2
Xanthomonas oryzae pv. oryzae strain DY89031(J18) chromosome,...	NA	64187	34.2	34.2	89%	47	100.00	4979456	CP064780.1
Citrobacter portucalensis strain PNUCL1 chromosome, complete...	NA	1639133	34.2	64.4	94%	47	100.00	4825730	CP048388.1
Salmonella enterica subsp. enterica strain P22 chromosome,...	NA	59201	34.2	34.2	89%	47	100.00	4936609	CP073326.1
Citrobacter sp. MGH103 chromosome, complete genome	NA	1686378	34.2	64.4	94%	47	100.00	4923318	CP073043.1
Citrobacter sp. BIDMC108 chromosome, complete genome	NA	1686385	34.2	64.4	94%	47	100.00	5145556	CP073007.1
Klebsiella pneumoniae strain 3347689I chromosome, complete genome	NA	573	34.2	34.2	89%	47	100.00	5620512	CP071086.1
Aspergillus sydowii CBS 593.65 uncharacterized protein...	NA	1036612	34.2	34.2	89%	47	100.00	2055	XM_040846660.1
Aspergillus versicolor CBS 583.65 uncharacterized protein...	NA	1036611	34.2	34.2	89%	47	100.00	1590	XM_040814545.1
Escherichia coli strain QDFD216 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4577885	CP053211.1
Escherichia coli strain ESBL_DR28 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4803708	CP067250.1
Escherichia coli strain OW1E2 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4820906	CP067245.1
Xanthomonas oryzae pv. oryzae strain T7133 chromosome, complet...	NA	64187	34.2	34.2	89%	47	100.00	4978475	CP071891.1
Leclercia sp. 4-9-1-25 chromosome, complete genome	NA	2815358	34.2	34.2	89%	47	100.00	4392178	CP071383.1
Citrobacter freundii strain zone4 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4919686	CP045726.1
Enterobacter cloacae En37 DNA, complete genome	NA	550	34.2	34.2	89%	47	100.00	4846950	AP024495.1
Citrobacter freundii strain CF50935 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4984319	CP070559.1
Citrobacter freundii strain CF49969 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5098771	CP070549.1
Citrobacter freundii strain CF48846 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4977086	CP070544.1

Citrobacter sp. BIDMC107 strain Colony252 chromosome	NA	1686384	34.2	34.2	89%	47	100.00	4477298	CP070240.1
Salmonella enterica subsp. enterica strain Se29 chromosome,...	NA	59201	34.2	34.2	89%	47	100.00	4859543	CP070222.1
Xylota sylvarum genome assembly, chromosome: 4	NA	374264	34.2	34.2	89%	47	100.00	77113630	LR999960.1
Citrobacter sp. B72 chromosome, complete genome	NA	2807631	34.2	64.4	94%	47	100.00	5030371	CP069801.1
Citrobacter cronae strain Colony303 chromosome	NA	1748967	34.2	34.2	89%	47	100.00	5080150	CP069786.1
Citrobacter braakii strain Colony488 chromosome	NA	57706	34.2	64.4	94%	47	100.00	4917491	CP069788.1
Citrobacter freundii strain Colony306 chromosome	NA	546	34.2	64.4	94%	47	100.00	5070621	CP069787.1
Citrobacter braakii strain Colony205 chromosome	NA	57706	34.2	64.4	94%	47	100.00	5070624	CP069780.1
Citrobacter braakii strain Colony237 chromosome	NA	57706	34.2	64.4	94%	47	100.00	5080025	CP069769.1
Citrobacter braakii strain Colony229 chromosome	NA	57706	34.2	64.4	94%	47	100.00	5070622	CP069771.1
Citrobacter braakii strain Colony228 chromosome	NA	57706	34.2	64.4	94%	47	100.00	5098585	CP069772.1
Citrobacter werkmanii strain Colony242 chromosome	NA	67827	34.2	34.2	89%	47	100.00	5070622	CP069767.1
Citrobacter cronae strain Colony458 chromosome	NA	1748967	34.2	34.2	89%	47	100.00	5098182	CP069783.1
Citrobacter braakii strain Colony209 chromosome	NA	57706	34.2	64.4	94%	47	100.00	5096346	CP069775.1
Citrobacter cronae strain Colony510 chromosome	NA	1748967	34.2	34.2	89%	47	100.00	5070622	CP069781.1
Citrobacter cronae strain Colony241 chromosome	NA	1748967	34.2	34.2	89%	47	100.00	5070623	CP069768.1
Citrobacter cronae strain Colony226 chromosome	NA	1748967	34.2	34.2	89%	47	100.00	5070622	CP069784.1
Citrobacter cronae strain Colony233 chromosome	NA	1748967	34.2	34.2	89%	47	100.00	5070623	CP069770.1
Citrobacter cronae strain Colony473 chromosome	NA	1748967	34.2	34.2	89%	47	100.00	5070620	CP069782.1
Citrobacter cronae strain Colony506 chromosome	NA	1748967	34.2	34.2	89%	47	100.00	5070622	CP069779.1
Citrobacter braakii strain Colony193 chromosome	NA	57706	34.2	64.4	94%	47	100.00	5070624	CP069776.1
Citrobacter cronae strain Colony478 chromosome	NA	1748967	34.2	34.2	89%	47	100.00	5079087	CP069763.1
Citrobacter braakii strain Colony244 chromosome	NA	57706	34.2	64.4	94%	47	100.00	5098585	CP069765.1
Citrobacter cronae strain Colony267 chromosome	NA	1748967	34.2	34.2	89%	47	100.00	5070621	CP069764.1
Citrobacter werkmanii strain Colony247 chromosome	NA	67827	34.2	34.2	89%	47	100.00	5070622	CP069762.1
Citrobacter braakii strain Colony215 chromosome	NA	57706	34.2	64.4	94%	47	100.00	5094434	CP069774.1
Citrobacter braakii strain Colony191 chromosome	NA	57706	34.2	64.4	94%	47	100.00	5070624	CP069761.1
Escherichia coli strain E41 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4861324	CP069707.1
Xanthomonas oryzae pv. oryzae strain LN4 chromosome, complete...	NA	64187	34.2	34.2	89%	47	100.00	5012583	CP045452.1
Escherichia coli strain MS1170 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4735839	CP056077.1

Acidovorax sp. KKS102, complete genome	NA	358220	34.2	64.4	89%	47	100.00	5196935	CP003872.1
Citrobacter freundii strain PSV genome assembly, chromosome: PSV	NA	546	34.2	64.4	94%	47	100.00	5233206	LR881934.1
Escherichia coli isolate strain_Ecoli_008 genome assembly,...	NA	562	34.2	34.2	89%	47	100.00	4847870	LR880734.1
Corynebacterium glucuronolyticum strain FDAARGOS_1111...	NA	39791	34.2	34.2	89%	47	100.00	2921218	CP068162.1
Salmonella enterica subsp. enterica serovar Weltevreden strain...	NA	57743	34.2	34.2	89%	47	100.00	5047093	CP067990.1
Salmonella enterica subsp. enterica serovar Weltevreden strain...	NA	57743	34.2	34.2	89%	47	100.00	5047093	CP067988.1
Salmonella enterica subsp. enterica serovar Weltevreden strain...	NA	57743	34.2	34.2	89%	47	100.00	5047093	CP067980.1
Salmonella enterica subsp. enterica serovar Havana strain CVM...	NA	179997	34.2	34.2	89%	47	100.00	4788249	CP051407.1
Salmonella enterica subsp. enterica serovar Derby strain CVM...	NA	28144	34.2	34.2	89%	47	100.00	4865042	CP053048.1
Salmonella enterica subsp. enterica serovar Schwarzengrund...	NA	340190	34.2	34.2	89%	47	100.00	4654533	CP051350.1
Xanthomonas oryzae pv. oryzae strain BXO512 chromosome, comple...	NA	64187	34.2	34.2	89%	47	100.00	4934882	CP065228.1
Citrobacter koseri strain FDAARGOS_1029 chromosome, complete...	NA	545	34.2	34.2	89%	47	100.00	4721681	CP066089.1
Escherichia coli strain W60 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4808792	CP058342.1
Escherichia coli strain 18MD05VL07 005213EC chromosome, comple...	NA	562	34.2	34.2	89%	47	100.00	4973127	CP063729.1
Citrobacter freundii isolate MSB1_1H-sc-2280393 genome assembl...	NA	546	34.2	64.4	94%	47	100.00	4908711	LR890181.1
Escherichia coli isolate 2016-17-550 genome assembly,...	NA	562	34.2	34.2	89%	47	100.00	4712903	LR883965.1
Citrobacter freundii STW0522-19 DNA, complete genome	NA	546	34.2	34.2	89%	47	100.00	5044118	AP022384.1
Citrobacter freundii STW0522-01 DNA, complete genome	NA	546	34.2	34.2	89%	47	100.00	5055174	AP022380.1
Citrobacter freundii strain N16-03880 chromosome, complete genome	NA	546	34.2	98.6	94%	47	100.00	5268984	CP047269.1
Citrobacter koseri MPUCK001 DNA, complete genome	NA	545	34.2	34.2	89%	47	100.00	4925206	AP023452.1
Citrobacter freundii strain MGH281 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5128689	CP060662.1
Citrobacter freundii strain MGH281C chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5128186	CP060659.1
Citrobacter freundii strain MGH279 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5128721	CP060650.1

Citrobacter freundii strain MGH283 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5125085	CP060654.1
Citrobacter koseri strain UCICRE-127 chromosome	NA	545	34.2	34.2	89%	47	100.00	4567869	CP060484.1
Salmonella enterica strain FARPER-222 chromosome, complete genome	NA	28901	34.2	34.2	89%	47	100.00	4879141	CP041622.1
Citrobacter freundii strain N18-04078 chromosome, complete genome	NA	546	34.2	98.6	94%	47	100.00	5216668	CP047273.1
Citrobacter freundii strain N18-04085 chromosome, complete genome	NA	546	34.2	98.6	94%	47	100.00	5167126	CP047275.1
Citrobacter freundii strain N18-04128 chromosome, complete genome	NA	546	34.2	98.6	94%	47	100.00	5195939	CP047279.1
Escherichia coli strain 101.3 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4634466	CP059944.1
Escherichia coli strain 154AHL.1 chromosome	NA	562	34.2	34.2	89%	47	100.00	4722166	CP059988.1
Citrobacter freundii strain IDR1800045912-01-00 chromosome,...	NA	546	34.2	98.6	94%	47	100.00	4988401	CP054294.1
Citrobacter freundii strain IDR1900015725-01-02 chromosome,...	NA	546	34.2	64.4	94%	47	100.00	4995557	CP054278.1
Citrobacter sp. RHBSTW-00848 chromosome	NA	2742665	34.2	64.4	94%	47	100.00	5087483	CP055910.1
Escherichia coli strain RHB09-C16 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4777660	CP057941.1
Citrobacter freundii strain RHB12-C05 chromosome, complete genome	NA	546	34.2	34.2	89%	47	100.00	4904767	CP057868.1
Citrobacter freundii strain RHB12-C19 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4885177	CP057864.1
Citrobacter freundii strain RHB12-C20 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5359677	CP057863.1
Citrobacter freundii strain RHB14-C12 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5232071	CP057824.1
Citrobacter freundii strain CIFR51929 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5107866	CP059427.1
Escherichia fergusonii strain RHB26-C09 chromosome, complete...	NA	564	34.2	34.2	89%	47	100.00	4549178	CP057458.1
Escherichia coli strain RHB29-C09 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	5124687	CP057347.1
Escherichia coli strain RHB29-C10 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	5124640	CP057345.1
Escherichia coli strain RHB29-C16 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	5124691	CP057342.1
Escherichia coli strain RHB29-C18 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	5124674	CP057340.1

Escherichia coli strain RHB29-C23 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	5124691	CP057334.1
Citrobacter freundii strain RHB30-C04 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4928912	CP057319.1
Escherichia coli strain RHB31-C01 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4721910	CP057276.1
Citrobacter freundii strain RHB35-C18 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5112878	CP057149.1
Citrobacter sp. RHB35-C21 chromosome, complete genome	NA	2742626	34.2	64.4	94%	47	100.00	5152141	CP057147.1
Citrobacter freundii strain RHB35-C22 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5112880	CP057146.1
Citrobacter sp. RHB36-C18 chromosome, complete genome	NA	2742627	34.2	98.6	94%	47	100.00	4843970	CP057125.1
Escherichia coli strain RHB39-C18 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4670886	CP057055.1
Escherichia coli strain RHB41-C01 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4611954	CP057007.1
Citrobacter sp. RHBSTW-00017 chromosome, complete genome	NA	2742629	34.2	64.4	94%	47	100.00	5052482	CP056899.1
Citrobacter sp. RHBSTW-00021 chromosome, complete genome	NA	2742630	34.2	64.4	94%	47	100.00	5099714	CP056896.1
Citrobacter sp. RHBSTW-00053 chromosome, complete genome	NA	2742632	34.2	64.4	94%	47	100.00	5167268	CP056888.1
Citrobacter sp. RHBSTW-00107 chromosome, complete genome	NA	2742635	34.2	64.4	94%	47	100.00	5087383	CP056861.1
Citrobacter freundii strain RHBSTW-00126 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	4906122	CP056839.1
Citrobacter sp. RHBSTW-00127 chromosome, complete genome	NA	2742636	34.2	64.4	94%	47	100.00	5098550	CP056834.1
Citrobacter freundii strain RHBSTW-00135 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5136614	CP056827.1
Citrobacter sp. RHBSTW-00137 chromosome, complete genome	NA	2742638	34.2	64.4	94%	47	100.00	5138391	CP056822.1
Citrobacter freundii strain RHBSTW-00162 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5066655	CP056809.1
Citrobacter sp. RHBSTW-01044 chromosome, complete genome	NA	2742678	34.2	64.4	94%	47	100.00	4946286	CP056180.1
Citrobacter freundii strain RHBSTW-01016 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	4992760	CP056181.1
Citrobacter sp. RHBSTW-01013 chromosome, complete genome	NA	2742677	34.2	64.4	94%	47	100.00	5217381	CP056185.1
Citrobacter sp. RHBSTW-00986 chromosome, complete genome	NA	2742675	34.2	64.4	94%	47	100.00	4941540	CP056200.1
Citrobacter freundii strain RHBSTW-00985 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	4829251	CP056208.1
Citrobacter sp. RHBSTW-00599 chromosome, complete genome	NA	2742657	34.2	64.4	94%	47	100.00	5109855	CP056717.1
Citrobacter freundii strain RHBSTW-00502 chromosome,	NA	546	34.2	64.4	94%	47	100.00	4892927	CP056451.1

complete...									
Citrobacter freundii strain RHBSTW-00310 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5065503	CP056622.1
Citrobacter sp. RHBSTW-00229 chromosome, complete genome	NA	2742641	34.2	64.4	94%	47	100.00	5231053	CP056647.1
Citrobacter freundii strain RHBSTW-00214 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5056951	CP056653.1
Citrobacter freundii strain RHBSTW-00342 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5031983	CP056595.1
Citrobacter freundii strain RHBSTW-00350 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	4982711	CP056592.1
Enterobacter sp. RHBSTW-00422 chromosome, complete genome	NA	2742646	34.2	34.2	89%	47	100.00	5060999	CP056552.1
Citrobacter freundii strain RHBSTW-00435 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5087480	CP056527.1
Citrobacter freundii strain RHBSTW-00486 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5027895	CP056466.1
Citrobacter freundii strain RHBSTW-00449 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5205079	CP056505.1
Citrobacter sp. RHBSTW-00524 chromosome, complete genome	NA	2742653	34.2	64.4	94%	47	100.00	5251041	CP056421.1
Citrobacter sp. RHBSTW-00535 chromosome, complete genome	NA	2742654	34.2	64.4	94%	47	100.00	5051038	CP056409.1
Citrobacter sp. RHBSTW-00628 chromosome, complete genome	NA	2742658	34.2	64.4	94%	47	100.00	5041930	CP056381.1
Citrobacter sp. RHBSTW-00667 chromosome, complete genome	NA	2742659	34.2	64.4	94%	47	100.00	5054623	CP056361.1
Citrobacter freundii strain RHBSTW-00302 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5099027	CP056635.1
Citrobacter freundii strain RHBSTW-00370 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5126475	CP056573.1
Citrobacter sp. RHBSTW-00424 chromosome, complete genome	NA	2742647	34.2	64.4	94%	47	100.00	5365582	CP056546.1
Citrobacter sp. RHBSTW-00570 chromosome, complete genome	NA	2742655	34.2	64.4	94%	47	100.00	5103116	CP056399.1
Citrobacter freundii strain RHBSTW-00658 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5044080	CP056365.1
Citrobacter sp. RHBSTW-00678 chromosome, complete genome	NA	2742661	34.2	64.4	94%	47	100.00	5178534	CP056350.1
Citrobacter freundii strain RHBSTW-00697 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5084908	CP056336.1
Citrobacter sp. RHBSTW-00446 chromosome, complete genome	NA	2742648	34.2	64.4	94%	47	100.00	5162943	CP056508.1
Citrobacter sp. RHBSTW-00696 chromosome, complete genome	NA	2742662	34.2	64.4	94%	47	100.00	5331005	CP056341.1
Citrobacter sp. RHBSTW-00821 chromosome, complete genome	NA	2742663	34.2	64.4	94%	47	100.00	5161365	CP056321.1
Citrobacter freundii strain RHBSTW-00830 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	4983531	CP056314.1

Citrobacter sp. RHBSTW-00859 chromosome, complete genome	NA	2742666	34.2	64.4	94%	47	100.00	5163773	CP056284.1
Enterobacter roggenkampii strain RHBSTW-00872 chromosome,...	NA	1812935	34.2	34.2	89%	47	100.00	4844952	CP056148.1
Citrobacter sp. RHBSTW-00881 chromosome, complete genome	NA	2742667	34.2	64.4	94%	47	100.00	5224399	CP056269.1
Citrobacter sp. RHBSTW-00887 chromosome, complete genome	NA	2742668	34.2	64.4	94%	47	100.00	5327400	CP056267.1
Citrobacter freundii strain RHBSTW-00902 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5108587	CP056256.1
Citrobacter sp. RHBSTW-00903 chromosome, complete genome	NA	2742670	34.2	64.4	94%	47	100.00	5310160	CP056251.1
Citrobacter freundii strain RHBSTW-00915 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	4956708	CP056245.1
Citrobacter freundii strain RHBSTW-00935 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5103922	CP056238.1
Citrobacter freundii strain RHBSTW-00942 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5297052	CP056235.1
Citrobacter freundii strain RHBSTW-00965 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5167828	CP056232.1
Citrobacter sp. RHBSTW-00976 chromosome, complete genome	NA	2742674	34.2	64.4	94%	47	100.00	5082224	CP056219.1
Enterobacter hormaechei strain RHBSTW-00059 chromosome, comple...	NA	158836	34.2	34.2	89%	47	100.00	4769962	CP058167.1
Citrobacter sp. RHBSTW-00944 chromosome, complete genome	NA	2742671	34.2	64.4	94%	47	100.00	5145831	CP055418.1
Citrobacter freundii strain RHBSTW-00862 chromosome, complete...	NA	546	34.2	98.6	94%	47	100.00	4978770	CP055421.1
Citrobacter freundii strain RHBSTW-00153 chromosome, complete...	NA	546	34.2	64.4	94%	47	100.00	5163581	CP055564.1
Citrobacter freundii strain RHBSTW-00110 chromosome, complete...	NA	546	34.2	98.6	94%	47	100.00	5023392	CP055582.1
Citrobacter freundii strain RHBSTW-00084 chromosome, complete...	NA	546	34.2	98.6	94%	47	100.00	5024564	CP055588.1
Citrobacter sp. 172116965 chromosome, complete genome	NA	2683822	34.2	64.4	94%	47	100.00	5163174	CP046673.1
Escherichia coli strain 005008 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4848135	CP058661.1
Serratia symbiotica strain CWBI-2.3 chromosome, complete genome	NA	138074	34.2	34.2	89%	47	100.00	3351526	CP050855.1
Escherichia coli strain AMSCJX03 chromosome, complete genome	NA	562	34.2	34.2	89%	47	100.00	4618346	CP058355.1
Citrobacter freundii strain 111 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	4954350	CP046502.1
Citrobacter freundii strain M92 chromosome, complete genome	NA	546	34.2	64.4	94%	47	100.00	5338221	CP058318.1
Salmonella enterica subsp. enterica serovar Weltevreden str....	NA	936157	34.2	34.2	89%	47	100.00	353015	FR775246.1

Salmonella enterica subsp. enterica serovar Schwarzengrund str...	NA	439843	34.2	34.2	89%	47	100.00	4709075	CP001127.1
Pseudomonas putida GB-1 chromosome, complete genome	NA	76869	34.2	34.2	89%	47	100.00	6078430	CP000926.1
Citrobacter koseri ATCC BAA-895, complete genome	NA	290338	34.2	34.2	89%	47	100.00	4720462	CP000822.1
Xanthomonas oryzae pv. oryzae MAFF 311018 DNA, complete genome	NA	342109	34.2	34.2	89%	47	100.00	4940217	AP008229.1
Xanthomonas oryzae pv. oryzae KACC 10331, complete genome	NA	291331	34.2	34.2	89%	47	100.00	4941439	AE013598.1
PREDICTED: Drosophila subobscura prolow-density lipoprotein...	NA	7241	32.2	32.2	84%	186	100.00	15044	XM_034797968.1
PREDICTED: Drosophila subobscura prolow-density lipoprotein...	NA	7241	32.2	32.2	84%	186	100.00	15050	XM_034797967.1
Apiotrichum mycotoxinovorans strain CICC 1454 chromosome 2	NA	252803	32.2	32.2	84%	186	100.00	10254415	CP053621.1
Bacillus circulans strain GN03 chromosome, complete genome	NA	1397	32.2	32.2	84%	186	100.00	5217129	CP053315.1
PREDICTED: Drosophila guanche prolow-density lipoprotein...	NA	7266	32.2	32.2	84%	186	100.00	15030	XM_034286388.1
PREDICTED: Drosophila guanche prolow-density lipoprotein...	NA	7266	32.2	32.2	84%	186	100.00	15090	XM_034286387.1
Xylella fastidiosa subsp. multiplex strain LM10 chromosome,...	NA	644357	32.2	32.2	84%	186	100.00	2669650	CP052854.1
Xylella fastidiosa subsp. multiplex strain RH1 chromosome,...	NA	644357	32.2	32.2	84%	186	100.00	2678425	CP052853.1
Xylella fastidiosa subsp. multiplex strain Fillmore chromosome...	NA	644357	32.2	32.2	84%	186	100.00	2526544	CP052855.1
PREDICTED: Geotrypetes seraphini transmembrane protein 9...	NA	260995	32.2	32.2	84%	186	100.00	1642	XM_033918501.1
PREDICTED: Geotrypetes seraphini transmembrane protein 9...	NA	260995	32.2	32.2	84%	186	100.00	1660	XM_033918500.1
PREDICTED: Geotrypetes seraphini transmembrane protein 9...	NA	260995	32.2	32.2	84%	186	100.00	1727	XM_033918499.1
Pseudomonas sp. gcc21 chromosome, complete genome	NA	2726989	32.2	32.2	84%	186	100.00	3983233	CP051625.1
Enterobacter hormaechei strain AMS-38 chromosome, complete genome	NA	158836	32.2	32.2	84%	186	100.00	4914558	CP051132.1
Xylella fastidiosa strain ATCC 35879 chromosome, complete genome	NA	2371	32.2	32.2	84%	186	100.00	2565504	CP044352.1
Apiotrichum mycotoxinovorans strain GMU1709 chromosome IV	NA	252803	32.2	32.2	84%	186	100.00	10238178	CP049824.1
Bradyrhizobium sp. 6(2017) strain 1S3 chromosome, complete genome	NA	1197460	32.2	32.2	84%	186	100.00	10014235	CP049289.1
Xylella fastidiosa subsp. fastidiosa strain Bakersfield-1...	NA	644356	32.2	32.2	84%	186	100.00	2537329	CP040799.2
Pseudomonas sp. DTU12.1 chromosome, complete genome	NA	2654238	32.2	32.2	84%	186	100.00	5943629	CP045254.1
Aeromonas veronii strain AVNIH1 chromosome, complete genome	NA	654	32.2	32.2	84%	186	100.00	4807642	CP047155.1
Lentilactobacillus kefiri strain DH5 chromosome, complete genome	NA	33962	32.2	32.2	84%	186	100.00	2421275	CP029971.1

Paenibacillus sp. B01 chromosome, complete genome	NA	2660554	32.2	32.2	84%	186	100.00	5825233	CP045802.1
Rhizobium grahamii strain BG7 chromosome, complete genome	NA	1120045	32.2	32.2	84%	186	100.00	3927797	CP043498.1
Enterobacter hormaechei strain C45 chromosome, complete genome	NA	158836	32.2	32.2	84%	186	100.00	5068785	CP042551.1
Geotrypetes seraphini genome assembly, chromosome: 13	NA	260995	32.2	32.2	84%	186	100.00	83871185	LR699158.1
Euhalothece natronophila Z-M001 chromosome, complete genome	NA	522448	32.2	32.2	84%	186	100.00	3326959	CP042326.1
PREDICTED: Salmo trutta Tax1 binding protein 1 (tax1bp1), mRNA	river trout	8032	32.2	32.2	84%	186	100.00	3602	XM_029746696.1
Lysobacter enzymogenes strain YC36 chromosome, complete genome	NA	69	32.2	32.2	84%	186	100.00	6131517	CP040656.1
Syngnathus acus genome assembly, chromosome: 4	greater pipe...	161584	32.2	32.2	84%	186	100.00	12636307	LR594590.1
Salmo trutta genome assembly, chromosome: 3	river trout	8032	32.2	32.2	84%	186	100.00	74753489	LR584416.1
Scleropages formosus genome assembly, chromosome: 9	Asian bonyto...	113540	32.2	32.2	84%	186	100.00	32798776	LR584074.1
PREDICTED: Dendronephthya gigantea uncharacterized LOC11453563...	NA	151771	32.2	32.2	84%	186	100.00	1858	XM_028556920.1
PREDICTED: Dendronephthya gigantea uncharacterized LOC11453563...	NA	151771	32.2	32.2	84%	186	100.00	2300	XM_028556919.1
Bacillus circulans strain PK3_138 chromosome, complete genome	NA	1397	32.2	32.2	84%	186	100.00	5274417	CP026033.1
Bacillus circulans strain PK3_109 chromosome, complete genome	NA	1397	32.2	32.2	84%	186	100.00	5175203	CP026031.1
Halorubrum ezzemoulense strain Fb21 chromosome, complete genome	NA	337243	32.2	62.4	89%	186	100.00	3062294	CP034940.1
Caproiciproducens sp. NJN-50 chromosome, complete genome	NA	2507162	32.2	32.2	84%	186	100.00	3308050	CP035283.1
Eukaryotic synthetic construct chromosome 16	NA	111789	32.2	64.4	84%	186	100.00	98200793	CP034494.1
Slackia heliotrinireducens strain NCTC11029 genome assembly,...	NA	84110	32.2	32.2	84%	186	100.00	3166158	LR134379.1
Enterobacter hormaechei subsp. xiangfangensis strain Pb204...	NA	1296536	32.2	32.2	84%	186	100.00	4956155	CP030007.1
Xylella fastidiosa strain Fb7, complete genome	NA	2371	32.2	62.4	84%	186	100.00	2659912	CP010051.2
PREDICTED: Physcomitrella patens kinesin-like protein KIN-10A...	NA	3218	32.2	32.2	84%	186	100.00	4739	XM_024538146.1
PREDICTED: Physcomitrella patens photosystem I chlorophyll...	NA	3218	32.2	32.2	84%	186	100.00	1743	XM_024535798.1
PREDICTED: Physcomitrella patens photosystem I chlorophyll...	NA	3218	32.2	32.2	84%	186	100.00	1114	XM_024535797.1
PREDICTED: Physcomitrella patens photosystem I chlorophyll...	NA	3218	32.2	32.2	84%	186	100.00	1686	XM_024535796.1
PREDICTED: Physcomitrella patens photosystem I chlorophyll...	NA	3218	32.2	32.2	84%	186	100.00	1317	XM_024535795.1
PREDICTED: Physcomitrella patens photosystem I chlorophyll...	NA	3218	32.2	32.2	84%	186	100.00	1266	XM_024535794.1
Pulveribacter suum strain SC2-7 chromosome, complete genome	NA	2116657	32.2	32.2	84%	186	100.00	3358427	CP027792.1
Bacteroides heparinolyticus strain F0111 chromosome, complete...	NA	28113	32.2	62.4	89%	186	100.00	3608975	CP027234.1

Bacteroides zoogleoformans strain ATCC 33285 chromosome,...	NA	28119	32.2	32.2	84%	186	100.00	3361794	CP027231.1
Bos mutus isolate yakQH1 chromosome 16	wild yak	72004	32.2	32.2	84%	186	100.00	78623970	CP027084.1
Niveispirillum cyanobacteriorum strain TH16 chromosome eg_2,...	NA	1612173	32.2	32.2	84%	186	100.00	1254521	CP025612.1
Cordyceps militaris strain ATCC 34164 chromosome VII, complete...	NA	73501	32.2	32.2	84%	186	100.00	8286469	CP023324.1
Anabaena variabilis NIES-23 DNA, nearly complete genome	NA	1973479	32.2	32.2	84%	186	100.00	6411850	AP018216.1
Vibrio gazogenes strain ATCC 43942 chromosome 1, complete...	NA	687	32.2	32.2	84%	186	100.00	3471064	CP018835.1
Xylella fastidiosa strain Hib4 chromosome, complete genome	NA	2371	32.2	62.4	84%	186	100.00	2813297	CP009885.1
Xylella fastidiosa strain J1a12, complete genome	NA	2371	32.2	62.4	84%	186	100.00	2788789	CP009823.1
Xylella fastidiosa strain U24D, complete genome	NA	2371	32.2	62.4	84%	186	100.00	2681334	CP009790.1
Saitoella complicata NRRL Y-17804 glycoside hydrolase...	NA	698492	32.2	32.2	84%	186	100.00	2457	XM_019171936.1
Streptomyces lincolnensis strain NRRL 2936, complete genome	NA	1915	32.2	32.2	84%	186	100.00	10319054	CP016438.1
PREDICTED: Salmo salar tax1-binding protein 1 homolog B-like...	Atlantic salmon	8030	32.2	32.2	84%	186	100.00	3576	XM_014185549.1
PREDICTED: Salmo salar tax1-binding protein 1 homolog B-like...	Atlantic salmon	8030	32.2	32.2	84%	186	100.00	864	XM_014148252.1
PREDICTED: Salmo salar tax1-binding protein 1 homolog B-like...	Atlantic salmon	8030	32.2	32.2	84%	186	100.00	834	XM_014148243.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	32.2	32.2	84%	186	100.00	173785	LK068066.1
TPA: Neospora caninum Liverpool, chromosome chrII, complete...	NA	572307	32.2	32.2	84%	186	100.00	2174329	LN714476.1
Cucumis melo genomic chromosome, chr_11	muskmelon	3656	32.2	32.2	84%	186	100.00	31442130	LN713265.1
Cucumis melo genomic scaffold, anchoredscaffold00020	muskmelon	3656	32.2	32.2	84%	186	100.00	5729086	LN681918.1
PREDICTED: Tarenaya hassleriana probable serine/threonine...	NA	28532	32.2	32.2	84%	186	100.00	753	XM_010552312.1
PREDICTED: Gavia stellata dynein heavy chain 17, axonemal-like...	red-throated...	37040	32.2	32.2	84%	186	100.00	2672	XM_009811350.1
Xylella fastidiosa subsp. sandyi Ann-1, complete genome	NA	155920	32.2	32.2	84%	186	100.00	2750603	CP006696.1
Xylella fastidiosa MUL0034, complete genome	NA	1401256	32.2	32.2	84%	186	100.00	2642186	CP006740.1
Rhodosporidium toruloides strain CECT1137, genomic scaffold,...	NA	5286	32.2	32.2	84%	186	100.00	968495	LK052943.1
Pseudocercospora fijiensis CIRAD86 uncharacterized protein...	NA	383855	32.2	32.2	84%	186	100.00	2736	XM_007925185.1
Phaeoacremonium minimum UCRPA7 putative tartrate dehydrogenase...	NA	1286976	32.2	32.2	84%	186	100.00	1116	XM_007919159.1
Dichomitus squalens LYAD-421 SS1 uncharacterized protein...	NA	732165	32.2	32.2	84%	186	100.00	3268	XM_007367084.1
Kutzneria albida DSM 43870, complete genome	NA	1449976	32.2	32.2	84%	186	100.00	9874926	CP007155.1
Bacillus sp. NP157 chromosome, complete genome	NA	2846778	32.2	32.2	84%	186	100.00	4875246	CP076546.1

Paludibacterium sp. B53371 chromosome, complete genome	NA	2806263	32.2	32.2	84%	186	100.00	3626872	CP069163.1
Zeuzera pyrina genome assembly, chromosome: Z	NA	1101072	32.2	32.2	84%	186	100.00	28043699	OU015621.1
PREDICTED: Drosophila obscura prolow-density lipoprotein...	NA	7282	32.2	32.2	84%	186	100.00	15618	XM_022367044.2
Homo sapiens isolate CHM13 chromosome 16	human	9606	32.2	32.2	84%	186	100.00	96330374	CP068262.2
Xylella fastidiosa subsp. multiplex strain BB08-1 chromosome,...	NA	644357	32.2	32.2	84%	186	100.00	2553631	CP072932.1
Xylella fastidiosa subsp. multiplex strain AlmaEM3 chromosome,...	NA	644357	32.2	32.2	84%	186	100.00	2487451	CP072933.1
Halomonas sp. MCCC 1A13718 chromosome, complete genome	NA	2733488	32.2	32.2	84%	186	100.00	4572976	CP053383.1
Roseomonas sp. 1318 chromosome, complete genome	NA	2768161	32.2	62.4	84%	186	100.00	3565232	CP061091.1
PREDICTED: Bufo bufo ADAMTS like 4 (ADAMTSL4), transcript...	common toad	8384	32.2	32.2	84%	186	100.00	4507	XM_040412459.1
PREDICTED: Bufo bufo ADAMTS like 4 (ADAMTSL4), transcript...	common toad	8384	32.2	32.2	84%	186	100.00	7319	XR_005774884.1
PREDICTED: Bufo bufo ADAMTS like 4 (ADAMTSL4), transcript...	common toad	8384	32.2	32.2	84%	186	100.00	6208	XR_005774883.1
PREDICTED: Bufo bufo ADAMTS like 4 (ADAMTSL4), transcript...	common toad	8384	32.2	32.2	84%	186	100.00	6399	XM_040412458.1
Acinetobacter variabilis RYU24 DNA, complete genome	NA	70346	32.2	32.2	84%	186	100.00	3198423	AP024524.1
Hyphomicrobium denitrificans 1NES1, complete genome	NA	670307	32.2	32.2	84%	186	100.00	3808687	CP005587.1
Pyrochroa serraticornis genome assembly, chromosome: 6	NA	346838	32.2	32.2	84%	186	100.00	21990463	HG995157.1
Enterobacter hormaechei strain EC48293 chromosome, complete...	NA	158836	32.2	32.2	84%	186	100.00	4950181	CP070534.1
Spilosoma lubricipeda genome assembly, chromosome: 3	NA	875880	32.2	32.2	84%	186	100.00	24480163	HG992277.1
Rhizobium sp. BG6 chromosome, complete genome	NA	2613771	32.2	32.2	84%	186	100.00	3928948	CP044009.1
Streptomyces davawensis strain JCM 4913 complete genome	NA	1214101	32.2	32.2	84%	186	100.00	9466619	HE971709.1
Sphingomonas sp. DH-S5 chromosome, complete genome	NA	2759526	32.2	32.2	84%	186	100.00	3916662	CP061035.1
Luteimonas sp. MC1572 chromosome, complete genome	NA	2799325	32.2	62.4	89%	186	100.00	3020716	CP067112.1
1_Tps_b3v08	NA	170557	32.2	32.2	84%	186	100.00	4834	OD021736.1
Xylella fastidiosa subsp. fastidiosa strain Bakersfield-8...	NA	644356	32.2	32.2	84%	186	100.00	2553893	CP064334.1
Xylella fastidiosa subsp. fastidiosa strain Bakersfield-11...	NA	644356	32.2	32.2	84%	186	100.00	2554506	CP064332.1
Xylella fastidiosa subsp. multiplex strain Red Oak 2 chromosom...	NA	644357	32.2	32.2	84%	186	100.00	2476446	CP064325.1
Xylella fastidiosa subsp. multiplex strain Riv5 chromosome,...	NA	644357	32.2	32.2	84%	186	100.00	2499994	CP064326.1
Xylella fastidiosa subsp. fastidiosa strain Bakersfield-14...	NA	644356	32.2	32.2	84%	186	100.00	2536882	CP064328.1
Xylella fastidiosa subsp. fastidiosa strain Bakersfield-13...	NA	644356	32.2	32.2	84%	186	100.00	2537289	CP064330.1
Xylella fastidiosa strain 3124 chromosome, complete genome	NA	2371	32.2	62.4	84%	186	100.00	2748592	CP009829.2

Xylella fastidiosa strain Pr8x chromosome, complete genome	NA	2371	32.2	62.4	84%	186	100.00	2666240	CP009826.2
Spirodela intermedia genome assembly, chromosome: 1	NA	51605	32.2	32.2	84%	186	100.00	11466831	LR746264.1
Spirodela intermedia genome assembly, chromosome: 1	NA	51605	32.2	32.2	84%	186	100.00	11046452	LR743588.1
Enterobacter hormaechei STN0717-64 DNA, complete genome	NA	158836	32.2	32.2	84%	186	100.00	4979003	AP022510.1
Homo sapiens DNA, chromosome 16, nearly complete genome	human	9606	32.2	32.2	84%	186	100.00	94690957	AP023476.1
Xylella fastidiosa subsp. multiplex strain IVIA5901 chromosome...	NA	644357	32.2	32.2	84%	186	100.00	2559157	CP047134.1
Xylella fastidiosa subsp. fastidiosa strain IVIA5235 chromosom...	NA	644356	32.2	32.2	84%	186	100.00	2537917	CP047171.1
Acomys russatus genome assembly, chromosome: 3	golden spiny...	60746	32.2	32.2	84%	186	100.00	86290179	LR877214.1
Xylella fastidiosa subsp. fastidiosa strain GV230 chromosome,...	NA	644356	32.2	32.2	84%	186	100.00	2514993	CP060159.1
Sphingobium yanoikuyae strain A3 chromosome, complete genome	NA	13690	32.2	32.2	84%	186	100.00	6531504	CP060122.1
Mesorhizobium loti strain 582 chromosome, complete genome	NA	381	32.2	32.2	84%	186	100.00	7221895	CP050293.1
Pipistrellus pipistrellus genome assembly, chromosome: 8	common pipis...	59474	32.2	62.4	89%	186	100.00	83522093	LR862364.1
Anas platyrhynchos genome assembly, chromosome: 21	mallard	8839	32.2	32.2	84%	186	100.00	15673935	LS423631.1
Komagataeibacter medellinensis NBRC 3288 DNA, complete genome	NA	634177	32.2	32.2	84%	186	100.00	3136818	AP012159.1
Neospora caninum Liverpool complete genome, chromosome II	NA	572307	32.2	32.2	84%	186	100.00	2170133	FR823382.1
Xylella fastidiosa subsp. fastidiosa GB514, complete genome	NA	788929	32.2	32.2	84%	186	100.00	2491203	CP002165.1
Slackia heliotrinireducens DSM 20476, complete genome	NA	471855	32.2	32.2	84%	186	100.00	3165038	CP001684.1
Wolbachia endosymbiont of Culex quinquefasciatus Pel strain wP...	NA	570417	32.2	644	84%	186	100.00	1482455	AM999887.1
Physcomitrella patens mRNA for KINID1a, complete cds	NA	3218	32.2	32.2	84%	186	100.00	4242	AB434497.1
Xylella fastidiosa M23, complete genome	NA	405441	32.2	32.2	84%	186	100.00	2535690	CP001011.1
Xylella fastidiosa M12, complete genome	NA	405440	32.2	32.2	84%	186	100.00	2475130	CP000941.1
Aspergillus niger contig An08c0150, genomic contig	NA	5061	32.2	32.2	84%	186	100.00	38077	AM270170.1
Wolbachia endosymbiont of Culex pipiens quinquefasciatus...	NA	263437	32.2	32.2	84%	186	100.00	1812	DQ355378.1
Paenarthrobacter aurescens TC1, complete genome	NA	290340	32.2	32.2	84%	186	100.00	4597686	CP000474.1
Xylella fastidiosa 9a5c, complete genome	NA	160492	32.2	62.4	84%	186	100.00	2679306	AE003849.1
Homo sapiens chromosome 16 clone RP11-616M22, complete sequence	human	9606	32.2	32.2	84%	186	100.00	195680	AC120498.2
Homo sapiens 16p13.3 sequence section 5 of 8	human	9606	32.2	32.2	84%	186	100.00	265786	AE006466.1
Nostoc sp. PCC 7120 DNA, complete genome	NA	103690	32.2	32.2	84%	186	100.00	6413771	BA000019.2
Homo sapiens BAC clone RP11-635P21 from 2, complete	human	9606	32.2	32.2	84%	186	100.00	19494	AC104086.6

sequence									
Xylella fastidiosa Temecula1, complete genome	NA	183190	32.2	32.2	84%	186	100.00	2519802	AE009442.1
Human DNA sequence from clone LA16c-344F5 on chromosome 16,...	human	9606	32.2	32.2	84%	186	100.00	37305	AL031712.21
Marinomonas primoryensis strain KMM3633 chromosome, complete...	NA	178399	30.2	30.2	78%	735	100.00	4068722	CP054301.1
Achromobacter denitrificans strain FDAARGOS_787 chromosome,...	NA	32002	30.2	30.2	78%	735	100.00	6816538	CP054569.1
Dickeya solani strain IFB0421 chromosome, complete genome	NA	1089444	30.2	30.2	78%	735	100.00	4934537	CP051460.1
Dickeya solani strain IFB0417 chromosome, complete genome	NA	1089444	30.2	30.2	78%	735	100.00	4924102	CP051459.1
Dickeya solani strain IFB0231 chromosome, complete genome	NA	1089444	30.2	30.2	78%	735	100.00	4924702	CP051458.1
Dickeya solani strain IFB0167 chromosome, complete genome	NA	1089444	30.2	30.2	78%	735	100.00	4922289	CP051457.1
Ralstonia solanacearum strain FJAT1458.F1 chromosome, complete...	NA	305	30.2	30.2	78%	735	100.00	3984237	CP052120.1
Ralstonia solanacearum strain FJAT1458.F50 chromosome, complet...	NA	305	30.2	30.2	78%	735	100.00	3984236	CP052118.1
Ralstonia solanacearum strain FJAT1463.F1 chromosome, complete...	NA	305	30.2	30.2	78%	735	100.00	3984235	CP052116.1
Ralstonia solanacearum strain FJAT1463.F50 chromosome, complet...	NA	305	30.2	30.2	78%	735	100.00	3984235	CP052114.1
Ralstonia solanacearum strain FJAT15244.F1 chromosome, complet...	NA	305	30.2	30.2	78%	735	100.00	3788096	CP052112.1
Ralstonia solanacearum strain FJAT15244.F50 chromosome, comple...	NA	305	30.2	30.2	78%	735	100.00	3789233	CP052110.1
Ralstonia solanacearum strain FJAT15249.F1 chromosome, complet...	NA	305	30.2	30.2	78%	735	100.00	3984112	CP052108.1
Ralstonia solanacearum strain FJAT15249.F50 chromosome, comple...	NA	305	30.2	30.2	78%	735	100.00	3984230	CP052106.1
Ralstonia solanacearum strain FJAT15252.F1 chromosome, complet...	NA	305	30.2	30.2	78%	735	100.00	3984186	CP052104.1
Ralstonia solanacearum strain FJAT15252.F50 chromosome, comple...	NA	305	30.2	30.2	78%	735	100.00	3984237	CP052102.1
Ralstonia solanacearum strain FJAT448.F1 chromosome, complete...	NA	305	30.2	30.2	78%	735	100.00	3944010	CP052074.1
Ralstonia solanacearum strain FJAT448.F50 chromosome, complete...	NA	305	30.2	30.2	78%	735	100.00	3943689	CP052072.1
Ralstonia solanacearum strain FJAT454.F1 chromosome, complete...	NA	305	30.2	30.2	78%	735	100.00	3944010	CP052070.1
Achromobacter denitrificans strain FDAARGOS_786 chromosome,...	NA	32002	30.2	30.2	78%	735	100.00	6736870	CP053987.1
Achromobacter denitrificans strain FDAARGOS_788 chromosome,...	NA	32002	30.2	30.2	78%	735	100.00	6736877	CP053986.1

Felis catus Senzu DNA, chromosome: F2, American Shorthair breed	domestic cat	9685	30.2	30.2	78%	735	100.00	86116642	AP023169.1
Pseudomonas sp. B14-6 chromosome, complete genome	NA	2738843	30.2	30.2	78%	735	100.00	6766112	CP053929.1
Pseudomonas graminis strain PgKB30 chromosome, complete genome	NA	158627	30.2	30.2	78%	735	100.00	5521192	CP053746.1
PREDICTED: Trachemys scripta elegans rho-related GTP-binding...	NA	31138	30.2	30.2	78%	735	100.00	9199	XM_034781389.1
PREDICTED: Trachemys scripta elegans rho-related GTP-binding...	NA	31138	30.2	30.2	78%	735	100.00	8855	XM_034781386.1
Salmonella enterica subsp. diarizonae serovar 47:k:z35 strain...	NA	1192846	30.2	60.5	100%	735	100.00	4852711	CP053583.1
Salmonella enterica subsp. diarizonae serovar 47:k:z35 strain...	NA	1192846	30.2	60.5	100%	735	100.00	5183057	CP053335.1
Salmonella enterica subsp. diarizonae serovar 65:z10:e,n,x,z15...	NA	2577494	30.2	30.2	78%	735	100.00	4898988	CP053323.1
Klebsiella pneumoniae SMKP03 DNA, complete genome	NA	573	30.2	30.2	78%	735	100.00	5155320	AP023148.1
Herbaspirillum rubrisubalbicans Os34, complete genome	NA	1235827	30.2	30.2	78%	735	100.00	6122717	CP008956.1
PREDICTED: Arvicanthis niloticus FA complementation group A...	African gras...	61156	30.2	30.2	78%	735	100.00	4394	XM_034522211.1
Escherichia coli strain HB37 chromosome HB37, complete sequence	NA	562	30.2	30.2	78%	735	100.00	5307814	CP053080.1
PREDICTED: Thalassophryne amazonica sterile alpha motif...	NA	390379	30.2	30.2	78%	735	100.00	1180	XM_034172610.1
PREDICTED: Thalassophryne amazonica sterile alpha motif...	NA	390379	30.2	30.2	78%	735	100.00	1266	XM_034172609.1
Pseudomonas fluorescens strain G7 chromosome, complete genome	NA	294	30.2	30.2	78%	735	100.00	6336169	CP027561.1
Klebsiella pneumoniae strain F17KP0054 chromosome, complete...	NA	573	30.2	60.5	78%	735	100.00	5357257	CP052136.1
PREDICTED: Pecten maximus uncharacterized LOC117323518...	NA	6579	30.2	30.2	78%	735	100.00	11332	XM_033878782.1
PREDICTED: Pecten maximus uncharacterized LOC117323518...	NA	6579	30.2	30.2	78%	735	100.00	11366	XM_033878781.1
Pseudomonas umsongensis strain CY-1 chromosome, complete genome	NA	198618	30.2	30.2	78%	735	100.00	6690075	CP051487.1
Digitaria exilis annotation	NA	1010633	30.2	30.2	100%	735	94.74	28225861	LR792835.1
Digitaria exilis annotation	NA	1010633	30.2	30.2	100%	735	94.74	30797934	LR792834.1
Digitaria exilis annotation	NA	1010633	30.2	30.2	78%	735	100.00	38778756	LR792829.1
Digitaria exilis annotation	NA	1010633	30.2	30.2	78%	735	100.00	40393928	LR792828.1
Digitaria exilis annotation	NA	1010633	30.2	30.2	100%	735	94.74	42379666	LR792824.1
Mytilinidion resinicola FAD/NAD(P)-binding domain-containing...	NA	574789	30.2	30.2	78%	735	100.00	1262	XM_033723603.1
Neohortaea acidophila glyoxalase-like domain-containing protei...	NA	245834	30.2	30.2	78%	735	100.00	1222	XM_033732674.1
Dissoconium aciculare CBS 342.82 uncharacterized protein...	NA	1314786	30.2	30.2	78%	735	100.00	917	XM_033608729.1

Aspergillus tanneri DEAH-box RNA helicase prp16 (PRP16), parti...	NA	1220188	30.2	30.2	78%	735	100.00	2736	XM_033569133.1
PREDICTED: Epinephelus lanceolatus macrophage mannose receptor...	giant grouper	310571	30.2	30.2	78%	735	100.00	7243	XM_033647447.1
Digitaria exilis genome assembly, chromosome: 8B	NA	1010633	30.2	30.2	100%	735	94.74	28225861	LR761620.1
Digitaria exilis genome assembly, chromosome: 8A	NA	1010633	30.2	30.2	100%	735	94.74	30797934	LR761619.1
Digitaria exilis genome assembly, chromosome: 5B	NA	1010633	30.2	30.2	78%	735	100.00	38778756	LR761614.1
Digitaria exilis genome assembly, chromosome: 5A	NA	1010633	30.2	30.2	78%	735	100.00	40393928	LR761613.1
Digitaria exilis genome assembly, chromosome: 3A	NA	1010633	30.2	30.2	100%	735	94.74	42379666	LR761609.1
Chryseobacterium sp. NEB161 chromosome, complete genome	NA	2724619	30.2	30.2	78%	735	100.00	3543981	CP050993.1
Acinetobacter towneri strain 205 chromosome, complete genome	NA	202956	30.2	30.2	78%	735	100.00	2660496	CP048014.1
Klebsiella pneumoniae strain Bckp212 chromosome, complete genome	NA	573	30.2	60.5	78%	735	100.00	5204371	CP050826.1
Canis lupus familiaris breed Labrador retriever chromosome 18a	dog	9615	30.2	30.2	78%	735	100.00	55362250	CP050597.1
Canis lupus familiaris breed Labrador retriever chromosome 31a	dog	9615	30.2	30.2	78%	735	100.00	39430757	CP050592.1
Canis lupus familiaris breed Labrador retriever chromosome 37a	dog	9615	30.2	30.2	78%	735	100.00	35123412	CP050579.1
Canis lupus familiaris breed Labrador retriever chromosome 37b	dog	9615	30.2	30.2	78%	735	100.00	35118724	CP050638.1
Canis lupus familiaris breed Labrador retriever chromosome 31b	dog	9615	30.2	30.2	78%	735	100.00	39416698	CP050617.1
Canis lupus familiaris breed Labrador retriever chromosome 18b	dog	9615	30.2	30.2	78%	735	100.00	55343242	CP050607.1
HIV-1 isolate L718b from Argentina envelope glycoprotein (env)...	NA	11676	30.2	30.2	78%	735	100.00	540	MT121191.1
HIV-1 isolate L718a from Argentina envelope glycoprotein (env)...	NA	11676	30.2	30.2	78%	735	100.00	561	MT121190.1
Klebsiella aerogenes strain 035 chromosome, complete genome	NA	548	30.2	30.2	78%	735	100.00	4832387	CP050067.1
Citrobacter sp. Y3 chromosome, complete genome	NA	2716879	30.2	30.2	78%	735	100.00	5246113	CP050009.1
PREDICTED: Petromyzon marinus gap junction gamma-1 protein-lik...	sea lamprey	7757	30.2	30.2	78%	735	100.00	10755	XM_032945855.1
PREDICTED: Drosophila grimshawi uncharacterized LOC6562660...	NA	7222	30.2	30.2	78%	735	100.00	942	XM_032735769.1
Cutibacterium acnes SZ2 DNA, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2504552	AP022845.1
Cutibacterium acnes SZ1 DNA, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2494525	AP022844.1
Klebsiella aerogenes strain 18-	NA	548	30.2	30.2	78%	735	100.00	5241093	CP049600.1

2341 chromosome, complete genome									
Plectropomus leopardus DNA, chromosome 10, nearly complete...	leopard cora...	160734	30.2	30.2	78%	735	100.00	34657930	AP022709.1
Plectropomus leopardus DNA, chromosome 8, nearly complete...	leopard cora...	160734	30.2	30.2	78%	735	100.00	35874999	AP022707.1
Epinephelus fuscoguttatus DNA, LG19, complete sequence	brown-marble...	293821	30.2	30.2	78%	735	100.00	41259535	AP022693.1
Epinephelus fuscoguttatus DNA, LG15, complete sequence	brown-marble...	293821	30.2	30.2	78%	735	100.00	43073509	AP022689.1
Mesorhizobium sp. AA22 chromosome, complete genome	NA	1854057	30.2	30.2	78%	735	100.00	6611049	CP048406.1
Klebsiella pneumoniae strain 23 chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5287221	CP030320.1
Klebsiella pneumoniae strain 11311 chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5270063	CP030313.1
Mycobacterium mantenii JCM 18113 DNA, complete genome	NA	560555	30.2	30.2	100%	735	94.74	6185541	AP022590.1
Mycolicibacterium duvalii JCM 6396 DNA, complete genome	NA	39688	30.2	30.2	78%	735	100.00	5657388	AP022563.1
Malassezia globosa strain CBS7966 chromosome 7	NA	76773	30.2	30.2	78%	735	100.00	814315	CP046437.1
Cutibacterium acnes KPA171202 chromosome, complete genome	NA	267747	30.2	30.2	78%	735	100.00	2560634	CP025935.1
Cutibacterium acnes DSM 1897 chromosome, complete genome	NA	1122995	30.2	30.2	78%	735	100.00	2495002	CP025934.1
Shewanella sp. Arc9-LZ chromosome, complete genome	NA	2698686	30.2	30.2	78%	735	100.00	4911031	CP048031.1
Citrobacter portucalensis IOMTU157 DNA, complete genome	NA	1639133	30.2	30.2	78%	735	100.00	4987090	AP022378.1
Aspergillus caelatus P-loop containing nucleoside triphosphate...	NA	61420	30.2	30.2	78%	735	100.00	2476	XM_032066068.1
Aspergillus pseudotamarii P-loop containing nucleoside...	NA	132259	30.2	30.2	78%	735	100.00	2486	XM_032051251.1
HIV-1 isolate K104483R16 from Uganda gag protein (gag) gene,...	NA	11676	30.2	30.2	78%	735	100.00	6473	MN650569.1
Klebsiella aerogenes strain HNHF1 chromosome, complete genome	NA	548	30.2	30.2	78%	735	100.00	5253477	CP047669.1
Pseudomonas sp. S49 chromosome, complete genome	NA	1573720	30.2	30.2	78%	735	100.00	6659551	CP019432.1
Lutra lutra genome assembly, chromosome: 16	Eurasian riv...	9657	30.2	120	84%	735	100.00	61483029	LR738418.1
Lutra lutra genome assembly, chromosome: 15	Eurasian riv...	9657	30.2	30.2	78%	735	100.00	69992071	LR738417.1
Lutra lutra genome assembly, chromosome: 12	Eurasian riv...	9657	30.2	30.2	78%	735	100.00	96445735	LR738414.1
Citrobacter freundii strain LDL3-3 chromosome, complete genome	NA	546	30.2	30.2	78%	735	100.00	4878270	CP047247.1
Serratia marcescens strain N10A28 chromosome, complete genome	NA	615	30.2	30.2	78%	735	100.00	5276341	CP033623.1
Paraburkholderia acidiphila strain 7Q-K02 chromosome 1, comple...	NA	2571747	30.2	30.2	78%	735	100.00	3177533	CP046909.1
HIV-1 isolate MVC19_POSTMVC from Brazil envelope	NA	11676	30.2	30.2	78%	735	100.00	365	MK306287.1

glycoprotein...									
PREDICTED: Cucumis sativus probable receptor-like protein kina...	cucumber	3659	30.2	30.2	78%	735	100.00	1749	XM_031888355.1
Beggiatoa leptomitoformis strain D-401 chromosome, complete...	NA	288004	30.2	30.2	78%	735	100.00	4266350	CP018889.2
Beggiatoa leptomitoformis strain D-402 chromosome, complete...	NA	288004	30.2	30.2	78%	735	100.00	4265317	CP012373.2
Klebsiella aerogenes strain Y1 chromosome, complete genome	NA	548	30.2	30.2	78%	735	100.00	5295061	CP045870.1
Klebsiella aerogenes strain Y3 chromosome, complete genome	NA	548	30.2	30.2	78%	735	100.00	5272156	CP045869.1
Klebsiella aerogenes strain Y6 chromosome, complete genome	NA	548	30.2	30.2	78%	735	100.00	5266224	CP045868.1
Shewanella algae strain RQs-106 chromosome, complete genome	NA	38313	30.2	30.2	78%	735	100.00	4990025	CP046378.1
Citrobacter portucalensis strain FDAARGOS_738 chromosome,...	NA	1639133	30.2	30.2	78%	735	100.00	4998495	CP046348.1
Pantoea sp. MSR2 plasmid pMSR2A	NA	2052056	30.2	30.2	78%	735	100.00	656860	CP024637.1
Sciurus carolinensis genome assembly, chromosome: 15	gray squirrel	30640	30.2	30.2	78%	735	100.00	83138899	LR738605.1
Sciurus carolinensis genome assembly, chromosome: 14	gray squirrel	30640	30.2	30.2	78%	735	100.00	88654151	LR738604.1
Pecten maximus genome assembly, chromosome: 3	NA	6579	30.2	30.2	78%	735	100.00	53454838	LR736840.1
Acinetobacter towneri strain 19110F47 chromosome, complete genome	NA	202956	30.2	30.2	78%	735	100.00	2789147	CP046045.1
Alistipes sp. dk3624 chromosome, complete genome	NA	2662363	30.2	30.2	78%	735	100.00	3019767	CP045651.1
Klebsiella pneumoniae strain LH94 chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5300315	CP035202.1
Klebsiella pneumoniae strain LH102-A chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5153352	CP035194.1
Brucella anthropi strain T16R-87 chromosome 1, complete sequence	NA	529	30.2	30.2	78%	735	100.00	2645955	CP044970.1
Bradyrhizobium betae strain PL7HG1 chromosome, complete genome	NA	244734	30.2	30.2	78%	735	100.00	7150095	CP044543.1
Klebsiella aerogenes strain C9 chromosome, complete genome	NA	548	30.2	30.2	78%	735	100.00	5034705	CP042530.1
PREDICTED: Geospiza fortis alpha-1,3-mannosyl-glycoprotein...	medium groun...	48883	30.2	30.2	78%	735	100.00	2530	XM_031055309.1
Pseudomonas umsongensis strain GO16 chromosome	NA	198618	30.2	30.2	78%	735	100.00	7269974	CP044409.1
Cutibacterium acnes TP-CU389 DNA, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2494387	AP019664.1
Cutibacterium acnes strain ATCC 6919 chromosome, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2494216	CP044255.1
Klebsiella aerogenes strain KA_P10_L5_03.19 chromosome, comple...	NA	548	30.2	30.2	78%	735	100.00	5059877	CP044214.1
PREDICTED: Camarhynchus parvulus alpha-1,3-mannosyl-glycoprote...	NA	87175	30.2	30.2	78%	735	100.00	2659	XM_030957645.1

Klebsiella aerogenes strain FDAARGOS_641 chromosome, complete...	NA	548	30.2	30.2	78%	735	100.00	5286332	CP044083.1
PREDICTED: Chanos chanos metal regulatory transcription factor...	milkfish	29144	30.2	30.2	78%	735	100.00	2940	XM_030781814.1
PREDICTED: Chanos chanos family with sequence similarity 214...	milkfish	29144	30.2	30.2	78%	735	100.00	4030	XM_030764994.1
PREDICTED: Chanos chanos family with sequence similarity 214...	milkfish	29144	30.2	30.2	78%	735	100.00	4081	XM_030764993.1
Labrys sp. KNU-23 chromosome 2, complete sequence	NA	2789216	30.2	30.2	78%	735	100.00	2162438	CP043488.1
PREDICTED: Archocentrus centrarchus sterile alpha motif domain...	flier cichlid	63155	30.2	30.2	78%	735	100.00	2483	XM_030733686.1
PREDICTED: Archocentrus centrarchus sterile alpha motif domain...	flier cichlid	63155	30.2	30.2	78%	735	100.00	2331	XM_030733684.1
Azospirillum brasilense strain Cd chromosome 1, complete sequence	NA	192	30.2	30.2	78%	735	100.00	3035856	CP033318.1
Azospirillum brasilense strain Sp 7 chromosome 1, complete...	NA	192	30.2	30.2	78%	735	100.00	2983263	CP033312.1
Kushneria phosphatilytica strain YCWA18 chromosome, complete...	NA	657387	30.2	30.2	78%	735	100.00	3624619	CP043420.1
PREDICTED: Rhodamnia argentea E3 ubiquitin-protein ligase...	NA	178133	30.2	30.2	78%	735	100.00	678	XM_030662261.1
Citrobacter portucalensis strain WCHCP085039 chromosome,...	NA	1639133	30.2	30.2	78%	735	100.00	4813365	CP043009.1
Beijerinckiaceae bacterium RH AL1 isolate RH_AL1 genome...	NA	2572036	30.2	30.2	78%	735	100.00	4234359	LR590083.2
Chanos chanos genome assembly, chromosome: 8	milkfish	29144	30.2	30.2	78%	735	100.00	48343650	LR697113.1
Chanos chanos genome assembly, chromosome: 2	milkfish	29144	30.2	30.2	78%	735	100.00	59736555	LR697107.1
Burkholderia sp. KBS0801 chromosome 1, complete sequence	NA	1179675	30.2	30.2	78%	735	100.00	3530666	CP042177.1
Klebsiella pneumoniae strain KP14003 chromosome, complete genome	NA	573	30.2	60.5	78%	735	100.00	5293274	CP041934.1
Gimesia algae strain Pan161 chromosome	NA	2527971	30.2	30.2	100%	735	94.74	7929454	CP036343.1
Venturia effusa strain albino chromosome 12, complete sequence	NA	50376	30.2	30.2	78%	735	100.00	2088313	CP042196.1
Sparus aurata genome assembly, chromosome: 12	gilthead sea...	8175	30.2	30.2	78%	735	100.00	30193437	LR537132.1
Haemonchus contortus strain NZ_Hco_NP chromosome 3	barber pole ...	6289	30.2	60.5	78%	735	100.00	83970805	CP035802.1
Klebsiella aerogenes strain Ka37751 chromosome, complete genome	NA	548	30.2	30.2	78%	735	100.00	5183422	CP041925.1
Paraoceanicella profunda strain D4M1 chromosome, complete genome	NA	2579971	30.2	30.2	78%	735	100.00	4039866	CP040818.1
Pseudomonas aeruginosa strain AZPAE15042 chromosome,	NA	287	30.2	30.2	78%	735	100.00	6527298	CP041354.1

complete...									
Citrobacter amalonaticus strain 133355-SW-C4-Cam chromosome,...	NA	35703	30.2	30.2	78%	735	100.00	4722748	CP041362.1
Gadus morhua genome assembly, chromosome: 13	Atlantic cod	8049	30.2	30.2	78%	735	100.00	28829685	LR633955.1
Klebsiella grimontii strain 4928STDY7071187 genome assembly,...	NA	2058152	30.2	30.2	78%	735	100.00	7064570	LR607341.1
Klebsiella aerogenes strain 4928STDY7071344 genome assembly,...	NA	548	30.2	30.2	78%	735	100.00	5726555	LR607333.1
Serratia marcescens strain WVU-010 chromosome, complete genome	NA	615	30.2	30.2	78%	735	100.00	5324996	CP041134.1
Serratia marcescens strain WVU-007 chromosome, complete genome	NA	615	30.2	30.2	78%	735	100.00	5325027	CP041130.1
Serratia marcescens strain WVU-004 chromosome, complete genome	NA	615	30.2	30.2	78%	735	100.00	5307451	CP041125.1
Serratia marcescens strain WVU-002 chromosome, complete genome	NA	615	30.2	30.2	78%	735	100.00	5307415	CP041123.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 21	NA	223781	30.2	30.2	78%	735	100.00	24756580	LR606201.1
Sphaeramia orbicularis genome assembly, chromosome: 16	orbiculate c...	375764	30.2	30.2	78%	735	100.00	62079929	LR597473.1
Sphaeramia orbicularis genome assembly, chromosome: 6	orbiculate c...	375764	30.2	30.2	78%	735	100.00	58172481	LR597463.1
Salarias fasciatus genome assembly, chromosome: 12	jewelled blenny	181472	30.2	60.5	78%	735	100.00	32729575	LR597447.1
PREDICTED: Rhinatrema bivittatum DEP domain-containing...	two-lined ca...	194408	30.2	30.2	78%	735	100.00	2630	XM_029611966.1
Myxococcus xanthus strain KF3.2.8c11, complete genome	NA	34	30.2	30.2	78%	735	100.00	8952969	CP017171.1
Paremcibacter congregatus strain ZYLT chromosome, complete genome	NA	2043170	30.2	30.2	78%	735	100.00	4189011	CP041025.1
Alistipes onderdonkii subsp. vulgaris 5NYCFAH2 DNA, complete...	NA	2585117	30.2	30.2	78%	735	100.00	3312682	AP019738.1
Alistipes onderdonkii subsp. vulgaris 5CPYCFAH4 DNA, complete...	NA	2585117	30.2	30.2	78%	735	100.00	3312673	AP019737.1
Alistipes dispar 5CPEGH6 DNA, complete genome	NA	2585119	30.2	30.2	78%	735	100.00	2962376	AP019736.1
Alistipes onderdonkii subsp. vulgaris 3BBH6 DNA, complete genome	NA	2585117	30.2	30.2	78%	735	100.00	3507492	AP019734.1
Hymenobacter jejuensis strain 17J68-5 chromosome, complete genome	NA	2502781	30.2	30.2	78%	735	100.00	5086993	CP040896.1
Cutibacterium acnes subsp. acnes NBRC 107605 DNA, complete genome	NA	1734925	30.2	30.2	78%	735	100.00	2494738	AP019723.1
Moorella thermoacetica strain 39073-HH chromosome, complete...	NA	1525	30.2	30.2	78%	735	100.00	2645661	CP031054.1

Klebsiella quasipneumoniae isolate SGM81 genome assembly,...	NA	1463165	30.2	30.2	78%	735	100.00	5186362	LT898450.1
Pseudomonas sp. MPC6 chromosome, complete genome	NA	2498848	30.2	30.2	78%	735	100.00	6841168	CP034783.1
Streptopelia turtur genome assembly, chromosome: 22	NA	177155	30.2	30.2	78%	735	100.00	4500174	LR594577.1
Streptopelia turtur genome assembly, chromosome: 8	NA	177155	30.2	30.2	78%	735	100.00	34574536	LR594559.1
Schaalia cardiffensis F0333 chromosome, complete genome	NA	888050	30.2	30.2	78%	735	100.00	2230588	CP040505.1
PREDICTED: Arachis hypogaea glycerol-3-phosphate dehydrogenase...	peanut	3818	30.2	30.2	78%	735	100.00	2614	XM_025777152.2
PREDICTED: Arachis hypogaea glycerol-3-phosphate dehydrogenase...	peanut	3818	30.2	30.2	78%	735	100.00	2590	XR_003165745.2
PREDICTED: Arachis hypogaea glycerol-3-phosphate dehydrogenase...	peanut	3818	30.2	30.2	78%	735	100.00	2614	XR_003165744.2
PREDICTED: Arachis hypogaea glycerol-3-phosphate dehydrogenase...	peanut	3818	30.2	30.2	78%	735	100.00	2702	XM_025777151.2
PREDICTED: Arachis hypogaea glycerol-3-phosphate dehydrogenase...	peanut	3818	30.2	30.2	78%	735	100.00	3354	XM_025793044.2
PREDICTED: Arachis hypogaea glycerol-3-phosphate dehydrogenase...	peanut	3818	30.2	30.2	78%	735	100.00	2199	XM_025793031.2
PREDICTED: Scleropages formosus sterile alpha motif...	Asian bonyto...	113540	30.2	30.2	78%	735	100.00	1502	XM_018756613.2
PREDICTED: Scleropages formosus sterile alpha motif...	Asian bonyto...	113540	30.2	30.2	78%	735	100.00	828	XM_029249821.1
Brenneria nigrifluens DSM 30175 = ATCC 13028 chromosome,...	NA	1121120	30.2	30.2	78%	735	100.00	4891702	CP034036.1
Salinivibrio kushneri strain AL184 chromosome 1, complete...	NA	1908198	30.2	30.2	78%	735	100.00	2840906	CP040021.1
Azospirillum brasilense strain MTCC4039 chromosome, complete...	NA	192	30.2	30.2	78%	735	100.00	2941886	CP032345.1
Azospirillum brasilense strain MTCC4038 chromosome, complete...	NA	192	30.2	30.2	78%	735	100.00	3007857	CP032339.1
Muribaculum gordoncarteri strain TLL-A4 chromosome	NA	2530390	30.2	30.2	78%	735	100.00	3306969	CP039393.1
Citrobacter portucalensis strain Effluent_1 chromosome, comple...	NA	1639133	30.2	30.2	78%	735	100.00	5018095	CP039327.1
Desulfovibrio desulfuricans strain IC1 chromosome, complete...	NA	876	30.2	30.2	78%	735	100.00	3251440	CP036295.1
Klebsiella pneumoniae strain 121 chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5180019	CP031849.1
Scleropages formosus genome assembly, chromosome: 16	Asian bonyto...	113540	30.2	30.2	78%	735	100.00	27323948	LR584081.1
Echeneis naucrates genome assembly, chromosome: 22	live sharksu...	173247	30.2	30.2	78%	735	100.00	21968004	LR584063.1
HIV-1 isolate HLJ16303 from China envelope glycoprotein (env)...	NA	11676	30.2	30.2	78%	735	100.00	492	MK703757.1
HIV-1 isolate HLJ13009 from China envelope glycoprotein	NA	11676	30.2	30.2	78%	735	100.00	519	MK703142.1

(env)...									
Paracoccus liaowanqingii strain 2251 chromosome, complete genome	NA	2560053	30.2	30.2	78%	735	100.00	3271357	CP038439.1
Herbaspirillum huttiense strain NFYY 53159 chromosome, complet...	NA	863372	30.2	30.2	78%	735	100.00	5691775	CP037993.1
Talaromyces funiculosus strain X33 chromosome 2	NA	28572	30.2	30.2	78%	735	100.00	3232346	CP036224.1
Enterobacter hormaechei strain NCTC11571 genome assembly,...	NA	158836	30.2	60.5	78%	735	100.00	4552052	LR134164.1
Salmonella enterica subsp. arizonae strain NCTC10047 genome...	NA	59203	30.2	30.2	78%	735	100.00	4930903	LR134156.1
Klebsiella aerogenes strain NCTC10006 genome assembly,...	NA	548	30.2	30.2	78%	735	100.00	1497228	LR134123.1
Gouania willdenowi genome assembly, chromosome: 13	blunt-snoute...	441366	30.2	30.2	78%	735	100.00	44521366	LR131999.1
Undibacterium parvum strain DSM 23061 chromosome, complete genome	NA	401471	30.2	30.2	78%	735	100.00	4910324	CP034464.1
Pyxidicoccus sp. strain MCy9557 t3pks biosynthetic gene cluste...	NA	2023737	30.2	30.2	78%	735	100.00	58302	MH908914.1
Mesorhizobium sp. M6A.T.Cr.TU.016.01.1.1 chromosome	NA	2493677	30.2	30.2	78%	735	100.00	6784580	CP034452.1
Mesorhizobium sp. M7D.F.Ca.US.005.01.1.1 chromosome	NA	2493678	30.2	30.2	78%	735	100.00	7168230	CP034453.1
PREDICTED: Penaeus vannamei NPC intracellular cholesterol...	Pacific whit...	6689	30.2	30.2	78%	735	100.00	649	XM_027379918.1
PREDICTED: Penaeus vannamei 5'-nucleotidase domain-containing...	Pacific whit...	6689	30.2	30.2	78%	735	100.00	2141	XM_027367669.1
PREDICTED: Penaeus vannamei 5'-nucleotidase domain-containing...	Pacific whit...	6689	30.2	30.2	78%	735	100.00	2151	XM_027367668.1
PREDICTED: Penaeus vannamei 5'-nucleotidase domain-containing...	Pacific whit...	6689	30.2	30.2	78%	735	100.00	2202	XM_027367667.1
PREDICTED: Penaeus vannamei 5'-nucleotidase domain-containing...	Pacific whit...	6689	30.2	30.2	78%	735	100.00	2211	XM_027367666.1
PREDICTED: Coffea arabica uncharacterized LOC113709974...	coffee	13443	30.2	30.2	78%	735	100.00	4467	XM_027232822.1
Cutibacterium acnes strain FDAARGOS_503 chromosome, complete...	NA	1747	30.2	30.2	78%	735	100.00	2494539	CP033842.1
Klebsiella aerogenes strain FDAARGOS_513 chromosome, complete...	NA	548	30.2	30.2	78%	735	100.00	5259024	CP033817.1
Achromobacter denitrificans strain PheN1 chromosome, complete...	NA	32002	30.2	30.2	78%	735	100.00	7010850	CP033730.1
Cutibacterium acnes strain FDAARGOS_577 chromosome, complete...	NA	1747	30.2	30.2	78%	735	100.00	2495332	CP033718.1
Brassica oleracea HDEM genome, scaffold: C2	wild cabbage	3712	30.2	30.2	78%	735	100.00	63782621	LR031874.1
Leishmania donovani strain LdCL chromosome LdCL_33, complete...	NA	5661	30.2	30.2	78%	735	100.00	1490978	CP029532.1

Dickeya solani strain IFB0223 chromosome, complete genome	NA	1089444	30.2	30.2	78%	735	100.00	4937554	CP024710.1
Herbaspirillum rubrisubalbicans strain DSM 11543 chromosome,...	NA	80842	30.2	30.2	78%	735	100.00	5617593	CP024996.1
Dickeya solani strain IFB 0099 chromosome, complete genome	NA	1089444	30.2	30.2	78%	735	100.00	4932920	CP024711.1
Podospora comata strain T genome assembly, chromosome: 2	NA	48703	30.2	30.2	78%	735	100.00	5052399	LR026965.1
Burkholderia stabilis genome assembly, chromosome: I	NA	95485	30.2	30.2	78%	735	100.00	3705321	LR025742.1
PREDICTED: Zonotrichia albicollis...	white-throat...	44394	30.2	30.2	78%	735	100.00	2617	XM_005483645.3
Aspergillus welwitschiae amine oxidase (BDQ94DRAFT_186017),...	NA	1341132	30.2	30.2	78%	735	100.00	1667	XM_026775033.1
Pseudomonas sp. K2W31S-8 chromosome, complete genome	NA	2320867	30.2	30.2	78%	735	100.00	4949615	CP032419.1
Alteromonas sp. RKMC-009 chromosome, complete genome	NA	2267264	30.2	30.2	78%	735	100.00	4934803	CP031010.1
Klebsiella aerogenes strain FDAARGOS_327 chromosome, complete...	NA	548	30.2	30.2	78%	735	100.00	5387939	CP031756.1
Uncultured bacterium contig00108, complete sequence	NA	77133	30.2	30.2	78%	735	100.00	15754	MG852072.1
Haemonchus contortus, ISE/inbred ISE, WGS project CAVP01000000...	barber pole ...	6289	30.2	30.2	78%	735	100.00	43560352	LS997564.1
PREDICTED: Astatotilapia calliptera sterile alpha motif domain...	eastern happy	8154	30.2	30.2	78%	735	100.00	2500	XM_026153894.1
PREDICTED: Astatotilapia calliptera sterile alpha motif domain...	eastern happy	8154	30.2	30.2	78%	735	100.00	2510	XM_026153893.1
PREDICTED: Astatotilapia calliptera sterile alpha motif domain...	eastern happy	8154	30.2	30.2	78%	735	100.00	2454	XM_026153892.1
Klebsiella variicola strain X39 chromosome, complete genome	NA	244366	30.2	30.2	78%	735	100.00	5641443	CP018307.1
Escherichia coli strain Combat2C1 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	5202049	CP019243.1
Pseudomonas sp. ACM7 chromosome	NA	2052956	30.2	30.2	78%	735	100.00	6602660	CP024866.1
Escherichia coli strain BR02-DEC chromosome	NA	562	30.2	30.2	78%	735	100.00	5025753	CP035320.1
Escherichia coli strain BR07-DEC chromosome	NA	562	30.2	30.2	78%	735	100.00	5052397	CP035322.1
Escherichia coli strain BR03-DEC chromosome	NA	562	30.2	30.2	78%	735	100.00	5038603	CP035321.1
PREDICTED: **Falco** cherrug mitochondrial antiviral signaling...	Saker falcon	345164	30.2	30.2	78%	735	100.00	5285	XM_005435440.3
PREDICTED: **Falco** cherrug mitochondrial antiviral signaling...	Saker falcon	345164	30.2	30.2	78%	735	100.00	5499	XM_027799969.1
PREDICTED: **Falco** peregrinus mitochondrial antiviral signaling...	peregrine fa...	8954	30.2	30.2	78%	735	100.00	4229	XM_005230659.3
PREDICTED: **Falco** peregrinus mitochondrial antiviral signaling...	peregrine fa...	8954	30.2	30.2	78%	735	100.00	3908	XM_027777185.1
PREDICTED: **Falco** peregrinus mitochondrial antiviral signaling...	peregrine fa...	8954	30.2	30.2	78%	735	100.00	4443	XM_027777184.1
Lateolabrax maculatus linkage group 4 sequence	spotted sea ...	315492	30.2	30.2	78%	735	100.00	28631555	CP032601.1

Lateolabrax maculatus linkage group 15 sequence	spotted sea ...	315492	30.2	30.2	78%	735	100.00	23369250	CP032589.1
Lateolabrax maculatus linkage group 12 sequence	spotted sea ...	315492	30.2	30.2	78%	735	100.00	24885600	CP032586.1
Lateolabrax maculatus chromosome Lm19	spotted sea ...	315492	30.2	30.2	78%	735	100.00	22343975	CP027280.1
Lateolabrax maculatus chromosome Lm12	spotted sea ...	315492	30.2	30.2	78%	735	100.00	23523986	CP027273.1
Lateolabrax maculatus chromosome Lm5	spotted sea ...	315492	30.2	30.2	78%	735	100.00	21471159	CP027266.1
Pseudomonas sp. RU47 chromosome, complete genome	NA	2005388	30.2	30.2	78%	735	100.00	6663463	CP022411.1
Pseudomonas aeruginosa strain LW chromosome, complete genome	NA	287	30.2	30.2	100%	735	94.74	6824837	CP022478.1
Glycocaulis alkaliphilus strain 6B-8, complete genome	NA	1434191	30.2	30.2	78%	735	100.00	3019659	CP018911.1
Pseudomonas poae strain CAP-2018 chromosome, complete genome	NA	200451	30.2	30.2	78%	735	100.00	7371963	CP034537.1
Citrobacter portucalensis strain NCTC11104 genome assembly,...	NA	1639133	30.2	30.2	78%	735	100.00	4694654	LR134214.1
Phoenix dactylifera clone dpS5560CH2 sex-determination region...	date palm	42345	30.2	30.2	78%	735	100.00	1269680	MH680991.1
Phoenix dactylifera clone dpS5560CH1 sex-determination region...	date palm	42345	30.2	30.2	78%	735	100.00	1274508	MH680988.1
Cutibacterium acnes strain KCOM 1315 chromosome, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2560321	CP031442.1
PREDICTED: Apteryx rowi nuclear factor I C (NFIC), mRNA	Okarito brow...	308060	30.2	30.2	78%	735	100.00	2094	XM_026084138.1
PREDICTED: Oreochromis niloticus sterile alpha motif domain...	Nile tilapia	8128	30.2	30.2	78%	735	100.00	2498	XM_013274244.2
PREDICTED: Oreochromis niloticus sterile alpha motif domain...	Nile tilapia	8128	30.2	30.2	78%	735	100.00	2568	XM_025901587.1
PREDICTED: Oreochromis niloticus butyrophilin-like protein 2...	Nile tilapia	8128	30.2	30.2	78%	735	100.00	2698	XM_025904296.1
PREDICTED: Oreochromis niloticus butyrophilin-like protein 2...	Nile tilapia	8128	30.2	30.2	78%	735	100.00	3025	XM_005465897.4
Arachis hypogaea cultivar Shitouqi chromosome A02	peanut	3818	30.2	30.2	78%	735	100.00	99791824	CP030984.1
Salmonella enterica strain SA20021456 chromosome, complete genome	NA	28901	30.2	30.2	78%	735	100.00	5431908	CP030219.1
Aspergillus sclerotioniger CBS 115572 DNA lyase Apn2...	NA	1450535	30.2	30.2	78%	735	100.00	2053	XM_025617347.1
Aspergillus ibericus CBS 121593 DNA lyase Apn2...	NA	1448316	30.2	30.2	78%	735	100.00	2476	XM_025723611.1
Aspergillus niger CBS 101883 monoamine oxidase maoN...	NA	1450533	30.2	30.2	78%	735	100.00	1587	XM_025596928.1
Burkholderia sp. JP2-270 chromosome 1, complete sequence	NA	2217913	30.2	30.2	78%	735	100.00	3723585	CP029824.1
Scophthalmus maximus chromosome 7	turbot	52904	30.2	30.2	78%	735	100.00	26877711	CP026249.1

Scophthalmus maximus chromosome 4	turbot	52904	30.2	30.2	78%	735	100.00	30934145	CP026246.1
Flavobacterium pallidum strain HYN0049 chromosome, complete...	NA	2172098	30.2	30.2	78%	735	100.00	3552756	CP029187.1
Pseudomonas aeruginosa strain AR441 chromosome, complete genome	NA	287	30.2	30.2	78%	735	100.00	6584825	CP029093.1
Rhodobacter blasticus strain 28/5 chromosome, complete genome	NA	1075	30.2	30.2	78%	735	100.00	3548948	CP020470.1
Klebsiella aerogenes strain AR_0161 chromosome, complete genome	NA	548	30.2	30.2	78%	735	100.00	5086051	CP028951.1
Serratia marcescens strain AR_0130 chromosome, complete genome	NA	615	30.2	30.2	78%	735	100.00	5138817	CP028947.1
PREDICTED: Maylandia zebra obscurin-like (LOC112429874), mRNA	zebra mbuna	106582	30.2	30.2	78%	735	100.00	1403	XM_024800233.1
PREDICTED: Maylandia zebra obscurin (LOC101487466), mRNA	zebra mbuna	106582	30.2	30.2	78%	735	100.00	1356	XM_024799631.1
PREDICTED: Selaginella moellendorffii 3-ketoacyl-CoA thiolase ...	NA	88036	30.2	30.2	78%	735	100.00	1526	XM_002974789.2
PREDICTED: Selaginella moellendorffii pentatricopeptide...	NA	88036	30.2	30.2	78%	735	100.00	1131	XM_002967227.2
PREDICTED: Selaginella moellendorffii 3-ketoacyl-CoA thiolase ...	NA	88036	30.2	30.2	78%	735	100.00	1498	XM_002963707.2
PREDICTED: Selaginella moellendorffii pentatricopeptide...	NA	88036	30.2	30.2	78%	735	100.00	1917	XM_024676609.1
Dickeya dadantii strain DSM 18020 chromosome, complete genome	NA	204038	30.2	30.2	78%	735	100.00	4997541	CP023467.1
Cutibacterium acnes strain ATCC 6919 chromosome, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2495001	CP023676.1
Pseudomonas aeruginosa strain CR1 chromosome, complete genome	NA	287	30.2	30.2	78%	735	100.00	6118054	CP020560.1
Leishmania infantum strain TR01 isolate Lin_TR01 chromosome 33...	NA	5671	30.2	30.2	78%	735	100.00	1451830	CP027833.1
Linum usitatissimum chromosome Lu11	flax	4006	30.2	30.2	78%	735	100.00	19887771	CP027621.1
Lachnospiraceae bacterium oral taxon 500 strain W11650...	NA	712991	30.2	30.2	78%	735	100.00	3201383	CP027241.1
Pseudomonas aeruginosa strain AR_0356 chromosome, complete genome	NA	287	30.2	30.2	78%	735	100.00	6586916	CP027169.1
Xylella fastidiosa strain Salento-2 chromosome, complete genome	NA	2371	30.2	30.2	78%	735	100.00	2508296	CP016610.1
Xylella fastidiosa strain Salento-1 chromosome, complete genome	NA	2371	30.2	30.2	78%	735	100.00	2508097	CP016608.1
Citrobacter amalonaticus strain FDAARGOS_122, complete genome	NA	35703	30.2	30.2	78%	735	100.00	4904719	CP014015.2
Acinetobacter sp. SWBY1 chromosome, complete genome	NA	2079596	30.2	30.2	78%	735	100.00	2914878	CP026616.1
Citrobacter braakii strain FDAARGOS_253 chromosome, complete...	NA	57706	30.2	30.2	78%	735	100.00	5244290	CP020448.2

Klebsiella aerogenes strain AR_0062 chromosome, complete genome	NA	548	30.2	30.2	78%	735	100.00	5264003	CP026756.1
PREDICTED: Chrysemys picta bellii rho-related GTP-binding...	western pain...	8478	30.2	30.2	78%	735	100.00	5489	XM_005286049.2
Citrobacter amalonaticus strain FDAARGOS_165 chromosome,...	NA	35703	30.2	30.2	78%	735	100.00	5030678	CP014070.2
Arthrobacter agilis strain UMCV2 chromosome	NA	37921	30.2	30.2	78%	735	100.00	3482157	CP024915.1
Citrobacter sp. CFNIH10 chromosome, complete genome	NA	1920110	30.2	30.2	78%	735	100.00	5246201	CP026216.1
Klebsiella aerogenes strain FDAARGOS_152 chromosome, complete...	NA	548	30.2	30.2	78%	735	100.00	5317141	CP014029.2
Klebsiella aerogenes strain FDAARGOS_139 chromosome, complete...	NA	548	30.2	30.2	78%	735	100.00	5215793	CP014748.2
Sinorhizobium fredii strain NXT3 plasmid pSfreNXT3b, complete...	NA	380	30.2	30.2	78%	735	100.00	499999	CP024309.1
Ramularia collo-cygni related to class I alpha-mannosidase...	NA	112498	30.2	30.2	100 %	735	94.74	1842	XM_023776106.1
Citrobacter freundii complex sp. CFNIH9 chromosome, complete...	NA	2077149	30.2	30.2	78%	735	100.00	5016446	CP026238.1
Escherichia coli BH100N substr. MG2017, complete genome	NA	562	30.2	30.2	78%	735	100.00	5116034	CP025703.1
Nostoc sp. CENA543 chromosome, complete genome	NA	1869241	30.2	30.2	78%	735	100.00	6990729	CP023278.1
Larimichthys crocea genome assembly, chromosome: V	large yellow...	215358	30.2	30.2	78%	735	100.00	34017524	LT972194.1
Larimichthys crocea genome assembly, chromosome: XXII	large yellow...	215358	30.2	30.2	78%	735	100.00	20861818	LT972189.1
Larimichthys crocea genome assembly, chromosome: XVIII	large yellow...	215358	30.2	30.2	78%	735	100.00	12139166	LT972184.1
Escherichia coli BH100L substr. MG2017, complete genome	NA	562	30.2	30.2	78%	735	100.00	5033214	CP025716.1
PREDICTED: Dasypus novemcinctus paired box protein Pax-7...	nine-banded ...	9361	30.2	30.2	78%	735	100.00	1197	XM_012527771.2
Enterobacter sp. EA-1 chromosome, complete genome	NA	2057026	30.2	30.2	78%	735	100.00	5145523	CP025776.1
Citrobacter freundii complex sp. CFNIH2 chromosome, complete...	NA	2066049	30.2	30.2	78%	735	100.00	5277996	CP025757.1
Escherichia coli strain BH100 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	5072943	CP024650.2
Escherichia coli strain BH100 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	5131212	CP025251.1
Dickeya solani strain PPO 9019 chromosome, complete genome	NA	1089444	30.2	30.2	78%	735	100.00	4918850	CP017454.1
Dickeya solani D s0432-1 chromosome, complete genome	NA	1231725	30.2	30.2	78%	735	100.00	4919812	CP017453.1
Dickeya solani RNS 08.23.3.1.A chromosome, complete genome	NA	1240086	30.2	30.2	78%	735	100.00	4922468	CP016928.1
Santalum album AT1G32340 mRNA, partial sequence	white sandal...	35974	30.2	30.2	78%	735	100.00	1275	KY531726.1
Klebsiella aerogenes strain AR_0009 chromosome, complete genome	NA	548	30.2	30.2	78%	735	100.00	5323040	CP024885.1
Klebsiella aerogenes strain AR_0007 chromosome,	NA	548	30.2	30.2	78%	735	100.00	5118619	CP024883.1

complete genome									
Chryseobacterium camelliae strain Dolsongi-HT1, complete genome	NA	1265445	30.2	30.2	78%	735	100.00	4376354	CP022986.1
Klebsiella aerogenes strain FDAARGOS_363 chromosome, complete...	NA	548	30.2	30.2	78%	735	100.00	5245455	CP023963.1
PREDICTED: Seriola dumerili sterile alpha motif domain...	greater ambe...	41447	30.2	30.2	78%	735	100.00	1004	XM_022739232.1
PREDICTED: Astyanax mexicanus guanylyl cyclase domain containi...	Mexican tetra	7994	30.2	30.2	78%	735	100.00	2229	XM_007241806.3
PREDICTED: Astyanax mexicanus type I inositol...	Mexican tetra	7994	30.2	30.2	100 %	735	94.74	2935	XM_022663572.1
Pseudomonas frederiksbergensis strain KNU-15 chromosome,...	NA	104087	30.2	30.2	78%	735	100.00	6595804	CP023466.1
Aspergillus glaucus CBS 516.65 hypothetical protein...	NA	1160497	30.2	30.2	78%	735	100.00	1698	XM_022543662.1
Cohaesibacter sp. ES.047 genome assembly, chromosome: I	NA	1798205	30.2	30.2	78%	735	100.00	5110332	LT907844.1
Lupinus angustifolius cultivar Tanjil chromosome LG-15	narrow-leave...	3871	30.2	30.2	78%	735	100.00	24202101	CP023127.1
Dermatophilus congolensis strain NCTC13039 genome assembly,...	NA	1863	30.2	30.2	78%	735	100.00	2627820	LT906453.1
Ralstonia pseudosolanacearum strain RS 476, complete genome	NA	1310165	30.2	30.2	78%	735	100.00	3716422	CP021762.1
Leishmania donovani strain pasteur chromosome 33, complete...	NA	5661	30.2	30.2	78%	735	100.00	1561605	CP022648.1
Salmonella enterica subsp. enterica serovar Manhattan strain...	NA	340189	30.2	30.2	78%	735	100.00	4732484	CP022497.1
Serratia marcescens strain UMH6, complete genome	NA	615	30.2	30.2	78%	735	100.00	5192910	CP018926.1
Ralstonia solanacearum strain CQPS-1, complete genome	NA	305	30.2	30.2	78%	735	100.00	3832354	CP016914.1
Sinorhizobium meliloti strain CCMM B554 (FSM-MA), complete genome	NA	382	30.2	30.2	78%	735	100.00	3641423	CP019584.1
Salmonella enterica subsp. diarizonae serovar 50:k:z str....	NA	1243612	30.2	30.2	78%	735	100.00	5076950	CP022142.1
Citrobacter freundii strain 705SK3, complete genome	NA	546	30.2	30.2	78%	735	100.00	5242839	CP022151.1
Sinorhizobium meliloti RU11/001 plasmid pSmeRU11d, complete...	NA	1401243	30.2	30.2	78%	735	100.00	166875	CP021216.1
Citrobacter amalonaticus strain 92 genome assembly, chromosome...	NA	35703	30.2	30.2	78%	735	100.00	5109913	LT556085.1
Citrobacter amalonaticus strain 86 genome assembly, chromosome...	NA	35703	30.2	30.2	78%	735	100.00	5048670	LT556084.1
Croceicoccus marinus strain E4A9 chromosome, complete genome	NA	450378	30.2	30.2	78%	735	100.00	3001363	CP019602.1
PREDICTED: Columba livia phosphodiesterase 4B (PDE4B),...	rock pigeon	8932	30.2	30.2	78%	735	100.00	4079	XM_021296431.1
PREDICTED: Columba livia phosphodiesterase 4B (PDE4B),...	rock pigeon	8932	30.2	30.2	78%	735	100.00	4041	XM_021296426.1
PREDICTED: Heterocephalus glaber TATA-box binding protein...	naked mole-rat	10181	30.2	30.2	78%	735	100.00	6461	XM_004854687.2
PREDICTED: Heterocephalus glaber TATA-box binding protein...	naked mole-rat	10181	30.2	30.2	78%	735	100.00	6494	XM_004854686.3
PREDICTED: Heterocephalus glaber TATA-box binding protein...	naked mole-rat	10181	30.2	30.2	78%	735	100.00	6665	XM_021266432.1

PREDICTED: Heterocephalus glaber TATA-box binding protein...	naked mole-rat	10181	30.2	30.2	78%	735	100.00	6495	XM_021266431.1
PREDICTED: Heterocephalus glaber TATA-box binding protein...	naked mole-rat	10181	30.2	30.2	78%	735	100.00	6568	XM_004854684.2
Kluyveromyces lactis strain GG799 chromosome A, complete sequence	NA	28985	30.2	30.2	78%	735	100.00	1050866	CP021239.1
PREDICTED: Arachis duranensis glycerol-3-phosphate dehydrogena...	NA	130453	30.2	30.2	78%	735	100.00	2285	XM_016093854.2
PREDICTED: Arachis duranensis glycerol-3-phosphate dehydrogena...	NA	130453	30.2	30.2	78%	735	100.00	1731	XM_016093853.2
PREDICTED: Arachis duranensis glycerol-3-phosphate dehydrogena...	NA	130453	30.2	30.2	78%	735	100.00	2144	XM_016093852.2
PREDICTED: Arachis ipaensis glycerol-3-phosphate dehydrogenase...	NA	130454	30.2	30.2	78%	735	100.00	2538	XR_001617221.2
PREDICTED: Arachis ipaensis glycerol-3-phosphate dehydrogenase...	NA	130454	30.2	30.2	78%	735	100.00	2562	XR_002357528.1
PREDICTED: Arachis ipaensis glycerol-3-phosphate dehydrogenase...	NA	130454	30.2	30.2	78%	735	100.00	2679	XM_016327972.2
Xylella fastidiosa subsp. pauca strain De Donno chromosome,...	NA	698414	30.2	30.2	78%	735	100.00	2508465	CP020870.1
PREDICTED: Drosophila serrata methionine-R-sulfoxide reductase...	NA	7274	30.2	30.2	78%	735	100.00	1219	XM_020957641.1
PREDICTED: Drosophila serrata methionine-R-sulfoxide reductase...	NA	7274	30.2	30.2	78%	735	100.00	2837	XM_020957640.1
PREDICTED: Drosophila serrata methionine-R-sulfoxide reductase...	NA	7274	30.2	30.2	78%	735	100.00	1258	XM_020957639.1
Prosthecochloris sp. HL-130-GSB, complete genome	NA	1974213	30.2	30.2	100 %	735	94.74	2414726	CP020873.1
Rhizobium phaseoli Brasil 5, complete sequence	NA	526949	30.2	30.2	78%	735	100.00	4426693	CP020896.1
Pantoea alhagi strain LTYR-11Z, complete genome	NA	1891675	30.2	30.2	78%	735	100.00	4239970	CP019706.1
Streptomyces sp. S8, complete genome	NA	1837283	30.2	30.2	78%	735	100.00	7529075	CP015362.1
Gallus gallus (CB) class I like gene 8.4	chicken	9031	30.2	30.2	78%	735	100.00	3850	X75087.1
Gallus gallus (chicken) DNA sequence from a contig of cosmids...	NA	32630	30.2	30.2	78%	735	100.00	92863	AL023516.3
Paenalcaligenes hominis strain 15S00501, complete genome	NA	643674	30.2	30.2	78%	735	100.00	2688496	CP019697.1
Linum usitatissimum microsatellite 82921-84161 sequence	flax	4006	30.2	30.2	78%	735	100.00	343	KY327036.1
PREDICTED: Paralichthys olivaceus sterile alpha motif domain...	Japanese flo...	8255	30.2	30.2	78%	735	100.00	2249	XM_020095924.1
Leishmania donovani strain MHOM/IN/1983/AG83 isolate late...	NA	5661	30.2	30.2	78%	735	100.00	1450977	CP019542.1
Leishmania donovani strain MHOM/IN/1983/AG83 isolate early...	NA	5661	30.2	30.2	78%	735	100.00	1453464	CP018601.1

Trametes hirsuta strain 072 chromosome 8, complete sequence	NA	5327	30.2	60.5	78%	735	100.00	2614590	CP019381.1
Trametes hirsuta strain 072 chromosome 11, complete sequence	NA	5327	30.2	30.2	78%	735	100.00	2042872	CP019372.1
Fuerstia marisgermanicae strain NH11 chromosome, complete genome	NA	1891926	30.2	30.2	78%	735	100.00	8920478	CP017641.1
Salmonella enterica subsp. enterica serovar Yovokome str....	NA	1243600	30.2	30.2	78%	735	100.00	4640929	CP019418.1
Pseudomonas frederiksbergensis strain AS1, complete genome	NA	104087	30.2	30.2	78%	735	100.00	6126864	CP018319.1
Gramella flava JLT2011, complete genome	NA	1229726	30.2	30.2	78%	735	100.00	4007868	CP016359.1
Malassezia sympodialis ATCC 42132 genome assembly, chromosome: 1	NA	1230383	30.2	30.2	78%	735	100.00	1508930	LT671821.1
Malassezia sympodialis isolate KS292 genome assembly,...	NA	76777	30.2	30.2	78%	735	100.00	1507387	LT671813.1
Malassezia sympodialis isolate KS004 genome assembly,...	NA	76777	30.2	30.2	78%	735	100.00	1509448	LT671805.1
Malassezia sympodialis isolate KS327 genome assembly,...	NA	76777	30.2	30.2	78%	735	100.00	1509180	LT671797.1
Malassezia sympodialis isolate KS024 genome assembly,...	NA	76777	30.2	30.2	78%	735	100.00	1515123	LT671789.1
Streptomyces sp. Tue6075, complete genome	NA	1661694	30.2	30.2	78%	735	100.00	7931832	CP010833.1
Thalassolituus oleivorans strain K188 chromosome, complete genome	NA	187493	30.2	30.2	78%	735	100.00	3909699	CP017810.1
PREDICTED: Branchiostoma belcheri NADH dehydrogenase...	Belcher's la...	7741	30.2	30.2	78%	735	100.00	2042	XM_019777244.1
PREDICTED: Hipposideros armiger proprotein convertase...	great roundl...	186990	30.2	30.2	78%	735	100.00	2066	XM_019657367.1
PREDICTED: Hipposideros armiger proprotein convertase...	great roundl...	186990	30.2	30.2	78%	735	100.00	2189	XM_019657366.1
PREDICTED: Hipposideros armiger proprotein convertase...	great roundl...	186990	30.2	30.2	78%	735	100.00	2294	XM_019657365.1
PREDICTED: Hipposideros armiger proprotein convertase...	great roundl...	186990	30.2	30.2	78%	735	100.00	2369	XM_019657364.1
PREDICTED: Hipposideros armiger proprotein convertase...	great roundl...	186990	30.2	30.2	78%	735	100.00	2501	XM_019657363.1
PREDICTED: Hipposideros armiger proprotein convertase...	great roundl...	186990	30.2	30.2	78%	735	100.00	2516	XM_019657361.1
PREDICTED: Hipposideros armiger proprotein convertase...	great roundl...	186990	30.2	30.2	78%	735	100.00	2576	XM_019657360.1
PREDICTED: Hipposideros armiger proprotein convertase...	great roundl...	186990	30.2	30.2	78%	735	100.00	2576	XM_019657359.1
PREDICTED: Hipposideros armiger proprotein convertase...	great roundl...	186990	30.2	30.2	78%	735	100.00	2591	XM_019657358.1
Ochrobactrum anthropi genome assembly, chromosome: I	NA	529	30.2	30.2	78%	735	100.00	2754709	LT671861.1
Ralstonia solanacearum strain EP1, complete genome	NA	305	30.2	30.2	78%	735	100.00	3949527	CP015115.1
Salmonella enterica subsp. enterica serovar Newport str. Levin...	NA	930779	30.2	30.2	78%	735	100.00	4883715	CP015924.1
Bradyrhizobium lablabi strain MT34 genome assembly, chromosome: I	NA	722472	30.2	30.2	78%	735	100.00	8150968	LT670845.1
Ralstonia solanacearum FJAT-	NA	1130828	30.2	30.2	78%	735	100.00	3984240	CP016554.1

1458, complete genome									
Actinomyces sp. Marseille-P2985 strain Marseille-P2985T genome...	NA	1852377	30.2	30.2	78%	735	100.00	1892549	LT635457.1
Ralstonia solanacearum OE1-1, complete genome	NA	1429399	30.2	30.2	78%	735	100.00	3826396	CP009764.1
Moorella thermoacetica strain DSM 103284, complete genome	NA	1525	30.2	30.2	78%	735	100.00	2560375	CP017237.1
Paraburkholderia sprentiae WSM5005 chromosome 1, complete...	NA	754502	30.2	30.2	78%	735	100.00	3645501	CP017561.1
Marinobacter salinus strain Hb8 chromosome, complete genome	NA	1874317	30.2	30.2	78%	735	100.00	4121005	CP017715.1
Pseudomonas mandelii strain LMG 21607 genome assembly,...	NA	75612	30.2	30.2	78%	735	100.00	7041758	LT629796.1
Pseudomonas umsongensis strain BS3657 genome assembly,...	NA	198618	30.2	30.2	78%	735	100.00	6749275	LT629767.1
Pseudomonas lini strain BS3782 genome assembly, chromosome: I	NA	163011	30.2	30.2	78%	735	100.00	6529836	LT629746.1
Pseudomonas sp. bs2935 genome assembly, chromosome: I	NA	1761895	30.2	30.2	78%	735	100.00	5868846	LT629744.1
Bradyrhizobium ottawaense strain GAS524 genome assembly,...	NA	931866	30.2	30.2	78%	735	100.00	8339215	LT629693.1
PREDICTED: Scleropages formosus sterile alpha motif...	Asian bonyto...	113540	30.2	30.2	78%	735	100.00	1048	XM_018756612.1
PREDICTED: Scleropages formosus sterile alpha motif...	Asian bonyto...	113540	30.2	30.2	78%	735	100.00	815	XM_018756611.1
PREDICTED: Lates calcarifer WSC domain-containing protein 1-li...	barramundi p...	8187	30.2	30.2	78%	735	100.00	3029	XM_018692592.1
PREDICTED: Lates calcarifer sterile alpha motif domain...	barramundi p...	8187	30.2	30.2	78%	735	100.00	2862	XM_018686064.1
PREDICTED: Lates calcarifer sterile alpha motif domain...	barramundi p...	8187	30.2	30.2	78%	735	100.00	2857	XM_018686063.1
PREDICTED: Raphanus sativus uncharacterized LOC108850136...	radish	3726	30.2	30.2	78%	735	100.00	1373	XM_018623713.1
Microbulbifer aggregans strain CCB-MM1, complete genome	NA	1769779	30.2	30.2	78%	735	100.00	3864326	CP014143.1
Pseudomonas fluorescens strain Pt14, complete genome	NA	294	30.2	30.2	78%	735	100.00	5841722	CP017296.1
Novosphingobium resinovorum strain SA1 plasmid pSA1, complete...	NA	158500	30.2	30.2	78%	735	100.00	1756808	CP017076.1
Pochonia chlamydosporia 170 patatin-like serine hydrolase...	NA	1380566	30.2	30.2	78%	735	100.00	4536	XM_018283088.1
Moorella thermoacetica strain DSM 103132, complete genome	NA	1525	30.2	30.2	78%	735	100.00	2976077	CP017019.1
Paraphaeosphaeria sporulosa putative histidine kinase-like...	NA	1460663	30.2	30.2	78%	735	100.00	3671	XM_018187455.1
Burkholderia sp. BDU8 chromosome 1, complete sequence	NA	1385592	30.2	30.2	78%	735	100.00	4439942	CP013389.1
HIV-1 isolate BRRJTP133 from Brazil envelope glycoprotein (env...	NA	11676	30.2	30.2	78%	735	100.00	356	KT595560.1
Pseudomonas sp. TCU-HL1, complete genome	NA	1856685	30.2	30.2	78%	735	100.00	6244007	CP015992.1
Paenibacillus sp. BIHB4019, complete genome	NA	1870819	30.2	30.2	78%	735	100.00	7246671	CP016808.1
Comamonas aquatica strain CJG genome	NA	225991	30.2	60.5	100 %	735	100.00	3764434	CP016603.1

Fictibacillus arsenicus strain G25-54, complete genome	NA	255247	30.2	30.2	78%	735	100.00	4055461	CP016761.1
Serratia marcescens isolate PWN146_assembly genome assembly,...	NA	615	30.2	30.2	78%	735	100.00	5485668	LT575490.1
Escherichia coli strain K-15KW01, complete genome	NA	562	30.2	30.2	78%	735	100.00	5154641	CP016358.1
Escherichia coli strain ECONIH2, complete genome	NA	562	30.2	30.2	78%	735	100.00	5116831	CP014667.1
Rhizobium phaseoli strain N161, complete genome	NA	396	30.2	30.2	78%	735	100.00	4514436	CP013585.1
Rhizobium phaseoli strain N261, complete genome	NA	396	30.2	30.2	78%	735	100.00	4458726	CP013580.1
Rhizobium phaseoli strain N671, complete genome	NA	396	30.2	30.2	78%	735	100.00	4394011	CP013574.1
Rhizobium phaseoli strain N771, complete genome	NA	396	30.2	30.2	78%	735	100.00	4394302	CP013568.1
Rhizobium phaseoli strain N831, complete genome	NA	396	30.2	30.2	78%	735	100.00	4353903	CP013563.1
Rhizobium phaseoli strain N841, complete genome	NA	396	30.2	30.2	78%	735	100.00	4384120	CP013557.1
Rhizobium phaseoli strain N931, complete genome	NA	396	30.2	30.2	78%	735	100.00	4353948	CP013552.1
Rhizobium phaseoli strain R611, complete genome	NA	396	30.2	30.2	78%	735	100.00	4534235	CP013547.1
Rhizobium phaseoli strain R620, complete genome	NA	396	30.2	30.2	78%	735	100.00	4424308	CP013542.1
Rhizobium phaseoli strain R630, complete genome	NA	396	30.2	30.2	78%	735	100.00	4398888	CP013537.1
Rhizobium phaseoli strain R650, complete genome	NA	396	30.2	30.2	78%	735	100.00	4534235	CP013532.1
Rhizobium phaseoli strain R723, complete genome	NA	396	30.2	30.2	78%	735	100.00	4458723	CP013527.1
Rhizobium phaseoli strain R744, complete genome	NA	396	30.2	30.2	78%	735	100.00	4459165	CP013522.1
PREDICTED: Drosophila rhopaloa odorant receptor 42b...	NA	1041015	30.2	30.2	78%	735	100.00	1211	XM_017115062.1
Pseudomonas silesiensis strain A3, complete genome	NA	1853130	30.2	30.2	78%	735	100.00	6823539	CP014870.1
Dickeya solani IPO 2222, complete genome	NA	1225786	30.2	30.2	78%	735	100.00	4919833	CP015137.1
Cladophialophora bantiana CBS 173.52 hypothetical protein...	NA	1442370	30.2	30.2	78%	735	100.00	1155	XM_016761693.1
Abalone herpesvirus Taiwan/2005, partial genome	NA	1821058	30.2	30.2	78%	735	100.00	199102	KU096999.1
Acinetobacter sp. TGL-Y2, complete genome	NA	1407071	30.2	30.2	78%	735	100.00	3383728	CP015110.1
Zhongshania aliphaticivorans strain SM2, complete genome	NA	1470434	30.2	30.2	78%	735	100.00	4204359	CP014544.1
Enterobacter sp. FY-07, complete genome	NA	1692238	30.2	30.2	78%	735	100.00	5118646	CP012487.1
Klebsiella aerogenes strain G7 chromosome, complete genome	NA	548	30.2	30.2	78%	735	100.00	5452368	CP011539.1
PREDICTED: Panthera tigris altaica beta-site APP-cleaving enzy...	Amur tiger	74533	30.2	30.2	78%	735	100.00	2757	XM_015541200.1
Pseudomonas agarici strain NCPPB 2472 genome	NA	46677	30.2	30.2	78%	735	100.00	5502003	CP014135.1
PREDICTED: Lepisosteus oculatus ataxin 3 (atxn3), transcript...	spotted gar	7918	30.2	30.2	78%	735	100.00	2269	XM_015350922.1
PREDICTED: Lepisosteus	spotted gar	7918	30.2	30.2	78%	735	100.00	2349	XM_015350921.1

oculatus ataxin 3 (atxn3), transcript...									
Arthrobacter sp. A3, complete genome	NA	656366	30.2	30.2	78%	735	100.00	4264061	CP013745.1
Streptomyces globisporus C-1027, complete genome	NA	1172567	30.2	30.2	78%	735	100.00	7608611	CP013738.1
Herbaspirillum rubrisubalbicans M1, complete genome	NA	1078773	30.2	30.2	78%	735	100.00	5611261	CP013737.1
Cutibacterium acnes strain PA_15_1_R1 chromosome, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2493976	CP012355.1
Cutibacterium acnes strain PA_12_1_L1 chromosome, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2491961	CP012354.1
Cutibacterium acnes strain PA_12_1_R1 chromosome, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2470017	CP012353.1
Cutibacterium acnes strain PA_15_2_L1 chromosome, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2540008	CP012352.1
Cutibacterium acnes strain PA_21_1_L1 chromosome, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2560354	CP012351.1
Cutibacterium acnes strain PA_30_2_L1 chromosome, complete genome	NA	1747	30.2	30.2	78%	735	100.00	2530708	CP012350.1
PREDICTED: Poecilia latipinna sterile alpha motif domain...	sailfin molly	48699	30.2	30.2	78%	735	100.00	3159	XM_015054560.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : II	NA	305	30.2	30.2	78%	735	100.00	5839544	LN899820.1
Arthrobacter sp. YC-RL1, complete genome	NA	1652545	30.2	30.2	78%	735	100.00	3846272	CP013297.1
Mixia osmundae IAM 14324 hypothetical protein mRNA	NA	764103	30.2	30.2	78%	735	100.00	1380	XM_014713812.1
Mixia osmundae IAM 14324 hypothetical protein partial mRNA	NA	764103	30.2	30.2	78%	735	100.00	2226	XM_014711764.1
Azospirillum brasilense strain Sp7, complete sequence	NA	192	30.2	30.2	78%	735	100.00	3005726	CP012914.1
Oryza sativa Japonica Group DNA, chromosome 11, cultivar:...	Japanese rice	39947	30.2	30.2	78%	735	100.00	29021106	AP014967.1
PREDICTED: Haplochromis burtoni obscurin-like (LOC102293393),...	Burton's mou...	8153	30.2	30.2	78%	735	100.00	2341	XM_005951928.2
Psychrobacter urativorans strain R10.10B, complete genome	NA	45610	30.2	30.2	78%	735	100.00	2802354	CP012678.1
Arthrobacter sp. LS16, complete genome	NA	1690248	30.2	30.2	78%	735	100.00	3851242	CP012171.1
PREDICTED: Apteryx australis mantelli nuclear factor I/C...	NA	202946	30.2	30.2	78%	735	100.00	1485	XM_013944528.1
Litopenaeus vannamei 5'-nucleotidase domain-containing protein...	Pacific whit...	6689	30.2	30.2	78%	735	100.00	1960	KR676450.1
Nitrospira moscoviensis strain NSP M-1, complete genome	NA	42253	30.2	30.2	78%	735	100.00	4589485	CP011801.1
Moorella thermoacetica strain DSM 2955, complete genome	NA	1525	30.2	30.2	78%	735	100.00	2623349	CP012370.1
Moorella thermoacetica strain DSM 521, complete genome	NA	1525	30.2	30.2	78%	735	100.00	2527564	CP012369.1
Chondromyces crocatus strain Cm c5, complete genome	NA	52	30.2	30.2	78%	735	100.00	11388132	CP012159.1
Leptospirillum sp. Group II 'CF-1',	NA	1660083	30.2	30.2	78%	735	100.00	2709324	CP012147.1

complete genome									
HIV-1 isolate Chronic-AIDS17 from Cuba envelope glycoprotein...	NA	11676	30.2	30.2	78%	735	100.00	234	KP688216.1
Ovis canadensis canadensis isolate 43U chromosome 11 sequence	NA	112262	30.2	30.2	78%	735	100.00	62327148	CP011896.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	78%	735	100.00	22853255	LK064812.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	78%	735	100.00	42151	LK066650.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	78%	735	100.00	197644	LK064772.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	78%	735	100.00	9561987	LK064687.1
Thioalkalivibrio versutus strain D301, complete genome	NA	106634	30.2	30.2	78%	735	100.00	2969361	CP011367.1
Coccidioides immitis RS sorting nexin 3 (CIMG_00609), mRNA	NA	246410	30.2	30.2	78%	735	100.00	2039	XM_001246837.2
Fibroporia radiculosa predicted protein partial mRNA	NA	599839	30.2	30.2	78%	735	100.00	1125	XM_012323924.1
Uncultured bacterium clone contig18333 genomic sequence	NA	77133	30.2	30.2	78%	735	100.00	482	KP437236.1
Paraburkholderia fungorum strain ATCC BAA-463 chromosome 1,...	NA	134537	30.2	30.2	78%	735	100.00	4463161	CP010026.1
Burkholderia ambifaria AMMD chromosome 1, complete sequence	NA	339670	30.2	30.2	78%	735	100.00	3556555	CP009798.1
Rhizobium etli bv. phaseoli str. IE4803, complete genome	NA	1432049	30.2	30.2	78%	735	100.00	4598466	CP007641.1
Bradyrhizobium japonicum strain E109, complete genome	NA	375	30.2	30.2	78%	735	100.00	9224208	CP010313.1
Burkholderiales bacterium GJ-E10 DNA, complete genome	NA	1469502	30.2	30.2	78%	735	100.00	3276549	AP014683.1
Theileria orientalis strain Shintoku conserved hypothetical...	NA	869250	30.2	30.2	78%	735	100.00	8181	XM_009693583.1
Theileria orientalis strain Shintoku conserved hypothetical...	NA	869250	30.2	30.2	78%	735	100.00	6597	XM_009693544.1
Theileria orientalis strain Shintoku conserved hypothetical...	NA	869250	30.2	30.2	78%	735	100.00	8079	XM_009692339.1
PREDICTED: Struthio camelus australis nuclear factor I/C...	NA	441894	30.2	30.2	78%	735	100.00	1538	XM_009672862.1
Sphingomonas taxi strain ATCC 55669, complete genome	NA	1549858	30.2	30.2	78%	735	100.00	3859099	CP009571.1
Fonticula alba hypothetical protein mRNA	NA	691883	30.2	30.2	78%	735	100.00	2555	XM_009497625.1
Fonticula alba hypothetical protein mRNA	NA	691883	30.2	30.2	78%	735	100.00	2591	XM_009494177.1
Pseudomonas rhizosphaerae strain DSM 16299, complete genome	NA	216142	30.2	30.2	78%	735	100.00	4688635	CP009533.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	78%	735	100.00	1062	LN291765.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	78%	735	100.00	2172	LN169805.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	78%	735	100.00	3307	LN112703.1
Spirometra erinaceieuropaei genome assembly	NA	99802	30.2	30.2	100%	735	94.74	8054	LN028521.1

S_erinaceieuropaei...									
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	78%	735	100.00	13097	LN008572.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	78%	735	100.00	1172	LN272131.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common carp	7962	30.2	30.2	78%	735	100.00	553853	LN590794.1
Serratia sp. SCBI, complete genome	NA	488142	30.2	30.2	78%	735	100.00	5034688	CP003424.1
Ochrobactrum anthropi strain OAB chromosome 1, complete sequence	NA	529	30.2	30.2	78%	735	100.00	2708454	CP008820.1
Ralstonia phage RSY1 DNA, complete genome	NA	1530085	30.2	30.2	78%	735	100.00	40002	AB981169.1
Candidatus Nitrososphaera evergladensis SR1, complete genome	NA	1459636	30.2	30.2	78%	735	100.00	2954373	CP007174.1
Alcanivorax sp. NBRC 101098 DNA, complete genome	NA	1113728	30.2	30.2	78%	735	100.00	3095417	AP014613.1
Propionibacterium acnes hdn-1, complete genome	NA	1276648	30.2	30.2	78%	735	100.00	2494562	CP006032.1
Nitrososphaera viennensis EN76, complete genome	NA	926571	30.2	30.2	78%	735	100.00	2527938	CP007536.1
Rhizobium sp. IE4771 chromosome, complete genome	NA	1301032	30.2	30.2	78%	735	100.00	4475387	CP006986.1
Rhodosporidium toruloides strain CECT1137, genomic scaffold,...	NA	5286	30.2	30.2	78%	735	100.00	1440573	LK052938.1
Pseudomonas sp. WCS374 genome	NA	1495331	30.2	30.2	78%	735	100.00	6085054	CP007638.1
Leptospirillum ferriphilum YSK, complete genome	NA	1441628	30.2	30.2	78%	735	100.00	2330585	CP007243.1
Pseudomonas mandelii JR-1, complete genome	NA	1147786	30.2	30.2	78%	735	100.00	6778052	CP005960.1
Metarhizium acridum CQMa 102 F-box domain protein partial mRNA	NA	655827	30.2	30.2	78%	735	100.00	3525	XM_007814305.1
Coniophora puteana RWD-64-598 SS2 AAA-domain-containing protei...	NA	741705	30.2	30.2	78%	735	100.00	1592	XM_007769780.1
Cladophialophora yegresii CBS 114405 hypothetical protein...	NA	1182544	30.2	30.2	78%	735	100.00	4425	XM_007755985.1
Bradyrhizobium japonicum SEMIA 5079 genome	NA	476282	30.2	30.2	78%	735	100.00	9583027	CP007569.1
Candidatus Phaeomarinobacter ectocarpi complete genome	NA	1458461	30.2	30.2	78%	735	100.00	3415905	HG966617.1
Punctularia strigosozonata HHB-11173 SS5 tricalbin...	NA	741275	30.2	30.2	78%	735	100.00	4728	XM_007378525.1
Dichomitus squalens LYAD-421 SS1 pre-mRNA-splicing ATP-depende...	NA	732165	30.2	30.2	78%	735	100.00	2506	XM_007361173.1
Fomitiporia mediterranea MF3/22 MT-A70-domain-containing prote...	NA	694068	30.2	30.2	78%	735	100.00	1041	XM_007268234.1
Thalassolituus oleivorans R6-15, complete genome	NA	1208320	30.2	30.2	78%	735	100.00	3764053	CP006829.1
HIV-1 isolate S202022_39_MXR02_1 from Botswana envelope...	NA	11676	30.2	30.2	78%	735	100.00	1167	KF374291.1
Ruegeria pomeroyi DSS-3, complete genome	NA	246200	30.2	30.2	78%	735	100.00	4109437	CP000031.2

PREDICTED: Pundamilia nyererei sterile alpha motif domain...	NA	303518	30.2	30.2	78%	735	100.00	2516	XM_005740435.1
PREDICTED: Pundamilia nyererei sterile alpha motif domain...	NA	303518	30.2	30.2	78%	735	100.00	2319	XM_005740433.1
TPA: Myoviridae sp. isolate ctckC3, partial genome	NA	2202564	30.2	30.2	78%	735	100.00	39749	BK038103.1
Ruegeria pomeroyi strain DSS-3-B chromosome, complete genome	NA	89184	30.2	30.2	78%	735	100.00	4131101	CP076685.1
Paenibacillus sophorae strain DSM 23020 chromosome, complete...	NA	1333845	30.2	30.2	78%	735	100.00	5867720	CP076607.1
TPA: Siphoviridae sp. ctoD011, partial genome	NA	2828226	30.2	30.2	78%	735	100.00	41636	BK031254.1
Dickeya dadantii strain S3-1 chromosome, complete genome	NA	204038	30.2	30.2	78%	735	100.00	5065613	CP076386.1
TPA: Bacteriophage sp. isolate ctBkl3, partial genome	NA	38018	30.2	30.2	78%	735	100.00	24127	BK020204.1
TPA: Myoviridae sp. isolate ctjSP30, partial genome	NA	2202564	30.2	30.2	78%	735	100.00	40849	BK017714.1
Salmonella enterica strain CFSAN044888 chromosome, complete...	NA	28901	30.2	30.2	78%	735	100.00	4866315	CP075135.1
Gemmobacter sp. con5 chromosome, complete genome	NA	2840474	30.2	30.2	78%	735	100.00	3376470	CP076361.1
Salmonella enterica subsp. diarizonae strain CFSAN030538...	NA	59204	30.2	30.2	78%	735	100.00	4888508	CP075144.1
Salmonella enterica subsp. enterica serovar Rubislaw strain...	NA	598	30.2	30.2	78%	735	100.00	4863823	CP075129.1
Salmonella enterica strain CFSAN044945 chromosome, complete...	NA	28901	30.2	30.2	78%	735	100.00	4872383	CP075125.1
Salmonella enterica strain CFSAN029856 chromosome, complete...	NA	28901	30.2	30.2	78%	735	100.00	4595940	CP074653.1
Salmonella enterica strain CFSAN029865 chromosome, complete...	NA	28901	30.2	30.2	78%	735	100.00	4821427	CP074640.1
Salmonella enterica strain CFSAN029872 chromosome, complete...	NA	28901	30.2	30.2	78%	735	100.00	5041511	CP074633.1
Bradyrhizobium sp. S2-11-4 chromosome, complete genome	NA	2840473	30.2	30.2	78%	735	100.00	5477950	CP076136.1
Bradyrhizobium sp. S2-20-1 chromosome, complete genome	NA	2840469	30.2	30.2	78%	735	100.00	5554208	CP076134.1
Amycolatopsis sp. CA-230715 chromosome, complete genome	NA	2745196	30.2	30.2	78%	735	100.00	10363158	CP059997.1
Escherichia coli strain F11 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	5048308	CP076123.1
PREDICTED: Chelmon rostratus sterile alpha motif domain...	copperband b...	109905	30.2	30.2	78%	735	100.00	592	XM_041946601.1
Methanoculleus chikugoensis MG62 DNA, complete genome	NA	118126	30.2	30.2	78%	735	100.00	2622259	AP019781.1
Klebsiella pneumoniae strain RGF99-1 chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5205681	CP075552.1
Citrobacter freundii strain Colony300 chromosome	NA	546	30.2	30.2	78%	735	100.00	5016456	CP075521.1
PREDICTED: Drosophila kikkawai methionine-R-sulfoxide reductas...	NA	30033	30.2	30.2	78%	735	100.00	1465	XM_017176717.2
PREDICTED: Drosophila kikkawai methionine-R-sulfoxide reductas...	NA	30033	30.2	30.2	78%	735	100.00	1180	XM_017176716.2
PREDICTED: Drosophila kikkawai	NA	30033	30.2	30.2	78%	735	100.00	1227	XM_017176714.2

methionine-R-sulfoxide reductas...									
Salmonella enterica strain CFSAN029939 chromosome, complete...	NA	28901	30.2	30.2	78%	735	100.00	5033792	CP074623.1
Klebsiella pneumoniae strain RGF172-1 chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5205169	CP075275.1
Ochrobactrum sp. WY7 chromosome 1, complete sequence	NA	2708351	30.2	30.2	78%	735	100.00	2785871	CP049796.1
Pseudomonas lalucatii strain R1b52 chromosome	NA	1424203	30.2	30.2	78%	735	100.00	4619889	CP065340.1
Coccidioides posadasii str. Silveira chromosome 3	NA	443226	30.2	30.2	78%	735	100.00	6494557	CP075070.1
Eristalis pertinax genome assembly, chromosome: 5	NA	1572519	30.2	30.2	78%	735	100.00	72030237	OU026149.1
Eristalis pertinax genome assembly, chromosome: 4	NA	1572519	30.2	30.2	78%	735	100.00	73956772	OU026148.1
Eristalis pertinax genome assembly, chromosome: 2	NA	1572519	30.2	30.2	78%	735	100.00	79216483	OU026146.1
Blastobasis adustella genome assembly, chromosome: 9	NA	1869501	30.2	60.5	78%	735	100.00	20350496	OU026122.1
Danio rerio strain T5D chromosome 23	zebrafish	7955	30.2	30.2	78%	735	100.00	46207417	CP068757.1
Brachyptera putata genome assembly, chromosome: 13	NA	2065413	30.2	30.2	78%	735	100.00	16273929	OU015474.1
uncultured Rhodocyclaceae bacterium isolate DEC001_d71 genome...	NA	151985	30.2	30.2	78%	735	100.00	3463890	OU015322.1
Oikopleura dioica genome assembly, segment: PAR	NA	34765	30.2	30.2	78%	735	100.00	17092476	OU015568.1
PREDICTED: Ochotona princeps SLX1 homolog A, structure-specifi...	American pika	9978	30.2	30.2	78%	735	100.00	831	XM_004587128.1
Candidatus Saccharimonas aalborgensis isolate TM71 chromosome,...	NA	1332188	30.2	30.2	78%	735	100.00	1013781	CP005957.1
PREDICTED: Maylandia zebra sterile alpha motif domain containi...	zebra mbuna	106582	30.2	30.2	78%	735	100.00	2313	XM_004545986.1
Klebsiella sp. A52 chromosome, complete genome	NA	2834819	30.2	30.2	78%	735	100.00	5079954	CP074437.1
Shewanella algae TUM17378 DNA, complete genome	NA	38313	30.2	30.2	78%	735	100.00	4872739	AP024612.1
Salmonella enterica subsp. enterica serovar Rubislaw strain...	NA	598	30.2	30.2	78%	735	100.00	4649854	CP074267.1
PREDICTED: Gigantopelta aegis uncharacterized LOC121376191...	NA	1735272	30.2	30.2	78%	735	100.00	5331	XR_005958412.1
PREDICTED: Gigantopelta aegis uncharacterized LOC121376191...	NA	1735272	30.2	30.2	78%	735	100.00	4337	XR_005958411.1
PREDICTED: Gigantopelta aegis uncharacterized LOC121376191...	NA	1735272	30.2	30.2	78%	735	100.00	4449	XR_005958410.1
Chloracidobacterium sp. E chromosome 1, complete sequence	NA	2821541	30.2	30.2	78%	735	100.00	2677644	CP072644.1
Chloracidobacterium sp. N chromosome 1, complete sequence	NA	2821540	30.2	30.2	78%	735	100.00	2639773	CP072642.1
Chloracidobacterium sp. A chromosome 1, complete sequence	NA	2821539	30.2	30.2	78%	735	100.00	2661451	CP072640.1

Chloracidobacterium sp. S chromosome 1, complete sequence	NA	2821538	30.2	30.2	78%	735	100.00	2651488	CP072638.1
Chloracidobacterium sp. 2 chromosome 1, complete sequence	NA	2821537	30.2	30.2	78%	735	100.00	2663316	CP072636.1
Chloracidobacterium sp. D chromosome 1, complete sequence	NA	2821536	30.2	30.2	78%	735	100.00	2641344	CP072634.1
Chloracidobacterium thermophilum strain B chromosome 1, comple...	NA	458033	30.2	30.2	78%	735	100.00	2704697	CP072632.1
Klebsiella aerogenes strain Ka30434 chromosome	NA	548	30.2	30.2	78%	735	100.00	5116273	CP073780.1
PREDICTED: Polyodon spathula brain-specific angiogenesis...	Mississippi ...	7913	30.2	30.2	78%	735	100.00	3026	XM_041232402.1
Pseudomonas sp. Ost2 DNA, complete genome	NA	2678260	30.2	30.2	78%	735	100.00	7357961	AP021904.1
Salmonella enterica subsp. enterica strain B50 chromosome,...	NA	59201	30.2	30.2	78%	735	100.00	4875109	CP073323.1
Citrobacter amalonaticus JCM 1661 DNA, complete genome	NA	35703	30.2	30.2	78%	735	100.00	4717872	AP024585.1
PREDICTED: Toxotes jaculatrix sterile alpha motif domain...	banded arche...	941984	30.2	30.2	78%	735	100.00	645	XM_041055976.1
PREDICTED: Toxotes jaculatrix plakophilin-1 (LOC121189643),...	banded arche...	941984	30.2	30.2	78%	735	100.00	4852	XM_041050026.1
PREDICTED: Toxotes jaculatrix plakophilin-1 (LOC121189643),...	banded arche...	941984	30.2	30.2	78%	735	100.00	4962	XM_041050017.1
PREDICTED: Toxotes jaculatrix plakophilin-1 (LOC121189643),...	banded arche...	941984	30.2	30.2	78%	735	100.00	5001	XM_041050009.1
PREDICTED: Toxotes jaculatrix plakophilin-1 (LOC121189643),...	banded arche...	941984	30.2	30.2	78%	735	100.00	5006	XM_041049999.1
PREDICTED: Toxotes jaculatrix plakophilin-1 (LOC121189643),...	banded arche...	941984	30.2	30.2	78%	735	100.00	5154	XM_041049991.1
PREDICTED: Toxotes jaculatrix WSC domain containing 1b (wscd1b...	banded arche...	941984	30.2	30.2	78%	735	100.00	1722	XM_041051879.1
Clostridiales bacterium strain R-7 chromosome, complete genome	NA	1898207	30.2	30.2	78%	735	100.00	3390518	CP068393.1
Prevotella nigrescens strain F0109 chromosome 1, complete...	NA	28133	30.2	30.2	78%	735	100.00	2227666	CP072339.1
Prevotella nigrescens strain F0630 chromosome 1, complete...	NA	28133	30.2	30.2	78%	735	100.00	2204083	CP072335.1
Aspergillus ruber CBS 135680 Vps5-domain-containing protein...	NA	1388766	30.2	30.2	78%	735	100.00	1698	XM_040779222.1
Cucurbitaria berberidis CBS 394.84 uncharacterized protein...	NA	1168544	30.2	30.2	78%	735	100.00	588	XM_040933534.1
PREDICTED: Ochotona curzoniae probable E3 ubiquitin-protein...	black-lipped...	130825	30.2	30.2	78%	735	100.00	3134	XM_040997723.1
PREDICTED: Ochotona curzoniae probable E3 ubiquitin-protein...	black-lipped...	130825	30.2	30.2	78%	735	100.00	3275	XM_040997722.1
PREDICTED: Ochotona curzoniae SLX1 homolog A, structure-specif...	black-lipped...	130825	30.2	30.2	78%	735	100.00	1555	XM_040973094.1
PREDICTED: Ochotona curzoniae SLX1 homolog A, structure-specif...	black-lipped...	130825	30.2	30.2	78%	735	100.00	1903	XM_040973093.1
PREDICTED: Ochotona curzoniae probable E3 ubiquitin-protein...	black-lipped...	130825	30.2	30.2	78%	735	100.00	3134	XM_040972834.1
PREDICTED: Ochotona curzoniae probable E3 ubiquitin-protein...	black-lipped...	130825	30.2	30.2	78%	735	100.00	3275	XM_040972833.1

Comamonas aquatica strain NEB418 chromosome, complete genome	NA	225991	30.2	30.2	100 %	735	94.74	3969186	CP072916.1
Thiothrix sp. strain A52 chromosome, complete genome	NA	1032	30.2	30.2	78%	735	100.00	3546315	CP072800.1
PREDICTED: Gallus gallus poly(rC) binding protein 4 (PCBP4),...	chicken	9031	30.2	30.2	78%	735	100.00	1708	XM_040681899.1
PREDICTED: Gallus gallus poly(rC) binding protein 4 (PCBP4),...	chicken	9031	30.2	30.2	78%	735	100.00	2743	XM_040681898.1
PREDICTED: Gallus gallus poly(rC) binding protein 4 (PCBP4),...	chicken	9031	30.2	30.2	78%	735	100.00	2348	XM_040681897.1
PREDICTED: Gallus gallus poly(rC) binding protein 4 (PCBP4),...	chicken	9031	30.2	30.2	78%	735	100.00	2327	XM_040681896.1
PREDICTED: Gallus gallus poly(rC) binding protein 4 (PCBP4),...	chicken	9031	30.2	30.2	78%	735	100.00	1732	XM_040646560.1
PREDICTED: Gallus gallus poly(rC) binding protein 4 (PCBP4),...	chicken	9031	30.2	30.2	78%	735	100.00	2743	XM_040646559.1
PREDICTED: Gallus gallus poly(rC) binding protein 4 (PCBP4),...	chicken	9031	30.2	30.2	78%	735	100.00	2350	XM_015292855.3
PREDICTED: Gallus gallus poly(rC) binding protein 4 (PCBP4),...	chicken	9031	30.2	30.2	78%	735	100.00	2329	XM_015292856.3
Sus scrofa scrofa breed NS chromosome 18	NA	415978	30.2	30.2	78%	735	100.00	57355364	CP071569.1
PREDICTED: **Falco** naumanni mitochondrial antiviral signaling...	lesser kestrel	148594	30.2	30.2	78%	735	100.00	5388	XM_040591150.1
PREDICTED: **Falco** naumanni mitochondrial antiviral signaling...	lesser kestrel	148594	30.2	30.2	78%	735	100.00	5161	XM_040591139.1
PREDICTED: **Falco** naumanni mitochondrial antiviral signaling...	lesser kestrel	148594	30.2	30.2	78%	735	100.00	5038	XM_040591128.1
PREDICTED: **Falco** naumanni mitochondrial antiviral signaling...	lesser kestrel	148594	30.2	30.2	78%	735	100.00	5599	XM_040591118.1
Aphantopus hyperantus genome assembly, chromosome: 22	ringlet	2795564	30.2	30.2	78%	735	100.00	11669538	LR761669.2
Nitratireductor sp. isolate pb3 chromosome	NA	1872084	30.2	30.2	78%	735	100.00	3707227	CP051236.1
Ochrobactrum sp. EEELCW01 chromosome 1, complete sequence	NA	2696486	30.2	30.2	78%	735	100.00	2649164	CP047598.1
Klebsiella aerogenes strain G3_AM chromosome	NA	548	30.2	30.2	78%	735	100.00	5275806	CP072327.1
Leptidea sinapis genome assembly, chromosome: 24	NA	189913	30.2	30.2	78%	735	100.00	13606782	FR990177.1
Leptidea sinapis genome assembly, chromosome: Z	NA	189913	30.2	30.2	78%	735	100.00	36552532	FR990153.1
Ochlodes sylvanus genome assembly, chromosome: 15	NA	876063	30.2	30.2	78%	735	100.00	12826862	FR990138.1
Hedya salicella genome assembly, chromosome: 24	NA	1869985	30.2	30.2	78%	735	100.00	12337303	FR990120.1
Hedya salicella genome assembly, chromosome: 1	NA	1869985	30.2	30.2	78%	735	100.00	52607617	FR990097.1
Erannis defoliaria genome assembly, chromosome: 5	NA	104474	30.2	30.2	78%	735	100.00	21037887	FR990071.1
Erannis defoliaria genome assembly, chromosome: 1	NA	104474	30.2	30.2	78%	735	100.00	26948889	FR990066.1

Plebejus argus genome assembly, chromosome: 9	NA	242267	30.2	30.2	78%	735	100.00	16721534	FR989935.1
Plebejus argus genome assembly, chromosome: 8	NA	242267	30.2	30.2	78%	735	100.00	17023672	FR989934.1
Pheosia gnoma genome assembly, chromosome: 18	NA	988018	30.2	30.2	78%	735	100.00	8904324	FR989912.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	2731	XM_040424353.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	3420	XM_040424352.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	3444	XM_040424351.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	3517	XM_040424350.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	3530	XM_040424349.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	3647	XM_040424348.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	3606	XM_040424347.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	3534	XM_040424346.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	3549	XM_040424345.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	3558	XM_040424344.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	3600	XM_040424343.1
PREDICTED: Bufo bufo protein 4.1-like (LOC120995258), transcri...	common toad	8384	30.2	30.2	78%	735	100.00	3663	XM_040424342.1
Meleagris gallopavo genome assembly, chromosome: 16	turkey	9103	30.2	30.2	78%	735	100.00	15176134	HG999696.1
Meleagris gallopavo genome assembly, chromosome: 15	turkey	9103	30.2	30.2	78%	735	100.00	17861904	HG999695.1
Shewanella algae strain A59 chromosome, complete genome	NA	38313	30.2	30.2	78%	735	100.00	4817651	CP068227.1
Acinetobacter towneri strain GX7 chromosome, complete genome	NA	202956	30.2	30.2	78%	735	100.00	2841560	CP071771.1
Ottowia sp. 27C chromosome, complete genome	NA	2816950	30.2	30.2	78%	735	100.00	4320685	CP071796.1
Acinetobacter towneri strain GX5 chromosome, complete genome	NA	202956	30.2	30.2	78%	735	100.00	2630890	CP071770.1
Acinetobacter towneri strain GX3 chromosome, complete genome	NA	202956	30.2	30.2	78%	735	100.00	2597534	CP071766.1
PREDICTED: Xiphias gladius WSC domain containing 1b (wscd1b),...	swordfish	8245	30.2	30.2	78%	735	100.00	2270	XM_040150907.1
Podospora comata strain Wa139-chromosome 2, complete sequence	NA	48703	30.2	30.2	78%	735	100.00	5055838	CP071494.1

PREDICTED: Simochromis diagramma sterile alpha motif domain...	NA	43689	30.2	30.2	78%	735	100.00	2479	XM_040008324.1
PREDICTED: Simochromis diagramma obscurin-like (LOC120737772),...	NA	43689	30.2	30.2	78%	735	100.00	3600	XM_040038633.1
Pheosia tremula genome assembly, chromosome: 18	NA	988019	30.2	30.2	78%	735	100.00	9468769	HG995415.1
HIV-1 isolate T256254_03 from Thailand envelope glycoprotein...	NA	11676	30.2	30.2	78%	735	100.00	2589	KC748973.1
Propionibacterium acnes HL096PA1, complete genome	NA	1134454	30.2	30.2	78%	735	100.00	2494190	CP003293.1
Lycaena phlaeas genome assembly, chromosome: 1	common copper	282391	30.2	30.2	78%	735	100.00	26507414	HG995163.1
Pyrochroa serraticornis genome assembly, chromosome: 1	NA	346838	30.2	30.2	78%	735	100.00	50529459	HG995152.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	78%	735	100.00	30072609	HG994588.1
PREDICTED: Panicum virgatum B3 domain-containing protein...	switchgrass	38727	30.2	30.2	78%	735	100.00	1137	XM_039960614.1
PREDICTED: Panicum virgatum B3 domain-containing protein...	switchgrass	38727	30.2	30.2	78%	735	100.00	1246	XR_005676970.1
PREDICTED: Panicum virgatum B3 domain-containing protein...	switchgrass	38727	30.2	30.2	78%	735	100.00	1176	XM_039960613.1
PREDICTED: Panicum virgatum B3 domain-containing protein...	switchgrass	38727	30.2	30.2	78%	735	100.00	1152	XM_039960612.1
Canis lupus genome assembly, chromosome: 37	gray wolf	9612	30.2	30.2	78%	735	100.00	31495737	HG994418.1
Canis lupus genome assembly, chromosome: 31	gray wolf	9612	30.2	30.2	78%	735	100.00	44759192	HG994411.1
Canis lupus genome assembly, chromosome: 18	gray wolf	9612	30.2	30.2	78%	735	100.00	57593331	HG994402.1
Dickeya solani strain IPO2019 chromosome, complete genome	NA	1089444	30.2	30.2	78%	735	100.00	4919542	CP071062.1
Klebsiella pneumoniae strain JNQH116 chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5267247	CP070898.1
Klebsiella pneumoniae strain KP52813 chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5313559	CP070586.1
Pseudomonas sp. 15A4 chromosome, complete genome	NA	2804761	30.2	30.2	78%	735	100.00	5702273	CP068986.1
Klebsiella aerogenes strain Colony365 chromosome	NA	548	30.2	30.2	78%	735	100.00	3547674	CP070392.1
Klebsiella aerogenes strain Colony371 chromosome	NA	548	30.2	30.2	78%	735	100.00	3547674	CP070391.1
Glaciimonas sp. PAMC28666 chromosome, complete genome	NA	2807626	30.2	30.2	78%	735	100.00	5230360	CP070304.1
PREDICTED: Oreochromis aureus sterile alpha motif domain...	NA	47969	30.2	30.2	78%	735	100.00	2435	XM_031745508.2
Citrobacter sp. MGH 55 strain Colony470 chromosome	NA	1439319	30.2	30.2	78%	735	100.00	5087618	CP070239.1
Ceratobasidium sp. AG-Ba isolate LY chromosome 4	NA	170446	30.2	30.2	78%	735	100.00	3589637	CP059645.1
Klebsiella pneumoniae strain FDAARGOS_1329 chromosome, complet...	NA	573	30.2	30.2	78%	735	100.00	5379413	CP069992.1
Klebsiella pneumoniae strain FDAARGOS_1330 chromosome, complet...	NA	573	30.2	30.2	78%	735	100.00	5343616	CP070177.1
Noctua pronuba genome	large yellow...	214277	30.2	90.7	78%	735	100.00	1587969	LR999912.1

assembly, chromosome: 20								6	
Klebsiella pneumoniae strain strain	NA	573	30.2	30.2	78%	735	100.00	5351626	LR991401.1
Pieris napi genome assembly, chromosome: 9	NA	78633	30.2	30.2	78%	735	100.00	13392396	HG993171.1
Pyrenophora teres f. teres isolate W1-1 genome assembly,...	NA	97479	30.2	30.2	78%	735	100.00	7266427	HG992977.1
Nymphalis polychloros genome assembly, chromosome: 30	blackleg tor...	171594	30.2	30.2	78%	735	100.00	6077673	HG992271.1
Lysandra coridon genome assembly, chromosome: 68	NA	268709	30.2	30.2	78%	735	100.00	4853177	HG992123.1
Lysandra coridon genome assembly, chromosome: 25	NA	268709	30.2	30.2	78%	735	100.00	6205132	HG992080.1
Dyadobacter sp. Q3-56 chromosome, complete genome	NA	2747268	30.2	30.2	78%	735	100.00	6071216	CP056775.1
Citrobacter portucalensis strain Colony243 chromosome	NA	1639133	30.2	30.2	78%	735	100.00	5084410	CP069766.1
Citrobacter portucalensis strain Colony224 chromosome	NA	1639133	30.2	30.2	78%	735	100.00	5079742	CP069773.1
Citrobacter freundii strain Colony431 chromosome	NA	546	30.2	30.2	78%	735	100.00	5098587	CP069777.1
Escherichia coli strain FDAARGOS_1256 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	5082895	CP069451.1
Escherichia coli strain FDAARGOS_1257 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	5218953	CP069480.1
Citrobacter sp. R56 chromosome, complete genome	NA	1573676	30.2	30.2	78%	735	100.00	4652769	CP069159.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	78%	735	100.00	30072609	LR794192.1
Rhodobacteraceae bacterium C31 chromosome, complete genome	NA	2692755	30.2	30.2	78%	735	100.00	4129092	CP047166.1
Methylobacterium aquaticum strain BG2 chromosome, complete genome	NA	270351	30.2	30.2	78%	735	100.00	6988191	CP043627.1
Escherichia coli strain RIVM_C014187 chromosome	NA	562	30.2	30.2	78%	735	100.00	3797082	CP068993.1
Escherichia coli strain RIVM_C018150 chromosome	NA	562	30.2	30.2	78%	735	100.00	4335633	CP068996.1
Escherichia coli strain RIVM_C014046 chromosome	NA	562	30.2	30.2	78%	735	100.00	1947521	CP068991.1
Digitaria exilis genome assembly, chromosome: 8B	NA	1010633	30.2	30.2	100%	735	94.74	28225861	LR994619.1
Digitaria exilis genome assembly, chromosome: 8A	NA	1010633	30.2	30.2	100%	735	94.74	30797934	LR994618.1
Digitaria exilis genome assembly, chromosome: 5B	NA	1010633	30.2	30.2	78%	735	100.00	38778756	LR994613.1
Digitaria exilis genome assembly, chromosome: 5A	NA	1010633	30.2	30.2	78%	735	100.00	40393928	LR994612.1
Digitaria exilis genome assembly, chromosome: 3A	NA	1010633	30.2	30.2	100%	735	94.74	42379666	LR994608.1
Cyaniris semiargus genome assembly, chromosome: 9	NA	988025	30.2	30.2	78%	735	100.00	19361588	LR994555.1
Escherichia coli strain RIVM_C017887 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	5227631	CP068799.1
Escherichia coli strain RIVM_C028620 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	5192168	CP068815.1
Escherichia coli strain RIVM_C028786 chromosome,	NA	562	30.2	30.2	78%	735	100.00	5220173	CP068817.1

complete genome									
Escherichia coli strain RIVM_C028724 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	5165070	CP068816.1
Escherichia coli strain RIVM_C028497 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	5086007	CP068809.1
Escherichia coli strain RIVM_C029324 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	5191412	CP068822.1
5_Tge_b3v08	NA	629358	30.2	30.2	100 %	735	94.74	264555	OE839782.1
Trachurus trachurus genome assembly, chromosome: 7	Atlantic hor...	36212	30.2	30.2	78%	735	100.00	35447499	LR991638.1
Trachurus trachurus genome assembly, chromosome: 5	Atlantic hor...	36212	30.2	30.2	78%	735	100.00	36888734	LR991633.1
Lymantria monacha genome assembly, chromosome: Z	black-arched...	78897	30.2	30.2	78%	735	100.00	62811790	LR991081.1
Notocelia uddmanniana genome assembly, chromosome: 9	NA	1594315	30.2	30.2	78%	735	100.00	29116541	LR991061.1
Mamestra brassicae genome assembly, chromosome: 25	cabbage moth	55057	30.2	30.2	78%	735	100.00	13925230	LR991012.1
Noctua fimbriata genome assembly, chromosome: 30	NA	753202	30.2	30.2	78%	735	100.00	10789098	LR990951.1
Pararge aegeria genome assembly, chromosome: 26	specked wood...	116150	30.2	30.2	78%	735	100.00	9871873	LR990917.1
Aricia agestis genome assembly, chromosome: 9	brown argus	91739	30.2	30.2	78%	735	100.00	18581481	LR990265.1
Thalassolituus oleivorans MIL-1 complete genome	NA	1298593	30.2	30.2	78%	735	100.00	3920328	HF680312.1
Enterobacter aerogenes EA1509E complete genome	NA	935296	30.2	30.2	78%	735	100.00	5419609	FO203355.1
Singulisphaera acidiphila DSM 18658, complete genome	NA	886293	30.2	30.2	78%	735	100.00	9629675	CP003364.1
Oscillatoria nigro-viridis PCC 7112 chromosome, complete genome	NA	179408	30.2	30.2	78%	735	100.00	7479014	CP003614.1
Calothrix sp. PCC 6303, complete genome	NA	1170562	30.2	30.2	78%	735	100.00	6767834	CP003610.1
Abalone herpesvirus Victoria/AUS/2009, complete genome	NA	1241371	30.2	30.2	78%	735	100.00	211518	JX453331.1
Propionibacterium acnes C1, complete genome	NA	1234380	30.2	30.2	78%	735	100.00	2519002	CP003877.1
Saccharothrix espanaensis DSM 44229 complete genome	NA	1179773	30.2	30.2	78%	735	100.00	9360653	HE804045.1
Leptospirillum ferriphilum ML-04, complete genome	NA	1048260	30.2	30.2	78%	735	100.00	2406157	CP002919.1
Theileria orientalis strain Shintoku DNA, chromosome 3, comple...	NA	869250	30.2	60.5	78%	735	100.00	2000793	AP011948.1
Theileria orientalis strain Shintoku DNA, chromosome 2, comple...	NA	869250	30.2	30.2	78%	735	100.00	2216979	AP011947.1
Human immunodeficiency virus 1 partial Env gene for envelope...	NA	11676	30.2	30.2	78%	735	100.00	390	HE972507.1
Leishmania donovani hypothetical protein, conserved...	NA	5661	30.2	30.2	78%	735	100.00	1626	XM_003863985.1
Blastobasis lacticolella genome assembly, chromosome: 11	NA	2561016	30.2	30.2	78%	735	100.00	20671567	LR990050.1
Laspeyria flexula genome assembly, chromosome: 7	NA	938238	30.2	30.2	78%	735	100.00	17356636	LR989956.1
Pieris brassicae genome assembly, chromosome: 2	large cabbag...	7116	30.2	30.2	78%	735	100.00	23112875	LR989933.1

Scaeva pyrastri genome assembly, chromosome: 3	NA	219539	30.2	30.2	78%	735	100.00	84566249	LR989929.1
Endotricha flammealis genome assembly, chromosome: 13	NA	1101095	30.2	30.2	78%	735	100.00	16153102	LR990865.1
Nibea albiflora genome assembly, chromosome: 14	white flower...	240163	30.2	30.2	78%	735	100.00	23007688	LR699037.1
Nibea albiflora genome assembly, chromosome: 7	white flower...	240163	30.2	30.2	78%	735	100.00	25201542	LR699030.1
Pseudomonas aeruginosa strain A39-1 chromosome, complete genome	NA	287	30.2	30.2	78%	735	100.00	6374121	CP068238.1
Klebsiella quasipneumoniae strain YDKL-002 chromosome, complet...	NA	1463165	30.2	30.2	78%	735	100.00	5445419	CP068237.1
Pseudomonas fluorescens strain FDAARGOS_1088 chromosome,...	NA	294	30.2	30.2	78%	735	100.00	6134597	CP068151.1
Candidatus Saccharibacteria bacterium isolate...	NA	2026720	30.2	30.2	78%	735	100.00	936132	CP065017.1
Candidatus Saccharibacteria bacterium isolate...	NA	2026720	30.2	30.2	78%	735	100.00	1006672	CP065015.1
Candidatus Saccharibacteria bacterium isolate...	NA	2026720	30.2	30.2	78%	735	100.00	979137	CP064959.1
Myxococcus xanthus strain e-3-1 chromosome, complete genome	NA	34	30.2	30.2	78%	735	100.00	9251369	CP068048.1
Klebsiella pneumoniae strain LYS105A chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5259276	CP068033.1
Lysobacter enzymogenes strain CX06 chromosome, complete genome	NA	69	30.2	30.2	78%	735	100.00	6206196	CP067396.1
Entomomonas sp. F2A chromosome, complete genome	NA	2785331	30.2	30.2	78%	735	100.00	3236906	CP067393.1
Pseudomonas sp. SW-3 chromosome, complete genome	NA	147212	30.2	30.2	78%	735	100.00	6538059	CP067098.1
PREDICTED: Canis lupus familiaris uncharacterized LOC111094361...	dog	9615	30.2	30.2	78%	735	100.00	4623	XR_005308558.1
PREDICTED: Canis lupus familiaris uncharacterized LOC111094361...	dog	9615	30.2	30.2	78%	735	100.00	4623	XR_005318356.1
PREDICTED: Scyliorhinus canicula E3 SUMO-protein ligase...	smaller spot...	7830	30.2	30.2	78%	735	100.00	2578	XR_005463135.1
Micropterus salmoides WSC domain-containing protein 1 (wscd1b)...	largemouth bass	27706	30.2	30.2	78%	735	100.00	2964	XM_038707510.1
Mycobacteroides chelonae strain Myco1 chromosome	NA	1774	30.2	30.2	78%	735	100.00	4958937	CP050223.1
Candidatus Levybacteria bacterium isolate...	NA	2052151	30.2	30.2	78%	735	100.00	762565	CP066685.1
Aspergillus felis strain FM324 chromosome 6	NA	1287682	30.2	30.2	78%	735	100.00	4028693	CP066508.1
Brucella anthropi strain FDAARGOS_1039 chromosome 1, complete...	NA	529	30.2	30.2	78%	735	100.00	2887297	CP066050.1
Burkholderia ambifaria strain FDAARGOS_1027 chromosome 1,...	NA	152480	30.2	30.2	78%	735	100.00	3556545	CP066037.1
3_Tce_b3v08	NA	61476	30.2	30.2	78%	735	100.00	325023	OC316969.1
3_Tms_b3v08	NA	170555	30.2	30.2	78%	735	100.00	108058	OB795269.1

Mesorhizobium sp. L-2-11 DNA, complete genome	NA	2744521	30.2	30.2	78%	735	100.00	6652372	AP023257.1
Citrobacter freundii strain Cfr-13 chromosome, complete genome	NA	546	30.2	30.2	78%	735	100.00	5050163	CP047773.1
Corynebacterium lizhenjunii strain ZJ-599 chromosome, complete...	NA	2709394	30.2	30.2	78%	735	100.00	2607882	CP064954.1
PREDICTED: Glossina fuscipes BTB/POZ domain-containing protein...	NA	7396	30.2	30.2	78%	735	100.00	4698	XM_038029318.1
Nitrospira sp. isolate H3_NOB1 chromosome, complete genome	NA	70125	30.2	30.2	78%	735	100.00	4156062	CP054184.1
Gammaproteobacteria bacterium isolate H2_PRO1 chromosome	NA	1913989	30.2	30.2	78%	735	100.00	3105598	CP054183.1
Ignavibacteriales bacterium isolate H2_BAC3 chromosome, comple...	NA	2049428	30.2	30.2	78%	735	100.00	4212902	CP054182.1
Nitrosomonas sp. H1_AOB3 chromosome	NA	2741553	30.2	30.2	78%	735	100.00	2841842	CP054389.1
Rhizobium phaseoli strain BS3 chromosome, complete genome	NA	396	30.2	30.2	78%	735	100.00	4537630	CP064931.1
PREDICTED: Kryptolebias marmoratus sterile alpha motif domain...	mangrove riv...	37003	30.2	30.2	78%	735	100.00	1888	XM_017414930.3
Cyprideis torosa	NA	163714	30.2	30.2	78%	735	100.00	5578	OB668962.1
Darwinula stevensoni	NA	69355	30.2	30.2	78%	735	100.00	21811	LR903997.1
PREDICTED: Penaeus monodon 5'-nucleotidase domain-containing...	black tiger ...	6687	30.2	30.2	78%	735	100.00	2122	XM_037946969.1
PREDICTED: Penaeus monodon 5'-nucleotidase domain-containing...	black tiger ...	6687	30.2	30.2	78%	735	100.00	2129	XM_037946968.1
PREDICTED: Nematolebias whitei sterile alpha motif domain...	Rio pearlfish	451745	30.2	30.2	78%	735	100.00	1174	XM_037684079.1
Klebsiella pneumoniae strain 33Kpn9 chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5464147	CP064296.1
Rhizobium sp. 007 plasmid unnamed4	NA	2785056	30.2	30.2	78%	735	100.00	441467	CP064191.1
Citrobacter amalonaticus strain CA71 chromosome, complete genome	NA	35703	30.2	30.2	78%	735	100.00	4906411	CP064180.1
Brucella anthropi strain PBO chromosome 2, complete sequence	NA	529	30.2	30.2	78%	735	100.00	2733385	CP064063.1
PREDICTED: **Falco** rusticolus mitochondrial antiviral signaling...	gyrfalcon	120794	30.2	30.2	78%	735	100.00	5361	XM_037387669.1
PREDICTED: **Falco** rusticolus mitochondrial antiviral signaling...	gyrfalcon	120794	30.2	30.2	78%	735	100.00	5158	XM_037387660.1
PREDICTED: **Falco** rusticolus mitochondrial antiviral signaling...	gyr**Falcon**	120794	30.2	30.2	78%	735	100.00	5021	XM_037387650.1
Bradyrhizobium sp. CCBAU 53421 chromosome, complete genome	NA	1325120	30.2	30.2	78%	735	100.00	9259049	CP030047.1
Klebsiella pneumoniae strain S183-1 chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5167418	CP063927.1
Klebsiella pneumoniae strain M63-1 chromosome, complete genome	NA	573	30.2	30.2	78%	735	100.00	5309740	CP063863.1
PREDICTED: Pollicipes pollicipes diacylglycerol lipase-beta-li...	NA	41117	30.2	30.2	78%	735	100.00	4282	XM_037217851.1
Rhodococcus pyridinivorans strain 5Ap chromosome, complete	NA	103816	30.2	30.2	78%	735	100.00	5220735	CP063450.1

genome									
Klebsiella pneumoniae isolate INF065-sc-2279980 genome assembl...	NA	573	30.2	30.2	78%	735	100.00	5318175	LR890665.1
Klebsiella pneumoniae isolate INF182-sc-2280049 genome assembl...	NA	573	30.2	30.2	78%	735	100.00	5369040	LR890554.1
Klebsiella pneumoniae isolate INF192-sc-2280058 genome assembl...	NA	573	30.2	30.2	78%	735	100.00	5242271	LR890225.1
Macrobrachium nipponense isolate FS-2020 chromosome 27	NA	159736	30.2	30.2	78%	735	100.00	77890169	CP062030.1
Macrobrachium nipponense isolate FS-2020 chromosome 43	NA	159736	30.2	30.2	78%	735	100.00	53539879	CP062054.1
Macrobrachium nipponense isolate FS-2020 chromosome 45	NA	159736	30.2	30.2	78%	735	100.00	52246884	CP062043.1
Macrobrachium nipponense isolate FS-2020 chromosome 37	NA	159736	30.2	30.2	78%	735	100.00	66757347	CP062039.1
Rubrivivax gelatinosus IL144 DNA, complete genome	NA	983917	30.2	30.2	78%	735	100.00	5043253	AP012320.1
Gallus gallus TAP binding protein (TAPBP), transcript variant ...	chicken	9031	30.2	30.2	78%	735	100.00	1033	NM_001206611.2
Gallus gallus TAP binding protein (TAPBP), transcript variant ...	chicken	9031	30.2	30.2	78%	735	100.00	1378	NM_001034816.3
Propionibacterium acnes TypeIA2 P.acn33, complete genome	NA	1114966	30.2	30.2	78%	735	100.00	2489623	CP003195.1
Propionibacterium acnes TypeIA2 P.acn17, complete genome	NA	1114967	30.2	30.2	78%	735	100.00	2522885	CP003196.1
Propionibacterium acnes TypeIA2 P.acn31, complete genome	NA	1114969	30.2	30.2	78%	735	100.00	2498766	CP003197.1
Leishmania donovani BPK282A1 complete genome, chromosome 33	NA	5661	30.2	30.2	78%	735	100.00	1453978	FR799620.2
Ralstonia solanacearum MAFF 301560 DNA, complete genome	NA	305	30.2	30.2	78%	735	100.00	3826386	AP024103.1
Citrobacter portucalensis STN0717-72 DNA, complete genome	NA	1639133	30.2	30.2	78%	735	100.00	5094093	AP022513.1
Citrobacter portucalensis STN0717-36 DNA, complete genome	NA	1639133	30.2	30.2	78%	735	100.00	4981812	AP022494.1
Citrobacter portucalensis STN0717-27 DNA, complete genome	NA	1639133	30.2	30.2	78%	735	100.00	4980066	AP022486.1
Citrobacter portucalensis STW0522-30 DNA, complete genome	NA	1639133	30.2	30.2	78%	735	100.00	4988881	AP022399.1
Citrobacter portucalensis STW0522-27 DNA, complete genome	NA	1639133	30.2	30.2	78%	735	100.00	5040467	AP022394.1
Citrobacter portucalensis STW0522-26 DNA, complete genome	NA	1639133	30.2	30.2	78%	735	100.00	5126826	AP022389.1
Pseudomonas allokribbensis strain IzPS23 chromosome, complete...	NA	2774460	30.2	30.2	78%	735	100.00	6565027	CP062252.1
Pseudomonas sp. IzPS59 chromosome, complete genome	NA	2774459	30.2	30.2	78%	735	100.00	6381635	CP062251.1
PREDICTED: Octopus sinensis uncharacterized LOC118763626...	East Asian c...	2607531	30.2	30.2	78%	735	100.00	2093	XR_004999387.1
PREDICTED: Octopus sinensis chitinase-like protein 3...	East Asian c...	2607531	30.2	30.2	78%	735	100.00	2969	XM_036507005.1

Paenibacillus sp. JNUCC-31 chromosome, complete genome	NA	2777983	30.2	30.2	78%	735	100.00	7551121	CP062165.1
Ochrobactrum sp. MT180101 chromosome 1, complete sequence	NA	2726427	30.2	30.2	78%	735	100.00	2794467	CP061772.1
PREDICTED: Rousettus aegyptiacus ER degradation enhancing...	Egyptian rou...	9407	30.2	30.2	78%	735	100.00	5284	XM_016133154.2
Prevotella copri strain YF2 chromosome	NA	165179	30.2	30.2	78%	735	100.00	3748729	CP042464.1
Ralstonia solanacearum strain FJAT454.F50-1 chromosome, comple...	NA	305	30.2	30.2	78%	735	100.00	3941499	CP060701.1
Leishmania chagasi strain MCER/BR/1981/M6445/Salvaterra isolat...	NA	44271	30.2	30.2	78%	735	100.00	1448125	CP048198.1
Leishmania chagasi strain MHOM/HD/2017/M32502/Amapala isolate...	NA	44271	30.2	30.2	78%	735	100.00	1448064	CP048162.1
PREDICTED: Sander lucioperca WD repeat domain 83 opposite stra...	pikeperch	283035	30.2	30.2	78%	735	100.00	875	XM_036000922.1
Pyrenophora teres f. maculata isolate P-A14 chromosome 1	NA	97480	30.2	30.2	78%	735	100.00	6261937	CP060568.1
Pyrenophora teres f. maculata isolate FGOB10Ptm-1 chromosome 1	NA	97480	30.2	30.2	78%	735	100.00	5291235	CP060556.1
Pyrenophora teres f. maculata isolate NZKF2 chromosome 1	NA	97480	30.2	30.2	78%	735	100.00	6687509	CP060547.1
Pyrenophora teres f. maculata isolate DEN2.6 chromosome 1	NA	97480	30.2	30.2	78%	735	100.00	6460204	CP060535.1
Streptomyces libani subsp. rufus NBRC 15424 plasmid pSP90 DNA,...	NA	249582	30.2	30.2	100%	735	94.74	89961	AP023409.1
Klebsiella aerogenes strain MGH232 chromosome	NA	548	30.2	30.2	78%	735	100.00	5088348	CP060486.1
Serratia marcescens strain MGH246 chromosome	NA	615	30.2	30.2	78%	735	100.00	5262921	CP060487.1
Pseudomonas protegens strain H1F10A chromosome, complete genome	NA	380021	30.2	30.2	78%	735	100.00	6817972	CP060289.1
Serratia ureilytica strain CC119 chromosome, complete genome	NA	300181	30.2	30.2	78%	735	100.00	5091032	CP060276.1
PREDICTED: Neolamprologus brichardi sterile alpha motif domain...	NA	32507	30.2	30.2	78%	735	100.00	2551	XM_006796329.2
Acomys russatus genome assembly, chromosome: 5	golden spiny...	60746	30.2	30.2	78%	735	100.00	79927262	LR877216.1
Shewanella algae strain 2NE11 chromosome, complete genome	NA	38313	30.2	30.2	78%	735	100.00	5030813	CP055159.1
Pseudomonas protegens strain H1F5C chromosome, complete genome	NA	380021	30.2	30.2	78%	735	100.00	6818519	CP060201.1
PREDICTED: Folsomia candida transmembrane protease serine...	NA	158441	30.2	30.2	78%	735	100.00	1628	XM_022096857.2
Ciceribacter thiooxidans strain F43B chromosome, complete genome	NA	1969821	30.2	30.2	78%	735	100.00	3661327	CP059896.1
Spirosoma sp. PL0136 chromosome, complete genome	NA	2710596	30.2	30.2	78%	735	100.00	8853064	CP059732.1
Pipistrellus pipistrellus genome assembly, chromosome: 16	common pipis...	59474	30.2	30.2	78%	735	100.00	46231460	LR862372.1

Gammaproteobacteria bacterium isolate MH-Pat-all_autometa_1-2...	NA	1913989	30.2	30.2	78%	735	100.00	2650119	CP046178.1
Klebsiella grimontii strain RHBSTW-00494 chromosome	NA	2058152	30.2	30.2	78%	735	100.00	6029240	CP055991.1
Citrobacter freundii strain RHB12-C12 chromosome, complete genome	NA	546	30.2	30.2	78%	735	100.00	4889917	CP057867.1
Citrobacter freundii strain RHB12-C18 chromosome, complete genome	NA	546	30.2	30.2	78%	735	100.00	4889497	CP057866.1
Citrobacter freundii strain RHB16-C09 chromosome, complete genome	NA	546	30.2	30.2	78%	735	100.00	4936996	CP057746.1
Citrobacter sp. RHB20-C15 chromosome, complete genome	NA	2742620	30.2	30.2	78%	735	100.00	4886739	CP057632.1
Citrobacter sp. RHB20-C16 chromosome, complete genome	NA	2742621	30.2	30.2	78%	735	100.00	4885668	CP057630.1
Citrobacter freundii strain RHB30-C03 chromosome, complete genome	NA	546	30.2	30.2	78%	735	100.00	5062205	CP057323.1
Citrobacter sp. RHB35-C17 chromosome, complete genome	NA	2742625	30.2	30.2	78%	735	100.00	4737278	CP057150.1
Citrobacter freundii strain RHB36-C06 chromosome, complete genome	NA	546	30.2	30.2	78%	735	100.00	5042664	CP057136.1
Bradyrhizobium japonicum strain 5038 chromosome, complete genome	NA	375	30.2	30.2	78%	735	100.00	9226248	CP058354.1
Escherichia coli strain RHBSTW-00386 chromosome, complete genome	NA	562	30.2	30.2	78%	735	100.00	4818714	CP056565.1
Klebsiella oxytoca strain RHBSTW-00432 chromosome, complete...	NA	571	30.2	30.2	78%	735	100.00	5721466	CP056539.1
Klebsiella pneumoniae strain RHBSTW-00515 chromosome, complete...	NA	573	30.2	30.2	78%	735	100.00	5494507	CP056425.1
Citrobacter freundii strain RHBSTW-00857 chromosome, complete...	NA	546	30.2	30.2	78%	735	100.00	4920836	CP056293.1
Citrobacter freundii strain RHBSTW-00858 chromosome, complete...	NA	546	30.2	30.2	78%	735	100.00	4920836	CP056289.1
Klebsiella aerogenes strain RHBSTW-00898 chromosome, complete...	NA	548	30.2	30.2	78%	735	100.00	5404196	CP056260.1
Ralstonia solanacearum strain FJAT15244-F8 chromosome, complet...	NA	305	30.2	30.2	78%	735	100.00	3787707	CP059376.1
PREDICTED: Scophthalmus maximus WSC domain containing 1b...	turbot	52904	30.2	30.2	78%	735	100.00	2891	XM_035626915.1
PREDICTED: Scophthalmus maximus WSC domain containing 1b...	turbot	52904	30.2	30.2	78%	735	100.00	2926	XM_035626914.1
PREDICTED: Scophthalmus maximus WSC domain containing 1b...	turbot	52904	30.2	30.2	78%	735	100.00	3364	XM_035626913.1
PREDICTED: Scophthalmus maximus WSC domain containing 1b...	turbot	52904	30.2	30.2	78%	735	100.00	3399	XM_035626912.1

PREDICTED: Scophthalmus maximus WSC domain containing 1b...	turbot	52904	30.2	30.2	78%	735	100.00	3459	XM_035626911.1
Citrobacter freundii strain RHBSTW-00398 chromosome, complete...	NA	546	30.2	30.2	78%	735	100.00	5067906	CP055538.1
Citrobacter freundii strain RHB16-C02 chromosome, complete genome	NA	546	30.2	30.2	78%	735	100.00	4938195	CP055702.1
Klebsiella aerogenes DNA, complete genome, strain: WP5-W18-CRE-01	NA	548	30.2	30.2	78%	735	100.00	5135838	AP022108.1
Candidatus Fermentimicrarchaeum limneticum isolate Sv326...	NA	2795018	30.2	30.2	78%	735	100.00	1178830	CP058998.1
Nostoc sp. C052 plasmid pC052_B, complete sequence	NA	2576902	30.2	30.2	78%	735	100.00	336425	CP040274.1
Paraburkholderia fungorum strain UM_TBK chromosome 1	NA	134537	30.2	30.2	78%	735	100.00	4463444	CP028829.1
Paenibacillus sp. URB8-2 DNA, complete genome	NA	2741301	30.2	30.2	78%	735	100.00	5583866	AP023239.1
Danio rerio genome assembly, chromosome: 23	zebrafish	7955	30.2	30.2	78%	735	100.00	47467499	LR812060.1
Danio rerio genome assembly, chromosome: 23	zebrafish	7955	30.2	30.2	78%	735	100.00	45104559	LR812616.1
Leishmania infantum genome assembly, chromosome: 33	NA	5671	30.2	30.2	78%	735	100.00	1532318	LR812966.1
Leishmania donovani genome assembly, chromosome: 33	NA	5661	30.2	30.2	78%	735	100.00	1553627	LR812653.1
Danio rerio strain Nadia (NA) genome assembly, chromosome: 23	zebrafish	7955	30.2	30.2	78%	735	100.00	45548233	LR812591.1
Danio rerio strain Cooch Behar (CB) genome assembly, chromosom...	zebrafish	7955	30.2	30.2	78%	735	100.00	43617724	LR812566.1
Danio kyathit genome assembly, chromosome: 8	NA	242068	30.2	30.2	78%	735	100.00	67457037	LR812526.1
Danio kyathit genome assembly, chromosome: 7	NA	242068	30.2	30.2	78%	735	100.00	89469171	LR812525.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged...	house mouse	10090	30.2	30.2	78%	735	100.00	37956	JN944968.1
Bradyrhizobium japonicum USDA 6 DNA, complete genome	NA	1037409	30.2	30.2	78%	735	100.00	9207384	AP012206.1
Chloracidobacterium thermophilum B chromosome 1, complete...	NA	981222	30.2	30.2	78%	735	100.00	2683362	CP002514.1
Myceliophthora thermophila ATCC 42464 chromosome 4, complete...	NA	573729	30.2	30.2	78%	735	100.00	4710208	CP003005.1
Myceliophthora thermophila ATCC 42464 chromosome 3, complete...	NA	573729	30.2	30.2	78%	735	100.00	5062665	CP003004.1
HIV-1 isolate 05CVHAN54 from Cape Verde envelope glycoprotein...	NA	11676	30.2	30.2	78%	735	100.00	406	JF267423.1
HIV-1 isolate 05CVHAN51 from Cape Verde envelope glycoprotein...	NA	11676	30.2	30.2	78%	735	100.00	407	JF267417.1
Abalone herpesvirus Taiwan/2004 isolate TC08, partial genome	NA	1003448	30.2	30.2	78%	735	100.00	21710	HQ890941.1
HIV-1 isolate 02PY.PSP0070 from Paraguay nonfunctional gag...	NA	11676	30.2	30.2	78%	735	100.00	8803	JN251899.1
Propionibacterium acnes 6609,	NA	1031709	30.2	30.2	78%	735	100.00	2560282	CP002815.1

complete genome									
Enterobacter aerogenes KCTC 2190, complete genome	NA	1028307	30.2	30.2	78%	735	100.00	5280350	CP002824.1
HIV-1 isolate PP45A-A0110-econBr1s1 from Kenya envelope...	NA	11676	30.2	30.2	78%	735	100.00	512	JF294818.1
Sphingobium chlorophenolicum L-1 chromosome 2, complete sequence	NA	690566	30.2	30.2	78%	735	100.00	1368670	CP002799.1
Methanobacterium paludis strain SWAN1, complete genome	NA	868131	30.2	30.2	78%	735	100.00	2546541	CP002772.1
Pseudomonas fulva 12-X, complete genome	NA	743720	30.2	30.2	78%	735	100.00	4920769	CP002727.1
Propionibacterium acnes 266, complete genome	NA	909952	30.2	30.2	78%	735	100.00	2494578	CP002409.1
Gallibacterium anatis UMN179, complete genome	NA	1005058	30.2	30.2	78%	735	100.00	2687335	CP002667.1
Gallus gallus DNA, BAC clone: 77C10 and 108G03, MHC region, fr...	chicken	9031	30.2	30.2	78%	735	100.00	167464	AP011531.1
HIV-1 isolate 07MYKT016 from Malaysia, complete genome	NA	11676	30.2	30.2	78%	735	100.00	8893	GQ175882.1
Leishmania infantum JPCM5 genome chromosome 33	NA	435258	30.2	30.2	78%	735	100.00	1448148	FR796465.1
Desulfobulbus propionicus DSM 2032, complete genome	NA	577650	30.2	30.2	78%	735	100.00	3851869	CP002364.1
Dickeya dadantii 3937, complete genome	NA	198628	30.2	30.2	78%	735	100.00	4922802	CP002038.1
Coccidioides posadasii C735 delta SOWgp PX domain containing...	NA	222929	30.2	30.2	78%	735	100.00	1895	XM_003066374.1
Fusarium vanettenii 77-13-4 uncharacterized protein...	NA	660122	30.2	30.2	78%	735	100.00	2667	XM_003045197.1
Abalone herpesvirus Victoria/AUS/2007 AbHVscaffold_3197-3033,...	NA	860344	30.2	30.2	78%	735	100.00	59682	HM631981.1
Candidatus Nitrospira defluvii chromosome, complete genome	NA	330214	30.2	30.2	78%	735	100.00	4317083	FP929003.1
Uncultured phage MedDCM-OCT-S05-C64 genomic sequence	NA	743563	30.2	30.2	78%	735	100.00	15496	GU943026.1
Propionibacterium acnes SK137, complete genome	NA	553199	30.2	30.2	78%	735	100.00	2495334	CP001977.1
Gallus gallus haplotype BR2 hypothetical protein (B-BTN2) gene...	chicken	9031	30.2	30.2	78%	735	100.00	61173	FJ770459.1
Gallus gallus haplotype BR4 hypothetical protein (B-BTN2) gene...	chicken	9031	30.2	30.2	78%	735	100.00	61406	FJ770458.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	58890	AB426154.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	59096	AB426153.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	59434	AB426152.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	58697	AB426151.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	59441	AB426150.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	59134	AB426149.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	60383	AB426148.1

Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	58685	AB426147.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	59423	AB426146.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	59361	AB426145.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	59413	AB426144.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	58942	AB426143.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	59136	AB426142.1
Gallus gallus genes, MHC region, partial and complete cds,...	chicken	9031	30.2	30.2	78%	735	100.00	58820	AB426141.1
HIV-1 isolate A097M from Kenya nonfunctional envelope...	NA	11676	30.2	30.2	78%	735	100.00	509	EU603144.1
HIV-1 isolate A027M from Kenya nonfunctional envelope...	NA	11676	30.2	30.2	78%	735	100.00	405	EU602500.1
Rhizobium etli CIAT 652, complete genome	NA	491916	30.2	30.2	78%	735	100.00	4513324	CP001074.1
Pyrenophora tritici-repentis Pt-1C-BFP long-chain-fatty-acid-C...	NA	426418	30.2	30.2	78%	735	100.00	1313	XM_001932497.1
Burkholderia ambifaria MC40-6 chromosome 1, complete sequence	NA	398577	30.2	30.2	78%	735	100.00	3443583	CP001025.1
Malassezia globosa CBS 7966 hypothetical protein MGL_4103...	NA	425265	30.2	30.2	78%	735	100.00	1581	XM_001728716.1
Canis familiaris, clone XX-92L16, complete sequence	dog	9615	30.2	30.2	78%	735	100.00	199653	AC198339.7
Xanthobacter autotrophicus Py2, complete genome	NA	78245	30.2	30.2	78%	735	100.00	5308934	CP000781.1
Parvibaculum lavamentivorans DS-1, complete genome	NA	402881	30.2	30.2	78%	735	100.00	3914745	CP000774.1
Ochrobactrum anthropi ATCC 49188 chromosome 1, complete sequence	NA	439375	30.2	30.2	78%	735	100.00	2887297	CP000758.1
Pseudomonas aeruginosa PA7, complete genome	NA	381754	30.2	30.2	78%	735	100.00	6588339	CP000744.1
Nitrosomonas europaea ATCC 19718, complete genome	NA	228410	30.2	30.2	78%	735	100.00	2812094	AL954747.1
Gallus gallus genes, MHC region, partial and complete cds	chicken	9031	30.2	30.2	78%	735	100.00	241833	AB268588.1
Thermotoga petrophila RKU-1, complete genome	NA	390874	30.2	30.2	78%	735	100.00	1823511	CP000702.1
Leishmania infantum JPCM5 conserved hypothetical protein parti...	NA	435258	30.2	30.2	78%	735	100.00	1626	XM_001468240.1
Aspergillus niger CBS 513.88 monoamine oxidase N, mRNA	NA	425011	30.2	30.2	78%	735	100.00	1488	XM_001395369.1
Aspergillus niger contig An12c0090, genomic contig	NA	5061	30.2	30.2	78%	735	100.00	115809	AM270266.1
Gallus gallus TPN gene for tapasin, haplotype B21, strain line...	chicken	9031	30.2	30.2	78%	735	100.00	5027	AM403082.1
Gallus gallus TPN gene for tapasin, haplotype B21, strain line...	chicken	9031	30.2	30.2	78%	735	100.00	5029	AM403081.1
Gallus gallus TPN gene for tapasin, haplotype Scandinavian B19...	chicken	9031	30.2	30.2	78%	735	100.00	5034	AM403080.1
Gallus gallus TPN gene for tapasin, haplotype B15, strain	chicken	9031	30.2	30.2	78%	735	100.00	5013	AM403079.1

line...									
Gallus gallus TPN gene for tapasin, haplotype B14, strain line...	chicken	9031	30.2	30.2	78%	735	100.00	5021	AM403078.1
Gallus gallus TPN gene for tapasin, haplotype B12, strain line...	chicken	9031	30.2	30.2	78%	735	100.00	5034	AM403077.1
Gallus gallus TPN gene for tapasin, haplotype B4, strain line...	chicken	9031	30.2	30.2	78%	735	100.00	5024	AM403076.1
Gallus gallus TPN gene for tapasin, haplotype B2, strain line...	chicken	9031	30.2	30.2	78%	735	100.00	5025	AM403074.1
Gallus gallus mRNA for tapasin (TPN gene), haplotype B21, stra...	chicken	9031	30.2	30.2	78%	735	100.00	1293	AM403072.1
Gallus gallus mRNA for tapasin (TPN gene), haplotype B12, stra...	chicken	9031	30.2	30.2	78%	735	100.00	1293	AM403068.1
Gallus gallus mRNA for tapasin (TPN gene), haplotype B15, stra...	chicken	9031	30.2	30.2	78%	735	100.00	1293	AM403070.1
Gallus gallus mRNA for tapasin (TPN gene), haplotype B14, stra...	chicken	9031	30.2	30.2	78%	735	100.00	1293	AM403069.1
Gallus gallus mRNA for tapasin (TPN gene), haplotype B4, strai...	chicken	9031	30.2	30.2	78%	735	100.00	1293	AM403067.1
Gallus gallus mRNA for tapasin (TPN gene), haplotype B2, strai...	chicken	9031	30.2	30.2	78%	735	100.00	1293	AM403065.1
Aspergillus niger PEPAc (pepAc) gene, complete cds	NA	5061	30.2	30.2	78%	735	100.00	7341	EF140758.1
Burkholderia ambifaria AMMD chromosome 1, complete sequence	NA	339670	30.2	30.2	78%	735	100.00	3556545	CP000440.1
Maricaulis maris MCS10 chromosome, complete genome	NA	394221	30.2	30.2	78%	735	100.00	3368780	CP000449.1
Alcanivorax borkumensis SK2, complete genome	NA	393595	30.2	30.2	78%	735	100.00	3120143	AM286690.1
HIV-1 isolate patient M59 from Brazil envelope glycoprotein...	NA	11676	30.2	30.2	78%	735	100.00	541	AY929004.1
Ralstonia solanacearum GMI1000 chromosome complete sequence	NA	267608	30.2	30.2	78%	735	100.00	3716413	AL646052.1
Chromohalobacter salexigens DSM 3043, complete genome	NA	290398	30.2	30.2	78%	735	100.00	3696649	CP000285.1
Mus musculus BAC clone RP23-332A4 from chromosome 6, complete...	house mouse	10090	30.2	30.2	78%	735	100.00	195179	AC163104.2
Nitrosococcus oceani ATCC 19707, complete genome	NA	323261	30.2	30.2	78%	735	100.00	3481691	CP000127.1
Oryza sativa Japonica Group cultivar Nipponbare chromosome 11...	Japanese rice	39947	30.2	30.2	78%	735	100.00	175425	AC108223.5
Propionibacterium acnes KPA171202, complete genome	NA	267747	30.2	30.2	78%	735	100.00	2560265	AE017283.1
Mus musculus chromosome 3, clone RP23-20F10, complete sequence	house mouse	10090	30.2	30.2	78%	735	100.00	183455	AC157379.7
Nitrobacter winogradskyi Nb-255, complete genome	NA	323098	30.2	30.2	78%	735	100.00	3402093	CP000115.1
Mus musculus BAC clone RP23-301C7 from 6, complete sequence	house mouse	10090	30.2	30.2	78%	735	100.00	224182	AC127311.3
HIV-1 clone 93SE.CII7eP from Sweden envelope glycoprotein, V3...	NA	11676	30.2	30.2	78%	735	100.00	307	AF397960.1
Moorella thermoacetica ATCC 39073, complete genome	NA	264732	30.2	30.2	78%	735	100.00	2628784	CP000232.1
Synechococcus sp. JA-3-3Ab, complete genome	NA	321327	30.2	30.2	78%	735	100.00	2932766	CP000239.1

HIV-1 isolate 02thmeno1006 from Thailand envelope glycoprotein...	NA	11676	30.2	30.2	78%	735	100.00	345	AY248134.1
Sus scrofa, clone RP44-428N16, complete sequence	pig	9823	30.2	30.2	78%	735	100.00	154348	AC129961.2
V.faba mRNA for an RNA- or ssDNA-binding protein	NA	3907	30.2	30.2	78%	735	100.00	1131	X97905.1
HIV-1 isolate ARGSM-SN-MT2 from Argentina envelope glycoprotei...	NA	11676	30.2	30.2	78%	735	100.00	105	DQ059521.1
Kluyveromyces lactis strain NRRL Y-1140 chromosome A complete...	NA	28985	30.2	30.2	78%	735	100.00	1062590	CR382121.1
Pan troglodytes chromosome 22 clone:PTB-015O01, map 22, comple...	chimpanzee	9598	30.2	30.2	78%	735	100.00	155412	BS000191.1
HIV-1 clone M3 from Tanzania envelope glycoprotein (env) gene,...	NA	11676	30.2	30.2	78%	735	100.00	384	AF439654.1
HIV-1 subtype F isolate M11 from France envelope glycoprotein...	NA	11676	30.2	30.2	78%	735	100.00	523	AY010337.1
Human immunodeficiency virus type 1 proviral partial env gene...	NA	11676	30.2	30.2	78%	735	100.00	548	AM086516.1
Mus musculus chromosome 3, clone RP24-137C19, complete sequence	house mouse	10090	30.2	30.2	78%	735	100.00	181758	AC113990.10
Human immunodeficiency virus type 1 proviral partial env gene...	NA	11676	30.2	30.2	78%	735	100.00	616	AJ554714.1
HIV-1 isolate ARMA159 from Argentina, complete genome	NA	11676	30.2	30.2	78%	735	100.00	9704	AF385936.1
Gallus gallus tapasin gene, complete CDS	chicken	9031	30.2	30.2	78%	735	100.00	4710	AJ004999.1
Gallus gallus mRNA for Tapasin, T8.4	chicken	9031	30.2	30.2	78%	735	100.00	866	AJ005072.1
Human immunodeficiency virus type 1 partial env gene, V3 regio...	NA	11676	30.2	30.2	78%	735	100.00	255	AJ228156.1
Aspergillus niger monoamine oxidase N (mao-N) mRNA, complete cds	NA	5061	30.2	30.2	78%	735	100.00	2193	L38858.1

SELEZIONE DI ALLINEAMENTI SIGNIFICATIVI

Oricola thermophila strain MEBiC13590 chromosome, complete genome
Sequence ID: CP054836.1Length: 3998539Number of Matches: 2
Range 1: 2324255 to 2324272 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
36.2 bits(18)	12	18/18(100%)	0/18(0%)	Plus/Minus

```
CDS: Putative 1        5            C   H   G   D   Q
Query                  1         ACGCAATGCCCGTCCTGG  18
                                 ||||||||||||||||||
Sbjct                  2324272   ACGCAATGCCCGTCCTGG  2324255
CDS:ROK family trans   116       V  C   H   G   D   Q
```

/prodotto = "ROK family transcriptional regulator"

Approfondimenti: https://www.ebi.ac.uk/interpro/entry/InterPro/IPR000600/

Range 2: 2595323 to 2595337 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	735	15/15(100%)	0/15(0%)	Plus/Minus

```
CDS: Putative 1        1           R   N   A   R   P
Query                  1         ACGCAATGCCCGTCC  15
                                 |||||||||||||||
Sbjct                  2595337   ACGCAATGCCCGTCC  2595323
CDS:hypothetical pro   120         R   N   A   R   P
```

Citrobacter freundii strain FDAARGOS_61 chromosome, complete genome
Sequence ID: CP026045.1Length: 5258481Number of Matches: 2
Range 1: 3903444 to 3903461 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
36.2 bits(18)	12	18/18(100%)	0/18(0%)	Plus/Plus

```
CDS: Putative 1        1          R   N   A   R   P   G
Query                  2         CGCAATGCCCGTCCTGGT  19
                                 ||||||||||||||||||
Sbjct                  3903444   CGCAATGCCCGTCCTGGT  3903461
CDS:superoxide dismu   168        R   N   A   R   P   G
```

/prodotto = "superoxide dismutase [Fe]"

Le mutazioni nel primo enzima **SOD (SOD1)** possono causare *la sclerosi laterale amiotrofica familiare* (**SLA**, una forma di malattia del motoneurone). La mutazione più comune negli Stati Uniti è A4V, mentre la più studiata è G93A (https://en.wikipedia.org/wiki/Superoxide_dismutase).

Pseudomonas xanthomarina strain LMG 23572 genome assembly, chromosome: I

Sequence ID: LT629970.1Length: 4332289Number of Matches: 1

Range 1: 204827 to 204844 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
36.2 bits(18)	12	18/18(100%)	0/18(0%)	Plus/Plus

```
CDS: Putative 1        1          Q   C   P   S   W
Query                  2        CGCAATGCCCGTCCTGGT  19
                                ||||||||||||||||||
Sbjct                  204827   CGCAATGCCCGTCCTGGT  204844
CDS:succinate dehydr   154      S   Q   C   P   S   W
```

/prodotto = "**succinate dehydrogenase/fumarate reductase iron-sulfur subunit**"

Approfondimenti:
https://string-db.org/newstring_cgi/show_network_section.pl?identifier=succinate%20dehydrogenase%20iron-sulfur%20subunit

PREDICTED: Dermochelys coriacea leukocyte immunoglobulin-like receptor subfamily A member 6 (LOC119847459), mRNA

NCBI Reference Sequence: XM_038382257.1

FASTA Graphics

Go to:

```
LOCUS       XM_038382257              18 bp    mRNA    linear   VRT 28-DEC-2020
DEFINITION  PREDICTED: Dermochelys coriacea leukocyte immunoglobulin-like
            receptor subfamily A member 6 (LOC119847459), mRNA.
ACCESSION   XM_038382257 REGION: 2101..2118
VERSION     XM_038382257.1
DBLINK      BioProject: PRJNA655518
KEYWORDS    RefSeq; includes ab initio.
SOURCE      Dermochelys coriacea (leatherback sea turtle)
  ORGANISM  Dermochelys coriacea
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archelosauria; Testudinata; Testudines; Cryptodira; Durocryptodira;
            Americhelydia; Chelonioidea; Dermochelyidae; Dermochelys.
COMMENT     MODEL REFSEQ:  This record is predicted by automated computational
            analysis. This record is derived from a genomic sequence
            (NC_050090.1) annotated using gene prediction method: Gnomon.
            Also see:
                Documentation of NCBI's Annotation Process

            ##Genome-Annotation-Data-START##
            Annotation Provider            :: NCBI
            Annotation Status              :: Full annotation
            Annotation Name                :: Dermochelys coriacea Annotation
                                              Release 100
```

```
            Annotation Version          :: 100
            Annotation Pipeline         :: NCBI eukaryotic genome annotation
                                           pipeline
            Annotation Software Version :: 8.5
            Annotation Method           :: Best-placed RefSeq; Gnomon
            Features Annotated          :: Gene; mRNA; CDS; ncRNA
            ##Genome-Annotation-Data-END##

            ##RefSeq-Attributes-START##
            ab initio :: 21% of CDS bases
            ##RefSeq-Attributes-END##
FEATURES             Location/Qualifiers
     source          1..18
                     /organism="Dermochelys coriacea"
                     /mol_type="mRNA"
                     /isolate="rDerCor1"
                     /db_xref="taxon:27794"
                     /chromosome="23"
                     /sex="male"
                     /tissue_type="blood"
                     /dev_stage="adult"
                     /country="USA: Half Moon Bay, California"
                     /lat_lon="37.46311 N 122.4293 W"
                     /collection_date="26-Sep-2017"
                     /collected_by="Lisa Komoroske"
     gene            <1..>18
                     /gene="LOC119847459"
                     /note="Derived by automated computational analysis using
                     gene prediction method: Gnomon. Supporting evidence
                     includes similarity to: 41 Proteins, and 78% coverage of
                     the annotated genomic feature by RNAseq alignments"
                     /db_xref="GeneID:119847459"
     CDS             <1..>18
                     /gene="LOC119847459"
                     /codon_start=3
                     /product="leukocyte immunoglobulin-like receptor
                      subfamily A member 6"
                     /protein_id="XP_038238185.1"
                     /db_xref="GeneID:119847459"
                     /translation="MASALTALLLGCWLAGRSGVSGEGSTPKPSISISPGGVIPMGGN
                     VTIRCRHQHLGMRILLYKDGDRNHLTYTDPAGSEAEFPVTSARREQGGSYTCRYSYRT
                     GPAAYSEPSDPVQIIVADPSLPRPSISVSLASVTASGADVTIQCQGQGRDVRFFLHKA
                     GDLNLPRHMDPAGDGAEFHIPTVGRQHGGSYSCSYRPRSEPFVSSQPSDPVQLVVAGS
                     SYSKPSISLSPSGEIAPGTDVSISCHGPRQGVRFKMYRSGVARWHMEPAGSTAEFAIP
                     NIRREDGGTYTCSYESLTEPPVSSPHSDPVQLVVAAHFSKPSISLSPSGEIAPGTDVS
```

```
                    ISCHGPRQGVRFKLYRAGVARWHTEPAGSTAEFRIPNVRREDGGSYTCSYESLREPPI
                    SSPHSDPMQLVVAGAGSGPTRGSDPTHPGAVLAPTLPGSTQPGAPPRQDYTPFAIVRL
                    SLAVGVLLVLVLVLAEAAYSWKRTPHPLIPPRPSGEQSQQPEGQMETPVLDLQPPQIP
                    ARSLGTGTAGHAHQGGWVGAIGPTGPSSLVSPPHSPAPPSPPQIRFMGPSTPIHGPIY
                    TGIPAPLPTPPDQIHGPIDTVAMVQEETRSYPCEASAPSHRIDLPPDAGEGDRKMQWV
                    YGNTAIATYPPSRHLPSVLDVGGWGISVTSCMNLTLLEFDAMPVLGASWSGTRVTCST
                    LTPTVPGDTRLETQVSLLN"
ORIGIN
        1 acgcaatgcc cgtcctgg
//
```

Sequence ID: XM_038382257.1Length: 2216Number of Matches: 1

Range 1: 2101 to 2118 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
36.2 bits(18)	12	18/18(100%)	0/18(0%)	Plus/Plus

```
CDS: Putative 1       1         A   M   P   V   L
Query                 1      ACGCAATGCCCGTCCTGG  18
                             ||||||||||||||||||
Sbjct                 2101   ACGCAATGCCCGTCCTGG  2118
CDS:leukocyte immuno  664    D   A   M   P   V   L
```

/prodotto = "leukocyte immunoglobulin-like receptor subfamily A member 6"

LILRA6 (**Leukocyte Immunoglobulin Like Receptor A6**) è un gene che codifica per proteine. Le malattie associate a ***LILRA6*** includono il fenomeno Shwartzman (https://www.genecards.org/cgi-bin/carddisp.pl?gene=LILRA6).. Il **fenomeno di Shwartzman** è una rara reazione di un corpo a particolari tipi di tossine, chiamate **endotossine**, che causano **trombosi nel tessuto colpito**. L'eliminazione della trombosi determina un **blocco reticoloendoteliale**, che impedisce la ripulitura della trombosi causata da un'introduzione ripetuta della tossina. Ciò causerà la *necrosi dei tessuti*. Il *fenomeno di Shwartzman* si osserva solitamente durante il ***parto*** o l'***aborto***, quando *corpi estranei* vengono introdotti nei tessuti del sistema riproduttivo femminile. Shwartzman fu il primo a sviluppare il concetto di ***ipersensibilità del sistema immunitario*** negli anni '20. Questa reazione è stata sperimentata utilizzando l'*endotossina di Neisseria meningitidis* (https://en.wikipedia.org/wiki/Shwartzman_phenomenon). Il **fenomeno Shwartzman** (https://www.malacards.org/card/shwartzman_phenomenon), noto anche come *reazione di shwartzman* , è correlato alla *granulocitopenia* e *alla reazione di arthus* [nota anche come *orticaria tipo Arthus*, è una malattia da reazione di ipersensibilità di tipo III caratterizzata da **vasculiti** (**assolutamente da approfondire: *vasculitis***) locali, accompagnate da sintomi dolorosi, edema, emorragia o necrosi e ha una base fisica nella deposizione di complessi immuni antigene-anticorpo nelle pareti vascolari o sierose. Un'importante gene associato con la reazione Arthus è SELL (Selectin L), e tra i suoi percorsi correlati/supercorrelati sono *Sistema Immunitario Innato* e *Segnalazione RANK negli Osteoclasti* (*RANK Signaling in Osteoclasts*). I tessuti affiliati includono *pelle*, *neutrofili* e *polmoni*, e i fenotipi correlati sono il *sistema ematopoietico* e *cellulare*. **Approfondimenti:** *https://en.wikipedia.org/wiki/Arthus_reaction*]. Un gene importante associato al fenomeno Shwartzman è **ITGAM** (**Integrin Subunit Alpha M**), e tra i suoi percorsi/superpercorsi correlati ci sono il *sistema immunitario innato* e la *segnalazione di citochine nel sistema immunitario*. Un'importante **paralogo** di questo gene è LILRB3 (https://www.genecards.org/cgi-bin/carddisp.pl?gene=LILRA6). **Approfondimenti**: https://www.uniprot.org/uniprot/Q6PI73.

Shigella sonnei strain SE6-1 chromosome, complete genome

Sequence ID: CP055292.1Length: 4762774Number of Matches: 1

Range 1: 960731 to 960747 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Minus

```
CDS: Putative 1       1          R  N  A  R  P
Query                 1       ACGCAATGCCCGTCCTG  17
                              |||||||||||||||||
Sbjct                 960747  ACGCAATGCCCGTCCTG  960731
CDS:host cell divisi  18         R  N  A  R  P
```

/prodotto = ”**host cell division inhibitor Icd-like protein**”

Approfondimenti:
https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=411097
https://0-www-ncbi-nlm-nih-gov.brum.beds.ac.uk/genome/annotation_prok/evidence/NF033153/
https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=cl41269&spf=1
https://pubmed.ncbi.nlm.nih.gov/8491703/
https://pfam.xfam.org/family/PF10554
https://assets.website-files.com/5fee4d603d8f86745bf69089/60afc3cf8f2eab1e8316526a_Rao%20et%20al%2C%202021%20Selective%20cell%20death%20in%20**HIV-1**%20infected%20cells%20by%20DDX3%20inhibitors.pdf

Xanthomonas oryzae pv. oryzae strain K1 chromosome, complete genome

Sequence ID: CP049205.1Length: 4981423Number of Matches: 1

Range 1: 922183 to 922199 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Minus

```
CDS: Putative 1       1         R  N  A  R  P  G
Query                 2       CGCAATGCCCGTCCTGG  18
                              |||||||||||||||||
Sbjct                 922199  CGCAATGCCCGTCCTGG  922183
CDS:8-oxo-dGTP dipho  26        R  N  A  R  P  G
```

/prodotto = ”**8-oxo-dGTP diphosphatase**”

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=239519

Klebsiella pneumoniae strain YML0508 chromosome, complete genome

Sequence ID: CP045193.1Length: 5352780Number of Matches: 1

Range 1: 4255376 to 4255392 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
Query  1        ACGCAATGCCCGTCCTG  17
                |||||||||||||||||
Sbjct  4255376  ACGCAATGCCCGTCCTG  4255392
```

Citrobacter portucalensis strain FDAARGOS_617 chromosome, complete genome
Sequence ID: CP044098.1Length: 4926736Number of Matches: 2
Range 2: 4480428 to 4480442 GenBank Graphics

```
Score           Expect  Identities      Gaps        Strand

30.2 bits(15)  735     15/15(100%)  0/15(0%)  Plus/Plus

CDS: Putative 1       5          R  L  A  R  G
Query                 1         ACGCAATGCCCGTCC  15
                                |||||||||||||||
Sbjct                 4480428   ACGCAATGCCCGTCC  4480442
CDS:hypothetical pro  34         R  L  A  R  G
```

Stieleria maiorica strain Mal15 chromosome
Sequence ID: CP036264.1Length: 9894293Number of Matches: 1
Range 1: 4906885 to 4906901 GenBank Graphics

```
Score           Expect  Identities      Gaps        Strand

34.2 bits(17)  47      17/17(100%)  0/17(0%)  Plus/Plus

CDS: Putative 1       1          T  Q  C  P  S
Query                 1         ACGCAATGCCCGTCCTG  17
                                |||||||||||||||||
Sbjct                 4906885   ACGCAATGCCCGTCCTG  4906901
CDS:hypothetical pro  24         T  Q  C  P  S  C
```

Thermaerobacter sp. FW80 chromosome, complete genome
Sequence ID: CP037895.1Length: 2953026Number of Matches: 1
Range 1: 2857087 to 2857103 GenBank Graphics

```
Score           Expect  Identities      Gaps        Strand

34.2 bits(17)  47      17/17(100%)  0/17(0%)  Plus/Plus

CDS: Putative 1       5            C  H  G  D  Q
Query                 1         ACGCAATGCCCGTCCTG  17
                                |||||||||||||||||
Sbjct                 2857087   ACGCAATGCCCGTCCTG  2857103
CDS:dCMP deaminase f  56        V  C  H  G  D  Q
```

/prodotto = "dCMP deaminase family protein"

Questo enzima lega **Zn++**, necessario per l'attività catalitica (https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=238613). Tutti i membri sono dipendenti dallo **Zn**. Lo **ione zinco** nel sito attivo svolge un ruolo centrale nel meccanismo catalitico proposto, attivando una molecola d'acqua per formare uno ione idrossido che esegue un attacco nucleofilo sul substrato (https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=238406).

Halomonas sp. hl-4 genome assembly, chromosome: I

GenBank: LT907845.1

FASTA Graphics

Go to:

```
LOCUS       LT907845                  17 bp    DNA     linear   BCT 06-SEP-2017
DEFINITION  Halomonas sp. hl-4 genome assembly, chromosome: I.
ACCESSION   LT907845 REGION: 2200308..2200324
VERSION     LT907845.1
DBLINK      BioProject: PRJEB22442
            BioSample: SAMN04488142
KEYWORDS    .
SOURCE      Halomonas sp. hl-4
  ORGANISM  Halomonas sp. hl-4
            Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
            Halomonadaceae; Halomonas.
REFERENCE   1
  AUTHORS   Varghese,N. and Submissions,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-SEP-2017) DOE - JOINT GENOME INSTITUTE, LBNL, 2800
            Mitchell Drive, Walnut Creek, CA 94598, USA
FEATURES             Location/Qualifiers
     source          1..17
                     /organism="Halomonas sp. hl-4"
                     /mol_type="genomic DNA"
                     /strain="HL-4"
                     /db_xref="taxon:1761789"
                     /chromosome="I"
     gene            <1..>17
                     /locus_tag="SAMN04488142_2115"
     CDS             <1..>17
                     /locus_tag="SAMN04488142_2115"
                     /codon_start=1
                     /transl_table=11
                     /product="Nuclease-related domain-containing protein"
                     /protein_id="SNY97525.1"
                     /translation="MIWLEYLLPLIFLFPMAAMGGIVLALRSLHDARVQSPFDTPLRE
                     PGRALRHRLDQAFSSLFLNGALGPLISLAPLVYGMGRMLFVDKQDWVEWALYGLLSTL
                     LVLAFSLLLVRDYQRIRRLKLGLACELAVGQELERLIRPDAHPYYVFHDVPTDSFTID
                     HVVVTPHGVFVVETRARTVPISSDGRELNTVAVERERLRFPYWQERRPLHKTRQGVNW
                     LSQWLEQRCGVPVPVQGVLVLPGWDINNDEAAPDILVARGDVLSKQLTELTPGKLSDP
                     IHDKIINTLLERAKLMELKHLRQPSV"
ORIGIN
        1 ccaggacggg cattgcg
//
```

Range 1: 2200308 to 2200324 GenBank Graphics

```
Score           Expect  Identities        Gaps        Strand

34.2 bits(17)  47     17/17(100%)  0/17(0%)  Plus/Minus

CDS: Putative 1         5              L   A   R   G   P
Query                   2          CGCAATGCCCGTCCTGG  18
                                   |||||||||||||||||
Sbjct                   2200324    CGCAATGCCCGTCCTGG  2200308
CDS:Nuclease-related    50         R   L   A   R   G   P
```

/prodotto ="Nuclease-related domain-containing protein"

Il **dominio correlato alla nucleasi** (**NERD**) si trova in una serie di proteine batteriche, archeali e vegetali https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=377990. Nell'articolo intitolato "**NERD: un dominio correlato all'elaborazione del DNA presente nel plasmide di virulenza dell'ANTRACE, pXO1** (NERD: a DNA processing-related domain present in the anthrax virulence plasmid, pXO1.) gli autori affermano di aver "….identificato un nuovo dominio in un'ampia gamma di proteine batteriche, così come singole archaeal e vegetali. La sua presenza nel **plasmide pXO1 correlato alla *virulenza*** di **Bacillus anthracis** (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5026784/; https://www.ncbi.nlm.nih.gov/pmc/articles/PMC103788/) e in molti altri agenti patogeni lo rende un possibile bersaglio di farmaci. Chiamiamo il nuovo dominio correlato alla *nucleasi* (**NERD**) a causa della sua lontana somiglianza con le **endonucleasi**" (https://pubmed.ncbi.nlm.nih.gov/15055202/).

Escherichia coli strain S50, complete genome

Sequence ID: CP010238.1Length: 4797106Number of Matches: 1

Range 1: 480657 to 480673 GenBank Graphics

```
Score           Expect  Identities        Gaps        Strand

34.2 bits(17)  47     17/17(100%)  0/17(0%)  Plus/Plus

CDS: Putative 1         1            R   N   A   R   P
Query                   1          ACGCAATGCCCGTCCTG  17
                                   |||||||||||||||||
Sbjct                   480657     ACGCAATGCCCGTCCTG  480673
CDS:HAD family hydro    18           R   N   A   R   P
```

/prodotto ="HAD family hydrolase"
/nome della regione ="phage_ICD_like"
/note ="host cell division inhibitor Icd domain; NF033153"

Pseudomonas putida strain PP112420, complete genome

Sequence ID: CP017073.1Length: 6031212Number of Matches: 1

Range 1: 1884957 to 1884973 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand


34.2 bits(17)  47     17/17(100%)  0/17(0%)  Plus/Minus


CDS: Putative 1        1           A   M   P   V   L

Query                  2         CGCAATGCCCGTCCTGG  18

                                 |||||||||||||||||

Sbjct                  1884973   CGCAATGCCCGTCCTGG  1884957

CDS:AraC family tran   78          A   M   P   V   L
```

/prodotto ="AraC family transcriptional regulator"

Approfondimenti:

https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=225117

The araC gene of Escherichia coli: transcriptional and translational start-points and complete nucleotide sequence. Gene 1980 Dec; 12(3-4): 179-90.

Purification and regulatory properties of MarA protein, a transcriptional activator of Escherichia coli multiple antibiotic and superoxide resistance promoters.J Bacteriol 1995 Dec ; 177(24):7100-4

Activation of multiple antibiotic resistance and binding of stress-inducible promoters by Escherichia coli Rob protein.J Bacteriol 1995 Apr ; 177(7):1655-61

Isolation, characterization, and nucleotide sequence of appY, a regulatory gene for growth-phase-dependent gene expression in Escherichia coli.J Bacteriol 1989 Mar ; 171(3):1683-91

A novel DNA-binding motif in MarA: the first structure for an AraC family transcriptional activator.Proc Natl Acad Sci U S A 1998 Sep 01; 95(18):10413-8

Pseudomonas sp. MRSN12121, complete genome

Sequence ID: CP010892.1Length: 6929263Number of Matches: 2

Range 1: 421278 to 421294 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand


34.2 bits(17)  47     17/17(100%)  0/17(0%)  Plus/Minus


CDS: Putative 1        1           Q   C   P   S   W

Query                  2       CGCAATGCCCGTCCTGG  18

                               |||||||||||||||||

Sbjct                  421294  CGCAATGCCCGTCCTGG  421278

CDS:chorismate mutas   145     P   Q   C   P   S   W
```

/prodotto ="chorismate mutase"

Approfondimenti:

https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=236441

https://www.ncbi.nlm.nih.gov/Structure/cdd/cl00693

https://en.wikipedia.org/wiki/Chorismate_mutase

https://pubmed.ncbi.nlm.nih.gov/28202315/

Range 2: 102557 to 102571 GenBank Graphics

Score Expect Identities Gaps Strand

30.2 bits(15) 735 15/15(100%) 0/15(0%) Plus/Plus

```
CDS: Putative 1        4          H   G   D   Q
Query                  5        AATGCCCGTCCTGGT  19
                                |||||||||||||||
Sbjct                  102557   AATGCCCGTCCTGGT  102571
CDS:peptidase M16 [P   392        H   G   D   Q   Y
```

/prodotto ="peptidase M16"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=223685

Aspergillus sydowii CBS 593.65 uncharacterized protein (ASPSYDRAFT_43463), mRNA

Sequence ID: XM_040846660.1Length: 2055Number of Matches: 1

Range 1: 971 to 987 GenBank Graphics

Score Expect Identities Gaps Strand

34.2 bits(17) 47 17/17(100%) 0/17(0%) Plus/Plus

```
CDS: Putative 1        1        A   M   P   V   L
Query                  1     ACGCAATGCCCGTCCTG  17
                             |||||||||||||||||
Sbjct                  971   ACGCAATGCCCGTCCTG  987
CDS:uncharacterized    206   D   A   M   P   V   L
```

Acidovorax sp. KKS102, complete genome

Sequence ID: CP003872.1Length: 5196935Number of Matches: 2

Range 1: 3971641 to 3971657 GenBank Graphics

Score Expect Identities Gaps Strand

34.2 bits(17) 47 17/17(100%) 0/17(0%) Plus/Plus

```
CDS: Putative 1        1          R   N   A   R   P   G
Query                  2         CGCAATGCCCGTCCTGG  18
                                 |||||||||||||||||
Sbjct                  3971641   CGCAATGCCCGTCCTGG  3971657
CDS:phage tail tape    435        R   N   A   R   P   G
```

/prodotto ="phage tail tape measure protein"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=227606

```
Range 2: 3912560 to 3912574 GenBank Graphics
Score            Expect  Identities        Gaps        Strand

30.2 bits(15)  735    15/15(100%)  0/15(0%)  Plus/Minus

CDS: Putative 1        1            Q   C   P   S
Query                  2        CGCAATGCCCGTCCT  16
                                |||||||||||||||
Sbjct                  3912574  CGCAATGCCCGTCCT  3912560
CDS:regulatory prote   112      A   Q   C   P   S
```

/prodotto ="regulatory protein"
/nome della regione ="HTH_MerR-like_sg6"
/note ="Dominio di legame al DNA Helix-Turn-Helix di presunti regolatori di trascrizione della superfamiglia MerR"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=133408

PREDICTED: Drosophila subobscura prolow-density lipoprotein receptor-related protein 1 (LOC117892042), transcript variant X2, mRNA
Sequence ID: XM_034797968.1Length: 15044Number of Matches: 1

```
Range 1: 9166 to 9181 GenBank Graphics
Score            Expect  Identities        Gaps        Strand

32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Minus

CDS: Putative 1        5       C   H   G   D   Q
Query                  3      GCAATGCCCGTCCTGG  18
                              ||||||||||||||||
Sbjct                  9181   GCAATGCCCGTCCTGG  9166
CDS:prolow-density 1   2896    C   H   G   D   Q
```

/prodotto ="prolow-density lipoprotein receptor-related protein 1 isoform X2"

La proteina 1 correlata al recettore delle lipoproteine a bassa densità (**LRP1**), nota anche come *recettore alfa-2-macroglobulina* (**A2MR**), *recettore dell'apolipoproteina E* (**APOER**) o cluster di *differenziazione 91* (**CD91**), è una proteina che forma un recettore presente nella membrana plasmatica di cellule coinvolte nell'endocitosi mediata da recettori. Nell'uomo, la proteina LRP1 è codificata dal gene LRP1. LRP1 è anche una *chiave proteina di segnalazione* e, quindi, coinvolta in vari processi biologici, come il metabolismo delle lipoproteine e la motilità cellulare, e **malattie, come le malattie neurodegenerative, l'aterosclerosi e il cancro** (https://en.wikipedia.org/wiki/LRP1). *Svolge funzioni di recettore per l'esotossina A di Pseudomonas aeruginosa.* (https://www.uniprot.org/uniprot/Q07954).

Bacillus circulans strain GN03 chromosome, complete genome

Sequence ID: CP053315.1Length: 5217129Number of Matches: 1

Range 1: 1127996 to 1128011 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Plus

```
CDS: Putative 1       5          R  L  A  R  G
Query                 1        ACGCAATGCCCGTCCT  16
                               ||||||||||||||||
Sbjct                 1127996  ACGCAATGCCCGTCCT  1128011
CDS:aldo/keto reduct  75         R  L  A  R  G
```

/prodotto ="aldo/keto reductase"

Approfondimenti: https://en.wikipedia.org/wiki/Aldo-keto_reductase

Xylella fastidiosa subsp. multiplex strain Fillmore chromosome, complete genome

Sequence ID: CP052855.1Length: 2526544Number of Matches: 1

Range 1: 2050639 to 2050654 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Plus

```
CDS: Putative 1       1             A  M  P  V  L
Query                 1        ACGCAATGCCCGTCCT  16
                               ||||||||||||||||
Sbjct                 2050639  ACGCAATGCCCGTCCT  2050654
CDS:hypothetical pro  38         H  A  M  P  V  L
```

PREDICTED: Geotrypetes seraphini transmembrane protein 9 (TMEM9), transcript variant X3, mRNA

Sequence ID: XM_033918501.1Length: 1642Number of Matches: 1

Range 1: 246 to 261 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Plus

```
CDS: Putative 1       1        M  P  V  L  V
Query                 4    CAATGCCCGTCCTGGT  19
                           ||||||||||||||||
Sbjct                 246  CAATGCCCGTCCTGGT  261
CDS:transmembrane pr  66   P  M  P  V  L  V
```

/prodotto ="transmembrane protein 9"

Approfondimenti: https://www.uniprot.org/uniprot/Q9P0T7

Bradyrhizobium sp. 6(2017) strain 1S3 chromosome, complete genome
Sequence ID: CP049289.1Length: 10014235Number of Matches: 1
Range 1: 1766030 to 1766045 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Plus

Features:
aec family transporter

```
CDS: Putative 1        1            A   M   P   V   L
Query                  2          CGCAATGCCCGTCCTG  17
                                  ||||||||||||||||
Sbjct                  1766030    CGCAATGCCCGTCCTG  1766045
CDS:AEC family trans   236          A   M   P   V   L
```

/prodotto ="AEC family transporter"

Approfondimenti: http://www.tcdb.org/search/result.php?tc=2.A.69

Pseudomonas sp. DTU12.1 chromosome, complete genome
Sequence ID: CP045254.1Length: 5943629Number of Matches: 1
Range 1: 5128536 to 5128551 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Plus

```
CDS: Putative 1        4              H   G   D   Q
Query                  4          CAATGCCCGTCCTGGT  19
                                  ||||||||||||||||
Sbjct                  5128536    CAATGCCCGTCCTGGT  5128551
CDS:TIGR02099 family   131        W   H   G   D   Q   D
```

/prodotto ="TIGR02099 family protein"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=273971

Aeromonas veronii strain AVNIH1 chromosome, complete genome
Sequence ID: CP047155.1Length: 4807642Number of Matches: 1
Range 1: 3429200 to 3429215 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Plus

```
CDS: Putative 1        1            N   A   R   P   G
Query                  4          CAATGCCCGTCCTGGT  19
                                  ||||||||||||||||
Sbjct                  3429200    CAATGCCCGTCCTGGT  3429215
CDS:alpha-L-glutamat   273          N   A   R   P   G
```

/prodotto ="alpha-L-glutamate ligase-like protein"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=418439

Rhizobium grahamii strain BG7 chromosome, complete genome

GenBank: CP043498.1 FASTA Graphics

Go to:

```
LOCUS       CP043498                  16 bp    DNA     linear   BCT 04-NOV-2019
DEFINITION  Rhizobium grahamii strain BG7 chromosome, complete genome.
ACCESSION   CP043498 REGION: 2600333..2600348
VERSION     CP043498.1
DBLINK      BioProject: PRJNA563034
            BioSample: SAMN12661675
KEYWORDS    .
SOURCE      Rhizobium grahamii
  ORGANISM  Rhizobium grahamii
            Bacteria; Proteobacteria; Alphaproteobacteria; Hyphomicrobiales;
            Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Ali,R., Chaluvadi,S.R. and Wang,X.
  TITLE     Prosopis cineraria nodule microbiome
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 16)
  AUTHORS   Ali,R., Chaluvadi,S.R. and Wang,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-AUG-2019) Genetics, University of Georgia, 120 Green
            Street, Athens, GA 30602, USA
COMMENT     Bacteria and source DNA available from Rashid Ali.
            The annotation was added by the NCBI Prokaryotic Genome Annotation
            Pipeline (PGAP). Information about PGAP can be found here:
            https://www.ncbi.nlm.nih.gov/genome/annotation_prok/
            ##Genome-Assembly-Data-START##
            Assembly Date          :: 2019
            Assembly Method        :: Canu v. 1.8
            Genome Representation  :: Full
            Expected Final Version :: Yes
            Genome Coverage        :: 100.0x
            Sequencing Technology  :: PacBio RSII
            ##Genome-Assembly-Data-END##
            ##Genome-Annotation-Data-START##
            Annotation Provider               :: NCBI
            Annotation Date                   :: 09/03/2019 16:26:22
            Annotation Pipeline               :: NCBI Prokaryotic Genome
                                                 Annotation Pipeline (PGAP)
            Annotation Method                 :: Best-placed reference protein
                                                 set; GeneMarkS-2+
            Annotation Software revision      :: 4.9
            Features Annotated                :: Gene; CDS; rRNA; tRNA; ncRNA;
                                                 repeat_region
```

```
            Genes (total)                      :: 5,574
            CDSs (total)                       :: 5,505
            Genes (coding)                     :: 5,181
            CDSs (with protein)                :: 5,181
            Genes (RNA)                        :: 69
            rRNAs                              :: 4, 4, 4 (5S, 16S, 23S)
            complete rRNAs                     :: 4, 4, 4 (5S, 16S, 23S)
            tRNAs                              :: 53
            ncRNAs                             :: 4
            Pseudo Genes (total)               :: 324
            CDSs (without protein)             :: 324
            Pseudo Genes (ambiguous residues) :: 0 of 324
            Pseudo Genes (frameshifted)        :: 280 of 324
            Pseudo Genes (incomplete)          :: 48 of 324
            Pseudo Genes (internal stop)       :: 12 of 324
            Pseudo Genes (multiple problems)   :: 15 of 324
            ##Genome-Annotation-Data-END##
FEATURES             Location/Qualifiers
     source          1..16
                     /organism="Rhizobium grahamii"
                     /mol_type="genomic DNA"
                     /strain="BG7"
                     /isolation_source="nodule"
                     /host="Prosopis cineraria"
                     /db_xref="taxon:1120045"
                     /altitude="16 m"
                     /collection_date="2014"
     gene            <1..>16
                     /locus_tag="FZ934_12695"
     CDS             <1..>16
                     /locus_tag="FZ934_12695"
                     /inference="COORDINATES: similar to AA
                     sequence:RefSeq:WP_003564676.1"
                     /note="Derived by automated computational analysis using
                     gene prediction method: Protein Homology."
                     /codon_start=2
                     /transl_table=11
                     /product="transglutaminase-like cysteine peptidase"
                     /protein_id="QFY61182.1"
                     /translation="MRTSLILSMLAAALTMLPSEGSAGSMLRASRSIGAPIGFPSACA
                     RYAWLCHNQGGGKISDDAAMPVLQRVNRSVNASVRPALDISTSGKSEYWSLPIDNRGD
                     CEDYALLKLKTLLDAGFPSNKLSMSVVLDRRGNNHVVLLARLNAGDYVLDNLSGSVRT
                     WESTGYTFLASQNFSNKGAWQVTLAGPRAGQFSGT"
ORIGIN
        1 cgcaatgccc gtcctg //
```

Range 1: 2600333 to 2600348 GenBank Graphics

```
Score          Expect  Identities        Gaps        Strand

32.2 bits(16)  186     16/16(100%)  0/16(0%)  Plus/Plus

CDS: Putative 1        1            A   M   P   V   L
Query                  2          CGCAATGCCCGTCCTG   17
                                  ||||||||||||||||
Sbjct                  2600333    CGCAATGCCCGTCCTG   2600348
CDS:transglutaminase   63           A   M   P   V   L
```

/prodotto ="transglutaminase-like cysteine peptidase"

Transglutaminase-like cysteine peptidase (Superfamiglia simile alla transglutaminasi)

Questa famiglia comprende le transglutaminasi animali e altre proteine batteriche di funzione sconosciuta. La conservazione della sequenza in questa superfamiglia coinvolge principalmente tre motivi che ruotano attorno ai residui conservati di cisteina, istidina e aspartato che formano la **triade catalitica nella transglutaminasi strutturalmente caratterizzata,** ***il fattore XIIIa della coagulazione del sangue umano***. Sulla base dell'attività dimostrata sperimentalmente della pseudomureina endoisopeptidasi del fago Methanobacterium, si propone che molti, se non tutti, gli omologhi microbici delle transglutaminasi siano proteasi e che le transglutaminasi eucariotiche si siano evolute da una proteasi ancestrale (https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=418444).

Enterobacter hormaechei strain C45 chromosome, complete genome

Sequence ID: CP042551.1Length: 5068785Number of Matches: 1

Range 1: 3192399 to 3192414 GenBank Graphics

```
Score          Expect  Identities        Gaps        Strand

32.2 bits(16)  186     16/16(100%)  0/16(0%)  Plus/Minus

CDS: Putative 1        4              I   G   T   R
Query                  3          GCAATGCCCGTCCTGG   18
                                  ||||||||||||||||
Sbjct                  3192414    GCAATGCCCGTCCTGG   3192399
CDS:two-component sy   283        A   I   G   T   R   S
```

/prodotto ="two-component system sensor histidine kinase DcuS"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=236839

Euhalothece natronophila Z-M001 chromosome, complete genome
Sequence ID: CP042326.1Length: 3326959Number of Matches: 1
Range 1: 2218370 to 2218385 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Plus

```
CDS: Putative 1       1           R  N  A  R  P
Query                 1         ACGCAATGCCCGTCCT  16
                                ||||||||||||||||
Sbjct                 2218370   ACGCAATGCCCGTCCT  2218385
CDS:DNA-directed RNA  944         R  N  A  R  P
```

/prodotto ="DNA-directed RNA polymerase subunit beta"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=235052

Lysobacter enzymogenes strain YC36 chromosome, complete genome
Sequence ID: CP040656.1Length: 6131517Number of Matches: 1
Range 1: 3354016 to 3354031 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Plus

```
CDS: Putative 1   1           Q  C  P  S  W
Query             3         GCAATGCCCGTCCTGG  18
                            ||||||||||||||||
Sbjct             3354016   GCAATGCCCGTCCTGG  3354031
CDS: pseudouridi  516         Q  C  P  S  W
```

/prodotto ="pseudouridine synthase"

Approfondimenti: https://www.sciencedirect.com/science/article/pii/S1074552106003425

Bacillus circulans strain PK3_138 chromosome, complete genome
Sequence ID: CP026033.1Length: 5274417Number of Matches: 1
Range 1: 2129190 to 2129205 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Minus

```
CDS: Putative 1       5          R  L  A  R  G
Query                 1         ACGCAATGCCCGTCCT  16
                                ||||||||||||||||
Sbjct                 2129205   ACGCAATGCCCGTCCT  2129190
CDS:alcohol dehydrog  75         R  L  A  R  G
```

/prodotto ="alcohol dehydrogenase"

Approfondimenti:
https://en.wikipedia.org/wiki/Alcohol_dehydrogenase#:~:text=Alcohol%20dehydrogenases%20(ADH)%20(EC,(NAD%2B)%20to%20NADH.

Caproiciproducens sp. NJN-50 chromosome, complete genome
Sequence ID: CP035283.1Length: 3308050Number of Matches: 1
Range 1: 2048822 to 2048837 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand


32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Plus


CDS: Putative 1        1          A   M   P   V   L
Query                  3         GCAATGCCCGTCCTGG  18
                                 ||||||||||||||||
Sbjct                  2048822   GCAATGCCCGTCCTGG  2048837
CDS:S58 family pepti   138        A   M   P   V   L
```

/prodotto ="S58 family peptidase"

Questo gruppo di **serina peptidasi** appartiene alla famiglia delle peptidasi **MEROPS S58**. (https://www.ebi.ac.uk/interpro/entry/InterPro/IPR005321/)

Slackia heliotrinireducens strain NCTC11029 genome assembly, chromosome: 1
Sequence ID: LR134379.1Length: 3166158Number of Matches: 1
Range 1: 443784 to 443799 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand


32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Plus


CDS: Putative 1        1         R   N   A   R   P
Query                  2        CGCAATGCCCGTCCTG  17
                                ||||||||||||||||
Sbjct                  443784   CGCAATGCCCGTCCTG  443799
CDS:Phenylalanine--t   704       R   N   A   R   P
```

/prodotto ="Phenylalanine--tRNA ligase beta subunit"

Approfondimenti: https://enzyme.expasy.org/EC/6.1.1.20

PREDICTED: Physcomitrella patens kinesin-like protein KIN-10A (LOC112291113), mRNA
Sequence ID: XM_024538146.1Length: 4739Number of Matches: 1
Related Information Gene-associated gene details Genome Data Viewer-aligned genomic context
Range 1: 2262 to 2277 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand


32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Plus


CDS: Putative 1        1       N   A   R   P   G
Query                  4      CAATGCCCGTCCTGGT  19
                              ||||||||||||||||
Sbjct                  2262   CAATGCCCGTCCTGGT  2277
CDS:kinesin-like pro   518     N   A   R   P   G
```

Prodotto ="kinesin-like protein KIN-10A"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=330404

PREDICTED: Physcomitrella patens photosystem I chlorophyll a/b-binding protein 2, chloroplastic-like (LOC112289979), transcript variant X5, mRNA
Sequence ID: XM_024535798.1Length: 1743Number of Matches: 1
Related Information Gene-associated gene details Genome Data Viewer-aligned genomic context
Range 1: 354 to 369 GenBank Graphics

```
Score            Expect  Identities         Gaps         Strand

32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Minus

CDS: Putative 1        4        L   A   R   G
Query                  2     CGCAATGCCCGTCCTG  17
                             ||||||||||||||||
Sbjct                  369   CGCAATGCCCGTCCTG  354
CDS:photosystem I ch   40    R   L   A   R   G   S
```

/prodotto ="photosystem I chlorophyll a/b-binding protein 2, chloroplastic-like isoform X5"
Approfondimenti:https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=413511

Niveispirillum cyanobacteriorum strain TH16 chromosome eg_2, complete sequence
Sequence ID: CP025612.1Length: 1254521Number of Matches: 1
Range 1: 353618 to 353633 GenBank Graphics

```
Score            Expect  Identities         Gaps         Strand

32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Plus

CDS: Putative 1        1          Q   C   P   S   W
Query                  3        GCAATGCCCGTCCTGG  18
                                ||||||||||||||||
Sbjct                  353618   GCAATGCCCGTCCTGG  353633
CDS:arylmalonate dec   167        Q   C   P   S   W
```

/prodotto ="arylmalonate decarboxylase"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=321017

Saitoella complicata NRRL Y-17804 glycoside hydrolase (SAICODRAFT_94473), partial mRNA
Sequence ID: XM_019171936.1Length: 2457Number of Matches: 1
Related Information Gene-associated gene details Genome Data Viewer-aligned genomic context
Range 1: 2341 to 2356 GenBank Graphics

```
Score            Expect  Identities         Gaps         Strand

32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Minus

CDS: Putative 1        5        A   I   G   T   R
Query                  1      ACGCAATGCCCGTCCT  16
                              ||||||||||||||||
Sbjct                  2356   ACGCAATGCCCGTCCT  2341
CDS:glycoside hydrol   785      A   I   G   T   R
```

/prodotto ="glycoside hydrolase"

Approfondimenti: https://www.ebi.ac.uk/interpro/entry/InterPro/IPR004888/

Streptomyces lincolnensis strain NRRL 2936, complete genome
Sequence ID: CP016438.1Length: 10319054Number of Matches: 1
Range 1: 10038466 to 10038481 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Minus

Features: 3-oxoacyl-(acyl-carrier-protein) synthase iii

```
CDS: Putative 1        5           A   I   G   T   R
Query                  2          CGCAATGCCCGTCCTG  17
                                  ||||||||||||||||
Sbjct                  10038481   CGCAATGCCCGTCCTG  10038466
CDS:3-oxoacyl-(acyl-   245         A   I   G   T   R
```

/prodotto ="3-oxoacyl-(acyl-carrier-protein) synthase III"

Approfondimenti: https://www.ebi.ac.uk/interpro/entry/InterPro/IPR013751/

Phaeoacremonium minimum UCRPA7 putative tartrate dehydrogenase protein partial mRNA
Sequence ID: XM_007919159.1Length: 1116Number of Matches: 1
Related Information Gene-associated gene details Genome Data Viewer-aligned genomic context
Range 1: 490 to 505 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Minus

```
CDS: Putative 1        5       I   G   T   R   T
Query                  4     CAATGCCCGTCCTGGT  19
                             ||||||||||||||||
Sbjct                  505   CAATGCCCGTCCTGGT  490
CDS:putative tartrat   168     I   G   T   R   T
```

/prodotto ="putative tartrate dehydrogenase protein"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=294303

Bacillus sp. NP157 chromosome, complete genome
Sequence ID: CP076546.1Length: 4875246Number of Matches: 1
Range 1: 405023 to 405038 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	186	16/16(100%)	0/16(0%)	Plus/Minus

```
CDS: Putative 1        5          I   G   T   R   T
Query                  4        CAATGCCCGTCCTGGT  19
                                ||||||||||||||||
Sbjct                  405038   CAATGCCCGTCCTGGT  405023
CDS:type IV secretor   570        I   G   T   R   T
```

/prodotto ="type IV secretory system conjugative DNA transfer family protein"

I sistemi di secrezione di tipo IV (T4SS)

“**I sistemi di secrezione di tipo IV (T4SS)** sono grandi complessi proteici che attraversano l’involucro cellulare di molti batteri (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3070162/). ***Il sistema T4S è impiegato dai batteri patogeni per esportare DNA di virulenza e/o proteine direttamente dal citoplasma batterico nella cellula ospite***. Forma un grande complesso multiproteico costituito da 12 proteine denominate VirB1-11 e VirD4. VirB10, interagisce con VirB7 e VirB9, formando il “complesso centrale” (CC) che attraversa la membrana, attorno al quale si assemblano tutti gli altri componenti. Il CC è inserito sia nella membrana esterna che in quella interna, svolgendo un ruolo fondamentale come impalcatura per il resto dei componenti T4SS e partecipando attivamente al trasferimento del substrato T4S attraverso l’involucro batterico attraverso cambiamenti conformazionali che regolano l’apertura e la chiusura del canale (https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=319756). “**I sistemi di secrezione di tipo IV (T4SS)** contengono un canale attraverso il quale le proteine o i complessi proteina-DNA possono essere traslocati. Questa traslocazione è guidata da un numero di ATPasi citoplasmatiche che potrebbero stimolare grandi cambiamenti conformazionali nel complesso di traslocazione. La famiglia dei T4SS è molto versatile, come dimostra la grande varietà di funzioni tra i membri della famiglia. Come già detto, alcuni T4SS sono utilizzati da batteri patogeni Gram-negativi per traslocare un’ampia varietà di fattori di virulenza nella cellula ospite, mentre altri T4SS vengono utilizzati per mediare il trasferimento genico orizzontale, evento che facilita notevolmente l’adattamento ai cambiamenti ambientali ed è alla base della diffusione della resistenza agli antibiotici tra i batteri.” (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3070162/).

PREDICTED: Bufo bufo ADAMTS like 4 (ADAMTSL4), transcript variant X1, mRNA

NCBI Reference Sequence: XM_040412458.1

FASTA Graphics

Go to:

```
LOCUS       XM_040412458              16 bp    mRNA    linear   VRT 30-MAR-2021
DEFINITION  PREDICTED: Bufo bufo ADAMTS like 4 (ADAMTSL4), transcript variant
            X1, mRNA.
ACCESSION   XM_040412458 REGION: 1136..1151
VERSION     XM_040412458.1
DBLINK      BioProject: PRJNA713386
KEYWORDS    RefSeq.
SOURCE      Bufo bufo (common toad)
  ORGANISM  Bufo bufo
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Bufonidae;
            Bufo.
COMMENT     MODEL REFSEQ:  This record is predicted by automated computational
            analysis. This record is derived from a genomic sequence
            (NC_053399.1) annotated using gene prediction method: Gnomon.
            Also see:
                Documentation of NCBI's Annotation Process

            ##Genome-Annotation-Data-START##
            Annotation Provider         :: NCBI
```

```
            Annotation Status           :: Full annotation
            Annotation Name             :: Bufo bufo Annotation Release 100
            Annotation Version          :: 100
            Annotation Pipeline         :: NCBI eukaryotic genome annotation
                                           pipeline
            Annotation Software Version :: 8.6
            Annotation Method           :: Best-placed RefSeq; Gnomon
            Features Annotated          :: Gene; mRNA; CDS; ncRNA
            ##Genome-Annotation-Data-END##
FEATURES             Location/Qualifiers
     source          1..16
                     /organism="Bufo bufo"
                     /mol_type="mRNA"
                     /db_xref="taxon:8384"
                     /chromosome="11"
     gene            <1..>16
                     /gene="ADAMTSL4"
                     /note="Derived by automated computational analysis using
                     gene prediction method: Gnomon. Supporting evidence
                     includes similarity to: 13 long SRA reads, 12 Proteins,
                     and 100% coverage of the annotated genomic feature by
                     RNAseq alignments, including 8 samples with support for
                     all annotated introns"
                     /db_xref="GeneID:120982372"
     CDS             <1..>16
                     /gene="ADAMTSL4"
                     /codon_start=1
                     /product="ADAMTS-like protein 4 isoform X1"
                     /protein_id="XP_040268392.1"
                     /db_xref="GeneID:120982372"
                     /translation="MSNFQSLFLHLLILHLCHGSEKVSHRRSRQTVEDDPVENKIAGT
                     WGSWGPWSSCSQTCGVGVIERSRSCLSPYQQVPWVPRSEPSPHNIQPHPEPPFRDERG
                     SIYSMGPARPLYPLHIEREIAAPFVEPYVPRNPPPSRYNQFNRNAREEVFAGGSQPTY
                     ARREQPPYQRSTSNRGRTAPQSPETLWQASPLDMPFRQDALRAPETISIHRKPHQDVP
                     FNRRNNSRVDDSSWPFFPDSIPLLKPESWEEANPGRALPPLSPTKESRFSRRSRVRNA
                     IKPGRYGYGKVPFALPLLTEQDESQRFKRHHKLMTFGTTAIPRREKKKDLTATRKSLD
                     SPGEHGSESPGQAVDFPGTSSKTRAPSLRKTKRSSQTDYPSWPKESVNSSAQKMLYGF
                     QPSQHEGESSEHESPVVGEADSVLMVGRQIFNHGKTDTNLEADLSGMETEKEEDDPTE
                     NRNSGTLHGFSTSKTLEEKTPSTQSPPLKRASRPMQSDIVVQRMDIVIRKLASSHQSF
                     NGKNSHDEQVAQPQRQSKTPLQNSHATSDEEVKHGQDNHKSDSSHRPRSRSQRQSPYR
                     HSTDGSRAYQSIFRDHPSRPVQGDTWASLGGNPSLTFERGQDPRQSHHPNSDVPLSLY
                     NPGTEEFHCAGPKKQYKSCTQEPCPPGQPDARTLQCSTFNNQEFMGRLYQWEAFTEVS
                     GNQRCALNCRPIGYRFYVRHTEKVQDGTPCEAGSVDVCVDGQCLSPGCDGILGSNSTL
                     DTCGVCGGDGSTCKFITGTFKDTNIPIGYHKILEIPKGATQISVRELTWSPNYLALRN
                     RSGKPIINGNWAVDPPGKYEVGSTVFTYNQPGREEQEGESFTAPGPTSEALDVYMIFQ
```

```
                     QDNPGVSFQYFISSPPGSDNPSHISHVPQQENGPLRSMPSSSSLPQTNLRNNPVEERI
                     RVPPPQARPPRPAGTLQRNVRIPPLAAPPVPYWPEQPQFFWRRVGNTPCSVTCGKGFW
                     YPIYQCASRSSLDEVNEEECDSSTKPFPQEEACNTQPCPAFWDAGNWSVCSRTCGSGI
                     QHRQVLCRQMYANRTTMVHPQRCSHLVKPNVTQTCQLRICSQWEIQSNWSSCSVMCGL
                     GQRTRHVRCVSNQGDVIGEGECSNRLRPRTNEVCDMGPCVRSWFHNHWGSSCSSECGP
                     GIQRRSVFCLSSSSTDESQDGCPGNKPSDMRVCNSGPCERTVKWYTGPWSQCSTDCDE
                     GSQRRDVICISKMGSDFNVTDPSECAHLEKPPSLQSCNAGPCGSRWFTTPWSTCSQSC
                     EGGVQVREVRCLAADKTYSQQCDLDSKPDEKRACNPQPCSSVVDNNCRDLYHNCAVVV
                     QARLCVYAYYKQACCSSCAHSLQRRTSESR"
ORIGIN
        1 ccaggacggg cattgc
//
```

Range 1: 1136 to 1151 GenBank Graphics

```
Score         Expect  Identities     Gaps        Strand

32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Minus

CDS: Putative 1       5        L   A   R   G   P
Query                 3      GCAATGCCCGTCCTGG  18
                             ||||||||||||||||
Sbjct                 1151   GCAATGCCCGTCCTGG  1136
CDS:ADAMTS-like prot  256      L   A   R   G   P
```

/prodotto="ADAMTS-like protein 4 isoform X1"

ADAMTS-like protein 4

La **proteina simile ad ADAMTS 4** è una proteina che nell'uomo è codificata dal gene **ADAMTSL4**. Questo gene è un membro della **famiglia di geni ADAMTS** (*una disintegrina e metalloproteinasi con motivi di trombospondina*) e codifica per una proteina con sette ripetizioni di **trombospondina di tipo 1**. Il dominio ripetuto della trombospondina di tipo 1 si trova in molte proteine con diverse funzioni biologiche tra cui l'*adesione cellulare*, l'*angiogenesi* e il *patterning del sistema nervoso in via di sviluppo*. Sono state caratterizzate varianti di splicing trascrizionale alternative, codificanti diverse isoforme (https://en.wikipedia.org/wiki/ADAMTSL4). La proteina simile ad ADAMTS 4 è coinvolta nella *regolazione positiva dell'apoptosi* e può *facilitare la biogenesi delle microfibrille FBN1* (https://www.uniprot.org/uniprot/Q6UY14). Diverse proteine ADAMTS sono pesantemente implicate nei disordini genetici e acquisiti umani e animali (https://link.springer.com/protocol/10.1007/978-1-4939-9698-8_1).

Approfondimenti:
https://www.ncbi.nlm.nih.gov/gene?Db=gene&Cmd=DetailsSearch&Term=54507
https://www.sciencedirect.com/science/article/pii/S0021925819576487

Hyphomicrobium denitrificans 1NES1, complete genome
Sequence ID: CP005587.1Length: 3808687Number of Matches: 1
Range 1: 614719 to 614734 GenBank Graphics

```
Score           Expect  Identities       Gaps         Strand

32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Plus

CDS: Putative 1         5          A   I   G   T   R
Query                   2        CGCAATGCCCGTCCTG  17
                                 ||||||||||||||||
Sbjct                   614719   CGCAATGCCCGTCCTG  614734
CDS:major facilitato    205        A   I   G   T   R
```

/prodotto="major facilitator superfamily protein"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=304372

Luteimonas sp. MC1572 chromosome, complete genome
Sequence ID: CP067112.1Length: 3020716Number of Matches: 2
Range 1: 3007143 to 3007158 GenBank Graphics

```
Score           Expect  Identities       Gaps         Strand

32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Plus

CDS: Putative 1         1             M   P   V   L   V
Query                   4          CAATGCCCGTCCTGGT  19
                                   ||||||||||||||||
Sbjct                   3007143    CAATGCCCGTCCTGGT  3007158
CDS:winged helix-tur    162        P   M   P   V   L   V
```

/prodotto="winged helix-turn-helix domain-containing protein"

Approfondimenti: https://www.jbc.org/article/S0021-9258(19)54323-X/fulltext

Range 2: 1463044 to 1463058 GenBank Graphics

```
Score           Expect  Identities       Gaps         Strand

30.2 bits(15)  735    15/15(100%)  0/15(0%)  Plus/Plus

CDS: Putative 1         1           Q   C   P   S
Query                   3          GCAATGCCCGTCCTG  17
                                   |||||||||||||||
Sbjct                   1463044    GCAATGCCCGTCCTG  1463058
CDS:lipopolysacchari    373         Q   C   P   S   C
```

/prodotto="lipopolysaccharide assembly protein LapB"

Approfondimenti: https://www.uniprot.org/uniprot/P0AB60

Komagataeibacter medellinensis NBRC 3288 DNA, complete genome
Sequence ID: AP012159.1Length: 3136818Number of Matches: 1
Range 1: 3069479 to 3069494 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand


32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Minus


CDS: Putative 1       5          A   I   G   T   R

Query                 2         CGCAATGCCCGTCCTG  17

                                ||||||||||||||||

Sbjct                 3069494   CGCAATGCCCGTCCTG  3069479

CDS:cellulose syntha  892        A   I   G   T   R
```

/prodotto ="cellulose synthase operon protein C"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=377509

Wolbachia endosymbiont of Culex quinquefasciatus Pel strain wPip complete genome
Sequence ID: AM999887.1Length: 1482455Number of Matches: 20
Range 1: 46988 to 47003 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand


32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Minus


CDS: Putative 1   4          C   H   G   D

Query             1       ACGCAATGCCCGTCCT  16

                          ||||||||||||||||

Sbjct             47003   ACGCAATGCCCGTCCT  46988

CDS: transposase  187     V   C   H   G   D   E
```

/prodotto ="transposase (pseudogene)"

Lo studio della **trasposasi Tn5** è di importanza generale a causa delle sue somiglianze con l'**HIV -1** e altre **malattie retrovirali**. Studiando Tn5, si può scoprire molto anche su altre trasposasi e sulle loro attività (https://en.wikipedia.org/wiki/Transposase).

Physcomitrella patens mRNA for KINID1a, complete cds
Sequence ID: AB434497.1Length: 4242Number of Matches: 1
Related Information Gene-associated gene details
Range 1: 1752 to 1767 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand


32.2 bits(16)  186    16/16(100%)  0/16(0%)  Plus/Plus


CDS: Putative 1       1        N   A   R   P   G

Query                 4      CAATGCCCGTCCTGGT  19

                             ||||||||||||||||

Sbjct                 1752   CAATGCCCGTCCTGGT  1767

CDS:KINID1a [Physcom  518      N   A   R   P   G
```

/prodotto ="KINID1a"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=330404

Marinomonas primoryensis strain KMM3633 chromosome, complete genome
Sequence ID: CP054301.1Length: 4068722Number of Matches: 1
Range 1: 1210133 to 1210147 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	735	15/15(100%)	0/15(0%)	Plus/Minus

```
CDS: Putative 1       4          H   G   D   Q
Query                 4        CAATGCCCGTCCTGG  18
                               |||||||||||||||
Sbjct                 1210147  CAATGCCCGTCCTGG  1210133
CDS:D-erythritol 1-p  188      W   H   G   D   Q
```

/prodotto ="D-erythritol 1-phosphate dehydrogenase"

Approfondimenti: https://www.genome.jp/dbget-bin/www_bget?ec:1.1.1.402

Ralstonia solanacearum strain FJAT1458.F1 chromosome, complete genome
Sequence ID: CP052120.1Length: 3984237Number of Matches: 1
Range 1: 1674158 to 1674172 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	735	15/15(100%)	0/15(0%)	Plus/Plus

```
CDS: Putative 1       1          Q   C   P   S
Query                 3        GCAATGCCCGTCCTG  17
                               |||||||||||||||
Sbjct                 1674158  GCAATGCCCGTCCTG  1674172
CDS:toprim domain-co  30         Q   C   P   S   C
```

/prodotto ="toprim domain-containing protein"

Approfondimenti: http://www.ebi.ac.uk/interpro/entry/InterPro/IPR006171/

Pseudomonas sp. B14-6 chromosome, complete genome
Sequence ID: CP053929.1Length: 6766112Number of Matches: 1
Range 1: 5966259 to 5966273 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	735	15/15(100%)	0/15(0%)	Plus/Minus

```
CDS: Putative 1       1         R   N   A   R   P
Query                 2        CGCAATGCCCGTCCT  16
                               |||||||||||||||
Sbjct                 5966273  CGCAATGCCCGTCCT  5966259
CDS:DNA mismatch rep  357       R   N   A   R   P
```

/prodotto ="DNA mismatch repair protein MutS"

DNA mismatch repair protein MutS

MutS (**Mutator S**) è una ***proteina di riparazione del DNA di mismatch***, originariamente descritta in Escherichia coli. La riparazione del disadattamento contribuisce alla fedeltà complessiva della replicazione del DNA ed è essenziale per combattere gli effetti negativi dei danni al genoma. **Implica la correzione di coppie di basi non corrispondenti che sono state perse dall'elemento di correzione** (frammento di Klenow) del **complesso della DNA polimerasi**. Il Mismatch Repair System post-replicativo (**MMRS**) di Escherichia coli coinvolge le proteine MutS (Mutator S), MutL e MutH e agisce per correggere mutazioni puntiformi o piccoli loop di inserimento/delezione prodotti durante la replicazione del DNA (https://en.wikipedia.org/wiki/MutS-1).

Herbaspirillum rubrisubalbicans Os34, complete genome

Sequence ID: CP008956.1Length: 6122717Number of Matches: 1

Range 1: 5109907 to 5109921 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	735	15/15(100%)	0/15(0%)	Plus/Plus

```
CDS: Putative 1        1          Q  C  P  S
Query                  3         GCAATGCCCGTCCTG  17
                                 |||||||||||||||
Sbjct                  5109907   GCAATGCCCGTCCTG  5109921
CDS:excinuclease ABC   409        Q  C  P  S  C
```

/prodotto ="excinuclease ABC subunit UvrA"

Approfondimenti:
https://www.wikigenes.org/e/gene/e/914295.html
https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=234734
https://www.uniprot.org/uniprot/K7A743

Escherichia coli strain HB37 chromosome HB37, complete sequence

GenBank: CP053080.1

FASTA Graphics

Go to:

```
LOCUS       CP053080                  15 bp    DNA     linear   BCT 10-MAY-2020
DEFINITION  Escherichia coli strain HB37 chromosome HB37, complete sequence.
ACCESSION   CP053080 REGION: 4114372..4114386
VERSION     CP053080.1
DBLINK      BioProject: PRJNA629661
            BioSample: SAMN14785846
KEYWORDS    .
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (bases 1 to 15)
```

```
  AUTHORS   Pan,Y. and He,D.
  TITLE     Characterization of an E. coli strain HB37 carrying blaCTX-M-123
            and rmtB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 15)
  AUTHORS   Pan,Y. and He,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAY-2020) College of Animal Science and Veterinary
            Medicine, Henan Agricultural University, Wenhua Road No. 95,
            Zhengzhou, Henan 450002, China
COMMENT     The annotation was added by the NCBI Prokaryotic Genome Annotation
            Pipeline (PGAP). Information about PGAP can be found here:
            https://www.ncbi.nlm.nih.gov/genome/annotation_prok/

            ##Genome-Assembly-Data-START##
            Assembly Method       :: HGAP v. 2.3.0
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage       :: 152.1x
            Sequencing Technology :: Illumina NovaSeq; PacBio RSII
            ##Genome-Assembly-Data-END##
            ##Genome-Annotation-Data-START##
            Annotation Provider               :: NCBI
            Annotation Date                   :: 05/04/2020 14:08:26
            Annotation Pipeline               :: NCBI Prokaryotic Genome
                                                 Annotation Pipeline (PGAP)
            Annotation Method                 :: Best-placed reference protein
                                                 set; GeneMarkS-2+
            Annotation Software revision      :: 4.11
            Features Annotated                :: Gene; CDS; rRNA; tRNA; ncRNA;
                                                 repeat_region
            Genes (total)                     :: 5,379
            CDSs (total)                      :: 5,264
            Genes (coding)                    :: 4,962
            CDSs (with protein)               :: 4,962
            Genes (RNA)                       :: 115
            rRNAs                             :: 8, 7, 7 (5S, 16S, 23S)
            complete rRNAs                    :: 8, 7, 7 (5S, 16S, 23S)
            tRNAs                             :: 87
            ncRNAs                            :: 6
            Pseudo Genes (total)              :: 302
            CDSs (without protein)            :: 302
            Pseudo Genes (ambiguous residues) :: 0 of 302
            Pseudo Genes (frameshifted)       :: 188 of 302
            Pseudo Genes (incomplete)         :: 133 of 302
```

```
            Pseudo Genes (internal stop)      :: 41 of 302
            Pseudo Genes (multiple problems)  :: 52 of 302
            ##Genome-Annotation-Data-END##
FEATURES             Location/Qualifiers
     source          1..15
                     /organism="Escherichia coli"
                     /mol_type="genomic DNA"
                     /strain="HB37"
                     /host="chicken"
                     /db_xref="taxon:562"
                     /chromosome="HB37"
                     /country="China: Zhengzhou"
                     /collection_date="May-2017"
     gene            complement(<1..>15)
                     /locus_tag="HKW69_19850"
     CDS             complement(<1..>15)
                     /locus_tag="HKW69_19850"
                     /inference="COORDINATES: similar to AA
                     sequence:RefSeq:NP_414749.2"
                     /note="Derived by automated computational analysis using
                     gene prediction method: Protein Homology."
                     /codon_start=2
                     /transl_table=11
                     /product="class I SAM-dependent methyltransferase"
                     /protein_id="QJR26747.1"
                     /translation="MKPARVPQTVVAPDCWGDLPWGELYRKALERQLNPWFTKMYGFH
                     LLKIGNLSAEINCEACAVSHQVNVSAQGMPVLVQADPLHLPFADKSVDVCLLAHTLPW
                     CTDPHRLLREADRVLIDDGWLVISGFNPISLMGLRKLVPVLRKTSPYNSRMFTLMRQL
                     DWLSLLNFEVLHASRFHVLPWNKHGGKLLNAHIPALGCLQLIVARKRTIPLTLNPMKQ
                     SKNKPRIRQAVGATRQCRKPQA"
ORIGIN
            1 accaggacgg gcatt
//
```

Range 1: 4114372 to 4114386 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	735	15/15(100%)	0/15(0%)	Plus/Minus

```
CDS: Putative 1        1          M  P  V  L  V
Query                  5        AATGCCCGTCCTGGT  19
                                |||||||||||||||
Sbjct                  4114386  AATGCCCGTCCTGGT  4114372
CDS:class I SAM-depe   73         M  P  V  L  V
```

/prodotto="class I SAM-dependent methyltransferase"

Class I SAM-dependent methyltransferase

Le **metiltransferasi dipendenti dalla S- adenosil- L- metionina** (**SAM**) sono oggetto di studi approfonditi perché svolgono ruoli importanti nella metilazione delle biomolecole in tutti i domini della vita (https://pubs.acs.org/doi/10.1021/acschembio.8b00958). Le **metiltransferasi** sono un ampio gruppo di enzimi che **metilano** [nei sistemi biologici, la **metilazione** è compiuta dagli enzimi. La metilazione può modificare i metalli pesanti, regolare l'espressione genica, l'elaborazione dell'RNA e la funzione delle proteine. È stato riconosciuto come un processo chiave alla base dell'*epigenetica* (https://en.wikipedia.org/wiki/Methylation)]. Le **metiltransferasi** sono un ampio gruppo di enzimi che metilano tutti i loro substrati ma possono essere suddivisi in diverse sottoclassi in base alle loro caratteristiche strutturali (https://en.wikipedia.org/wiki/Methyltransferase). La **metilazione**, così come altre *modificazioni epigenetiche*, influenza la *trascrizione*, la *stabilità genica* e l'*imprinting parentale*. Ha un impatto diretto sulla *struttura della cromatina* e può modulare la *trascrizione genica*, o addirittura **silenziare o attivare completamente i geni**, **senza mutazioni nel gene stesso**. Sebbene i meccanismi di questo controllo genetico siano complessi, **l'ipo e l'ipermetilazione del DNA sono implicate in molte malattie** (https://en.wikipedia.org/wiki/Methyltransferase). Come con qualsiasi processo biologico che regola l'espressione e/o la funzione genica, la **metilazione anomala del DNA** è associata a **disordini genetici** come **ICF**, **sindrome di Rett** e **sindrome dell'X fragile** (https://en.wikipedia.org/wiki/Methyltransferase). Le **cellule cancerose** in genere mostrano una minore attività di metilazione del DNA in generale, sebbene spesso ipermetilazione in siti che non sono metilati nelle cellule normali; questa sovrametilazione spesso funziona come un modo per inattivare i **geni oncosoppressori** (https://en.wikipedia.org/wiki/Methyltransferase; https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=400514; https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=cl17173&spf=1; https://www.ebi.ac.uk/interpro/entry/InterPro/IPR002935/).

PREDICTED: Thalassophryne amazonica sterile alpha motif domain-containing protein 10-like (LOC117512513), transcript variant X2, mRNA

Sequence ID: XM_034172610.1Length: 1180Number of Matches: 1

Range 1: 639 to 653 GenBank Graphics

```
Score           Expect  Identities      Gaps        Strand

30.2 bits(15)  735    15/15(100%)  0/15(0%)  Plus/Minus

CDS: Putative 1        4       L  A  R  G
Query                  3     GCAATGCCCGTCCTG  17
                             |||||||||||||||
Sbjct                  653   GCAATGCCCGTCCTG  639
CDS:sterile alpha mo   126     L  A  R  G  T
```

/prodotto ="sterile alpha motif domain-containing protein 10-like"

Approfondimenti:

https://www.uniprot.org/uniprot/Q9BYL1

https://en.wikipedia.org/wiki/Sterile_alpha_motif

Aspergillus tanneri DEAH-box RNA helicase prp16 (PRP16), partial mRNA
Sequence ID: [XM_033569133.1](XM_033569133.1)Length: 2736Number of Matches: 1
Range 1: 2718 to 2732 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	735	15/15(100%)	0/15(0%)	Plus/Minus

```
CDS: Putative 1         4         A   R   G   P
Query                   5      AATGCCCGTCCTGGT  19
                               |||||||||||||||
Sbjct                   2732   AATGCCCGTCCTGGT  2718
CDS:DEAH-box RNA hel    911    F   A   R   G   P
```

/prodotto ="DEAH-box RNA helicase prp16"

Approfondimenti:

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1369694/
https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=224557

https://www.sciencedirect.com/science/article/pii/S0960982298701782

https://www.sciencedirect.com/science/article/abs/pii/S0968000420302681

PREDICTED: Epinephelus lanceolatus macrophage mannose receptor 1 (LOC117270034), mRNA
Sequence ID: XM_033647447.1Length: 7243Number of Matches: 1
Range 1: 1247 to 1261 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	735	15/15(100%)	0/15(0%)	Plus/Minus

```
CDS: Putative 1         4        H   G   D   Q
Query                   5      AATGCCCGTCCTGGT  19
                               |||||||||||||||
Sbjct                   1261   AATGCCCGTCCTGGT  1247
CDS:macrophage manno    381      H   G   D   Q   D
```

/prodotto ="macrophage mannose receptor 1"

Approfondimenti: https://www.uniprot.org/uniprot/P22897; https://www.genecards.org/cgi-bin/carddisp.pl?gene=MRC1

https://en.wikipedia.org/wiki/Mannose_receptor

Chryseobacterium sp. NEB161 chromosome, complete genome
Sequence ID: CP050993.1Length: 3543981Number of Matches: 1
Range 1: 3138059 to 3138073 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	735	15/15(100%)	0/15(0%)	Plus/Plus

```
CDS: Putative 1        1          N  A  R  P  G
Query                  4         CAATGCCCGTCCTGG  18
                                 |||||||||||||||
Sbjct                  3138059   CAATGCCCGTCCTGG  3138073
CDS:OmpH family oute   179        N  A  R  P  G
```

/prodotto ="OmpH family outer membrane protein"

Approfondimenti: https://pfam.xfam.org/family/OmpH; https://pubmed.ncbi.nlm.nih.gov/10085039/

Acinetobacter towneri strain 205 chromosome, complete genome
Sequence ID: CP048014.1Length: 2660496Number of Matches: 1
Range 1: 1392028 to 1392042 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	735	15/15(100%)	0/15(0%)	Plus/Plus

```
CDS: Putative 1        1         N  A  R  P  G
Query                  5         AATGCCCGTCCTGGT  19
                                 |||||||||||||||
Sbjct                  1392028   AATGCCCGTCCTGGT  1392042
CDS:YqiJ family prot   141       N  A  R  P  G
```

/prodotto ="YqiJ family protein"

Approfondimenti: https://www.uniprot.org/uniprot/P76657

Klebsiella pneumoniae strain FDAARGOS_1329 chromosome, complete genome
Sequence ID: CP069992.1Length: 5379413Number of Matches: 1
Range 1: 1962441 to 1962455GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	730	15/15(100%)	0/15(0%)	Plus/Plus

```
CDS: Putative 1        4          H  G  D  Q
Query                  1         AATGCCCGTCCTGGT  15
                                 |||||||||||||||
Sbjct                  1962441   AATGCCCGTCCTGGT  1962455
CDS:peptidoglycan DD   572        H  G  D  Q  N
```

/prodotto ="peptidoglycan DD-metalloendopeptidase family protein"

Approfondimenti: https://biocyc.org/gene?orgid=META&id=EG10013-MONOMER#tab=showAll

HIV-1 isolate L718b from Argentina envelope glycoprotein (env) gene, partial cds

GenBank: MT121191.1

FASTA Graphics PopSet

Go to:

```
LOCUS       MT121191                  15 bp    DNA     linear   VRL 29-MAR-2020
DEFINITION  HIV-1 isolate L718b from Argentina envelope glycoprotein (env)
            gene, partial cds.
ACCESSION   MT121191 REGION: 105..119
VERSION     MT121191.1
KEYWORDS    .
SOURCE      Human immunodeficiency virus 1 (HIV-1)
  ORGANISM  Human immunodeficiency virus 1
            Viruses; Riboviria; Pararnavirae; Artverviricota; Revtraviricetes;
            Ortervirales; Retroviridae; Orthoretrovirinae; Lentivirus.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Golemba,M.D., Aulicino,P.C. and Mangano,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-FEB-2020) Laboratorio de Biologia Celular y
            Retrovirus, Hospital de Pediatria 'Prof. Dr. Juan P. Garrahan',
            Combate de los Pozos 1881, Buenos Aires C1245AAM, Argentina
COMMENT     ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..15
                     /organism="Human immunodeficiency virus 1"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="L718b"
                     /isolation_source="PBMC"
                     /host="Homo sapiens"
                     /db_xref="taxon:11676"
                     /country="Argentina"
                     /collection_date="04-Mar-2008"
                     /note="subtype: F"
     gene            <1..>15
                     /gene="env"
     CDS             <1..>15
                     /gene="env"
                     /codon_start=2
                     /product="envelope glycoprotein"
                     /protein_id="QIQ19348.1"
                     /translation="NIQENTKTIIVQLKEPVQINCTRPNNNTRTSIQMGPGRAFYATG
                     DIIGDIRKAYCTVNKSHWNATLERVRAKLKDLFPNGTIKFASPPPGGDLEITMHHFSC
                     RGEFFYCNTSGLFNNSLVNGTINGTTYKGNETITLPCRIKQMINMWQQVGRAMYAAPI
```

```
                     AGKITCNSNITGLLLTRDGG"
ORIGIN
        1 accaggacgg gcatt //
```

Sequence ID: MT121191.1Length: 540Number of Matches: 1

See all Identical Proteins(IPG)

Range 1: 105 to 119 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand

30.2 bits(15)  735    15/15(100%)  0/15(0%)  Plus/Minus

CDS: Putative 1       4       A   R   G   P
Query                 5     AATGCCCGTCCTGGT   19
                            |||||||||||||||
Sbjct                 119   AATGCCCGTCCTGGT   105
CDS:envelope glycopr  40    F   A   R   G   P
```

/prodotto ="envelope glycoprotein"

Envelope glycoprotein

Envelope glycoprotein (*glicoproteina dell'involucro*) del **gene Env** (un *gene virale* che codifica per la proteina che forma l'**involucro virale**) [(https://en.wikipedia.org/wiki/Env_(gene)) e (https://en.wikipedia.org/wiki/Viral_envelope)].
Un **involucro virale** è lo strato più esterno di molti tipi di virus. Esso protegge il materiale genetico nel suo ciclo di vita quando viaggia tra le *cellule ospiti*. Gli involucri sono tipicamente derivati da *porzioni delle membrane delle cellule ospiti*, ma includono alcune glicoproteine *virali*. **Possono aiutare i virus a evitare il** sistema immunitario dell'ospite. Le **glicoproteine sulla superficie dell'involucro** servono per identificare e legarsi ai *siti recettori* sulla membrana dell'ospite. L'*involucro virale* si fonde quindi con la membrana dell'ospite, consentendo al *capside* (un altro *strato proteico*, tra l'*involucro* e il *genoma*) e al *genoma virale* di **entrare e infettare l'ospite**. La cellula da cui germoglia un virus spesso muore o si indebolisce e rilascia più **particelle virali** per un periodo prolungato (https://en.wikipedia.org/wiki/Viral_envelope). L'*involucro* del **doppio strato lipidico** di questi virus è relativamente sensibile all'*essiccazione*, al *calore*, al *sapone* e ai *detergenti*, quindi questi virus sono più facili da sterilizzare rispetto ai *virus senza involucro*, hanno una sopravvivenza limitata al di fuori degli ambienti dell'ospite e in genere devono trasferirsi direttamente da ospite a ospite. Tra i **Virus con involucro** (https://en.wikipedia.org/wiki/Viral_envelope), tra gli altri, annoveriamo i *Virus a DNA* (Herpesvirus), i Retrovirus (come l'*HIV*) e i Coronavirus (*Virus a RNA*). **I virus avvolti possiedono una grande adattabilità, possono cambiare in breve tempo per eludere il sistema immunitario e causare** *infezioni persistenti* (https://en.wikipedia.org/wiki/Viral_envelope), quelle che si verificano perché il corpo non è in grado di eliminare l'organismo dopo l'infezione iniziale (https://en.wikipedia.org/wiki/Infection#Persistent_infection). Il prodotto maturo del **gene *Env*** è la **proteina virale spike** (la cui notorietà ha raggiunto il grande pubblico perché molto nominata dall'inizio della ***pandemia del SARS-CoV-2***), che ha **due parti principali**: la *proteina di superficie* (SU) e la *proteina transmembrana* (TM). Il tropismo del virus (costituito dalle cellule e dai tessuti di un ospite che supportano la crescita di un particolare virus o batterio) è determinato dal dominio della **proteina SU** perché è responsabile della *funzione di legame del recettore del virus*. **Il dominio SU determina quindi la specificità del virus per una singola molecola recettoriale** (https://en.wikipedia.org/wiki/Env_(gene)).

Mycolicibacterium duvalii JCM 6396 DNA, complete genome
Sequence ID: AP022563.1Length: 5657388Number of Matches: 1
Range 1: 4573756 to 4573770 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand

30.2 bits(15)  735    15/15(100%)  0/15(0%)  Plus/Plus

CDS: Putative 1       1            M   P   V   L   V
Query                 5          AATGCCCGTCCTGGT   19
                                 |||||||||||||||
Sbjct                 4573756    AATGCCCGTCCTGGT   4573770
CDS:thiol reductase   54           M   P   V   L   V
```

/prodotto ="thiol reductase thioredoxin"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=412351

Cutibacterium acnes KPA171202 chromosome, complete genome
Sequence ID: CP025935.1Length: 2560634Number of Matches: 1
Range 1: 39242 to 39256 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand

30.2 bits(15)  739    15/15(100%)  0/15(0%)  Plus/Minus

CDS: Putative 1       4          C   H   G   D
Query                 1       ACGCAATGCCCGTCC   15
                              |||||||||||||||
Sbjct                 39256   ACGCAATGCCCGTCC   39242
CDS:CpaF family prot  335     V   C   H   G   D
```

/prodotto ="CpaF family protein"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=410874

Alistipes sp. dk3624 chromosome, complete genome
Sequence ID: CP045651.1Length: 3019767Number of Matches: 1
Range 1: 2013659 to 2013673 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand

30.2 bits(15)  739    15/15(100%)  0/15(0%)  Plus/Minus

CDS: Putative 1       1            Q   C   P   S
Query                 3          GCAATGCCCGTCCTG   17
                                 |||||||||||||||
Sbjct                 2013673    GCAATGCCCGTCCTG   2013659
CDS:DNA polymerase I  63           Q   C   P   S   C
```

/prodotto ="DNA polymerase III subunit delta"

Approfondimenti: https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=273213

Pipistrellus pipistrellus genome assembly, chromosome: 8

Sequence ID: LR862364.1Length: 83522093Number of Matches: 2

Range 1: 42830883 to 42830898 GenBank Graphics

```
Score             Expect  Identities        Gaps        Strand


32.2 bits(16)  187    16/16(100%)  0/16(0%)  Plus/Plus


Query   4          CAATGCCCGTCCTGGT   19
                   ||||||||||||||||
Sbjct   42830883   CAATGCCCGTCCTGGT   42830898
```

Range 2: 13360371 to 13360385 GenBank Graphics

```
Score             Expect  Identities        Gaps        Strand


30.2 bits(15)  739    15/15(100%)  0/15(0%)  Plus/Minus


Query   3          GCAATGCCCGTCCTG   17
                   |||||||||||||||
Sbjct   13360385   GCAATGCCCGTCCTG   13360371
```

PREDICTED: Falco cherrug mitochondrial antiviral signaling protein (MAVS), transcript variant X1, mRNA

Sequence ID: XM_027799969.1Length: 5499Number of Matches: 1

Related Information Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 885 to 899 GenBank Graphics

```
Score             Expect  Identities        Gaps        Strand


30.2 bits(15)  739    15/15(100%)  0/15(0%)  Plus/Plus


CDS: Putative 1         1       N  A  R  P
Query                   3    GCAATGCCCGTCCTG   17
                             |||||||||||||||
Sbjct                   885  GCAATGCCCGTCCTG   899
CDS:mitochondrial an    112  S  N  A  R  P
```

/prodotto ="mitochondrial antiviral-signaling protein"

Mitochondrial antiviral-signaling protein (MAVS)

La **proteina di segnalazione antivirale mitocondriale (MAVS)** è una proteina essenziale per l'**immunità innata antivirale**. **MAVS** si trova nella membrana esterna dei mitocondri, dei perossisomi e del reticolo endoplasmatico (ER). Dopo l'***infezione virale***, un gruppo di *proteine citosoliche* rileverà la presenza del virus e si legherà a MAVS, attivando così MAVS. L'attivazione di MAVS porta la cellula infettata da virus a secernere **citochine**. Ciò induce una risposta immunitaria che uccide le cellule infette viralmente dell'ospite, con conseguente eliminazione del virus (https://en.wikipedia.org/wiki/Mitochondrial_antiviral-signaling_protein). **La proteina MAVS induce l'apoptosi nelle cellule ospiti infettate da virus interagendo con una proteasi chiamata caspasi 8**. L'attivazione dell'apoptosi da parte della caspasi 8 è indipendente dalla via apoptotica Bax/Bak, la via principale dell'apoptosi nelle cellule. Alcuni **virus**, come il **citomegalovirus umano (HCMV)** e l'**epatite**

C (HCV), si sono adattati per sopprimere la funzione di MAVS nella **risposta immunitaria innata antivirale**, favorendo la replicazione virale. **HCMV** altera MAVS attraverso l'**inibitore della proteina dell'apoptosi (vMIA)** localizzato nei mitocondri virali, riducendo così la risposta delle citochine pro-infiammatorie. **vMIA** si localizza anche nel perossisoma dove vMIA interagisce con la proteina chaperone citoplasmatica Pex19, disabilitando il meccanismo di trasporto delle proteine di membrana dei perossisomi. Il *ceppo HCV NS3-NS4A* inattiva la segnalazione MAVS scindendo la proteina MAVS direttamente a monte del dominio di targeting della membrana MAVS nel MAM e nel perossisoma, prevenendo la segnalazione MAVS a valle (https://en.wikipedia.org/wiki/Mitochondrial_antiviral-signaling_protein). **L'espressione e la funzione di MAVS sono regolate a livello trascrizionale, post-trascrizionale e post-traduzionale**. A **livello trascrizionale**, le *specie reattive dell'ossigeno* (ROS) generate durante la risposta antivirale agiscono come un regolatore negativo. MAVS, inoltre, codifica una serie di varianti di splicing che sono state proposte per regolare MAVS. A **livello post-trascrizionale**, ci sono due siti traduzionali presenti su MAVS che possono generare due proteine di MAVS. Il sito di traduzione alternativo risiede a monte, con conseguente espressione di sMAVS. A **livello traslazionale**, proteine come una *famiglia di ubiquitina E3 ligasi* regolano l'attività di MAVS (https://en.wikipedia.org/wiki/Mitochondrial_antiviral-signaling_protein).

PREDICTED: Lepisosteus oculatus ataxin 3 (atxn3), transcript variant X2, mRNA
Sequence ID: XM_015350922.1Length: 2269Number of Matches: 1
Related Information
Gene-associated gene details Genome Data Viewer-aligned genomic context
Range 1: 1083 to 1097 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand


30.2 bits(15)  739     15/15(100%)  0/15(0%)  Plus/Plus


Query   2      CGCAATGCCCGTCCT   16
               |||||||||||||||
Sbjct   1083   CGCAATGCCCGTCCT   1097
```

ataxin 3 (atxn3)

Approfondimenti:https://www.uniprot.org/uniprot/P54252

PREDICTED: Toxotes jaculatrix plakophilin-1 (LOC121189643), transcript variant X1, mRNA
Sequence ID: XM_041049991.1Length: 5154Number of Matches: 1
Range 1: 1286 to 1300 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand


30.2 bits(15)  739     15/15(100%)  0/15(0%)  Plus/Plus


CDS: Putative 1        1      A  M  P  V  L
Query                  3     GCAATGCCCGTCCTG   17
                             |||||||||||||||
Sbjct                  1286  GCAATGCCCGTCCTG   1300
CDS:plakophilin-1 is   368    A  M  P  V  L
```

/prodotto ="plakophilin-1 isoform X1"

Plakophilin-1 è una proteina che nell'uomo è codificata dal ***gene PKP1***. Questo gene codifica per un **membro delle famiglie di geni arm-repeat** (armadillo) e **placofilina**. Le **proteine della placofilina** contengono numerose ripetizioni di armadillo, si localizzano nei desmosomi e nei nuclei cellulari e partecipano al collegamento delle caderine ai filamenti intermedi nel citoscheletro. Questa proteina può essere coinvolta nel reclutamento molecolare e nella stabilizzazione durante la formazione dei desmosomi. Le mutazioni in questo gene sono state associate alla ***sindrome da displasia ectodermica/fragilità cutanea***. **PKP1** ha dimostrato di interagire con la **Desmoplachina**. La **Desmoplachina** è una proteina nell'uomo codificata dal **gene DSP** (https://en.wikipedia.org/wiki/Plakophilin-1). *Le mutazioni in questo gene sono la causa di diverse cardiomiopatie, tra cui la cardiomiopatia dilatativa e la cardiomiopatia aritmogena del ventricolo destro* (https://en.wikipedia.org/wiki/Desmoplakin). Le mutazioni nel DSP sono state anche associate al *cheratoderma palmoplantare striato*. La *sindrome di Carvajal* deriva da una mutazione autosomica recessiva di un frameshift (7901delG) in DSP che si traduce in una combinazione delle condizioni di cui sopra, inclusa la *cardiomiopatia dilatativa*, *cheratoderma* e *capelli lanosi*. I pazienti con *sindrome di Carvajal* spesso soffrono di *insufficienza cardiaca in adolescenza*. È stato riportato un caso di eterozigosi composta per due mutazioni nonsenso del DSP con conseguente *epidermolisi bollosa acantolitica letale*. *Gli autoanticorpi contro la DSP sono un segno distintivo del pemfigo paraneoplastico della malattia autoimmune*. È stata riscontrata una **diminuzione dell'espressione della desmoplachina in pazienti con cancro orofaringeo e cancro al seno, che può alterare le proprietà di adesione cellula-cellula e propagare metastasi** (https://en.wikipedia.org/wiki/Desmoplakin).

Klebsiella pneumoniae strain 33Kpn9 chromosome, complete genome
Sequence ID: CP064296.1Length: 5464147Number of Matches: 1
Range 1: 2399506 to 2399520GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	730	15/15(100%)	0/15(0%)	Plus/Minus

```
CDS: Putative 1        4           H   G   D   Q
Query                  1         AATGCCCGTCCTGGT  15
                                 |||||||||||||||
Sbjct                  2399520   AATGCCCGTCCTGGT  2399506
CDS:Lysozyme RrrD [K   572         H   G   D   Q   N
```

/prodotto ="Lysozyme RrrD"

Lysozyme RrrD

Essenziale per la lisi della parete cellulare batterica, mostrando *attività idrolizzante della parete cellulare*. Esibisce attività litica contro il substrato della parete cellulare di E.coli e S.typhi. ArrD(YbcS) e ArrQ(YdfQ) sono omologhi distanti della proteina fago lambda lisozima R, come evidenziato da tutte e tre le corrispondenze con il profilo pfam00959 (valori E per pfam00959 risultati utilizzando la ricerca NCBI Conserved Domain (CD): [maggiori informazioni sono disponibili su EcoGene: EG13635] YbcS è un'endolisina codificata dal criptico profago lambdoide DLP12 [maggiori informazioni sono disponibili su EcoCyc: G6310] (https://www.mybiosource.com/recombinant-protein/probable-lysozyme-from-lambdoid-prophage-dlp12-arrd/1084992).

Approfondimenti: https://www.uniprot.org/uniprot/A0A066R5P2;

https://www.ebi.ac.uk/QuickGO/term/GO:0003796;

https://string-db.org/network/511145.b0555

Pipistrellus pipistrellus genome assembly, chromosome: 16
Sequence ID: LR862372.1Length: 46231460Number of Matches: 1
Range 1: 36121439 to 36121453 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	739	15/15(100%)	0/15(0%)	Plus/Minus

```
Query  4          CAATGCCCGTCCTGG  18
                  |||||||||||||||
Sbjct  36121453   CAATGCCCGTCCTGG  36121439
```

Klebsiella grimontii strain RHBSTW-00494 chromosome
Sequence ID: CP055991.1Length: 6029240Number of Matches: 1
Range 1: 1148221 to 1148235 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	730	15/15(100%)	0/15(0%)	Plus/Plus

```
CDS: Putative 1       4            H  G  D  Q
Query                 1          AATGCCCGTCCTGGT  15
                                 |||||||||||||||
Sbjct                 1148221    AATGCCCGTCCTGGT  1148235
CDS:DUF3380 domain-c  572          H  G  D  Q  N
```

/prodotto ="DUF3380 domain-containing protein"

Approfondimenti:

https://pubmed.ncbi.nlm.nih.gov/29109551/; https://pubmed.ncbi.nlm.nih.gov/27287318/

Human immunodeficiency virus type 1 proviral partial env gene for gp120 protein, V3V5 sequence, isolate 98CM.MP1020

GenBank: AJ554714.1

FASTA Graphics

Go to:

```
LOCUS       AJ554714                  15 bp    DNA     linear   VRL 25-JUL-2016
DEFINITION  Human immunodeficiency virus type 1 proviral partial env gene for
            gp120 protein, V3V5 sequence, isolate 98CM.MP1020.
ACCESSION   AJ554714 REGION: 142..156
VERSION     AJ554714.1
KEYWORDS    env gene; gp120 protein.
SOURCE      Human immunodeficiency virus 1 (HIV-1)
  ORGANISM  Human immunodeficiency virus 1
            Viruses; Riboviria; Pararnavirae; Artverviricota; Revtraviricetes;
            Ortervirales; Retroviridae; Orthoretrovirinae; Lentivirus.
REFERENCE   1
```

```
  AUTHORS   Vergne,L., Bourgeois,A., Mpoudi-Ngole,E., Mougnutou,R.,
            Mbuagbaw,J., Liegois,F., Laurent,C., Butel,C., Zekeng,L.,
            Delaporte,E. and Peeters,M.
  TITLE     Biological and genetic characteristics of HIV infections in
            Cameroon reveals dual group M and O infections and a correlation
            between SI-inducing phenotype of the predominant CRF02_AG variant
            and disease stage
  JOURNAL   Virology 310 (2), 254-266 (2003)
   PUBMED   12781713
REFERENCE   2  (bases 1 to 15)
  AUTHORS   Vergne,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAR-2003) Vergne L., UR36, IRD, 911 Av. Agropolis
            BP64501, 34394 Montpellier cedex 5, FRANCE
FEATURES             Location/Qualifiers
     source          1..15
                     /organism="Human immunodeficiency virus 1"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolate="98CM.MP1020"
                     /db_xref="taxon:11676"
                     /country="Cameroon"
                     /note="V3V5 sequence"
     gene            <1..>15
                     /gene="env"
     CDS             <1..>15
                     /gene="env"
                     /codon_start=2
                     /product="gp120 protein"
                     /protein_id="CAD87023.1"
                     /db_xref="GOA:Q70RB9"
                     /db_xref="InterPro:IPR000777"
                     /db_xref="UniProtKB/TrEMBL:Q70RB9"
                     /translation="HCSRRIIIVRSENITDNAKTIIIQFVEPVNITCIRPNNSTRKSI
                     YIGPGRAFYATDRIIGDIRKAHCIVSRAAWNKTLQKVGEQLRKYFNNKTIIFTKSSGG
                     DIEITTHSFNCGGEFFYCYTSGLFNSTWNGTVSSDTNNTENITLPCRIKQIVHMWQRV
                     GQAMYAPPIPGVIKCESNITGLLLTRDGGNGNHSQNETFRPGGGI"
ORIGIN
            1 accaggacgg gcatt
//
```

Sequence ID: AJ554714.1Length: 616Number of Matches: 1
Range 1: 142 to 156 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	739	15/15(100%)	0/15(0%)	Plus/Minus

```
CDS: Putative 1        4       A   R   G   P
Query                  5    AATGCCCGTCCTGGT  19
                            |||||||||||||||
Sbjct                  156  AATGCCCGTCCTGGT  142
CDS:gp120 protein, p   52   F   A   R   G   P
```

/prodotto ="gp120 protein"

Envelope glycoprotein, gp120

“L’ingresso del **virus dell’immunodeficienza umana (HIV)** nelle cellule richiede l’interazione sequenziale della **glicoproteina dell’involucro esterno virale, gp120**, con la **glicoproteina CD4** e un **recettore per le chemochine sulla superficie cellulare**. Queste interazioni avviano una fusione delle membrane virali e cellulari. Sebbene **gp120 possa suscitare anticorpi neutralizzanti il virus**, **l’HIV sfugge al sistema immunitario**.” (https://pubmed.ncbi.nlm.nih.gov/9641677/).

3.2 LA SEQUENZA "AES (1)" E I RISULTATI DELLA RICERCA BLAST

Quella mostrata qui di seguito è la sequenza totale del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*.

C TCGAGCTGGT ACTGCATGC**A** 3900
CGCAATGCTA GCTGCCCCTT TCCCGTCCTG GGTACCCCGA GTCTCCCCCG 3950
ACCTCGGGTC CCAGGTATGC TCCCACCTCC ACCTGCCCCA CTCACCACCT 4000
CTGCTAGTTC CAGACACCTC CCAAGCACGC AGCAATGCAG CTCAAAACGC 4050
TTAGCCTAGC CACACCCCCA CGGGAAACAG CAGTGATTAA CCTTTAGCAA 4100
TAAACGAAAG TTTAACTAAG CTATACTAAC CCCAGGGTTG GTCAATTTCG 4150
TGCCAGCCAC ACCCTGGAGC TAGC

Le **lettere nere in grassetto** sono le lettere poste tra i **TRE spezzoni di sequenza** che costituiscono la **Sequenza "HIV-1"** (la sequenza discussa nel paragrafo precedente). La sequenza **Query** ("**ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGGT**") mostrata sotto è formata dai segmenti della **Sequenza "HIV-1"** e dalle lettere che li dividono. Questa nuova sequenza è stata definita **Sequenza "AES (1)"** (***Amino-terminal Enhancer of Split*** *o potenziatore ammino-terminale dell'mRNA diviso*. Per il significato di **AES** si rimanda allo studio del Capitolo II di questo documento). Questa sequenza è stata sottoposta ad una ricerca BLAST e nelle pagine seguenti sono mostrati gli *allineamenti significativi* ottenuti e gli "**organismi**" e i "**prodotti**" a cui tali allineamenti si riferiscono. **I risultati dei "prodotti" identificati dalla ricerca BLAST sono coerenti** (ovvero l'atteso ***Amino-terminal Enhancer of Split***, uno dei componenti principali del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*) **con quanto dichiarato nel documento scaricato dalla WHO** (https://berthub.eu/articles/11889.doc), documento relativo al "codice sorgente" integrale del Vaccino mRNA Sars-Cov-2 BioNTech/Pfizer (BNT162b2). In altri termini, le **sorprese** mostrate nel paragrafo precedente dalla ricerca BLAST su alcune parti costituenti la **Sequenza "AES (1)"** (le parti corrispondenti alla **Sequenza "HIV-1"**) emergono **SOLO** se alcuni elementi costitutivi della stessa (le **lettere in grassetto**) vengono omessi, ottenendo così la **Sequenza "HIV-1"**.

QUERY: ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGGT

earch Parameters

Program	blastn
Word size	28
Expect value	0.05
Hitlist size	**5000**
Match/Mismatch scores	1,-2
Gapcosts	0,2.5
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

SEQUENCES SELECTED: 32

Description	Name	Taxid	Score	Score	cover	Value	Ident	Len	Accession
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	65.9	65.9	97%	8,00E-08	100.00	1805	XM_034945921.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	62.1	62.1	97%	4,00E-07	100.00	1805	XM_034945921.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	62.1	62.1	97%	4,00E-07	100.00	1808	XM_034945920.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	62.1	62.1	97%	4,00E-07	100.00	1731	XM_034945919.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	62.1	62.1	97%	4,00E-07	100.00	1891	XM_034945918.1
PREDICTED: Hylobates moloch TLE family member 5, transcription...	silvery gibbon	81572	62.1	62.1	97%	4,00E-07	100.00	1672	XM_032176817.1
PREDICTED: Nomascus leucogenys TLE family member 5,...	northern whi...	61853	62.1	62.1	97%	4,00E-07	100.00	1839	XM_030795556.1
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	62.1	62.1	97%	4,00E-07	100.00	1798	NM_001130.6
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	62.1	62.1	97%	4,00E-07	100.00	1795	NM_198970.2
Eukaryotic synthetic construct chromosome 19	NA	111789	62.1	124	97%	4,00E-07	100.00	64242768	CP034522.1
Eukaryotic synthetic construct chromosome 19	NA	111789	62.1	124	97%	4,00E-07	100.00	64242768	CP034497.1
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	62.1	62.1	97%	4,00E-07	100.00	1512	XM_016937029.2
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	62.1	62.1	97%	4,00E-07	100.00	1683	XM_016937028.2
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	62.1	62.1	97%	4,00E-07	100.00	1693	XM_016937027.2
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	62.1	62.1	97%	4,00E-07	100.00	1888	XM_024351913.1
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	62.1	62.1	97%	4,00E-07	100.00	1891	XM_024351912.1
Homo sapiens chromosome 19 groucho protein homolog (AES) gene,...	human	9606	62.1	62.1	97%	4,00E-07	100.00	12683	AH007143.2
PREDICTED: Homo sapiens TLE family member 5, transcriptional...	human	9606	62.1	62.1	97%	4,00E-07	100.00	1881	XM_006722664.1
Homo sapiens isolate CHM13 chromosome 19	human	9606	62.1	62.1	97%	4,00E-07	100.00	61707364	CP068259.2
Homo sapiens DNA, chromosome 19, nearly complete genome	human	9606	62.1	62.1	97%	4,00E-07	100.00	59105444	AP023479.1
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	62.1	62.1	97%	4,00E-07	100.00	17057	NG_029870.1
Homo sapiens cDNA clone IMAGE:3464459, **** WARNING: chimeric...	human	9606	62.1	62.1	97%	4,00E-07	100.00	2395	BC040415.1
Homo sapiens cDNA clone IMAGE:4120426, **** WARNING: chimeric...	human	9606	62.1	62.1	97%	4,00E-07	100.00	3387	BC007797.1
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	62.1	62.1	97%	4,00E-07	100.00	1754	NM_198969.1
Homo sapiens cDNA FLJ37835 fis, clone BRSSN2010110, weakly...	human	9606	62.1	62.1	97%	4,00E-07	100.00	3276	AK095154.1
Homo sapiens cDNA FLJ37272 fis, clone BRAMY2012091,	human	9606	62.1	62.1	97%	4,00E-07	100.00	1884	AK094591.1

highly...									
Homo sapiens PP2150 mRNA, complete cds	human	9606	62.1	62.1	97%	4,00E-07	100.00	1035	AF269289.1
Homo sapiens chromosome 19, cosmid F23613, complete sequence	human	9606	62.1	62.1	97%	4,00E-07	100.00	42301	AC005944.1
Homo sapiens gp130 associated protein GAM mRNA, complete cds	human	9606	62.1	62.1	97%	4,00E-07	100.00	1317	AF072902.1
Human homolog of Drosophila enhancer of split m9/m10 mRNA,...	human	9606	62.1	62.1	97%	4,00E-07	100.00	1288	U04241.1
PREDICTED: Gorilla gorilla gorilla TLE family member 5,...	western lowl...	9595	56.5	56.5	97%	2,00E-05	96.97	1586	XM_031007483.1
PREDICTED: Gorilla gorilla gorilla TLE family member 5,...	western lowl...	9595	56.5	56.5	97%	2,00E-05	96.97	1804	XM_031007481.1
PREDICTED: Gorilla gorilla gorilla TLE family member 5,...	western lowl...	9595	56.5	56.5	97%	2,00E-05	96.97	1807	XM_031007480.1

SELEZIONE DI ALLINEAMENTI SIGNIFICATIVI

PREDICTED: Pan paniscus TLE family member 5, transcriptional modulator (TLE5), transcript variant X1, mRNA

Sequence ID: XM_034945918.1Length: 1891Number of Matches: 1

Range 1: 1384 to 1416 GenBank Graphics

```
Score           Expect  Identities        Gaps          Strand


62.1 bits(33)  4e-07  33/33(100%)  0/33(0%)  Plus/Plus


Query  1      ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
              |||||||||||||||||||||||||||||||||
Sbjct  1384   ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  1416
```

PREDICTED: Hylobates moloch TLE family member 5, transcriptional modulator (TLE5), mRNA

Sequence ID: XM_032176817.1Length: 1672Number of Matches: 1

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Range 1: 1161 to 1193 GenBank Graphics

```
Score           Expect  Identities        Gaps          Strand


62.1 bits(33)  4e-07  33/33(100%)  0/33(0%)  Plus/Plus


Query  1      ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
              |||||||||||||||||||||||||||||||||
Sbjct  1161   ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  1193
```

PREDICTED: Nomascus leucogenys TLE family member 5, transcriptional modulator (TLE5), mRNA

Sequence ID: XM_030795556.1Length: 1839Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 1329 to 1361 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
62.1 bits(33)	4e-07	33/33(100%)	0/33(0%)	Plus/Plus

```
Query  1     ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
             |||||||||||||||||||||||||||||||||
Sbjct  1329  ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  1361
```

Eukaryotic synthetic construct chromosome 19

Sequence ID: CP034522.1Length: 64242768Number of Matches: 2

Range 1: 2993384 to 2993416GenBankGraphicsNext MatchPrevious Match

Score	Expect	Identities	Gaps	Strand
62.1 bits(33)	4e-07	33/33(100%)	0/33(0%)	Plus/Minus

```
Query  1        ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
                |||||||||||||||||||||||||||||||||
Sbjct  2993416  ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  2993384
```

Range 2: 61383254 to 61383286 GenBank Graphics

Alignment statistics for match #2

Score	Expect	Identities	Gaps	Strand
62.1 bits(33)	4e-07	33/33(100%)	0/33(0%)	Plus/Minus

```
Query  1         ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
                 |||||||||||||||||||||||||||||||||
Sbjct  61383286  ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  61383254
```

PREDICTED: Pan troglodytes amino-terminal enhancer of split (AES), transcript variant X1, mRNA

Sequence ID: XM_024351912.1Length: 1891Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 1384 to 1416 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
62.1 bits(33)	4e-07	33/33(100%)	0/33(0%)	Plus/Plus

```
Query  1     ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
             |||||||||||||||||||||||||||||||||
Sbjct  1384  ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  1416
```

Homo sapiens chromosome 19 groucho protein homolog (AES) gene, complete cds GenBank: AH007143.2

FASTA Graphics

Go to:

```
LOCUS       AH007143                  33 bp    DNA     linear   PRI 10-JUN-2016
DEFINITION  Homo sapiens chromosome 19 groucho protein homolog (AES) gene,
            complete cds.
ACCESSION   AH007143 REGION: 11846..11878
VERSION     AH007143.2
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Miyasaka,H., Choudhury,B.K., Hou,E.W. and Li,S.S.
  TITLE     Molecular cloning and expression of mouse and human cDNA encoding
            AES and ESG proteins with strong similarity to Drosophila enhancer
            of split groucho protein
  JOURNAL   Eur. J. Biochem. 216 (1), 343-352 (1993)
   PUBMED   8365415
REFERENCE   2  (bases 1 to 33)
  AUTHORS   Hou,E.W. and Li,S.S.-L.
  TITLE     Genomic organization and in situ localization to chromosome 19p13.3
            of human AES gene: the gene product exhibiting strong similarity to
            the amino-terminal domain of Drosophila enhancer of split groucho
            protein
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 33)
  AUTHORS   Hou,E.W. and Li,S.S.-L.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-FEB-1997) Laboratory of Molecular Genetics, National
             Institute of Environmental Health Science, Mail Drop D3-05, P.O.
             Box 12233, Research Triangle Park, NC 27709, USA
COMMENT     On or before Jun 10, 2016 this sequence version replaced U88831.1,
            U88832.1, AH007143.1.
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /map="19p13.3"
                     /tissue_type="lymphocyte and umbilical cord"
ORIGIN
        1 acgcaatgct agctgcccct ttcccgtcct ggg
```

Homo sapiens chromosome 19 groucho protein homolog (AES) gene, complete cds

Sequence ID: AH007143.2Length: 12683Number of Matches: 1

Related Information
Gene-associated gene details
GEO Profiles-microarray expression data
Range 1: 11846 to 11878 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
62.1 bits(33)	4e-07	33/33(100%)	0/33(0%)	Plus/Plus

```
Query  1      ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
              |||||||||||||||||||||||||||||||||
Sbjct  11846  ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  11878
```

PREDICTED: Homo sapiens TLE family member 5, transcriptional modulator (TLE5), transcript variant X1, mRNA

NCBI Reference Sequence: XM_006722664.1

FASTA Graphics

Go to:

```
LOCUS       XM_006722664              33 bp    mRNA    linear   PRI 16-MAY-2021
DEFINITION  PREDICTED: Homo sapiens TLE family member 5, transcriptional
            modulator (TLE5), transcript variant X1, mRNA.
ACCESSION   XM_006722664 REGION: 1373..1405
VERSION     XM_006722664.1
DBLINK      BioProject: PRJNA168
KEYWORDS    RefSeq.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
COMMENT     MODEL REFSEQ:  This record is predicted by automated computational
            analysis. This record is derived from a genomic sequence
            (NC_000019.10) annotated using gene prediction method: Gnomon,
            supported by mRNA and EST evidence.
            Also see:
                Documentation of NCBI's Annotation Process

            ##Genome-Annotation-Data-START##
            Annotation Provider         :: NCBI
            Annotation Status           :: Updated annotation
            Annotation Name             :: Homo sapiens Updated Annotation
                                           Release 109.20210514
            Annotation Version          :: 109.20210514
            Annotation Pipeline         :: NCBI eukaryotic genome annotation
                                           pipeline
```

```
            Annotation Software Version :: 8.6
            Annotation Method           :: Best-placed RefSeq; propagated
                                           RefSeq model
            Features Annotated          :: Gene; mRNA; CDS; ncRNA
            ##Genome-Annotation-Data-END##
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="19"
     gene            <1..>33
                     /gene="TLE5"
                     /gene_synonym="AES; AES-1; AES-2; ESP1; GRG; Grg-5; GRG5"
                     /note="TLE family member 5, transcriptional modulator;
                        Derived by automated computational analysis using gene
                        prediction method: Gnomon. Supporting evidence includes
                        similarity to: 1 mRNA, 340 ESTs, 104 long SRA reads, and
                        100% coverage of the annotated genomic feature by RNAseq
                        alignments, including 150 samples with support for all
                        annotated introns"
                     /db_xref="GeneID:166"
                     /db_xref="HGNC:HGNC:307"
                     /db_xref="MIM:600188"
ORIGIN
        1 acgcaatgct agctgcccct ttcccgtcct ggg
//
```

PREDICTED: Homo sapiens TLE family member 5, transcriptional modulator (TLE5), transcript variant X1, mRNA

Sequence ID: XM_006722664.1Length: 1881Number of Matches: 1

Related Information

Gene-associated gene details

PubChem BioAssay-bioactivity screening

Genome Data Viewer-aligned genomic context

Range 1: 1373 to 1405 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
62.1 bits(33)	4e-07	33/33(100%)	0/33(0%)	Plus/Plus

```
Query  1     ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
             |||||||||||||||||||||||||||||||||
Sbjct  1373  ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  1405
```

Homo sapiens isolate CHM13 chromosome 19

Sequence ID: CP068259.2Length: 61707364Number of Matches: 1

Range 1: 3026839 to 3026871 GenBank Graphics

```
Score          Expect  Identities      Gaps        Strand

62.1 bits(33)  4e-07  33/33(100%)  0/33(0%)  Plus/Minus

Query  1         ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
                 |||||||||||||||||||||||||||||||||
Sbjct  3026871   ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  3026839
```

Homo sapiens DNA, chromosome 19, nearly complete genome

Sequence ID: AP023479.1Length: 59105444Number of Matches: 1

Range 1: 2910646 to 2910678 GenBank Graphics

```
Score          Expect  Identities      Gaps        Strand

62.1 bits(33)  4e-07  33/33(100%)  0/33(0%)  Plus/Minus

Query  1         ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
                 |||||||||||||||||||||||||||||||||
Sbjct  2910678   ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  2910646
```

Homo sapiens TLE family member 5, transcriptional modulator (TLE5), RefSeqGene on chromosome 19

Sequence ID: NG_029870.1Length: 17057Number of Matches: 1

Range 1: 14549 to 14581 GenBank Graphics

```
Score          Expect  Identities      Gaps        Strand

62.1 bits(33)  4e-07  33/33(100%)  0/33(0%)  Plus/Plus

Query  1       ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
               |||||||||||||||||||||||||||||||||
Sbjct  14549   ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  14581
```

Homo sapiens cDNA clone IMAGE:3464459, **** WARNING: chimeric clone ****

Sequence ID: BC040415.1Length: 2395Number of Matches: 1

Related Information

GEO Profiles-microarray expression data

Range 1: 1299 to 1331 GenBank Graphics

```
Score          Expect  Identities      Gaps        Strand

62.1 bits(33)  4e-07  33/33(100%)  0/33(0%)  Plus/Minus

Query  1      ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
              |||||||||||||||||||||||||||||||||
Sbjct  1331   ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  1299
```

Homo sapiens cDNA clone IMAGE:4120426, **** WARNING: chimeric clone ****

Sequence ID: BC007797.1Length: 3387Number of Matches: 1

Related Information GEO Profiles-microarray expression data
Range 1: 3110 to 3142 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
62.1 bits(33)	4e-07	33/33(100%)	0/33(0%)	Plus/Plus

```
Query  1     ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
             |||||||||||||||||||||||||||||||||
Sbjct  3110  ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  3142
```

Homo sapiens cDNA FLJ37835 fis, clone BRSSN2010110, weakly similar to GRG PROTEIN

Sequence ID: AK095154.1Length: 3276Number of Matches: 1

Related Information Gene-associated gene details PubChem BioAssay-bioactivity screening
Range 1: 2768 to 2800 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
62.1 bits(33)	4e-07	33/33(100%)	0/33(0%)	Plus/Plus

```
Query  1     ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
             |||||||||||||||||||||||||||||||||
Sbjct  2768  ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  2800
```

Homo sapiens cDNA FLJ37272 fis, clone BRAMY2012091, highly similar to Homo sapiens amino-terminal enhancer of split (AES), transcript variant 1, mRNA

Sequence ID: AK094591.1Length: 1884Number of Matches: 1

Related Information Gene-associated gene details PubChem BioAssay-bioactivity screening
Range 1: 1377 to 1409 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
62.1 bits(33)	4e-07	33/33(100%)	0/33(0%)	Plus/Plus

```
Query  1     ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
             |||||||||||||||||||||||||||||||||
Sbjct  1377  ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  1409
```

Homo sapiens PP2150 mRNA, complete cds

GenBank: AF269289.1

FASTA Graphics

Go to:

```
LOCUS       AF269289                  33 bp    mRNA    linear   PRI 15-JAN-2002
DEFINITION  Homo sapiens PP2150 mRNA, complete cds.
ACCESSION   AF269289 REGION: 684..716
VERSION     AF269289.1
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Zhang,P.P., Zhou,X.M., Jiang,H.Q., Huang,Y., Qin,W.X., Wan,D.F. and
            Gu,J.R.
  TITLE     Novel Human cDNA clones with function of inhibiting cancer cell
            growth
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 33)
  AUTHORS   Zhang,P.P., Zhou,X.M., Jiang,H.Q., Huang,Y., Qin,W.X., Wan,D.F. and
            Gu,J.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-2000) National Laboratory For Oncogenes & Related
             Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, Shanghai
             200032, P. R. China
FEATURES             Location/Qualifiers
     source          1..33
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     gene            <1..>33
                     /gene="PP2150"
     CDS             <1..>33
                     /gene="PP2150"
                     /codon_start=3
                     /product="unknown"
                     /protein_id="AAG23172.1"
                     /translation="MGDQVPREQDLAKRSSPGPSPVLNMCNRQSAWATALSPWYCMHA
                      MLAAPFPSWAPRVSPDPGSQVCSHLHLPHSPPLLVPDTSTPTWSSPIAHKRGGTRDELS"
ORIGIN
        1 acgcaatgct agctgcccct ttcccgtcct ggg
//
```

Related Information Gene-associated gene details GEO Profiles-microarray expression data
PubChem BioAssay-bioactivity screening
Range 1: 684 to 716 GenBank Graphics

```
Score           Expect  Identities       Gaps        Strand

62.1 bits(33)  4e-07  33/33(100%)  0/33(0%)  Plus/Plus

CDS: Putative 1        1        A  M  L  A  A  P  F  P  S  W
Query                    1     ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
                               |||||||||||||||||||||||||||||||||
Sbjct                    684   ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  716
CDS:unknown [Homo sa     43    H  A  M  L  A  A  P  F  P  S  W
```

Homo sapiens chromosome 19, cosmid F23613, complete sequence

Sequence ID: AC005944.1Length: 42301Number of Matches: 1

Related Information Genome Data Viewer-aligned genomic context
Range 1: 4634 to 4666 GenBank Graphics

```
Score            Expect  Identities        Gaps        Strand


62.1 bits(33)  4e-07  33/33(100%)  0/33(0%)  Plus/Minus


Query  1      ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33

              |||||||||||||||||||||||||||||||||

Sbjct  4666   ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  4634
```

Homo sapiens gp130 associated protein GAM mRNA, complete cds

Sequence ID: AF072902.1Length: 1317Number of Matches: 1

Related Information Gene-associated gene details GEO Profiles-microarray expression data
PubChem BioAssay-bioactivity screening
Range 1: 1071 to 1103 GenBank Graphics

```
Score            Expect  Identities        Gaps        Strand


62.1 bits(33)  4e-07  33/33(100%)  0/33(0%)  Plus/Plus


Query  1      ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33

              |||||||||||||||||||||||||||||||||

Sbjct  1071   ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  1103
```

La glicoproteina 130 (nota anche come **gp130**, **IL6ST**, **IL6-beta** o **CD130**) è una proteina transmembrana che è il membro fondatore della classe di tutti i **recettori delle citochine**. Forma una subunità del recettore delle **citochine di tipo I** all'interno della **famiglia dei recettori IL-6**. Viene spesso definita **subunità gp130** comune ed è importante per la **trasduzione del segnale dopo l'impegno delle citochine** (https://en.wikipedia.org/wiki/Glycoprotein_130). Come con altri *recettori delle citochine di tipo I*, *gp130* possiede un motivo amminoacidico *WSXWS* che assicura il corretto ripiegamento delle proteine e legame del ligando. Interagisce con le **Janus chinasi** per suscitare un segnale intracellulare a seguito dell'interazione del recettore con il suo ligando. Strutturalmente, gp130 è composto da **cinque domini di fibronectina di tipo III** e un **dominio di tipo C2 simile a immunoglobulina** (immunoglobulin-like) **nella sua porzione extracellulare** (https://en.wikipedia.org/wiki/Glycoprotein_130). **I membri della famiglia dei recettori IL-6 complessi con gp130 sono utilizzati per la trasduzione del segnale**. Ad esempio, IL-6 si lega al recettore IL-6. Il complesso di queste due proteine si associa quindi a gp130. Questo complesso di 3 proteine poi omodimerizza per formare un complesso esamerica che può produrre segnali a valle. Ci sono molte altre proteine che si associano a gp130, come la **cardiotropina 1 (CT-1)**, il **fattore inibitorio della leucemia (LIF)**, il **fattore neurotrofico ciliare (CNTF)**, **l'oncostatina M (OSM) e IL-11**. Ci sono anche molte altre proteine che hanno una somiglianza strutturale con gp130 e contengono il motivo WSXWS e residui di cisteina conservati. I membri di questo gruppo includono LIF-R, OSM-R e G-CSF-R (https://en.wikipedia.org/wiki/Glycoprotein_130). gp130 è una parte importante di molti diversi tipi di complessi di segnalazione. *L'inattivazione di gp130 è letale per i* ***topi***. I topi omozigoti che nascono mostrano una serie di difetti compreso lo *sviluppo alterato del miocardio ventricolare*. Gli *effetti ematopoietici* includevano un *numero ridotto di cellule staminali nella milza e nel fegato*. gp130 non ha attività tirosina chinasi intrinseca. Viene invece fosforilata sui residui di tirosina dopo la complessazione con altre proteine. La fosforilazione porta all'associazione con le tirosin chinasi JAK /Tyk e con i fattori di trascrizione della proteina STAT. In particolare, viene attivato STAT-3 che porta all'attivazione di molti geni a valle. Altre vie attivate includono la segnalazione RAS e MAPK (https://en.wikipedia.org/wiki/Glycoprotein_130).

Human homolog of Drosophila enhancer of split m9/m10 mRNA, complete cds

Sequence ID: U04241.1Length: 1288Number of Matches: 1

Related Information Gene-associated gene details
GEO Profiles-microarray expression data PubChem BioAssay-bioactivity screening
Range 1: 1032 to 1064 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
62.1 bits(33)	4e-07	33/33(100%)	0/33(0%)	Plus/Plus

```
Query  1     ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
             |||||||||||||||||||||||||||||||||
Sbjct  1032  ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  1064
```

PREDICTED: Gorilla gorilla gorilla TLE family member 5, transcriptional modulator (TLE5), transcript variant X1, mRNA

Sequence ID: XM_031007480.1Length: 1807Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 1301 to 1333 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
56.5 bits(30)	2e-05	32/33(97%)	0/33(0%)	Plus/Plus

```
Query  1     ACGCAATGCTAGCTGCCCCTTTCCCGTCCTGGG  33
             || ||||||||||||||||||||||||||||||
Sbjct  1301  ACACAATGCTAGCTGCCCCTTTCCCGTCCTGGG  1333
```

CAPITOLO IV

LA SEQUENZA “ANTHRAX”, “AES (2)” E I RISULTATI DELLE RICERCHE BLAST

OBIETTIVI DEL CAPITOLO IV

In questo capitolo sono mostrati i risultati delle ricerche BLAST effettuate su **due sequenze**:

1) la **Sequenza "ANTHRAX"** (**CCGTCCTGGAGACACCTCCC**), la **seconda sequenza** ottenuta dalla fusione di **DUE** segmenti di sequenza non contigui del *3'-UTR*;

2) la **Sequenza "AES (2)"** (**CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCG GGTCCCAGGTATGCTCCCACCTCCACCTGCCCCACTCACCACCTCTGCTA GTTCCAGACACCTCC**), l'***Amino-terminal Enhancer of Split*** *o potenziatore ammino-terminale dell'mRNA diviso*, uno dei componenti principali del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer* (per il significato di **AES** si rimanda allo studio del Capitolo II di questo documento).

La **Sequenza "ANTHRAX"** è così chiamata perché i **Bacilli Paranthracis** e, soprattutto, **Anthracis** sono i ***due organismi*** più sconcertanti identificati dalla ricerca BLAST. Sono state riscontrate **10** sequenze del batterio **Paranthracis** e ben **155** sequenze del batterio **Anthracis** (quest'ultimo è considerato una temibile arma batteriologica ed è stato già ampiamente discusso in "I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis). I **5 aminoacidi**, che sono parte del "prodotto" dei due organismi sopra identificati, si riferiscono alla "*50S ribosomal protein L19*". Una **proteina ribosomiale** è una delle qualsiasi proteine che, insieme all'**RNA Ribosomiale** (**rRNA**), costituiscono le subunità ribosomiali coinvolte nel *processo cellulare di traduzione*. **L19** contribuisce all'assemblaggio della ***subunità ribosomiale 50S***. La **subunità grande 50S** è presente in ***E. coli, altri batteri e Archaea***, mentre gli **esseri umani** e i **lieviti** hanno **una subunità grande 60S**. **La proteina ribosomiale L19/L19e è assente nei batteri** (si noti che i **Bacilli Paranthracis** e **Anthracis** sono **batteri** e la **subunità grande 50S** **NON è presente nell'UOMO**). Tuttavia, in un **mutante di Escherichia coli** (un batterio) è stata evidenziata una forma **drasticamente alterata della proteina L19 presente sul ribosoma**. **La proteina ribosomiale L19** era situata alla **base della particella 50 S**. ***50S*** *è il sito di inibizione per gli antibiotici come i macrolidi, il cloramfenicolo, la clindamicina e le pleuromutiline*. Le malattie associate alla **Proteina Ribosomiale L19** (**RPL19**) includono la **psoriasi 13** e l'**adenoma del retto** [l'*espressione fecale* di **RPL19** è associata a *stadi avanzati del cancro del colon-retto (**CRC**)* e dipende dai *livelli sierici dell'antigene carcinoembrionario* (**CEA**) nel predire la prognosi dei pazienti con *CRC*]. Inoltre, è stato accertato che i livelli dell'**mRNA** che codifica per la **RPL19** è più abbondante nei campioni di **cancro al seno** che esprimono alti livelli del gene **erbB-2**. **RPL19** è *sovraespresso* anche nelle **cellule prostatiche umane maligne**, rivelando che RPL19 è un predittore sensibile della progressione del **cancro alla prostata**. Tra i percorsi correlati a **RPL19** vi sono il **metabolismo delle proteine** e il **ciclo di vita dell'HIV**. Questo gene ha espressione ubiquitaria nell'**ovaio**, nel **linfonodo** e in altri **25 tessuti** (Per approfondimenti su S50 e L19 si veda pagina 304).

La **Sequenza "ANTHRAX"** ha evidenziato allineamenti significativi con parti della **Proteina del gruppo G dell'Anemia di Fanconi** (codificata dal **gene FANCG**), una **proteina di riparazione del DNA** che può operare in una riparazione postreplicazione o in una funzione di checkpoint del ciclo cellulare. **FANCG** è un ***Gene candidato come soppressore del tumore***. Le **proteine AF (Anemia di Fanconi)** interagiscono attraverso una via multi proteica che coinvolge ***il gene 1 di suscettibilità al cancro al seno (BRCA1)***, mentre di **perdita di FANCG** provoca l'**apoptosi dei progenitori neurali** durante lo sviluppo del proencefalo. I topi mutanti FANCG maschi e femmine hanno **gametogenesi difettosa**, **ipogonadismo** e **fertilità ridotta**, coerenti con il fenotipo dei pazienti con **AF** (Per approfondimenti si veda pagina 286).

Qui di seguito sono mostrati altri allineamenti significativi della **Sequenza "ANTHRAX"**.

Protein Turtle Homolog A è membro della **superfamiglia delle immunoglobuline 9 (IGSF9A)**. Un'importante **paralogo** (*un gene, o una sequenza di DNA, appartenente a un gruppo di sequenze omologhe all'interno della stessa specie*) di **IGSF9A** è **IGSF9B** (**Immunoglobulin Superfamily Member 9B**). Le malattie associate a IGSF9B includono il **Cancro Ovarico** (Per approfondimenti si veda pagina 287).

Kringle containing transmembrane protein 1 (KREMEN1) è un gene che codifica per un **recettore transmembrana** implicato indirettamente con la **genesi dei tumori**. **KREMEN1** può innescare anche l'**apoptosi** (Per approfondimenti si veda pagina 288).

ADAM 17-like protease, chiamata anche **TACE** (*enzima di conversione del fattore di necrosi tumorale α*), è un enzima che appartiene alla **famiglia delle proteine ADAM delle disintegrine e delle metalloproteasi**. **Si ritiene che ADAM17 sia coinvolto nell'elaborazione del fattore di necrosi tumorale alfa (TNF-α) sulla superficie della cellula e dall'interno delle membrane intracellulari della rete trans-Golgi**. Si ritiene che svolga anche un ruolo nel **rilascio di una varietà diversificata di citochine ancorate alla membrana**, **molecole di adesione cellulare, recettori, ligandi ed enzimi**. Infine, è stato dimostrato che **la radioterapia attiva ADAM17** nel **carcinoma polmonare non a piccole cellule**, causando gravi conseguenze (Per approfondimenti si veda pagina 289).

Integrin subunit beta 8 (ITGB8), gene membro della **famiglia della catena beta dell'integrina**, codifica per una **proteina di membrana di tipo I**. **Questo complesso gioca un ruolo nella proliferazione epiteliale delle vie aeree umane**. **ITGB8** è richiesto durante la **vasculogenesi**. Le malattie associate a *ITGB8* includono la **malformazione arterovenosa** e la **cardiomiopatia ventricolare destra aritmogena**. **ITGB8** è paralogo di **ITGB5**, le cui *malattie associate includono l'**adenocarcinoma dei villi** e l'**osteopetrosi**, **autosomica dominante 2***. **ITGB8** ha relazioni indirette con geni le cui malattie associate includono la ***tromboastenia di Glanzmann 2***, il ***disturbo emorragico**, **di tipo piastrinico, 24***, mentre ***ITGAV:ITGB3*** è un *recettore per il **fattore di von Willebrand*** (Per approfondimenti si veda pagina 290).

L’**invasione del linfoma T e la proteina 1** che induce la **metastasi (Tiam1)** è coinvolta nei **processi di tumorigenesi**, *tra cui migrazione cellulare, adesione e invasione, proteolisi, riorganizzazione del citoscheletro, trasformazione morfologica cellulare e segnalazione intracellulare*. Questi processi sono anche fondamentali per l’**impianto dell’embrione** (Per approfondimenti si veda pagina 299).

Il **recettore 2 della vasopressina (V2R)**, o **recettore 2 della vasopressina dell'arginina** (**AVPR2**), è una proteina che agisce come **recettore per la vasopressina**. L’**AVPR2** è espresso, tra l’altro, *nel* ***cancro del polmone***. **AVPR2 è espresso anche al di fuori del rene nell’endotelio vascolare**. **La stimolazione provoca il rilascio del fattore di von Willebrand e del fattore VIII dalle cellule endoteliali**. Quando la **funzione di AVPR2** viene persa, si manifesta la **malattia diabete insipido nefrogenico (NDI)**. La **funzione del recettore 2 della vasopressina** è influenzata in modo deleterio da **mutazioni puntiformi nel suo gene**. Alcune di queste mutazioni, quando espresse, fanno sì che il *recettore rimanga nel citosol* (Per approfondimenti si veda pagina 300).

Inoltre, sono stati identificati numerosi
allineamenti significativi con diverse specie di **PIPISTRELLI**

- **Pipistrellus pipistrellus**
- **Pteropus alecto**
- **Pteropus vampyrus**
- **Pteropus giganteus**
- **Pipistrellus pipistrellus**
- **Rhinolophus ferrumequinum**
- **Myotis brandtii**
- **Rousettus aegyptiacus**
- **Pipistrellus kuhlii**
- **Eptesicus fuscus**

e con le due specie di **PANGOLINI** (**Malese e Cinese**)

- **Manis javanica**
- **Manis pentadactyla**

ATTEZIONE:

La necessità di pubblicare in fretta questo documento non ci ha consentito di approfondire **altri importanti allineamenti significativi**. Il ricercatore interessato potrà utilizzare le informazioni pubblicate nelle pagine successive e fare autonomamente gli approfondimenti desiderati.

4.1 LA SEQUENZA “ANTHRAX” E I RISULTATI DELLA RICERCA BLAST

Quella mostrata qui di seguito è la sequenza totale del *3’-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*. Le lettere colorate sono i **DUE segmenti di sequenza non contigui** che sono stati identificati in questa ricerca. Essi, uniti insieme, formano la **Sequenza “ANTHRAX”**. Questa sequenza è stata sottoposta ad una ricerca BLAST e nelle pagine seguenti sono mostrati gli *allineamenti significativi* ottenuti e gli “**organismi**” e i **prodotti** a cui tali allineamenti si riferiscono.

C TCGAGCTGGT ACTGCATGCA 3900
CGCAATGCTA GCTGCCCCTT TC**CCGTCCTG G**GTACCCCGA GTCTCCCCCG 3950
ACCTCGGGTC CCAGGTATGC TCCCACCTCC ACCTGCCCCA CTCACCACCT 4000
CTGCTAGTTC C**AGACACCTC CC**AAGCACGC AGCAATGCAG CTCAAAACGC 4050
TTAGCCTAGC CACACCCCCA CGGGAAACAG CAGTGATTAA CCTTTAGCAA 4100
TAAACGAAAG TTTAACTAAG CTATACTAAC CCCAGGGTTG GTCAATTTCG 4150
TGCCAGCCAC ACCCTGGAGC TAGC

QUERY : CCGTCCTGGAGACACCTCCC

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	**5000**
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F

SEQUENZE SELEZIONATE: 3820

Description	**Name**	Taxid	Score	Score	cover	Value	Ident	Len	**Accession**
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	36.2	36.2	90%	12	100.00	720	LK381162.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	36.2	36.2	90%	12	100.00	1035270	LK065015.1
Desulfitobacterium hafniense strain PCE-S genome assembly,...	NA	49338	36.2	36.2	90%	12	100.00	5594916	LK996017.1
Desulfitobacterium hafniense DCB-2, complete genome	NA	272564	36.2	36.2	90%	12	100.00	5279134	CP001336.1
Desulfitobacterium hafniense Y51 DNA, complete genome	NA	138119	36.2	36.2	90%	12	100.00	5727534	AP008230.1
PREDICTED: Dromaius novaehollandiae FA complementation group G...	emu	8790	36.2	36.2	90%	12	100.00	2420	XM_026108231.1
PREDICTED: Dromaius novaehollandiae FA complementation group G...	emu	8790	36.2	36.2	90%	12	100.00	2043	XM_026108230.1
PREDICTED: Apteryx rowi FA complementation group G (FANCG),...	Okarito brow...	308060	36.2	36.2	90%	12	100.00	1302	XM_026069218.1
PREDICTED: Apteryx australis	NA	202946	36.2	36.2	90%	12	100.00	1935	XM_013952848.1

mantelli Fanconi anemia,...									
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	36.2	36.2	90%	12	100.00	1733005	LK065073.1
PREDICTED: Phaethon lepturus Fanconi anemia, complementation...	White-tailed...	97097	36.2	36.2	90%	12	100.00	1515	XM_010283869.1
Erithacus rubecula genome assembly, chromosome: 4	European robin	37610	34.2	94.6	90%	47	100.00	68599267	LR812106.1
PREDICTED: Ailuropoda melanoleuca immunoglobulin superfamily...	giant panda	9646	34.2	34.2	85%	47	100.00	3814	XM_034667302.1
PREDICTED: Cyclopterus lumpus G protein-coupled receptor kinas...	lumpfish	8103	34.2	34.2	85%	47	100.00	5191	XM_034562422.1
PREDICTED: Orcinus orca immunoglobulin superfamily member 9...	killer whale	9733	34.2	34.2	85%	47	100.00	4158	XM_004284457.2
Canis lupus familiaris breed Labrador retriever chromosome 05a	dog	9615	34.2	126	95%	47	100.00	86926571	CP050595.1
Canis lupus familiaris breed Labrador retriever chromosome 38a	dog	9615	34.2	34.2	85%	47	100.00	24001931	CP050585.1
Canis lupus familiaris breed Labrador retriever chromosome 05b	dog	9615	34.2	126	95%	47	100.00	86915062	CP050642.1
Canis lupus familiaris breed Labrador retriever chromosome 38b	dog	9615	34.2	34.2	85%	47	100.00	23991203	CP050641.1
PREDICTED: Camelus ferus immunoglobulin superfamily member 9...	Wild Bactria...	419612	34.2	34.2	85%	47	100.00	4470	XM_032463943.1
PREDICTED: Camelus ferus immunoglobulin superfamily member 9...	Wild Bactria...	419612	34.2	34.2	85%	47	100.00	4540	XM_032463942.1
PREDICTED: Camelus ferus immunoglobulin superfamily member 9...	Wild Bactria...	419612	34.2	34.2	85%	47	100.00	4634	XM_032463941.1
PREDICTED: Camelus ferus immunoglobulin superfamily member 9...	Wild Bactria...	419612	34.2	34.2	85%	47	100.00	4659	XM_032463940.1
PREDICTED: Camelus ferus immunoglobulin superfamily member 9...	Wild Bactria...	419612	34.2	34.2	85%	47	100.00	4274	XM_032463939.1
PREDICTED: Camelus ferus immunoglobulin superfamily member 9...	Wild Bactria...	419612	34.2	34.2	85%	47	100.00	4276	XM_032463938.1
PREDICTED: Camelus ferus immunoglobulin superfamily member 9...	Wild Bactria...	419612	34.2	34.2	85%	47	100.00	4823	XM_032463937.1
PREDICTED: Camelus ferus immunoglobulin superfamily member 9...	Wild Bactria...	419612	34.2	34.2	85%	47	100.00	4752	XM_032463936.1
PREDICTED: Vicugna pacos immunoglobulin superfamily member 9...	alpaca	30538	34.2	34.2	85%	47	100.00	4524	XM_015249064.2
PREDICTED: Camelus dromedarius immunoglobulin superfamily memb...	Arabian camel	9838	34.2	34.2	85%	47	100.00	4538	XM_031435993.1
PREDICTED: Camelus dromedarius immunoglobulin superfamily memb...	Arabian camel	9838	34.2	34.2	85%	47	100.00	4656	XM_031435992.1
Salarias fasciatus genome assembly, chromosome: 13	jewelled blenny	181472	34.2	34.2	85%	47	100.00	29904995	LR597448.1
Salmo trutta genome assembly, chromosome: 35	river trout	8032	34.2	64.4	95%	47	100.00	41918599	LR584444.1
Cottoperca gobio genome assembly, chromosome: 8	NA	56716	34.2	34.2	85%	47	100.00	23432536	LR131938.1
Cottoperca gobio genome assembly, chromosome: 7	NA	56716	34.2	64.4	95%	47	100.00	23069680	LR131937.1
PREDICTED: Ursus arctos horribilis immunoglobulin superfamily...	NA	116960	34.2	34.2	85%	47	100.00	4308	XM_026487442.1
PREDICTED: Balaenoptera acutorostrata scammoni	NA	310752	34.2	34.2	85%	47	100.00	3737	XM_007171794.2

immunoglobulin...									
PREDICTED: Balaenoptera acutorostrata scammoni immunoglobulin...	NA	310752	34.2	34.2	85%	47	100.00	4114	XM_007171792.2
Eukaryotic synthetic construct chromosome 22	NA	111789	34.2	64.4	90%	47	100.00	35194566	CP034501.1
PREDICTED: Pteropus alecto immunoglobulin superfamily member 9...	black flying...	9402	34.2	34.2	85%	47	100.00	4122	**XM_015597873.2**
PREDICTED: Pteropus alecto immunoglobulin superfamily member 9...	black flying...	9402	34.2	34.2	85%	47	100.00	4149	**XM_015597872.2**
PREDICTED: Pteropus alecto immunoglobulin superfamily member 9...	black flying...	9402	34.2	34.2	85%	47	100.00	4290	**XM_015597871.2**
PREDICTED: Pteropus alecto immunoglobulin superfamily member 9...	black flying...	9402	34.2	34.2	85%	47	100.00	4350	**XM_015597868.2**
PREDICTED: Pteropus alecto immunoglobulin superfamily member 9...	black flying...	9402	34.2	34.2	85%	47	100.00	4302	**XM_006922907.3**
PREDICTED: Desmodus rotundus immunoglobulin superfamily member...	common vampi...	9430	34.2	34.2	85%	47	100.00	3990	XM_024571304.1
PREDICTED: Desmodus rotundus immunoglobulin superfamily member...	common vampi...	9430	34.2	34.2	85%	47	100.00	4038	XM_024571297.1
PREDICTED: Desmodus rotundus immunoglobulin superfamily member...	common vampi...	9430	34.2	34.2	85%	47	100.00	3804	XM_024571293.1
PREDICTED: Pteropus vampyrus immunoglobulin superfamily member...	large flying...	132908	34.2	34.2	85%	47	100.00	3916	**XM_023538320.1**
PREDICTED: Pteropus vampyrus immunoglobulin superfamily member...	large flying...	132908	34.2	34.2	85%	47	100.00	4332	**XM_023538319.1**
PREDICTED: Pteropus vampyrus immunoglobulin superfamily member...	large flying...	132908	34.2	34.2	85%	47	100.00	4359	**XM_011373093.2**
PREDICTED: Pteropus vampyrus immunoglobulin superfamily member...	large flying...	132908	34.2	34.2	85%	47	100.00	4500	**XM_023538318.1**
PREDICTED: Pteropus vampyrus immunoglobulin superfamily member...	large flying...	132908	34.2	34.2	85%	47	100.00	4558	**XM_023538317.1**
PREDICTED: Pteropus vampyrus immunoglobulin superfamily member...	large flying...	132908	34.2	34.2	85%	47	100.00	4510	**XM_011373091.2**
Oryzias latipes strain Hd-rR chromosome 17 sequence	Japanese medaka	8090	34.2	34.2	85%	47	100.00	31792230	CP020681.1
Homo sapiens kringle containing transmembrane protein 1...	human	9606	34.2	34.2	85%	47	100.00	102256	NG_052986.1
PREDICTED: Branchiostoma belcheri ADAM 17-like protease...	Belcher's la...	7741	34.2	34.2	85%	47	100.00	694	XM_019772757.1
PREDICTED: Hipposideros armiger immunoglobulin superfamily...	great roundl...	186990	34.2	34.2	85%	47	100.00	4589	XM_019649781.1
PREDICTED: Hipposideros armiger immunoglobulin superfamily...	great roundl...	186990	34.2	34.2	85%	47	100.00	4526	XM_019649780.1
PREDICTED: Hipposideros armiger immunoglobulin superfamily...	great roundl...	186990	34.2	34.2	85%	47	100.00	4727	XM_019649779.1
TPA: Oryzias latipes strain Hd-rR, complete genome assembly,...	Japanese medaka	8090	34.2	34.2	85%	47	100.00	31848461	HF933223.1
PREDICTED: Poecilia reticulata netrin-1-like (LOC103480490),...	guppy	8081	34.2	34.2	85%	47	100.00	2971	XM_008435452.2
PREDICTED: Erinaceus europaeus integrin subunit beta 8 (ITGB8)...	western Euro...	9365	34.2	34.2	85%	47	100.00	3622	XM_007532261.2

PREDICTED: Peromyscus maniculatus bairdii RIMS-binding protein...	prairie deer...	230844	34.2	34.2	85%	47	100.00	5301	XM_006993043.2
PREDICTED: Lepisosteus oculatus collagen alpha-6(VI) chain-lik...	spotted gar	7918	34.2	34.2	85%	47	100.00	9315	XM_015356881.1
PREDICTED: Lepisosteus oculatus collagen alpha-6(VI) chain-lik...	spotted gar	7918	34.2	34.2	85%	47	100.00	9330	XM_015356879.1
PREDICTED: Lepisosteus oculatus collagen alpha-6(VI) chain-lik...	spotted gar	7918	34.2	34.2	85%	47	100.00	9357	XM_015356878.1
PREDICTED: Lepisosteus oculatus collagen alpha-6(VI) chain-lik...	spotted gar	7918	34.2	34.2	85%	47	100.00	9372	XM_015356877.1
PREDICTED: Lepisosteus oculatus collagen alpha-6(VI) chain-lik...	spotted gar	7918	34.2	34.2	85%	47	100.00	9528	XM_015356876.1
PREDICTED: Lepisosteus oculatus collagen alpha-6(VI) chain-lik...	spotted gar	7918	34.2	34.2	85%	47	100.00	9645	XM_015356875.1
PREDICTED: Lepisosteus oculatus collagen alpha-6(VI) chain-lik...	spotted gar	7918	34.2	34.2	85%	47	100.00	9648	XM_015356874.1
PREDICTED: Lepisosteus oculatus collagen alpha-6(VI) chain-lik...	spotted gar	7918	34.2	34.2	85%	47	100.00	9543	XM_015356873.1
PREDICTED: Lepisosteus oculatus CTS telomere maintenance compl...	spotted gar	7918	34.2	34.2	85%	47	100.00	3774	XM_015340475.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	34.2	34.2	85%	47	100.00	278468	LK066323.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	34.2	34.2	85%	47	100.00	17125944	LK064712.1
PREDICTED: Mandrillus leucophaeus uncharacterized LOC105533645...	drill	9568	34.2	34.2	85%	47	100.00	2553	XM_011972125.1
PREDICTED: Camelus bactrianus immunoglobulin superfamily, memb...	Bactrian camel	9837	34.2	34.2	85%	47	100.00	3829	XM_010955625.1
PREDICTED: Balaenoptera acutorostrata scammoni immunoglobulin...	NA	310752	34.2	34.2	85%	47	100.00	4045	XM_007171793.1
Flammeovirga yaeyamensis strain NBRC:100898 chromosome 1,...	NA	367791	34.2	34.2	85%	47	100.00	5191010	CP076132.1
Fagus sylvatica genome assembly, chromosome: 5	European beech	28930	34.2	124	85%	47	100.00	46564878	OU015765.1
Homo sapiens isolate CHM13 chromosome 22	human	9606	34.2	64.4	90%	47	100.00	51324926	CP068256.2
PREDICTED: Ursus maritimus immunoglobulin superfamily member 9...	polar bear	29073	34.2	34.2	85%	47	100.00	3833	XM_040634478.1
Roseomonas sp. 1318 chromosome, complete genome	NA	2768161	34.2	34.2	85%	47	100.00	3565232	CP061091.1
PREDICTED: Oryx dammah immunoglobulin superfamily member 9...	scimitar-hor...	59534	34.2	34.2	85%	47	100.00	4134	XM_040230134.1
PREDICTED: Oryx dammah immunoglobulin superfamily member 9...	scimitar-hor...	59534	34.2	34.2	85%	47	100.00	6069	XM_040230133.1
Canis lupus genome assembly, chromosome: 38	gray wolf	9612	34.2	34.2	85%	47	100.00	26441244	HG994420.1
Canis lupus genome assembly, chromosome: 5	gray wolf	9612	34.2	157	95%	47	100.00	89778077	HG994385.1
PREDICTED: Pteropus giganteus immunoglobulin superfamily membe...	Indian flyin...	143291	34.2	34.2	85%	47	100.00	3888	*XM_039839994.1*
PREDICTED: Pteropus giganteus immunoglobulin superfamily membe...	Indian flyin...	143291	34.2	34.2	85%	47	100.00	4102	*XM_039839993.1*
PREDICTED: Pteropus giganteus immunoglobulin superfamily membe...	Indian flyin...	143291	34.2	34.2	85%	47	100.00	4305	*XM_039839992.1*
PREDICTED: Pteropus giganteus immunoglobulin superfamily	Indian flyin...	143291	34.2	34.2	85%	47	100.00	4332	*XM_039839991.1*

membe...									
PREDICTED: Pteropus giganteus immunoglobulin superfamily membe...	Indian flyin...	143291	34.2	34.2	85%	47	100.00	4473	XM_039839990.1
PREDICTED: Pteropus giganteus immunoglobulin superfamily membe...	Indian flyin...	143291	34.2	34.2	85%	47	100.00	4531	XM_039839989.1
PREDICTED: Pteropus giganteus immunoglobulin superfamily membe...	Indian flyin...	143291	34.2	34.2	85%	47	100.00	4483	XM_039839988.1
Cosmia trapezina genome assembly, chromosome: 26	dun-bar pinion	116126	34.2	34.2	85%	47	100.00	19015461	LR991045.1
PREDICTED: Canis lupus familiaris immunoglobulin superfamily...	dog	9615	34.2	34.2	85%	47	100.00	3496	XM_038448713.1
PREDICTED: Canis lupus familiaris immunoglobulin superfamily...	dog	9615	34.2	34.2	85%	47	100.00	4272	XM_038448712.1
PREDICTED: Canis lupus familiaris immunoglobulin superfamily...	dog	9615	34.2	34.2	85%	47	100.00	4189	XM_038448711.1
PREDICTED: Canis lupus familiaris immunoglobulin superfamily...	dog	9615	34.2	34.2	85%	47	100.00	4159	XM_038448710.1
PREDICTED: Canis lupus familiaris immunoglobulin superfamily...	dog	9615	34.2	34.2	85%	47	100.00	4325	XM_038448709.1
PREDICTED: Canis lupus familiaris immunoglobulin superfamily...	dog	9615	34.2	34.2	85%	47	100.00	3497	XM_038464119.1
PREDICTED: Canis lupus familiaris immunoglobulin superfamily...	dog	9615	34.2	34.2	85%	47	100.00	4271	XM_038464118.1
PREDICTED: Canis lupus familiaris immunoglobulin superfamily...	dog	9615	34.2	34.2	85%	47	100.00	4184	XM_038464117.1
PREDICTED: Canis lupus familiaris immunoglobulin superfamily...	dog	9615	34.2	34.2	85%	47	100.00	4154	XM_038464116.1
PREDICTED: Canis lupus familiaris immunoglobulin superfamily...	dog	9615	34.2	34.2	85%	47	100.00	4326	XM_038464115.1
PREDICTED: Chelonia mydas fatty acid 2-hydroxylase (FA2H), mRNA	Green sea tu...	8469	34.2	34.2	85%	47	100.00	4650	XM_037877813.1
PREDICTED: Peromyscus leucopus RIMS-binding protein 3-like...	white-footed...	10041	34.2	34.2	85%	47	100.00	5470	XM_028894712.2
PREDICTED: Artibeus jamaicensis immunoglobulin superfamily...	Jamaican fru...	9417	34.2	34.2	85%	47	100.00	3992	XM_037130718.1
PREDICTED: Artibeus jamaicensis immunoglobulin superfamily...	Jamaican fru...	9417	34.2	34.2	85%	47	100.00	4028	XM_037130717.1
PREDICTED: Artibeus jamaicensis immunoglobulin superfamily...	Jamaican fru...	9417	34.2	34.2	85%	47	100.00	4038	XM_037130716.1
PREDICTED: Artibeus jamaicensis immunoglobulin superfamily...	Jamaican fru...	9417	34.2	34.2	85%	47	100.00	4206	XM_037130715.1
PREDICTED: Artibeus jamaicensis immunoglobulin superfamily...	Jamaican fru...	9417	34.2	34.2	85%	47	100.00	4079	XM_037130714.1
PREDICTED: Artibeus jamaicensis immunoglobulin superfamily...	Jamaican fru...	9417	34.2	34.2	85%	47	100.00	4085	XM_037130713.1
PREDICTED: Artibeus jamaicensis immunoglobulin superfamily...	Jamaican fru...	9417	34.2	34.2	85%	47	100.00	4096	XM_037130712.1
PREDICTED: Artibeus jamaicensis immunoglobulin superfamily...	Jamaican fru...	9417	34.2	34.2	85%	47	100.00	4133	XM_037130711.1
PREDICTED: Sturnira hondurensis immunoglobulin superfamily...	NA	192404	34.2	34.2	85%	47	100.00	4123	XM_037059811.1
PREDICTED: Sturnira hondurensis immunoglobulin superfamily...	NA	192404	34.2	34.2	85%	47	100.00	4376	XM_037059810.1
PREDICTED: Sturnira hondurensis immunoglobulin superfamily...	NA	192404	34.2	34.2	85%	47	100.00	4189	XM_037059809.1
PREDICTED: Sturnira hondurensis immunoglobulin superfamily...	NA	192404	34.2	34.2	85%	47	100.00	4524	XM_037059807.1
PREDICTED: Sturnira hondurensis immunoglobulin superfamily...	NA	192404	34.2	34.2	85%	47	100.00	4085	XM_037059806.1
PREDICTED: Sturnira hondurensis immunoglobulin superfamily...	NA	192404	34.2	34.2	85%	47	100.00	4192	XM_037059805.1
PREDICTED: Sturnira hondurensis immunoglobulin superfamily...	NA	192404	34.2	34.2	85%	47	100.00	4528	XM_037059804.1
PREDICTED: Balaenoptera	Blue whale	9771	34.2	34.2	85%	47	100.00	4185	XM_036857303.1

musculus immunoglobulin superfamily...									
PREDICTED: Balaenoptera musculus immunoglobulin superfamily...	Blue whale	9771	34.2	34.2	85%	47	100.00	4133	XM_036857292.1
PREDICTED: Balaenoptera musculus immunoglobulin superfamily...	Blue whale	9771	34.2	34.2	85%	47	100.00	4438	XR_005020555.1
PREDICTED: Balaenoptera musculus immunoglobulin superfamily...	Blue whale	9771	34.2	34.2	85%	47	100.00	4046	XM_036857277.1
PREDICTED: Balaenoptera musculus immunoglobulin superfamily...	Blue whale	9771	34.2	34.2	85%	47	100.00	4132	XM_036857267.1
PREDICTED: Balaenoptera musculus immunoglobulin superfamily...	Blue whale	9771	34.2	34.2	85%	47	100.00	4110	XM_036857258.1
PREDICTED: Balaenoptera musculus immunoglobulin superfamily...	Blue whale	9771	34.2	34.2	85%	47	100.00	4307	XM_036857250.1
PREDICTED: Molossus molossus immunoglobulin superfamily member...	Pallas's mas...	27622	34.2	34.2	85%	47	100.00	3906	XM_036273383.1
PREDICTED: Molossus molossus immunoglobulin superfamily member...	Pallas's mas...	27622	34.2	34.2	85%	47	100.00	3893	XM_036273382.1
Homo sapiens DNA, chromosome 22, nearly complete genome	human	9606	34.2	64.4	90%	47	100.00	46684173	AP023482.1
PREDICTED: Onychomys torridus RIMS-binding protein 3-like...	southern gra...	38674	34.2	34.2	85%	47	100.00	5245	XM_036197710.1
Poecilia reticulata genome assembly, chromosome: 18	guppy	8081	34.2	34.2	85%	47	100.00	27716212	LR880662.1
PREDICTED: Phyllostomus discolor immunoglobulin superfamily...	pale spear-n...	89673	34.2	34.2	85%	47	100.00	4069	XM_036015562.1
PREDICTED: Phyllostomus discolor immunoglobulin superfamily...	pale spear-n...	89673	34.2	34.2	85%	47	100.00	4045	XM_036015561.1
PREDICTED: Phyllostomus discolor immunoglobulin superfamily...	pale spear-n...	89673	34.2	34.2	85%	47	100.00	4274	XM_036015560.1
PREDICTED: Phyllostomus discolor immunoglobulin superfamily...	pale spear-n...	89673	34.2	34.2	85%	47	100.00	4293	XM_028530555.2
PREDICTED: Phyllostomus discolor immunoglobulin superfamily...	pale spear-n...	89673	34.2	34.2	85%	47	100.00	4329	XM_036015559.1
PREDICTED: Phyllostomus discolor immunoglobulin superfamily...	pale spear-n...	89673	34.2	34.2	85%	47	100.00	4429	XM_036015558.1
PREDICTED: Phyllostomus discolor immunoglobulin superfamily...	pale spear-n...	89673	34.2	34.2	85%	47	100.00	4242	XM_036015557.1
PREDICTED: Phyllostomus discolor immunoglobulin superfamily...	pale spear-n...	89673	34.2	34.2	85%	47	100.00	4387	XM_036015556.1
PREDICTED: Phyllostomus discolor immunoglobulin superfamily...	pale spear-n...	89673	34.2	34.2	85%	47	100.00	4425	XM_036015555.1
PREDICTED: Branchiostoma floridae ADAM 17-like protease...	Florida lanc...	7739	34.2	34.2	85%	47	100.00	2504	XM_035802937.1
PREDICTED: Branchiostoma floridae ADAM 17-like protease...	Florida lanc...	7739	34.2	34.2	85%	47	100.00	5071	XM_035802936.1
PREDICTED: Branchiostoma floridae ADAM 17-like protease...	Florida lanc...	7739	34.2	34.2	85%	47	100.00	5086	XM_035802935.1
PREDICTED: Branchiostoma floridae ADAM 17-like protease...	Florida lanc...	7739	34.2	34.2	85%	47	100.00	5125	XM_035802934.1
PREDICTED: Branchiostoma floridae ADAM 17-like protease...	Florida lanc...	7739	34.2	34.2	85%	47	100.00	5140	XM_035802933.1
PREDICTED: Canis lupus dingo immunoglobulin superfamily member...	dingo	286419	34.2	34.2	85%	47	100.00	3484	XM_035711295.1

PREDICTED: Canis lupus dingo immunoglobulin superfamily member...	dingo	286419	34.2	34.2	85%	47	100.00	4112	XM_025420715.2
PREDICTED: Canis lupus dingo immunoglobulin superfamily member...	dingo	286419	34.2	34.2	85%	47	100.00	4256	XM_035711294.1
PREDICTED: Canis lupus dingo immunoglobulin superfamily member...	dingo	286419	34.2	34.2	85%	47	100.00	4190	XM_035711293.1
PREDICTED: Canis lupus dingo immunoglobulin superfamily member...	dingo	286419	34.2	34.2	85%	47	100.00	4160	XM_035711292.1
PREDICTED: Canis lupus dingo immunoglobulin superfamily member...	dingo	286419	34.2	34.2	85%	47	100.00	4314	XM_035711291.1
Human DNA sequence from clone CTA-57G9 on chromosome 22q12.1,...	human	9606	34.2	34.2	85%	47	100.00	113872	Z95116.1
PREDICTED: Marmota flaviventris G protein-coupled receptor 35...	yellow-belli...	93162	34.2	34.2	85%	47	100.00	5254	XM_027951751.2
PREDICTED: Marmota flaviventris G protein-coupled receptor 35...	yellow-belli...	93162	34.2	34.2	85%	47	100.00	5260	XM_027951749.2
Flammeovirga sp. MY04 chromosome 1, complete sequence	NA	1191459	34.2	34.2	85%	47	100.00	5056210	CP003560.2
Canis lupus familiaris breed Labrador retriever chromosome 09a	dog	9615	34.2	64.4	95%	47	100.00	60580822	CP050593.1
Canis lupus familiaris breed Labrador retriever chromosome 09b	dog	9615	34.2	64.4	95%	47	100.00	60598474	CP050635.1
Lutra lutra genome assembly, chromosome: 16	Eurasian riv...	9657	34.2	64.4	85%	47	100.00	61483029	LR738418.1
PREDICTED: Oncorhynchus kisutch...	coho salmon	8019	34.2	34.2	85%	47	100.00	8993	XM_031810905.1
PREDICTED: Oncorhynchus kisutch...	coho salmon	8019	34.2	34.2	85%	47	100.00	9048	XM_031810904.1
PREDICTED: Oncorhynchus kisutch...	coho salmon	8019	34.2	34.2	85%	47	100.00	8990	XM_031810903.1
PREDICTED: Oncorhynchus kisutch...	coho salmon	8019	34.2	34.2	85%	47	100.00	8971	XM_020462491.2
Thalassophryne amazonica genome assembly, chromosome: 22	NA	390379	34.2	34.2	85%	47	100.00	39415425	LR722987.1
Asterias rubens genome assembly, chromosome: 12	European sta...	7604	34.2	34.2	85%	47	100.00	17180802	LR699103.1
PREDICTED: Microcaecilia unicolor U6 snRNA biogenesis...	NA	1415580	34.2	34.2	85%	47	100.00	2123	XM_030203583.1
PREDICTED: Microcaecilia unicolor U6 snRNA biogenesis...	NA	1415580	34.2	34.2	85%	47	100.00	2126	XM_030203582.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: Z	NA	223781	34.2	34.2	85%	47	100.00	88216475	LR606180.1
PREDICTED: Salmo trutta chromodomain-helicase-DNA-binding...	river trout	8032	34.2	34.2	85%	47	100.00	8951	XM_029705456.1
PREDICTED: Salmo trutta chromodomain-helicase-DNA-binding...	river trout	8032	34.2	34.2	85%	47	100.00	8766	XM_029705455.1
PREDICTED: Salmo trutta chromodomain-helicase-DNA-binding...	river trout	8032	34.2	34.2	85%	47	100.00	8824	XM_029705454.1
PREDICTED: Salmo trutta chromodomain-helicase-DNA-binding...	river trout	8032	34.2	34.2	85%	47	100.00	8954	XM_029705453.1
PREDICTED: Salmo trutta chromodomain-helicase-DNA-binding...	river trout	8032	34.2	34.2	85%	47	100.00	8947	XM_029725162.1
PREDICTED: Salmo trutta chromodomain-helicase-DNA-binding...	river trout	8032	34.2	34.2	85%	47	100.00	9004	XM_029725160.1
PREDICTED: Oncorhynchus nerka chromodomain-helicase-DNA-bindin...	sockeye salmon	8023	34.2	34.2	85%	47	100.00	8956	XM_029643104.1

PREDICTED: Oncorhynchus nerka chromodomain-helicase-DNA-bindin...	sockeye salmon	8023	34.2	34.2	85%	47	100.00	8945	XM_029623067.1
Salarias fasciatus genome assembly, chromosome: 14	jewelled blenny	181472	34.2	64.4	85%	47	100.00	41006365	LR597449.1
Scleropages formosus genome assembly, chromosome: 12	Asian bonyto...	113540	34.2	34.2	85%	47	100.00	29733308	LR584077.1
Echeneis naucrates genome assembly, chromosome: 16	live sharksu...	173247	34.2	64.4	85%	47	100.00	24564695	LR584057.1
Denticeps clupeoides genome assembly, chromosome: 4	denticle her...	299321	34.2	34.2	85%	47	100.00	35364899	LR535816.1
Lateolabrax maculatus chromosome Lm21	spotted sea ...	315492	34.2	34.2	85%	47	100.00	19085413	CP027282.1
PREDICTED: Alligator sinensis RNA polymerase III subunit E...	Chinese alli...	38654	34.2	34.2	85%	47	100.00	2865	XM_025207015.1
PREDICTED: Alligator sinensis RNA polymerase III subunit E...	Chinese alli...	38654	34.2	34.2	85%	47	100.00	2943	XM_006026117.3
PREDICTED: Oncorhynchus tshawytscha...	Chinook salmon	74940	34.2	34.2	85%	47	100.00	8769	XM_024391208.1
PREDICTED: Oncorhynchus tshawytscha...	Chinook salmon	74940	34.2	34.2	85%	47	100.00	8696	XM_024436087.1
PREDICTED: Oncorhynchus tshawytscha...	Chinook salmon	74940	34.2	34.2	85%	47	100.00	8032	XM_024436086.1
PREDICTED: Oncorhynchus tshawytscha...	Chinook salmon	74940	34.2	34.2	85%	47	100.00	8957	XM_024436085.1
PREDICTED: Oncorhynchus tshawytscha...	Chinook salmon	74940	34.2	34.2	85%	47	100.00	8063	XM_024436084.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8888	XM_023977114.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8942	XM_023977113.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8901	XM_023977112.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8858	XM_023977111.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8914	XM_023977110.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8955	XM_023977109.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8956	XM_023977108.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8945	XM_023977107.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8914	XM_024009712.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8804	XM_024009711.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8861	XM_024009709.1
PREDICTED: Salvelinus alpinus chromodomain-helicase-DNA-bindin...	Arctic char	8036	34.2	34.2	85%	47	100.00	8971	XM_024009708.1
PREDICTED: Salmo salar	Atlantic	8030	34.2	34.2	85%	47	100.00	8930	XM_014140808.1

chromodomain-helicase-DNA-binding prote...	salmon								
PREDICTED: Salmo salar chromodomain-helicase-DNA-binding prote...	Atlantic salmon	8030	34.2	34.2	85%	47	100.00	8793	XM_014140806.1
PREDICTED: Salmo salar chromodomain-helicase-DNA-binding prote...	Atlantic salmon	8030	34.2	34.2	85%	47	100.00	8797	XM_014140805.1
PREDICTED: Salmo salar chromodomain-helicase-DNA-binding prote...	Atlantic salmon	8030	34.2	34.2	85%	47	100.00	8933	XM_014140804.1
PREDICTED: Salmo salar chromodomain-helicase-DNA-binding prote...	Atlantic salmon	8030	34.2	34.2	85%	47	100.00	8930	XM_014191616.1
PREDICTED: Salmo salar chromodomain-helicase-DNA-binding prote...	Atlantic salmon	8030	34.2	34.2	85%	47	100.00	8236	XM_014191614.1
PREDICTED: Salmo salar chromodomain-helicase-DNA-binding prote...	Atlantic salmon	8030	34.2	34.2	85%	47	100.00	9026	XM_014191610.1
PREDICTED: Salmo salar chromodomain-helicase-DNA-binding prote...	Atlantic salmon	8030	34.2	34.2	85%	47	100.00	9026	XM_014191609.1
PREDICTED: Coregonus clupeaformis...	lake whitefish	59861	34.2	34.2	85%	47	100.00	9021	XM_041842871.1
Caprimulgus europaeus genome assembly, chromosome: 8	Eurasian nig...	111811	34.2	98.6	85%	47	100.00	50913645	OU015531.1
PREDICTED: Salvelinus namaycush...	lake trout	8040	34.2	34.2	85%	47	100.00	8849	XM_038963719.1
PREDICTED: Salvelinus namaycush...	lake trout	8040	34.2	34.2	85%	47	100.00	8462	XM_039004242.1
PREDICTED: Oncorhynchus mykiss chromodomain helicase DNA bindi...	rainbow trout	8022	34.2	34.2	85%	47	100.00	8955	XM_021589027.2
PREDICTED: Oncorhynchus mykiss chromodomain-helicase-DNA-bindi...	rainbow trout	8022	34.2	34.2	85%	47	100.00	8705	XM_036986234.1
PREDICTED: Oncorhynchus mykiss chromodomain-helicase-DNA-bindi...	rainbow trout	8022	34.2	34.2	85%	47	100.00	8716	XM_036986233.1
PREDICTED: Oncorhynchus mykiss chromodomain-helicase-DNA-bindi...	rainbow trout	8022	34.2	34.2	85%	47	100.00	8767	XM_036986232.1
PREDICTED: Oncorhynchus mykiss chromodomain-helicase-DNA-bindi...	rainbow trout	8022	34.2	34.2	85%	47	100.00	8809	XM_036986231.1
PREDICTED: Oncorhynchus mykiss chromodomain-helicase-DNA-bindi...	rainbow trout	8022	34.2	34.2	85%	47	100.00	8798	XM_036986230.1
PREDICTED: Oncorhynchus mykiss chromodomain-helicase-DNA-bindi...	rainbow trout	8022	34.2	34.2	85%	47	100.00	8856	XM_036986229.1
Poecilia reticulata genome assembly, chromosome: 19	guppy	8081	34.2	34.2	85%	47	100.00	25553809	LR880663.1
PREDICTED: Oncorhynchus keta chromodomain-helicase-DNA-binding...	chum salmon	8018	34.2	34.2	85%	47	100.00	9040	XR_004829494.1
Pipistrellus pipistrellus genome assembly, chromosome: 10	common pipis...	59474	34.2	124	95%	47	100.00	71504835	**LR862366.1**
Rattus norvegicus 3 BAC CH230-11N5 (Children's Hospital Oaklan...	Norway rat	10116	34.2	34.2	85%	47	100.00	238007	AC097745.8
Wallaby DNA sequence from clone MEKBa-201B9, complete sequence	tammar wallaby	9315	34.2	34.2	85%	47	100.00	194524	CR848708.12
Erithacus rubecula genome assembly, chromosome: 27	European robin	37610	32.2	32.2	80%	185	100.00	5428052	LR812131.1
Erithacus rubecula genome	Europe	37610	32.2	62.4	80%	185	100.00	17821735	LR812119.1

assembly, chromosome: 16	an robin								
Erithacus rubecula genome assembly, chromosome: 9	European robin	37610	32.2	94.6	90%	185	100.00	34931163	LR812111.1
Danio rerio genome assembly, chromosome: 14	zebrafish	7955	32.2	32.2	80%	185	100.00	53898899	LR812076.1
Canis lupus familiaris breed Labrador retriever chromosome 13a	dog	9615	32.2	62.4	90%	185	100.00	63905973	CP050604.1
Canis lupus familiaris breed Labrador retriever chromosome 28a	dog	9615	32.2	62.4	85%	185	100.00	41217541	CP050584.1
Canis lupus familiaris breed Labrador retriever chromosome 13b	dog	9615	32.2	62.4	90%	185	100.00	63899846	CP050644.1
Canis lupus familiaris breed Labrador retriever chromosome 28b	dog	9615	32.2	62.4	85%	185	100.00	41256193	CP050626.1
PREDICTED: Trachypithecus francoisi G protein-coupled receptor...	Francois's l...	54180	32.2	32.2	80%	185	100.00	2965	XM_033180016.1
PREDICTED: Trachypithecus francoisi G protein-coupled receptor...	Francois's l...	54180	32.2	32.2	80%	185	100.00	2996	XM_033180014.1
PREDICTED: Trachypithecus francoisi mediator of DNA damage...	Francois's l...	54180	32.2	32.2	80%	185	100.00	7117	XM_033219555.1
PREDICTED: Trachypithecus francoisi mediator of DNA damage...	Francois's l...	54180	32.2	32.2	80%	185	100.00	7089	XM_033219553.1
PREDICTED: Rhinolophus ferrumequinum immunoglobulin superfamil...	greater hors...	59479	32.2	32.2	80%	185	100.00	3900	**XM_033094038.1**
PREDICTED: Rhinolophus ferrumequinum immunoglobulin superfamil...	greater hors...	59479	32.2	32.2	80%	185	100.00	3936	**XM_033094037.1**
PREDICTED: Rhinolophus ferrumequinum immunoglobulin superfamil...	greater hors...	59479	32.2	32.2	80%	185	100.00	4053	**XM_033094036.1**
PREDICTED: Rhinolophus ferrumequinum immunoglobulin superfamil...	greater hors...	59479	32.2	32.2	80%	185	100.00	4160	**XM_033094034.1**
PREDICTED: Catharus ustulatus Snf2 related CREBBP activator...	Swainson's t...	91951	32.2	32.2	100%	185	95.00	6317	XM_033084517.1
PREDICTED: Catharus ustulatus microtubule associated...	Swainson's t...	91951	32.2	32.2	80%	185	100.00	9901	XM_033067136.1
PREDICTED: Catharus ustulatus microtubule associated...	Swainson's t...	91951	32.2	32.2	80%	185	100.00	10010	XM_033067135.1
PREDICTED: Tyto alba alba zinc finger protein 639 (ZNF639),...	NA	507980	32.2	32.2	80%	185	100.00	5893	XM_033006391.1
PREDICTED: Tyto alba alba zinc finger protein 639 (ZNF639),...	NA	507980	32.2	32.2	80%	185	100.00	7292	XR_004409055.1
Coregonus sp. 'balchen' genome assembly, chromosome: 5	NA	861768	32.2	32.2	80%	185	100.00	45591172	LR778257.1
PREDICTED: Chiroxiphia lanceolata leucine rich repeats and...	lance-tailed...	296741	32.2	32.2	80%	185	100.00	6396	XM_032698791.1
PREDICTED: Etheostoma spectabile collagen alpha-1(VII)...	orangethroat...	54343	32.2	32.2	80%	185	100.00	9627	XM_032505355.1
PREDICTED: Etheostoma spectabile collagen alpha-1(VII)...	orangethroat...	54343	32.2	32.2	80%	185	100.00	9669	XM_032505354.1
PREDICTED: Etheostoma spectabile collagen alpha-1(VII)...	orangethroat...	54343	32.2	32.2	80%	185	100.00	9672	XM_032505353.1
Epinephelus fuscoguttatus DNA, LG13, complete sequence	brown-marble...	293821	32.2	185	85%	185	100.00	43720812	AP022687.1
PREDICTED: Camelus ferus ataxin 7 (ATXN7), transcript variant...	Wild Bactria...	419612	32.2	32.2	80%	185	100.00	6922	XM_032458136.1
PREDICTED: Drosophila ananassae uncharacterized LOC6499470...	NA	7217	32.2	32.2	80%	185	100.00	5617	XM_014910592.2
PREDICTED: Drosophila ananassae uncharacterized LOC6499470...	NA	7217	32.2	32.2	80%	185	100.00	5686	XM_001954539.3

Mycolicibacterium tokaiense JCM 6373 DNA, nearly complete genome	NA	39695	32.2	32.2	80%	185	100.00	6328149	AP022600.1
Saprochaete ingens uncharacterized protein (SAPINGB_P004129),...	NA	2606893	32.2	32.2	80%	185	100.00	1032	XM_031998844.1
Lutra lutra genome assembly, chromosome: 17	Eurasian riv...	9657	32.2	32.2	80%	185	100.00	60348511	LR738419.1
Lutra lutra genome assembly, chromosome: 15	Eurasian riv...	9657	32.2	92.7	90%	185	100.00	69992071	LR738417.1
PREDICTED: Piliocolobus tephrosceles G protein-coupled recepto...	Ugandan red ...	591936	32.2	32.2	80%	185	100.00	2937	XM_023185134.3
PREDICTED: Anarrhichthys ocellatus SRY-box transcription facto...	wolf-eel	433405	32.2	32.2	80%	185	100.00	2961	XR_004213533.1
PREDICTED: Anarrhichthys ocellatus SRY-box transcription facto...	wolf-eel	433405	32.2	32.2	80%	185	100.00	3408	XR_004213532.1
PREDICTED: Anarrhichthys ocellatus SRY-box transcription facto...	wolf-eel	433405	32.2	32.2	80%	185	100.00	3264	XR_004213531.1
PREDICTED: Anarrhichthys ocellatus SRY-box transcription facto...	wolf-eel	433405	32.2	32.2	80%	185	100.00	7289	XR_004213530.1
PREDICTED: Anarrhichthys ocellatus SRY-box transcription facto...	wolf-eel	433405	32.2	32.2	80%	185	100.00	7231	XR_004213529.1
PREDICTED: Anarrhichthys ocellatus SRY-box transcription facto...	wolf-eel	433405	32.2	32.2	80%	185	100.00	7375	XR_004213528.1
Streptomyces ficellus strain NRRL 8067 chromosome, complete...	NA	1977088	32.2	32.2	80%	185	100.00	7078240	CP034279.1
PREDICTED: Vicugna pacos ataxin 7 (ATXN7), mRNA	alpaca	30538	32.2	32.2	80%	185	100.00	6506	XM_031686336.1
Sciurus vulgaris genome assembly, chromosome: 18	Eurasian red...	55149	32.2	62.4	80%	185	100.00	41577549	LR738629.1
Sciurus carolinensis genome assembly, chromosome: 18	gray squirrel	30640	32.2	62.4	80%	185	100.00	41557064	LR738608.1
PREDICTED: Papio anubis G protein-coupled receptor kinase 6...	olive baboon	9555	32.2	32.2	80%	185	100.00	2675	XM_031666624.1
PREDICTED: Papio anubis G protein-coupled receptor kinase 6...	olive baboon	9555	32.2	32.2	80%	185	100.00	3007	XM_003900593.5
PREDICTED: Papio anubis G protein-coupled receptor kinase 6...	olive baboon	9555	32.2	32.2	80%	185	100.00	2907	XR_002522893.2
PREDICTED: Phasianus colchicus pleckstrin homology domain...	Ring-necked ...	9054	32.2	32.2	80%	185	100.00	4908	XM_031597772.1
PREDICTED: Camelus dromedarius ataxin 7 (ATXN7), mRNA	Arabian camel	9838	32.2	32.2	80%	185	100.00	6778	XM_031470676.1
Streptomyces sp. C8S0 chromosome	NA	2585716	32.2	32.2	80%	185	100.00	6898902	CP045031.1
PREDICTED: Rhinopithecus roxellana G protein-coupled receptor...	golden snub-...	61622	32.2	32.2	80%	185	100.00	3171	XM_030926837.1
PREDICTED: Rhinopithecus roxellana G protein-coupled receptor...	golden snub-...	61622	32.2	32.2	80%	185	100.00	3177	XM_030926836.1
PREDICTED: Rhinopithecus roxellana G protein-coupled receptor...	golden snub-...	61622	32.2	32.2	80%	185	100.00	2939	XM_030926834.1
PREDICTED: Rhinopithecus roxellana G protein-coupled receptor...	golden snub-...	61622	32.2	32.2	80%	185	100.00	2893	XR_004056257.1
Chanos chanos genome assembly, chromosome: 6	milkfish	29144	32.2	32.2	80%	185	100.00	50300218	LR697111.1
Sparus aurata genome assembly, chromosome: 19	gilthead sea...	8175	32.2	122	80%	185	100.00	31047742	LR537139.1
Sparus aurata genome assembly,	gilthead	8175	32.2	185	85%	185	100.00	37104330	LR537138.1

chromosome: 18	sea...								
Sparus aurata genome assembly, chromosome: 9	gilthead sea...	8175	32.2	185	85%	185	100.00	37012328	LR537129.1
Sparus aurata genome assembly, chromosome: 6	gilthead sea...	8175	32.2	455	80%	185	100.00	40124345	LR537126.1
PREDICTED: Manacus vitellinus leucine rich repeats and...	golden-colla...	328815	32.2	32.2	80%	185	100.00	5986	XM_029958315.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 3	NA	223781	32.2	153	80%	185	100.00	79382107	LR606183.1
Sphaeramia orbicularis genome assembly, chromosome: 12	orbiculate c...	375764	32.2	62.4	80%	185	100.00	81199652	LR597469.1
Salarias fasciatus genome assembly, chromosome: 6	jewelled blenny	181472	32.2	124	90%	185	100.00	41296897	LR597441.1
PREDICTED: Echeneis naucrates toll-like receptor 2 type-1...	live sharksu...	173247	32.2	32.2	80%	185	100.00	3515	XM_029503567.1
PREDICTED: Echeneis naucrates toll-like receptor 2 type-1...	live sharksu...	173247	32.2	32.2	80%	185	100.00	3627	XM_029503566.1
PREDICTED: Denticeps clupeoides suppressor of cytokine signali...	denticle her...	299321	32.2	32.2	80%	185	100.00	3769	XM_028985117.1
PREDICTED: Denticeps clupeoides suppressor of cytokine signali...	denticle her...	299321	32.2	32.2	80%	185	100.00	3771	XM_028985116.1
PREDICTED: Denticeps clupeoides suppressor of cytokine signali...	denticle her...	299321	32.2	32.2	80%	185	100.00	3874	XM_028985115.1
PREDICTED: Denticeps clupeoides suppressor of cytokine signali...	denticle her...	299321	32.2	32.2	80%	185	100.00	3876	XM_028985114.1
PREDICTED: Macaca mulatta uncharacterized LOC114674783...	Rhesus monkey	9544	32.2	32.2	80%	185	100.00	1208	XR_003725896.1
PREDICTED: Macaca mulatta G protein-coupled receptor kinase 6...	Rhesus monkey	9544	32.2	32.2	80%	185	100.00	2818	XM_028849953.1
PREDICTED: Macaca mulatta G protein-coupled receptor kinase 6...	Rhesus monkey	9544	32.2	32.2	80%	185	100.00	3691	XM_015141518.2
PREDICTED: Macaca mulatta G protein-coupled receptor kinase 6...	Rhesus monkey	9544	32.2	32.2	80%	185	100.00	2988	XM_015141515.2
Takifugu rubripes genome assembly, chromosome: 6	torafugu	31033	32.2	94.6	80%	185	100.00	12913240	LR584250.1
Takifugu rubripes genome assembly, chromosome: 13	torafugu	31033	32.2	32.2	80%	185	100.00	21507415	LR584232.1
Echeneis naucrates genome assembly, chromosome: 24	live sharksu...	173247	32.2	32.2	80%	185	100.00	19509531	LR584065.1
Echeneis naucrates genome assembly, chromosome: 6	live sharksu...	173247	32.2	32.2	80%	185	100.00	24884894	LR584047.1
Homo sapiens chromosome 15 clone VMRC59-183F02, complete sequence	human	9606	32.2	32.2	80%	185	100.00	155330	AC279026.1
Homo sapiens chromosome 15 clone VMRC59-291C21, complete sequence	human	9606	32.2	32.2	80%	185	100.00	148395	AC278960.1
Pan troglodytes chromosome 15 clone CH251-115L20, complete...	chimpanzee	9598	32.2	32.2	80%	185	100.00	176604	AC278950.1
PREDICTED: Gouania willdenowi mitogen-activated protein kinase...	blunt-snoute...	441366	32.2	32.2	80%	185	100.00	3283	XM_028435586.1
PREDICTED: Gouania willdenowi mitogen-activated protein kinase...	blunt-snoute...	441366	32.2	32.2	80%	185	100.00	3286	XM_028435585.1
PREDICTED: Gouania willdenowi mitogen-activated protein kinase...	blunt-snoute...	441366	32.2	32.2	80%	185	100.00	3488	XM_028435584.1
PREDICTED: Gouania willdenowi mitogen-activated protein kinase...	blunt-snoute...	441366	32.2	32.2	80%	185	100.00	3834	XM_028435582.1
Gouania willdenowi genome assembly, chromosome: 21	blunt-snoute...	441366	32.2	32.2	80%	185	100.00	38978045	LR132001.1
Cottoperca gobio genome assembly, chromosome: 4	NA	56716	32.2	92.7	85%	185	100.00	28949045	LR131934.1

Cottoperca gobio genome assembly, chromosome: 17	NA	56716	32.2	32.2	80%	185	100.00	25156145	LR131924.1
Cottoperca gobio genome assembly, chromosome: 10	NA	56716	32.2	92.7	85%	185	100.00	27438269	LR131917.1
PREDICTED: Piliocolobus tephrosceles G protein-coupled recepto...	Ugandan red ...	591936	32.2	32.2	80%	185	100.00	3037	XM_023185133.2
PREDICTED: Empidonax traillii leucine rich repeats and...	willow flyca...	164674	32.2	32.2	80%	185	100.00	3627	XM_027889294.1
Lateolabrax maculatus linkage group 8 sequence	spotted sea ...	315492	32.2	32.2	80%	185	100.00	27526425	CP032605.1
PREDICTED: Corapipo altera leucine rich repeats and...	White-ruffed...	415028	32.2	32.2	80%	185	100.00	6395	XM_027640185.1
PREDICTED: Neopelma chrysocephalum threonine--tRNA ligase,...	saffron-cres...	114329	32.2	32.2	80%	185	100.00	838	XM_027707939.1
PREDICTED: Neopelma chrysocephalum leucine rich repeats and...	saffron-cres...	114329	32.2	32.2	80%	185	100.00	6400	XM_027700383.1
Eukaryotic synthetic construct chromosome 15	NA	111789	32.2	128	80%	185	100.00	82521392	CP034493.1
Streptomyces griseoviridis strain F1-27 chromosome, complete...	NA	45398	32.2	62.4	80%	185	100.00	8963414	CP034687.1
PREDICTED: Vulpes vulpes immunoglobulin superfamily member 9...	red fox	9627	32.2	32.2	80%	185	100.00	3999	XM_025986332.1
PREDICTED: Vulpes vulpes immunoglobulin superfamily member 9...	red fox	9627	32.2	32.2	80%	185	100.00	4856	XM_025986331.1
Paraburkholderia hospita strain mHSR1 chromosome mHSR1_C,...	NA	169430	32.2	32.2	80%	185	100.00	2509140	CP024939.1
PREDICTED: Theropithecus gelada G protein-coupled receptor...	gelada	9565	32.2	32.2	80%	185	100.00	2656	XM_025388320.1
PREDICTED: Theropithecus gelada G protein-coupled receptor...	gelada	9565	32.2	32.2	80%	185	100.00	2709	XM_025388317.1
PREDICTED: Theropithecus gelada G protein-coupled receptor...	gelada	9565	32.2	32.2	80%	185	100.00	2714	XM_025388316.1
PREDICTED: Pomacea canaliculata uncharacterized LOC112559175...	NA	400727	32.2	32.2	100%	185	95.00	224	XR_003098296.1
PREDICTED: Pomacea canaliculata uncharacterized LOC112559160...	NA	400727	32.2	32.2	100%	185	95.00	344	XR_003098293.1
PREDICTED: Pomacea canaliculata ADAM 17-like protease...	NA	400727	32.2	32.2	100%	185	95.00	1168	XM_025230052.1
PREDICTED: Pomacea canaliculata ADAM 17-like protease...	NA	400727	32.2	32.2	100%	185	95.00	2501	XM_025229985.1
PREDICTED: Pomacea canaliculata ADAM 17-like protease...	NA	400727	32.2	32.2	100%	185	95.00	2345	XM_025232134.1
PREDICTED: Pomacea canaliculata ADAM 17-like protease...	NA	400727	32.2	32.2	100%	185	95.00	869	XM_025232004.1
PREDICTED: Pomacea canaliculata ADAM 17-like protease...	NA	400727	32.2	32.2	100%	185	95.00	3309	XM_025231511.1
PREDICTED: Pelodiscus sinensis chondroitin sulfate synthase 3...	Chinese soft...	13735	32.2	32.2	80%	185	100.00	4249	XM_006131872.3
PREDICTED: Pelodiscus sinensis WD repeat domain,...	Chinese soft...	13735	32.2	32.2	80%	185	100.00	2429	XM_025180363.1
PREDICTED: Macaca nemestrina G protein-coupled receptor kinase...	pig-tailed m...	9545	32.2	32.2	80%	185	100.00	3692	XM_011745249.2
PREDICTED: Neophocaena asiaeorientalis asiaeorientalis PITPNM...	Yangtze finl...	1706337	32.2	32.2	80%	185	100.00	3999	XM_024736166.1
Bos mutus isolate yakQH1 chromosome 13	wild yak	72004	32.2	64.4	85%	185	100.00	75983851	CP027081.1
PREDICTED: Myotis lucifugus immunoglobulin superfamily member ...	little brown...	59463	32.2	32.2	80%	185	100.00	4182	XM_014462785.2
Larimichthys crocea genome assembly, chromosome: XVII	large yellow...	215358	32.2	32.2	80%	185	100.00	26353782	LT972183.1

Zymoseptoria tritici ST99CH_3D1 genome assembly, chromosome:...	NA	1276537	32.2	32.2	100%	185	95.00	3863243	LT854274.1
Zymoseptoria tritici ST99CH_1E4 genome assembly, chromosome:...	NA	1276532	32.2	32.2	100%	185	95.00	3718615	LT854254.1
Cystobacter fuscus strain DSM 52655 chromosome, complete genome	NA	43	32.2	62.4	80%	185	100.00	12349744	CP022098.1
PREDICTED: Crassostrea virginica solute carrier family 22 memb...	eastern oyster	6565	32.2	32.2	80%	185	100.00	1014	XM_022476645.1
Thermococcus thioreducens strain OGL-20P, complete genome	NA	277988	32.2	32.2	80%	185	100.00	2065932	CP015105.1
Zymoseptoria tritici ST99CH_1A5 genome assembly, chromosome: 2	NA	1276529	32.2	32.2	100%	185	95.00	3698724	LT882677.1
Zymoseptoria tritici ST99CH_3D7 genome assembly, chromosome: 2	NA	1276538	32.2	32.2	100%	185	95.00	3819071	LT853693.1
Avian orthoreovirus strain 878-Bi-05 core shell gene, partial cds	NA	38170	32.2	32.2	80%	185	100.00	3847	KX398252.1
Avian orthoreovirus strain 875-Bi-05 core shell gene, complete...	NA	38170	32.2	32.2	80%	185	100.00	3944	KX398242.1
PREDICTED: Rhinopithecus bieti G protein-coupled receptor kina...	black snub-n...	61621	32.2	32.2	80%	185	100.00	2760	XM_017896054.1
PREDICTED: Rhinopithecus bieti G protein-coupled receptor kina...	black snub-n...	61621	32.2	32.2	80%	185	100.00	2921	XM_017896053.1
PREDICTED: Rhinopithecus bieti G protein-coupled receptor kina...	black snub-n...	61621	32.2	32.2	80%	185	100.00	3711	XM_017896052.1
PREDICTED: Rhinopithecus bieti G protein-coupled receptor kina...	black snub-n...	61621	32.2	32.2	80%	185	100.00	2938	XM_017896050.1
PREDICTED: Lepidothrix coronata leucine rich repeats and...	blue-crowned...	321398	32.2	32.2	80%	185	100.00	5938	XM_017826881.1
Mycobacterium sp. djl-10, complete genome	NA	1879023	32.2	62.4	100%	185	100.00	6395946	CP016640.1
PREDICTED: Poecilia formosa M-phase phosphoprotein 9-like...	Amazon molly	48698	32.2	32.2	80%	185	100.00	4241	XM_016681099.1
PREDICTED: Poecilia formosa M-phase phosphoprotein 9-like...	Amazon molly	48698	32.2	32.2	80%	185	100.00	4619	XM_016681098.1
PREDICTED: Poecilia formosa M-phase phosphoprotein 9-like...	Amazon molly	48698	32.2	32.2	80%	185	100.00	4622	XM_007570828.2
PREDICTED: Poecilia formosa M-phase phosphoprotein 9-like...	Amazon molly	48698	32.2	32.2	80%	185	100.00	4622	XM_007570829.2
PREDICTED: Myotis davidii immunoglobulin superfamily member 9...	NA	225400	32.2	32.2	80%	185	100.00	4294	XM_015558592.1
PREDICTED: Macaca fascicularis G protein-coupled receptor kina...	crab-eating ...	9541	32.2	32.2	80%	185	100.00	2922	XM_015452313.1
PREDICTED: Macaca fascicularis G protein-coupled receptor kina...	crab-eating ...	9541	32.2	32.2	80%	185	100.00	3713	XM_015452312.1
PREDICTED: Macaca fascicularis G protein-coupled receptor kina...	crab-eating ...	9541	32.2	32.2	80%	185	100.00	3459	XM_015452311.1
PREDICTED: Macaca fascicularis G protein-coupled receptor kina...	crab-eating ...	9541	32.2	32.2	80%	185	100.00	2995	XM_005558651.2
PREDICTED: Poecilia mexicana M-phase phosphoprotein 9-like...	NA	48701	32.2	32.2	80%	185	100.00	4248	XM_014978308.1
PREDICTED: Poecilia mexicana M-phase phosphoprotein 9...	NA	48701	32.2	32.2	80%	185	100.00	4621	XM_014999435.1
PREDICTED: Poecilia mexicana M-phase phosphoprotein 9...	NA	48701	32.2	32.2	80%	185	100.00	3946	XM_014999434.1
PREDICTED: Poecilia mexicana M-phase phosphoprotein 9...	NA	48701	32.2	32.2	80%	185	100.00	3949	XM_014999433.1
PREDICTED: Poecilia latipinna M-phase phosphoprotein 9...	sailfin molly	48699	32.2	32.2	80%	185	100.00	4613	XM_015044530.1
PREDICTED: Poecilia latipinna M-phase phosphoprotein 9...	sailfin molly	48699	32.2	32.2	80%	185	100.00	4616	XM_015044529.1

PREDICTED: Poecilia latipinna M-phase phosphoprotein 9...	sailfin molly	48699	32.2	32.2	80%	185	100.00	4619	XM_015044528.1
PREDICTED: Sturnus vulgaris microtubule associated...	Common starling	9172	32.2	32.2	80%	185	100.00	9824	XM_014872052.1
PREDICTED: Sturnus vulgaris microtubule associated...	Common starling	9172	32.2	32.2	80%	185	100.00	9891	XM_014872051.1
PREDICTED: Sturnus vulgaris microtubule associated...	Common starling	9172	32.2	32.2	80%	185	100.00	10286	XM_014872050.1
PREDICTED: Sturnus vulgaris microtubule associated...	Common starling	9172	32.2	32.2	80%	185	100.00	12462	XM_014872049.1
PREDICTED: Sturnus vulgaris microtubule associated...	Common starling	9172	32.2	32.2	80%	185	100.00	10052	XM_014872048.1
PREDICTED: Sturnus vulgaris microtubule associated...	Common starling	9172	32.2	32.2	80%	185	100.00	10669	XM_014872047.1
PREDICTED: Sturnus vulgaris microtubule associated...	Common starling	9172	32.2	32.2	80%	185	100.00	10690	XM_014872046.1
PREDICTED: Myotis brandtii immunoglobulin superfamily, member ...	Brandt's bat	109478	32.2	32.2	80%	185	100.00	4037	**XM_014547596.1**
PREDICTED: Latimeria chalumnae GINS complex subunit 1 (Psf1...	coelacanth	7897	32.2	32.2	80%	185	100.00	2129	XM_006003644.2
PREDICTED: Latimeria chalumnae GINS complex subunit 1 (Psf1...	coelacanth	7897	32.2	32.2	80%	185	100.00	2281	XM_006003643.2
Ovis canadensis canadensis isolate 43U chromosome 18 sequence	NA	112262	32.2	32.2	80%	185	100.00	68687575	CP011903.1
Ovis canadensis canadensis isolate 43U chromosome 13 sequence	NA	112262	32.2	64.4	85%	185	100.00	83176208	CP011898.1
TPA: Toxoplasma gondii VEG, chromosome chrVIIb, complete genome	NA	432359	32.2	32.2	80%	185	100.00	5053590	LN714497.1
PREDICTED: Macaca nemestrina G protein-coupled receptor kinase...	pig-tailed m...	9545	32.2	32.2	80%	185	100.00	3452	XM_011745247.1
PREDICTED: Macaca nemestrina G protein-coupled receptor kinase...	pig-tailed m...	9545	32.2	32.2	80%	185	100.00	2988	XM_011745246.1
PREDICTED: Cercocebus atys G protein-coupled receptor kinase 6...	sooty mangabey	9531	32.2	32.2	80%	185	100.00	2661	XM_012051183.1
PREDICTED: Cercocebus atys G protein-coupled receptor kinase 6...	sooty mangabey	9531	32.2	32.2	80%	185	100.00	2897	XM_012051182.1
PREDICTED: Cercocebus atys G protein-coupled receptor kinase 6...	sooty mangabey	9531	32.2	32.2	80%	185	100.00	3713	XM_012051181.1
PREDICTED: Cercocebus atys G protein-coupled receptor kinase 6...	sooty mangabey	9531	32.2	32.2	80%	185	100.00	2988	XM_012051179.1
PREDICTED: Mandrillus leucophaeus G protein-coupled receptor...	drill	9568	32.2	32.2	80%	185	100.00	2658	XM_011989958.1
PREDICTED: Colius striatus immunoglobulin superfamily, member ...	speckled mou...	57412	32.2	32.2	80%	185	100.00	2367	XM_010205233.1
PREDICTED: Cuculus canorus mucin-17-like (LOC104054814), mRNA	common cuckoo	55661	32.2	62.4	80%	185	100.00	5115	XM_009555875.1
PREDICTED: Phalacrocorax carbo T-cell lymphoma invasion and...	great cormorant	9209	32.2	32.2	80%	185	100.00	4743	XM_009502555.1
PREDICTED: Acanthisitta chloris leucine-rich repeats and...	rifleman	57068	32.2	32.2	80%	185	100.00	1338	XM_009085189.1

PREDICTED: Callorhinchus milii E3 ubiquitin-protein ligase...	elephant shark	7868	32.2	128	80%	185	100.00	653	XM_007886546.1
PREDICTED: Vulpes lagopus immunoglobulin superfamily member 9...	Arctic fox	494514	32.2	32.2	80%	185	100.00	3405	XM_041773386.1
PREDICTED: Vulpes lagopus immunoglobulin superfamily member 9...	Arctic fox	494514	32.2	32.2	80%	185	100.00	4167	XM_041773385.1
PREDICTED: Vulpes lagopus immunoglobulin superfamily member 9...	Arctic fox	494514	32.2	32.2	80%	185	100.00	4213	XM_041773383.1
PREDICTED: Vulpes lagopus immunoglobulin superfamily member 9...	Arctic fox	494514	32.2	32.2	80%	185	100.00	4240	XM_041773382.1
PREDICTED: Vulpes lagopus immunoglobulin superfamily member 9...	Arctic fox	494514	32.2	32.2	80%	185	100.00	4212	XM_041773381.1
PREDICTED: Vulpes lagopus immunoglobulin superfamily member 9...	Arctic fox	494514	32.2	32.2	80%	185	100.00	4266	XM_041773380.1
Eristalis pertinax genome assembly, chromosome: 3	NA	1572519	32.2	32.2	80%	185	100.00	77495269	OU026147.1
Caprimulgus europaeus genome assembly, chromosome: 26	Eurasian nig...	111811	32.2	32.2	80%	185	100.00	7503399	OU015550.1
Caprimulgus europaeus genome assembly, chromosome: Z	Eurasian nig...	111811	32.2	92.7	90%	185	100.00	82627501	OU015527.1
Homo sapiens isolate CHM13 chromosome 15	human	9606	32.2	193	80%	185	100.00	99753195	CP068263.2
PREDICTED: Pyrgilauda ruficollis microtubule associated...	rufous-necke...	221976	32.2	32.2	80%	185	100.00	10132	XM_041483329.1
PREDICTED: Pyrgilauda ruficollis microtubule associated...	rufous-necke...	221976	32.2	32.2	80%	185	100.00	10269	XM_041483328.1
PREDICTED: Pyrgilauda ruficollis microtubule associated...	rufous-necke...	221976	32.2	32.2	80%	185	100.00	10097	XM_041483327.1
PREDICTED: Pyrgilauda ruficollis microtubule associated...	rufous-necke...	221976	32.2	32.2	80%	185	100.00	10289	XM_041483326.1
PREDICTED: Pyrgilauda ruficollis microtubule associated...	rufous-necke...	221976	32.2	32.2	80%	185	100.00	10116	XM_041483325.1
PREDICTED: Pyrgilauda ruficollis microtubule associated...	rufous-necke...	221976	32.2	32.2	80%	185	100.00	10236	XM_041483324.1
PREDICTED: Pyrgilauda ruficollis microtubule associated...	rufous-necke...	221976	32.2	32.2	80%	185	100.00	10207	XM_041483323.1
PREDICTED: Pyrgilauda ruficollis microtubule associated...	rufous-necke...	221976	32.2	32.2	80%	185	100.00	10325	XM_041483322.1
PREDICTED: Pyrgilauda ruficollis microtubule associated...	rufous-necke...	221976	32.2	32.2	80%	185	100.00	10482	XM_041483321.1
PREDICTED: Pyrgilauda ruficollis microtubule associated...	rufous-necke...	221976	32.2	32.2	80%	185	100.00	10305	XM_041483320.1
PREDICTED: Pyrgilauda ruficollis microtubule associated...	rufous-necke...	221976	32.2	32.2	80%	185	100.00	10499	XM_041483319.1
PREDICTED: Onychostruthus taczanowskii microtubule associated...	white-rumped ...	356909	32.2	32.2	80%	185	100.00	10076	XM_041421484.1
PREDICTED: Onychostruthus taczanowskii microtubule associated...	white-rumped ...	356909	32.2	32.2	80%	185	100.00	10109	XM_041421482.1
PREDICTED: Onychostruthus taczanowskii microtubule associated...	white-rumped ...	356909	32.2	32.2	80%	185	100.00	10053	XM_041421480.1
PREDICTED: Onychostruthus taczanowskii microtubule associated...	white-rumped ...	356909	32.2	32.2	80%	185	100.00	10073	XM_041421479.1
PREDICTED: Onychostruthus taczanowskii microtubule associated...	white-rumped ...	356909	32.2	32.2	80%	185	100.00	10281	XM_041421478.1
PREDICTED: Onychostruthus taczanowskii microtubule associated...	white-rumped ...	356909	32.2	32.2	80%	185	100.00	10293	XM_041421477.1

PREDICTED: Onychostruthus taczanowskii microtubule associated...	white-rumped ...	356909	32.2	32.2	80%	185	100.00	10296	XM_041421476.1
PREDICTED: Onychostruthus taczanowskii microtubule associated...	white-rumped ...	356909	32.2	32.2	80%	185	100.00	10314	XM_041421475.1
PREDICTED: Toxotes jaculatrix collagen type VII alpha 1-like...	banded arche...	941984	32.2	32.2	80%	185	100.00	9559	XM_041030596.1
Clostera curtula genome assembly, chromosome: 15	NA	987902	32.2	32.2	80%	185	100.00	17175963	FR997809.1
Zymoseptoria tritici isolate M4_64 chromosome 2	NA	1047171	32.2	32.2	100%	185	95.00	3820937	CP062503.1
Zymoseptoria tritici isolate M4_30 chromosome 2	NA	1047171	32.2	32.2	100%	185	95.00	3828741	CP062522.1
Zymoseptoria tritici isolate M4_9 chromosome 2	NA	1047171	32.2	32.2	100%	185	95.00	3688427	CP062542.1
Zymoseptoria tritici isolate M4_8 chromosome 2	NA	1047171	32.2	32.2	100%	185	95.00	3876196	CP062561.1
Zymoseptoria tritici isolate M3_45 chromosome 2	NA	1047171	32.2	32.2	100%	185	95.00	3845180	CP062580.1
Zymoseptoria tritici isolate M3_19 chromosome 2	NA	1047171	32.2	32.2	100%	185	95.00	3847015	CP062599.1
Zymoseptoria tritici isolate M2_11 chromosome 2	NA	1047171	32.2	32.2	100%	185	95.00	3690378	CP062619.1
Zymoseptoria tritici isolate M2_1 chromosome 2	NA	1047171	32.2	32.2	100%	185	95.00	3692739	CP062639.1
Zymoseptoria tritici isolate M1_A66.2 chromosome 2	NA	1047171	32.2	32.2	100%	185	95.00	3795481	CP062659.1
Zymoseptoria tritici isolate M1_A2.2 chromosome 2	NA	1047171	32.2	32.2	100%	185	95.00	3822579	CP062679.1
Erannis defoliaria genome assembly, chromosome: 23	NA	104474	32.2	32.2	80%	185	100.00	13382061	FR990089.1
Fabriciana adippe genome assembly, chromosome: 19	high brown f...	405009	32.2	32.2	80%	185	100.00	14936505	FR990000.1
Meleagris gallopavo genome assembly, chromosome: 7	turkey	9103	32.2	62.4	100%	185	100.00	36365977	HG999687.1
PREDICTED: Ictidomys tridecemlineatus uncharacterized...	thirteen-lin...	43179	32.2	32.2	80%	185	100.00	12946	XR_002483478.2
PREDICTED: Ictidomys tridecemlineatus uncharacterized...	thirteen-lin...	43179	32.2	32.2	80%	185	100.00	12838	XR_005728582.1
PREDICTED: Gasterosteus aculeatus aculeatus plectin b (plecb),...	three-spined...	481459	32.2	32.2	80%	185	100.00	15737	XM_040165185.1
PREDICTED: Gasterosteus aculeatus aculeatus plectin b (plecb),...	three-spined...	481459	32.2	32.2	80%	185	100.00	15755	XM_040165184.1
PREDICTED: Gasterosteus aculeatus aculeatus plectin b (plecb),...	three-spined...	481459	32.2	32.2	80%	185	100.00	15773	XM_040165183.1
PREDICTED: Gasterosteus aculeatus aculeatus plectin b (plecb),...	three-spined...	481459	32.2	32.2	80%	185	100.00	15785	XM_040165182.1
PREDICTED: Gasterosteus aculeatus aculeatus plectin b (plecb),...	three-spined...	481459	32.2	32.2	80%	185	100.00	15791	XM_040165180.1
PREDICTED: Gasterosteus aculeatus aculeatus plectin b (plecb),...	three-spined...	481459	32.2	32.2	80%	185	100.00	15804	XM_040165179.1
PREDICTED: Hirundo rustica microtubule associated...	Barn swallow	43150	32.2	32.2	80%	185	100.00	9804	XM_040072325.1
PREDICTED: Hirundo rustica microtubule associated...	Barn swallow	43150	32.2	32.2	80%	185	100.00	9945	XM_040072322.1
PREDICTED: Hirundo rustica microtubule associated...	Barn swallow	43150	32.2	32.2	80%	185	100.00	10032	XM_040072321.1
PREDICTED: Hirundo rustica microtubule associated...	Barn swallow	43150	32.2	32.2	80%	185	100.00	10050	XM_040072320.1
Canis lupus genome assembly, chromosome: 30	gray wolf	9612	32.2	126	85%	185	100.00	41615186	HG994415.1

Canis lupus genome assembly, chromosome: 26	gray wolf	9612	32.2	32.2	80%	185	100.00	46109286	HG994409.1
Canis lupus genome assembly, chromosome: 9	gray wolf	9612	32.2	62.4	95%	185	100.00	66787146	HG994394.1
PREDICTED: Passer montanus microtubule associated...	Eurasian tre...	9160	32.2	32.2	80%	185	100.00	10256	XM_039711653.1
PREDICTED: Passer montanus microtubule associated...	Eurasian tre...	9160	32.2	32.2	80%	185	100.00	10526	XM_039711651.1
PREDICTED: Passer montanus microtubule associated...	Eurasian tre...	9160	32.2	32.2	80%	185	100.00	10110	XM_039711649.1
PREDICTED: Passer montanus microtubule associated...	Eurasian tre...	9160	32.2	32.2	80%	185	100.00	9833	XM_039711648.1
PREDICTED: Passer montanus microtubule associated...	Eurasian tre...	9160	32.2	32.2	80%	185	100.00	10143	XM_039711645.1
PREDICTED: Passer montanus microtubule associated...	Eurasian tre...	9160	32.2	32.2	80%	185	100.00	9936	XM_039711644.1
PREDICTED: Passer montanus microtubule associated...	Eurasian tre...	9160	32.2	32.2	80%	185	100.00	10010	XM_039711643.1
PREDICTED: Passer montanus microtubule associated...	Eurasian tre...	9160	32.2	32.2	80%	185	100.00	10028	XM_039711642.1
PREDICTED: Passer montanus microtubule associated...	Eurasian tre...	9160	32.2	32.2	80%	185	100.00	10031	XM_039711641.1
PREDICTED: Passer montanus microtubule associated...	Eurasian tre...	9160	32.2	32.2	80%	185	100.00	10049	XM_039711640.1
Spilosoma lubricipeda genome assembly, chromosome: 29	NA	875880	32.2	32.2	80%	185	100.00	9330587	HG992303.1
PREDICTED: Pipra filicauda leucine rich repeats and...	Wire-tailed ...	649802	32.2	32.2	80%	185	100.00	6235	XM_027722955.2
Apotomis turbidana genome assembly, chromosome: 6	NA	1100916	32.2	64.4	80%	185	100.00	28902381	LR990286.1
Zymoseptoria tritici IPO323 uncharacterized protein...	NA	336722	32.2	32.2	100%	185	95.00	664	XM_003854739.1
Streptomyces sp. SN-593	NA	659352	32.2	32.2	100%	185	95.00	8833490	AP018365.1
3_Tms_b3v08	NA	170555	32.2	32.2	80%	185	100.00	468879	OB793032.1
PREDICTED: Motacilla alba alba heat shock protein family A...	NA	1094192	32.2	32.2	80%	185	100.00	4206	XM_038145393.1
PREDICTED: Chlorocebus sabaeus G protein-coupled receptor kina...	green monkey	60711	32.2	32.2	80%	185	100.00	3689	XM_008015433.2
PREDICTED: Chlorocebus sabaeus G protein-coupled receptor kina...	green monkey	60711	32.2	32.2	80%	185	100.00	2996	XM_008015430.2
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6061	XM_037838799.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	5925	XM_037838797.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	5965	XM_037838796.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6142	XM_037838795.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6473	XM_037838794.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6518	XM_037838793.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6533	XM_037838792.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6551	XM_037838791.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6632	XM_037838790.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6344	XM_037838789.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6507	XM_037838788.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6506	XM_037838787.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6530	XM_037838786.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6545	XM_037838784.1

PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6612	XM_037838783.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6449	XM_037838782.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6674	XM_037838781.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6150	XM_037838780.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6237	XM_037838779.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6245	XM_037838778.1
PREDICTED: Choloepus didactylus...	southern two...	27675	32.2	32.2	100%	185	95.00	6419	XM_037838777.1
PREDICTED: Sebastes umbrosus collagen type VII alpha 1-like...	honeycomb ro...	72105	32.2	32.2	80%	185	100.00	7541	XM_037761211.1
Avian orthoreovirus isolate ISR/3559/2020 lambda-1 gene, parti...	NA	38170	32.2	32.2	80%	185	100.00	361	MW057720.1
Letharia columbiana uncharacterized protein (HO173_000884),...	NA	112416	32.2	32.2	80%	185	100.00	3747	XM_037302831.1
Letharia lupina uncharacterized protein (HO133_005998), partia...	NA	560253	32.2	32.2	80%	185	100.00	3813	XM_037296901.1
PREDICTED: Acanthopagrus latus CLOCK-interacting pacemaker b...	yellowfin se...	8177	32.2	32.2	80%	185	100.00	6179	XM_037085890.1
PREDICTED: Acanthopagrus latus CLOCK-interacting pacemaker b...	yellowfin se...	8177	32.2	32.2	80%	185	100.00	6072	XM_037085889.1
PREDICTED: Acanthopagrus latus CLOCK-interacting pacemaker b...	yellowfin se...	8177	32.2	32.2	80%	185	100.00	6159	XM_037085888.1
PREDICTED: Acanthopagrus latus CLOCK-interacting pacemaker b...	yellowfin se...	8177	32.2	32.2	80%	185	100.00	7099	XM_037085887.1
Dicentrarchus labrax chromosome sequence corresponding to...	European sea...	13489	32.2	32.2	80%	185	100.00	14502917	FQ310508.3
Dicentrarchus labrax chromosome sequence corresponding to...	European sea...	13489	32.2	32.2	80%	185	100.00	14803407	FQ310507.3
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowfin se...	8177	32.2	62.4	85%	185	100.00	26170885	LR884481.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowfin se...	8177	32.2	213	95%	185	100.00	31735906	LR884477.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowfin se...	8177	32.2	62.4	80%	185	100.00	31321781	LR884470.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome: 9	yellowfin se...	8177	32.2	62.4	80%	185	100.00	30717905	LR884468.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome: 6	yellowfin se...	8177	32.2	153	80%	185	100.00	34040639	LR884465.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome: 5	yellowfin se...	8177	32.2	62.4	80%	185	100.00	31400991	LR884464.1
PREDICTED: Myotis myotis immunoglobulin superfamily member 9...	NA	51298	32.2	32.2	80%	185	100.00	4108	XM_036344201.1
PREDICTED: Myotis myotis immunoglobulin superfamily member 9...	NA	51298	32.2	32.2	80%	185	100.00	4370	XM_036344199.1
PREDICTED: Myotis myotis immunoglobulin superfamily member 9...	NA	51298	32.2	32.2	80%	185	100.00	4401	XM_036344198.1
PREDICTED: Myotis myotis immunoglobulin superfamily member 9...	NA	51298	32.2	32.2	80%	185	100.00	4546	XM_036344196.1
PREDICTED: Myotis myotis immunoglobulin superfamily member 9...	NA	51298	32.2	32.2	80%	185	100.00	4210	XM_036344195.1
PREDICTED: Myotis myotis immunoglobulin superfamily member 9...	NA	51298	32.2	32.2	80%	185	100.00	4553	XM_036344194.1

PREDICTED: Rousettus aegyptiacus immunoglobulin superfamily...	Egyptian rou...	9407	32.2	32.2	80%	185	100.00	4690	**XM_036235296.1**
PREDICTED: Rousettus aegyptiacus immunoglobulin superfamily...	Egyptian rou...	9407	32.2	32.2	80%	185	100.00	5868	**XM_016139315.2**
PREDICTED: Rousettus aegyptiacus immunoglobulin superfamily...	Egyptian rou...	9407	32.2	32.2	80%	185	100.00	3997	**XM_036235295.1**
PREDICTED: Rousettus aegyptiacus immunoglobulin superfamily...	Egyptian rou...	9407	32.2	32.2	80%	185	100.00	4346	**XM_016139295.2**
PREDICTED: Rousettus aegyptiacus immunoglobulin superfamily...	Egyptian rou...	9407	32.2	32.2	80%	185	100.00	4394	**XM_016139305.2**
Homo sapiens DNA, chromosome 15, nearly complete genome	human	9606	32.2	96.6	80%	185	100.00	95537968	AP023475.1
Peribacillus butanolivorans strain KJ40 chromosome, complete...	NA	421767	32.2	32.2	80%	185	100.00	5451105	CP050509.1
Acomys russatus genome assembly, chromosome: 31	golden spiny...	60746	32.2	32.2	80%	185	100.00	43509854	LR877242.1
Acomys russatus genome assembly, chromosome: 14	golden spiny...	60746	32.2	62.4	85%	185	100.00	62749011	LR877225.1
Acomys russatus genome assembly, chromosome: 11	golden spiny...	60746	32.2	32.2	80%	185	100.00	62768634	LR877222.1
Acomys russatus genome assembly, chromosome: 9	golden spiny...	60746	32.2	32.2	80%	185	100.00	66475698	LR877220.1
Acomys russatus genome assembly, chromosome: 4	golden spiny...	60746	32.2	94.6	90%	185	100.00	85305823	LR877215.1
Onychomys torridus genome assembly, chromosome: 12	southern gra...	38674	32.2	62.4	90%	185	100.00	75710165	LR877199.1
Arvicola amphibius genome assembly, chromosome: 16	Eurasian wat...	1047088	32.2	32.2	80%	185	100.00	51382976	LR862396.1
PREDICTED: Electrophorus electricus StAR-related lipid transfe...	electric eel	8005	32.2	32.2	80%	185	100.00	13571	XM_035532893.1
Danio rerio genome assembly, chromosome: 14	zebrafish	7955	32.2	32.2	80%	185	100.00	54753181	LR812051.1
Anas platyrhynchos genome assembly, chromosome: 19	mallard	8839	32.2	32.2	80%	185	100.00	12467114	LS423629.1
Danio rerio genome assembly, chromosome: 14	zebrafish	7955	32.2	32.2	80%	185	100.00	48960514	LR812607.1
Homo sapiens protein tyrosine phosphatase receptor type N2...	human	9606	32.2	64.4	85%	185	100.00	1055733	NG_029966.1
Trypanosoma congolense IL3000 annotated genomic contig,...	NA	1068625	32.2	32.2	80%	185	100.00	4815855	HE575324.1
Homo sapiens FOSMID clone ABC9-43868200G7 from chromosome 15,...	human	9606	32.2	64.4	80%	185	100.00	41802	AC231200.2
Zea mays uncharacterized LOC100279993 (LOC100279993), mRNA	NA	4577	32.2	32.2	100%	185	95.00	1524	NM_001152941.1
Zea mays clone 260621 MCM10 minichromosome maintenance deficie...	NA	4577	32.2	32.2	100%	185	95.00	1485	EU963299.1
Homo sapiens alpha-L-iduronidase (IDUA), RefSeqGene (LRG_1277)...	human	9606	32.2	32.2	80%	185	100.00	24533	NG_008103.1
Homo sapiens FOSMID clone ABC10-44749600O7 from chromosome...	human	9606	32.2	32.2	80%	185	100.00	42333	AC225832.2
Rhesus Macaque BAC CH250-271J18 () complete sequence	Rhesus monkey	9544	32.2	32.2	80%	185	100.00	191092	AC144026.2
Aspergillus niger contig An12c0020, genomic contig	NA	5061	32.2	32.2	100%	185	95.00	73518	AM270259.1
Homo sapiens chromosome 15, clone RP11-361M10, complete sequence	human	9606	32.2	32.2	80%	185	100.00	213746	AC009712.22

Cenarchaeum symbiosum B clone C15D08, complete sequence	NA	414005	32.2	32.2	80%	185	100.00	38754	DQ397852.1
Cenarchaeum symbiosum B clone C08E01, complete sequence	NA	414005	32.2	32.2	80%	185	100.00	37303	DQ397849.1
Mus musculus chromosome 5, clone RP24-84G9, complete sequence	house mouse	10090	32.2	32.2	80%	185	100.00	204954	AC116151.10
Pan troglodytes BAC clone RP43-20G17 from chromosome 7, comple...	chimpanzee	9598	32.2	32.2	80%	185	100.00	221255	AC145883.2
Homo sapiens mRNA for solute carrier family 26, member 1 isofo...	human	9606	32.2	32.2	80%	185	100.00	5597	AB208901.1
Homo sapiens 12 BAC RP13-977J11 (Roswell Park Cancer Institute...	human	9606	32.2	32.2	100%	185	95.00	129492	AC138466.12
Homo sapiens BAC clone RP11-460I19 from 4, complete sequence	human	9606	32.2	32.2	80%	185	100.00	177950	AC019103.8
Homo sapiens chromosome 15, clone RP11-2M12, complete sequence	human	9606	32.2	32.2	80%	185	100.00	162060	AC013486.12
Homo sapiens golgin-like protein (GLP) gene, complete cds	human	9606	32.2	32.2	80%	185	100.00	21500	AF266285.1
Mus musculus chromosome 3, clone RP23-427K12, complete sequence	house mouse	10090	32.2	32.2	80%	185	100.00	175075	AC116406.13
Mouse DNA sequence from clone RP23-44D10 on chromosome 4,...	house mouse	10090	32.2	32.2	80%	185	100.00	176816	AL806527.7
PREDICTED: Pan paniscus solute carrier family 26 member 1...	pygmy chimpa...	9597	32.2	32.2	80%	185	100.00	3634	XM_008963702.2
PREDICTED: Trachemys scripta elegans polyamine oxidase (PAOX),...	NA	31138	32.2	32.2	80%	185	100.00	1399	XM_034775004.1
PREDICTED: Trachemys scripta elegans polyamine oxidase (PAOX),...	NA	31138	32.2	32.2	80%	185	100.00	1895	XM_034775000.1
PREDICTED: Esox lucius CUE domain containing 1b (cuedc1b),...	northern pike	8010	32.2	32.2	80%	185	100.00	6148	XM_020050352.2
PREDICTED: Esox lucius CUE domain containing 1b (cuedc1b),...	northern pike	8010	32.2	32.2	80%	185	100.00	6384	XM_010873621.4
PREDICTED: Esox lucius CUE domain containing 1b (cuedc1b),...	northern pike	8010	32.2	32.2	80%	185	100.00	6334	XM_010873537.3
PREDICTED: Periophthalmus magnuspinnatus heterogeneous nuclear...	NA	409849	32.2	32.2	80%	185	100.00	1370	XM_033983607.1
PREDICTED: Orcinus orca C-X-C motif chemokine ligand 17...	killer whale	9733	32.2	32.2	100%	185	95.00	1025	XM_004271217.2
PREDICTED: Anabas testudineus chromodomain helicase DNA bindin...	climbing perch	64144	32.2	32.2	80%	185	100.00	12327	XM_026378661.2
Pseudochaenichthys georgianus genome assembly, chromosome: 12	South Georgi...	52239	32.2	62.4	85%	185	100.00	30946200	LR792557.1
Streptomyces griseoviridis strain K61 chromosome, complete genome	NA	45398	32.2	62.4	80%	185	100.00	8962736	CP029078.1
Canis lupus familiaris breed Labrador retriever chromosome 32a	dog	9615	32.2	62.4	100%	185	100.00	65817495	CP050598.1
Canis lupus familiaris breed Labrador retriever chromosome 06a	dog	9615	32.2	32.2	80%	185	100.00	81738426	CP050586.1
Canis lupus familiaris breed Labrador retriever chromosome 26a	dog	9615	32.2	32.2	80%	185	100.00	38035513	CP050570.1
Canis lupus familiaris breed Labrador retriever chromosome 32b	dog	9615	32.2	62.4	100%	185	100.00	65810985	CP050634.1
Canis lupus familiaris breed Labrador retriever chromosome 26b	dog	9615	32.2	32.2	80%	185	100.00	38033444	CP050610.1
PREDICTED: Brassica rapa type II inositol polyphosphate...	field mustard	3711	32.2	32.2	80%	185	100.00	3757	XM_009106907.3

Brevibacterium sp. o2 chromosome, complete genome	NA	2697565	32.2	32.2	80%	185	100.00	4253182	CP050154.1
Coregonus sp. 'balchen' genome assembly, chromosome: 6	NA	861768	32.2	32.2	80%	185	100.00	43692974	LR778258.1
PREDICTED: Chiroxiphia lanceolata NIPA like domain containing ...	lance-tailed...	296741	32.2	32.2	80%	185	100.00	5790	XM_032710073.1
PREDICTED: Phocoena sinus C-X-C motif chemokine ligand 17...	vaquita	42100	32.2	32.2	100%	185	95.00	492	XM_032614237.1
PREDICTED: Lynx canadensis thioesterase superfamily member 5...	Canada lynx	61383	32.2	32.2	80%	185	100.00	2431	XM_032594381.1
PREDICTED: Lynx canadensis thioesterase superfamily member 5...	Canada lynx	61383	32.2	32.2	80%	185	100.00	3363	XM_030325056.2
Epinephelus fuscoguttatus DNA, LG20, complete sequence	brown-marble...	293821	32.2	122	85%	185	100.00	39681369	AP022694.1
Epinephelus fuscoguttatus DNA, LG11, complete sequence	brown-marble...	293821	32.2	153	80%	185	100.00	44419306	AP022685.1
Epinephelus fuscoguttatus DNA, LG6, complete sequence	brown-marble...	293821	32.2	62.4	90%	185	100.00	47213327	AP022680.1
PREDICTED: Corvus moneduloides selectin P (SELP), transcript...	New Caledoni...	1196302	32.2	32.2	80%	185	100.00	2983	XM_032118227.1
PREDICTED: Corvus moneduloides selectin P (SELP), transcript...	New Caledoni...	1196302	32.2	32.2	80%	185	100.00	3234	XM_032118226.1
PREDICTED: Corvus moneduloides selectin P (SELP), transcript...	New Caledoni...	1196302	32.2	32.2	80%	185	100.00	3311	XM_032118225.1
PREDICTED: Corvus moneduloides selectin P (SELP), transcript...	New Caledoni...	1196302	32.2	32.2	80%	185	100.00	3124	XM_032118224.1
PREDICTED: Corvus moneduloides selectin P (SELP), transcript...	New Caledoni...	1196302	32.2	32.2	80%	185	100.00	6477	XM_032118223.1
PREDICTED: Corvus moneduloides selectin P (SELP), transcript...	New Caledoni...	1196302	32.2	32.2	80%	185	100.00	6660	XM_032118222.1
Aspergillus caelatus uncharacterized protein...	NA	61420	32.2	32.2	80%	185	100.00	948	XM_032068524.1
Aspergillus pseudotamarii uncharacterized protein...	NA	132259	32.2	32.2	80%	185	100.00	1084	XM_032054830.1
Lutra lutra genome assembly, chromosome: X	Eurasian riv...	9657	32.2	62.4	95%	185	100.00	99689450	LR738421.1
PREDICTED: Oncorhynchus kisutch vasopressin V2 receptor...	coho salmon	8019	32.2	32.2	80%	185	100.00	3004	XM_031803871.1
PREDICTED: Oncorhynchus kisutch vasopressin V2 receptor...	coho salmon	8019	32.2	32.2	80%	185	100.00	6187	XR_004205252.1
PREDICTED: Oncorhynchus kisutch vasopressin V2 receptor...	coho salmon	8019	32.2	32.2	80%	185	100.00	3042	XM_031803870.1
PREDICTED: Oncorhynchus kisutch vasopressin V2 receptor...	coho salmon	8019	32.2	32.2	80%	185	100.00	3045	XM_020460139.2
PREDICTED: Oncorhynchus kisutch vasopressin V2 receptor-like...	coho salmon	8019	32.2	32.2	80%	185	100.00	2288	XM_031794650.1
PREDICTED: Papio anubis interleukin 15 receptor subunit alpha...	olive baboon	9555	32.2	32.2	80%	185	100.00	1504	XM_031651935.1
PREDICTED: Gorilla gorilla gorilla solute carrier family 26...	western lowl...	9595	32.2	32.2	80%	185	100.00	5641	XM_019025220.2
PREDICTED: Gorilla gorilla gorilla solute carrier family 26...	western lowl...	9595	32.2	32.2	80%	185	100.00	6007	XM_019025218.2
Streptomyces fradiae ATCC 10745 = DSM 40063 strain ATCC 10745...	NA	1319510	32.2	32.2	100%	185	95.00	6725579	CP023696.1
PREDICTED: Globicephala melas C-X-C motif chemokine ligand 17...	long-finned ...	9731	32.2	32.2	100%	185	95.00	966	XM_030874076.1

PREDICTED: Strigops habroptila FA complementation group G...	Kakapo	2489341	32.2	32.2	80%	185	100.00	1677	XM_030470574.1
Geotrypetes seraphini genome assembly, chromosome: 13	NA	260995	32.2	32.2	80%	185	100.00	83871185	LR699158.1
Chanos chanos genome assembly, chromosome: 11	milkfish	29144	32.2	32.2	80%	185	100.00	25523583	LR697116.1
PREDICTED: Sphaeramia orbicularis cadherin-related family memb...	orbiculate c...	375764	32.2	32.2	80%	185	100.00	4407	XM_030148818.1
PREDICTED: Sphaeramia orbicularis cadherin-related family memb...	orbiculate c...	375764	32.2	32.2	80%	185	100.00	4401	XM_030148816.1
PREDICTED: Sphaeramia orbicularis cadherin-related family memb...	orbiculate c...	375764	32.2	32.2	80%	185	100.00	4299	XM_030148815.1
PREDICTED: Manacus vitellinus NIPA like domain containing 3...	golden-colla...	328815	32.2	32.2	80%	185	100.00	5560	XM_008920554.3
PREDICTED: Terrapene carolina triunguis peroxisomal...	Three-toed b...	2587831	32.2	32.2	80%	185	100.00	1589	XM_026653782.2
PREDICTED: Terrapene carolina triunguis peroxisomal...	Three-toed b...	2587831	32.2	32.2	80%	185	100.00	1592	XM_024210356.3
PREDICTED: Takifugu rubripes chromodomain helicase DNA binding...	torafugu	31033	32.2	32.2	80%	185	100.00	7842	XM_029846661.1
PREDICTED: Takifugu rubripes chromodomain helicase DNA binding...	torafugu	31033	32.2	32.2	80%	185	100.00	9762	XM_029846660.1
PREDICTED: Takifugu rubripes chromodomain helicase DNA binding...	torafugu	31033	32.2	32.2	80%	185	100.00	9542	XM_029846659.1
PREDICTED: Takifugu rubripes chromodomain helicase DNA binding...	torafugu	31033	32.2	32.2	80%	185	100.00	9545	XM_029846658.1
PREDICTED: Takifugu rubripes chromodomain helicase DNA binding...	torafugu	31033	32.2	32.2	80%	185	100.00	10179	XM_029846657.1
PREDICTED: Takifugu rubripes chromodomain helicase DNA binding...	torafugu	31033	32.2	32.2	80%	185	100.00	9596	XM_011609691.2
PREDICTED: Salmo trutta vasopressin V2 receptor-like...	river trout	8032	32.2	32.2	80%	185	100.00	1656	XM_029718637.1
PREDICTED: Oncorhynchus nerka vasopressin V2 receptor-like...	sockeye salmon	8023	32.2	32.2	80%	185	100.00	2426	XM_029622874.1
PREDICTED: Oncorhynchus nerka vasopressin V2 receptor-like...	sockeye salmon	8023	32.2	32.2	80%	185	100.00	3012	XM_029622873.1
PREDICTED: Oncorhynchus nerka vasopressin V2 receptor-like...	sockeye salmon	8023	32.2	32.2	80%	185	100.00	2712	XR_003859474.1
PREDICTED: Oncorhynchus nerka vasopressin V2 receptor-like...	sockeye salmon	8023	32.2	32.2	80%	185	100.00	3050	XM_029622872.1
PREDICTED: Oncorhynchus nerka vasopressin V2 receptor-like...	sockeye salmon	8023	32.2	32.2	80%	185	100.00	3053	XM_029622871.1
PREDICTED: Oncorhynchus nerka vasopressin V2 receptor-like...	sockeye salmon	8023	32.2	32.2	80%	185	100.00	1310	XM_029654336.1
Salarias fasciatus genome assembly, chromosome: 11	jewelled blenny	181472	32.2	183	95%	185	100.00	36057378	LR597446.1
Streptopelia turtur genome assembly, chromosome: 23	NA	177155	32.2	32.2	80%	185	100.00	5936520	LR594572.1
Streptopelia turtur genome assembly, chromosome: 8	NA	177155	32.2	94.6	90%	185	100.00	34574536	LR594559.1
Takifugu rubripes genome assembly, chromosome: 2	torafugu	31033	32.2	32.2	80%	185	100.00	15686389	LR584245.2
PREDICTED: Macaca mulatta interleukin 15 receptor subunit alph...	Rhesus monkey	9544	32.2	32.2	80%	185	100.00	1739	XM_028853491.1

PREDICTED: Macaca mulatta interleukin 15 receptor subunit alph...	Rhesus monkey	9544	32.2	32.2	80%	185	100.00	1838	XM_015146371.2
PREDICTED: Macaca mulatta interleukin 15 receptor subunit alph...	Rhesus monkey	9544	32.2	32.2	80%	185	100.00	1415	XM_015146370.2
PREDICTED: Macaca mulatta interleukin 15 receptor subunit alph...	Rhesus monkey	9544	32.2	32.2	80%	185	100.00	1514	XM_015146369.2
Streptomyces sp. SS52 chromosome, complete genome	NA	2563602	32.2	32.2	80%	185	100.00	8184045	CP039123.1
Salmo trutta genome assembly, chromosome: 16	river trout	8032	32.2	32.2	80%	185	100.00	61349433	LR584431.1
Salmo trutta genome assembly, chromosome: 28	river trout	8032	32.2	32.2	80%	185	100.00	46383311	LR584422.1
Byssochlamys spectabilis hypothetical protein...	NA	264951	32.2	32.2	80%	185	100.00	918	XM_028633273.1
Homo sapiens chromosome 15 clone VMRC59-114M16, complete sequence	human	9606	32.2	64.4	80%	185	100.00	149664	AC279104.1
Homo sapiens chromosome 15 clone VMRC59-148F23, complete sequence	human	9606	32.2	32.2	80%	185	100.00	108707	AC278993.1
Denticeps clupeoides genome assembly, chromosome: 7	denticle her...	299321	32.2	32.2	80%	185	100.00	25339795	LR535819.1
Streptomyces aquilus strain GGCR-6 chromosome, complete genome	NA	2548456	32.2	32.2	80%	185	100.00	10393987	CP034463.1
Parambassis ranga genome assembly, chromosome: 2	Indian glass...	210632	32.2	62.4	80%	185	100.00	46703924	LR131970.1
Parambassis ranga genome assembly, chromosome: 16	Indian glass...	210632	32.2	32.2	80%	185	100.00	22465611	LR131966.1
Parambassis ranga genome assembly, chromosome: 10	Indian glass...	210632	32.2	32.2	80%	185	100.00	24485510	LR131961.1
Cottoperca gobio genome assembly, chromosome: 14	NA	56716	32.2	92.7	85%	185	100.00	25704503	LR131921.1
Glaciecola amylolytica strain THG-3.7 chromosome, complete genome	NA	2489595	32.2	32.2	80%	185	100.00	4606342	CP034120.1
PREDICTED: Lagenorhynchus obliquidens C-X-C motif chemokine...	Pacific whit...	90247	32.2	32.2	100%	185	95.00	1074	XM_027079714.1
PREDICTED: Acinonyx jubatus thioesterase superfamily member 5...	cheetah	32536	32.2	32.2	80%	185	100.00	948	XM_015078033.2
PREDICTED: Acinonyx jubatus thioesterase superfamily member 5...	cheetah	32536	32.2	32.2	80%	185	100.00	1360	XM_015078027.2
PREDICTED: Frankliniella occidentalis uncharacterized...	western flow...	133901	32.2	32.2	80%	185	100.00	3883	XM_026424588.1
PREDICTED: Urocitellus parryii polycystin 1 like 1, transient...	Arctic groun...	9999	32.2	32.2	80%	185	100.00	8247	XM_026411621.1
PREDICTED: Anabas testudineus chromodomain helicase DNA bindin...	climbing perch	64144	32.2	32.2	80%	185	100.00	10527	XM_026378665.1
PREDICTED: Anabas testudineus chromodomain helicase DNA bindin...	climbing perch	64144	32.2	32.2	80%	185	100.00	10665	XM_026378664.1
PREDICTED: Anabas testudineus chromodomain helicase DNA bindin...	climbing perch	64144	32.2	32.2	80%	185	100.00	12275	XM_026378663.1
PREDICTED: Anabas testudineus chromodomain helicase DNA bindin...	climbing perch	64144	32.2	32.2	80%	185	100.00	12278	XM_026378662.1
PREDICTED: Anabas testudineus chromodomain helicase DNA bindin...	climbing perch	64144	32.2	32.2	80%	185	100.00	12326	XM_026378660.1
PREDICTED: Anabas testudineus chromodomain helicase DNA bindin...	climbing perch	64144	32.2	32.2	80%	185	100.00	12329	XM_026378659.1

PREDICTED: Balaenoptera acutorostrata scammoni C-X-C motif...	NA	310752	32.2	32.2	100%	185	95.00	858	XM_007168055.2
Lateolabrax maculatus linkage group 18 sequence	spotted sea ...	315492	32.2	32.2	80%	185	100.00	22499927	CP032592.1
Lateolabrax maculatus chromosome Lm15	spotted sea ...	315492	32.2	128	80%	185	100.00	23659279	CP027276.1
PREDICTED: Corapipo altera NIPA like domain containing 3...	White-ruffed...	415028	32.2	32.2	80%	185	100.00	5829	XM_027661195.1
Eukaryotic synthetic construct chromosome 14	NA	111789	32.2	62.4	80%	185	100.00	88289540	CP034492.1
Peribacillus butanolivorans strain PHB-7a chromosome, complete...	NA	421767	32.2	32.2	80%	185	100.00	5568346	CP030926.1
PREDICTED: Theropithecus gelada interleukin 15 receptor subuni...	gelada	9565	32.2	32.2	80%	185	100.00	1651	XM_025395871.1
PREDICTED: Theropithecus gelada interleukin 15 receptor subuni...	gelada	9565	32.2	32.2	80%	185	100.00	1750	XM_025395870.1
Streptomyces actuosus strain ATCC 25421 chromosome, complete...	NA	1885	32.2	32.2	80%	185	100.00	8145579	CP029788.1
PREDICTED: Alligator sinensis nuclear receptor binding protein...	Chinese alli...	38654	32.2	32.2	80%	185	100.00	8530	XM_025214240.1
PREDICTED: Macaca nemestrina interleukin 15 receptor subunit...	pig-tailed m...	9545	32.2	32.2	80%	185	100.00	1668	XM_011762731.2
PREDICTED: Macaca nemestrina interleukin 15 receptor subunit...	pig-tailed m...	9545	32.2	32.2	80%	185	100.00	1765	XM_011762729.2
PREDICTED: Macaca nemestrina interleukin 15 receptor subunit...	pig-tailed m...	9545	32.2	32.2	80%	185	100.00	1880	XM_011762726.2
PREDICTED: Neophocaena asiaeorientalis asiaeorientalis C-X-C...	Yangtze finl...	1706337	32.2	32.2	100%	185	95.00	777	XM_024768710.1
PREDICTED: Oncorhynchus tshawytscha vasopressin V2 receptor-li...	Chinook salmon	74940	32.2	32.2	80%	185	100.00	2385	XM_024383903.1
PREDICTED: Oncorhynchus tshawytscha vasopressin V2 receptor-li...	Chinook salmon	74940	32.2	32.2	80%	185	100.00	2558	XM_024383902.1
PREDICTED: Oncorhynchus tshawytscha vasopressin V2 receptor-li...	Chinook salmon	74940	32.2	32.2	80%	185	100.00	2964	XM_024383901.1
PREDICTED: Oncorhynchus tshawytscha vasopressin V2 receptor-li...	Chinook salmon	74940	32.2	32.2	80%	185	100.00	2729	XR_002949050.1
PREDICTED: Oncorhynchus tshawytscha vasopressin V2 receptor-li...	Chinook salmon	74940	32.2	32.2	80%	185	100.00	3002	XM_024383900.1
PREDICTED: Oncorhynchus tshawytscha vasopressin V2 receptor-li...	Chinook salmon	74940	32.2	32.2	80%	185	100.00	2671	XR_002949049.1
PREDICTED: Oncorhynchus tshawytscha vasopressin V2 receptor-li...	Chinook salmon	74940	32.2	32.2	80%	185	100.00	3005	XM_024383899.1
Bos mutus isolate yakQH1 chromosome 26	wild yak	72004	32.2	32.2	80%	185	100.00	16099052	CP027094.1
PREDICTED: Physeter catodon C-X-C motif chemokine ligand 17...	sperm whale	9755	32.2	32.2	100%	185	95.00	360	XM_024132473.1
PREDICTED: Bicyclus anynana putative ammonium transporter 3...	squinting bu...	110368	32.2	32.2	80%	185	100.00	1963	XM_024096581.1
PREDICTED: Salvelinus alpinus vasopressin V2 receptor...	Arctic char	8036	32.2	32.2	80%	185	100.00	3030	XM_024005006.1
PREDICTED: Cavia porcellus FERM domain containing 8 (Frmd8),...	domestic gui...	10141	32.2	32.2	80%	185	100.00	3280	XM_005002975.3
PREDICTED: Cavia porcellus FERM domain containing 8 (Frmd8),...	domestic gui...	10141	32.2	32.2	80%	185	100.00	3281	XM_003468229.4
PREDICTED: Felis	domestic cat	9685	32.2	32.2	80%	185	100.00	5781	XM_023254423.1

catus semaphorin 6A (SEMA6A), transcript...									
PREDICTED: Felis catus semaphorin 6A (SEMA6A), transcript...	domestic cat	9685	32.2	32.2	80%	185	100.00	5947	XM_023254419.1
PREDICTED: Felis catus semaphorin 6A (SEMA6A), transcript...	domestic cat	9685	32.2	32.2	80%	185	100.00	6000	XM_023254418.1
PREDICTED: Brassica napus type II inositol polyphosphate...	rape	3708	32.2	32.2	80%	185	100.00	3807	XM_013866985.2
PREDICTED: Brassica napus type II inositol polyphosphate...	rape	3708	32.2	32.2	80%	185	100.00	3613	XM_022689063.1
Oryzias latipes strain HSOK chromosome 3	Japanese medaka	8090	32.2	32.2	80%	185	100.00	39097270	CP020623.1
Oryzias latipes strain HNI chromosome 3	Japanese medaka	8090	32.2	32.2	80%	185	100.00	35737580	CP020781.1
Oryzias latipes strain HNI chromosome 2	Japanese medaka	8090	32.2	32.2	80%	185	100.00	21867142	CP020780.1
Oryzias latipes strain Hd-rR chromosome 3 sequence	Japanese medaka	8090	32.2	32.2	80%	185	100.00	38248663	CP020667.1
PREDICTED: Arabidopsis lyrata subsp. lyrata type II inositol...	NA	81972	32.2	32.2	80%	185	100.00	3810	XM_021034746.1
PREDICTED: Arabidopsis lyrata subsp. lyrata type II inositol...	NA	81972	32.2	32.2	80%	185	100.00	3749	XM_021034745.1
PREDICTED: Arabidopsis lyrata subsp. lyrata type II inositol...	NA	81972	32.2	32.2	80%	185	100.00	3793	XM_021034744.1
PREDICTED: Oryzias latipes uncharacterized LOC110017447...	Japanese medaka	8090	32.2	32.2	80%	185	100.00	1540	XR_002292853.1
Spirodela polyrhiza strain 9509 chromosome 4 sequence	great duckweed	29656	32.2	32.2	100%	185	95.00	8682450	CP019096.1
PREDICTED: Felis catus thioesterase superfamily member 5...	domestic cat	9685	32.2	32.2	80%	185	100.00	946	XM_006935156.2
PREDICTED: Felis catus thioesterase superfamily member 5...	domestic cat	9685	32.2	32.2	80%	185	100.00	1070	XM_003990639.4
PREDICTED: Branchiostoma belcheri uncharacterized LOC109468288...	Belcher's la...	7741	32.2	32.2	80%	185	100.00	4169	XM_019766544.1
PREDICTED: Branchiostoma belcheri uncharacterized LOC109468288...	Belcher's la...	7741	32.2	32.2	80%	185	100.00	4103	XM_019766543.1
PREDICTED: Branchiostoma belcheri uncharacterized LOC109468288...	Belcher's la...	7741	32.2	32.2	80%	185	100.00	4172	XM_019766542.1
PREDICTED: Alligator mississippiensis nuclear receptor binding...	American all...	8496	32.2	32.2	80%	185	100.00	7280	XM_014601724.2
PREDICTED: Aptenodytes forsteri **Fanconi anemia complementation...**	emperor penguin	9233	32.2	32.2	80%	185	100.00	1887	**XM_009288251.2**
PREDICTED: Lates calcarifer RAB3 GTPase activating protein...	barramundi p...	8187	32.2	32.2	80%	185	100.00	4597	XM_018666545.1
PREDICTED: Raphanus sativus type II inositol polyphosphate...	radish	3726	32.2	32.2	80%	185	100.00	1414	XM_018606089.1
Streptomyces rubrolavendulae strain MJM4426, complete genome	NA	285473	32.2	32.2	100%	185	95.00	6543262	CP017316.1
PREDICTED: Nanorana parkeri POU domain, class 5, transcription...	NA	125878	32.2	32.2	80%	185	100.00	1263	XM_018556760.1
Streptomyces fodineus strain TW1S1 chromosome, complete genome	NA	1904616	32.2	32.2	80%	185	100.00	9698948	CP017248.1

Arabidopsis thaliana Endonuclease/exonuclease/phosphatase fami...	thale cress	3702	32.2	32.2	80%	185	100.00	3804	NM_001334216.1
Arabidopsis thaliana Endonuclease/exonuclease/phosphatase fami...	thale cress	3702	32.2	32.2	80%	185	100.00	3787	NM_105232.3
TPA: Oryzias latipes strain Hd-rR, complete genome assembly,...	Japanese medaka	8090	32.2	32.2	80%	185	100.00	36623554	HF933209.1
Variovorax sp. HW608 genome assembly, chromosome: I	NA	1034889	32.2	32.2	80%	185	100.00	7733665	LT607803.1
PREDICTED: Lepidothrix coronata NIPA like domain containing 3...	blue-crowned...	321398	32.2	32.2	80%	185	100.00	5812	XM_017836581.1
PREDICTED: Lepidothrix coronata NIPA like domain containing 3...	blue-crowned...	321398	32.2	32.2	80%	185	100.00	5755	XM_017836580.1
PREDICTED: Corvus brachyrhynchos selectin P (SELP), mRNA	American crow	85066	32.2	32.2	80%	185	100.00	3124	XM_017729691.1
PREDICTED: Poecilia reticulata zinc finger FYVE-type containin...	guppy	8081	32.2	32.2	80%	185	100.00	4356	XM_008400055.2
PREDICTED: Poecilia reticulata zinc finger FYVE-type containin...	guppy	8081	32.2	32.2	80%	185	100.00	4452	XM_008400054.2
PREDICTED: Tribolium castaneum protein DDI1 homolog 2...	red flour be...	7070	32.2	32.2	80%	185	100.00	1594	XM_008195012.2
PREDICTED: Tribolium castaneum protein DDI1 homolog 2...	red flour be...	7070	32.2	32.2	80%	185	100.00	2636	XM_008195011.2
PREDICTED: Tribolium castaneum protein DDI1 homolog 2...	red flour be...	7070	32.2	32.2	80%	185	100.00	2666	XM_008195008.2
PREDICTED: Diachasma alloeum uncharacterized LOC107048675...	NA	454923	32.2	32.2	80%	185	100.00	2932	XM_015271984.1
PREDICTED: Salmo salar vasopressin V2 receptor-like...	Atlantic salmon	8030	32.2	32.2	80%	185	100.00	2165	XM_014147112.1
PREDICTED: Brassica oleracea var. oleracea type II inositol...	NA	109376	32.2	32.2	80%	185	100.00	3747	XM_013736272.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	32.2	32.2	80%	185	100.00	18604806	LK064876.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	32.2	32.2	80%	185	100.00	847937	LK064862.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	32.2	32.2	80%	185	100.00	67200	LK070070.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	32.2	32.2	80%	185	100.00	10087767	LK064645.1
PREDICTED: Cercocebus atys interleukin 15 receptor, alpha...	sooty mangabey	9531	32.2	32.2	80%	185	100.00	1666	XM_012085753.1
PREDICTED: Mandrillus leucophaeus interleukin 15 receptor, alp...	drill	9568	32.2	32.2	80%	185	100.00	1882	XM_011974951.1
PREDICTED: Balearica regulorum gibbericeps **Fanconi anemia,...**	East African...	100784	32.2	32.2	80%	185	100.00	1769	**XM_010304489.1**
PREDICTED: Chlamydotis macqueenii **Fanconi anemia,...**	Macqueen's b...	187382	32.2	32.2	80%	185	100.00	1769	**XM_010115636.1**
PREDICTED: Antrostomus carolinensis **FA complementation group G...**	chuck-will's...	279965	32.2	32.2	80%	185	100.00	1271	**XM_010167765.1**
PREDICTED: Buceros rhinoceros silvestris **Fanconi anemia,...**	NA	175836	32.2	32.2	80%	185	100.00	1772	**XM_010142144.1**
PREDICTED: Tauraco erythrolophus **Fanconi anemia, complementati...**	red-crested ...	121530	32.2	32.2	80%	185	100.00	1754	**XM_009979471.1**
PREDICTED: Nestor notabilis **Fanconi anemia, complementation**...	Kea	176057	32.2	32.2	80%	185	100.00	1751	**XM_010015558.1**
PREDICTED: Gavia stellata **Fanconi anemia,**	red-throated...	37040	32.2	32.2	80%	185	100.00	1637	**XM_009811632.1**

complementation grou...									
PREDICTED: Nipponia nippon Fanconi anemia, complementation gro...	crested ibis	128390	32.2	32.2	80%	185	100.00	1195	XM_009475062.1
PREDICTED: Pygoscelis adeliae Fanconi anemia, complementation...	Adelie penguin	9238	32.2	32.2	80%	185	100.00	1802	XM_009330421.1
PREDICTED: Equus przewalskii transmembrane protease, serine 13...	Przewalski's...	9798	32.2	32.2	80%	185	100.00	3994	XM_008507339.1
Gloeophyllum trabeum ATCC 11539 heme peroxidase partial mRNA	NA	670483	32.2	32.2	80%	185	100.00	4289	XM_007869200.1
PREDICTED: Lipotes vexillifer chemokine (C-X-C motif) ligand 1...	Yangtze Rive...	118797	32.2	32.2	100%	185	95.00	406	XM_007458582.1
PREDICTED: Macaca fascicularis interleukin-15 receptor subunit...	crab-eating ...	9541	32.2	32.2	80%	185	100.00	1021	XM_005595185.1
PREDICTED: Corvus kubaryi selectin P (LOC121665529), transcrip...	Mariana crow	68294	32.2	32.2	80%	185	100.00	2983	XM_042029863.1
PREDICTED: Corvus kubaryi selectin P (LOC121665529), transcrip...	Mariana crow	68294	32.2	32.2	80%	185	100.00	2941	XM_042029861.1
PREDICTED: Corvus kubaryi selectin P (LOC121665529), transcrip...	Mariana crow	68294	32.2	32.2	80%	185	100.00	3234	XM_042029860.1
PREDICTED: Corvus kubaryi selectin P (LOC121665529), transcrip...	Mariana crow	68294	32.2	32.2	80%	185	100.00	3306	XM_042029859.1
PREDICTED: Corvus kubaryi selectin P (LOC121665529), transcrip...	Mariana crow	68294	32.2	32.2	80%	185	100.00	6675	XM_042029858.1
PREDICTED: Corvus kubaryi selectin P (LOC121665529), transcrip...	Mariana crow	68294	32.2	32.2	80%	185	100.00	3124	XM_042029857.1
PREDICTED: Coregonus clupeaformis chromodomain helicase DNA...	lake whitefish	59861	32.2	32.2	80%	185	100.00	9693	XM_041896533.1
PREDICTED: Coregonus clupeaformis CUE domain-containing protei...	lake whitefish	59861	32.2	32.2	80%	185	100.00	2599	XM_041877991.1
PREDICTED: Coregonus clupeaformis CUE domain-containing protei...	lake whitefish	59861	32.2	32.2	80%	185	100.00	2751	XM_041871551.1
PREDICTED: Coregonus clupeaformis CUE domain-containing protei...	lake whitefish	59861	32.2	32.2	80%	185	100.00	2949	XM_041871548.1
PREDICTED: Cheilinus undulatus chromodomain helicase DNA bindi...	humphead wrasse	241271	32.2	32.2	80%	185	100.00	10577	XM_041792998.1
PREDICTED: Cheilinus undulatus chromodomain helicase DNA bindi...	humphead wrasse	241271	32.2	32.2	80%	185	100.00	12139	XM_041792989.1
PREDICTED: Cheilinus undulatus chromodomain helicase DNA bindi...	humphead wrasse	241271	32.2	32.2	80%	185	100.00	12123	XM_041792982.1
PREDICTED: Cheilinus undulatus chromodomain helicase DNA bindi...	humphead wrasse	241271	32.2	32.2	80%	185	100.00	12190	XM_041792973.1
Danio rerio strain T5D chromosome 14	zebrafish	7955	32.2	32.2	80%	185	100.00	51872344	CP068748.1
Zygaena filipendulae genome assembly, chromosome: 4	NA	287375	32.2	32.2	80%	185	100.00	15029683	OU015652.1
Caprimulgus europaeus genome assembly, chromosome: 21	Eurasian nig...	111811	32.2	32.2	80%	185	100.00	12349417	OU015545.1
Caprimulgus europaeus genome assembly, chromosome: 28	Eurasian nig...	111811	32.2	32.2	80%	185	100.00	6036106	OU015552.1
Osmia bicornis bicornis genome assembly, chromosome: 16	NA	1437191	32.2	32.2	80%	185	100.00	8269188	OU015519.1

PREDICTED: Echinops telfairi chloride voltage-gated channel Ka...	small Madaga ...	9371	32.2	32.2	80%	185	100.00	1935	XM_004705161.1
PREDICTED: Echinops telfairi chloride voltage-gated channel Ka...	small Madaga ...	9371	32.2	32.2	80%	185	100.00	2064	XM_004705160.1
PREDICTED: Jaculus jaculus taste receptor type 2 member 136-li...	lesser Egypt...	51337	32.2	32.2	80%	185	100.00	900	XM_004668643.1
Streptopelia turtur genome assembly, chromosome: 4	NA	177155	32.2	62.4	80%	185	100.00	81365208	LR594554.2
PREDICTED: Puma yagouaroundi thioesterase superfamily member 5...	jaguarundi	1608482	32.2	32.2	80%	185	100.00	945	XM_040461287.1
PREDICTED: Puma yagouaroundi thioesterase superfamily member 5...	jaguarundi	1608482	32.2	32.2	80%	185	100.00	1063	XM_040461286.1
Meleagris gallopavo genome assembly, chromosome: 8	turkey	9103	32.2	32.2	80%	185	100.00	34787218	HG999688.1
PREDICTED: Ictidomys tridecemlineatus HUS1 checkpoint clamp...	thirteen-lin...	43179	32.2	32.2	80%	185	100.00	1570	XM_040291923.1
PREDICTED: Ictidomys tridecemlineatus HUS1 checkpoint clamp...	thirteen-lin...	43179	32.2	32.2	80%	185	100.00	1502	XM_040291922.1
Canis lupus genome assembly, chromosome: 13	gray wolf	9612	32.2	32.2	80%	185	100.00	65443671	HG994397.1
PREDICTED: Corvus cornix cornix selectin P (LOC104695430),...	NA	932674	32.2	32.2	80%	185	100.00	3234	XM_019291881.3
PREDICTED: Corvus cornix cornix selectin P (LOC104695430),...	NA	932674	32.2	32.2	80%	185	100.00	2971	XM_019291883.3
PREDICTED: Corvus cornix cornix selectin P (LOC104695430),...	NA	932674	32.2	32.2	80%	185	100.00	3302	XM_019291880.3
PREDICTED: Corvus cornix cornix selectin P (LOC104695430),...	NA	932674	32.2	32.2	80%	185	100.00	3113	XM_019291882.3
PREDICTED: Corvus cornix cornix selectin P (LOC104695430),...	NA	932674	32.2	32.2	80%	185	100.00	6485	XM_019291879.3
PREDICTED: Corvus cornix cornix selectin P (LOC104695430),...	NA	932674	32.2	32.2	80%	185	100.00	6488	XM_019291878.3
PREDICTED: Corvus cornix cornix selectin P (LOC104695430),...	NA	932674	32.2	32.2	80%	185	100.00	6671	XM_039556212.1
PREDICTED: Pipra filicauda NIPA like domain containing 3...	Wire-tailed ...	649802	32.2	32.2	80%	185	100.00	5758	XM_039381263.1
PREDICTED: Pipra filicauda NIPA like domain containing 3...	Wire-tailed ...	649802	32.2	32.2	80%	185	100.00	5780	XM_027740168.2
Trachurus trachurus genome assembly, chromosome: 14	Atlantic hor...	36212	32.2	62.4	80%	185	100.00	33713437	LR991640.1
Homo sapiens solute carrier family 26 member 1 (SLC26A1),...	human	9606	32.2	32.2	80%	185	100.00	21364	NG_033042.1
Cronobacter phage vB_CsaM_GAP31, complete genome	NA	1141135	32.2	32.2	80%	185	100.00	147940	JN882284.1
Nibea albiflora genome assembly, chromosome: 14	white flower...	240163	32.2	32.2	80%	185	100.00	23007688	LR699037.1
PREDICTED: Salvelinus namaycush vasopressin V2 receptor-like...	lake trout	8040	32.2	32.2	80%	185	100.00	1221	XM_039010011.1
3_Tce_b3v08	NA	61476	32.2	32.2	80%	185	100.00	835	OC377792.1
3_Tce_b3v08	NA	61476	32.2	32.2	80%	185	100.00	61105	OC320535.1
Scyliorhinus canicula chromosome 31	smaller spot...	7830	32.2	32.2	80%	185	100.00	12109206	LR744060.1
PREDICTED: Motacilla alba alba uncharacterized LOC119699751...	NA	1094192	32.2	32.2	80%	185	100.00	837	XR_005256519.1
PREDICTED: Chlorocebus sabaeus interleukin 15 receptor subunit...	green monkey	60711	32.2	32.2	80%	185	100.00	1384	XM_008002188.2
PREDICTED: Chlorocebus sabaeus interleukin 15 receptor subunit...	green monkey	60711	32.2	32.2	80%	185	100.00	1534	XM_008002187.2
PREDICTED: Chlorocebus sabaeus interleukin 15 receptor subunit...	green monkey	60711	32.2	32.2	80%	185	100.00	1483	XM_008002186.2
PREDICTED: Chlorocebus sabaeus	green	60711	32.2	32.2	80%	185	100.00	1598	XM_008002185.2

interleukin 15 receptor subunit...	monkey								
PREDICTED: Chlorocebus sabaeus interleukin 15 receptor subunit...	green monkey	60711	32.2	32.2	80%	185	100.00	1582	XM_008002183.2
PREDICTED: Penaeus monodon galactosylgalactosylxylosylprotein...	black tiger ...	6687	32.2	32.2	80%	185	100.00	2072	XM_037947800.1
PREDICTED: Oncorhynchus mykiss vasopressin V2 receptor...	rainbow trout	8022	32.2	32.2	80%	185	100.00	2731	XM_036946831.1
PREDICTED: Oncorhynchus mykiss vasopressin V2 receptor...	rainbow trout	8022	32.2	32.2	80%	185	100.00	3063	XM_036946830.1
PREDICTED: Oncorhynchus mykiss vasopressin V2 receptor...	rainbow trout	8022	32.2	32.2	80%	185	100.00	3101	XM_036946829.1
PREDICTED: Oncorhynchus mykiss vasopressin V2 receptor...	rainbow trout	8022	32.2	32.2	80%	185	100.00	3058	XM_021565826.2
PREDICTED: Oncorhynchus mykiss vasopressin V2 receptor...	rainbow trout	8022	32.2	32.2	80%	185	100.00	3104	XM_036946828.1
Macrobrachium nipponense isolate FS-2020 chromosome 14	NA	159736	32.2	32.2	80%	185	100.00	99588160	CP062014.1
Macrobrachium nipponense isolate FS-2020 chromosome 31	NA	159736	32.2	92.7	100%	185	95.00	73203386	CP062049.1
PREDICTED: Balaenoptera musculus C-X-C motif chemokine ligand ...	Blue whale	9771	32.2	32.2	100%	185	95.00	859	XM_036834491.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowfin se...	8177	32.2	92.7	80%	185	100.00	25616698	LR884475.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome: 4	yellowfin se...	8177	32.2	153	80%	185	100.00	35910746	LR884463.1
PREDICTED: Onychomys torridus scribble planar cell polarity...	southern gra...	38674	32.2	32.2	80%	185	100.00	5478	XM_036209090.1
PREDICTED: Onychomys torridus scribble planar cell polarity...	southern gra...	38674	32.2	32.2	80%	185	100.00	5474	XM_036209089.1
PREDICTED: Onychomys torridus scribble planar cell polarity...	southern gra...	38674	32.2	32.2	80%	185	100.00	5537	XM_036209088.1
PREDICTED: Onychomys torridus scribble planar cell polarity...	southern gra...	38674	32.2	32.2	80%	185	100.00	5546	XM_036209087.1
PREDICTED: Onychomys torridus scribble planar cell polarity...	southern gra...	38674	32.2	32.2	80%	185	100.00	5618	XM_036209086.1
PREDICTED: Onychomys torridus scribble planar cell polarity...	southern gra...	38674	32.2	32.2	80%	185	100.00	5621	XM_036209085.1
Poecilia reticulata genome assembly, chromosome: 22	guppy	8081	32.2	32.2	80%	185	100.00	24441338	LR880666.1
Acomys russatus genome assembly, chromosome: 24	golden spiny...	60746	32.2	64.4	85%	185	100.00	60479378	LR877235.1
Acomys russatus genome assembly, chromosome: 16	golden spiny...	60746	32.2	62.4	80%	185	100.00	47487087	LR877227.1
Acomys russatus genome assembly, chromosome: 6	golden spiny...	60746	32.2	62.4	80%	185	100.00	89442464	LR877217.1
PREDICTED: Oncorhynchus keta uncharacterized LOC118360505...	chum salmon	8018	32.2	32.2	80%	185	100.00	1572	XM_035739750.1
PREDICTED: Oncorhynchus keta vasopressin V2 receptor-like...	chum salmon	8018	32.2	32.2	80%	185	100.00	4936	XR_004820816.1
PREDICTED: Oncorhynchus keta vasopressin V2 receptor-like...	chum salmon	8018	32.2	32.2	80%	185	100.00	2444	XM_035739309.1
PREDICTED: Oncorhynchus keta vasopressin V2 receptor-like...	chum salmon	8018	32.2	32.2	80%	185	100.00	2791	XM_035739308.1
PREDICTED: Oncorhynchus keta vasopressin V2 receptor-like...	chum salmon	8018	32.2	32.2	80%	185	100.00	4887	XM_035739307.1
PREDICTED: Oncorhynchus keta vasopressin V2 receptor-like...	chum salmon	8018	32.2	32.2	80%	185	100.00	3279	XM_035739305.1
PREDICTED: Oncorhynchus keta vasopressin V2 receptor-like...	chum salmon	8018	32.2	32.2	80%	185	100.00	3282	XM_035739304.1
PREDICTED: Oncorhynchus keta vasopressin V2 receptor-like...	chum salmon	8018	32.2	32.2	80%	185	100.00	3240	XM_035739303.1
Arvicola amphibius genome assembly, chromosome: 13	Eurasian wat...	1047088	32.2	62.4	80%	185	100.00	75712621	LR862393.1
PREDICTED: Cricetulus griseus solute carrier family 5 member 5...	Chinese hamster	10029	32.2	32.2	80%	185	100.00	5835	XM_035451284.1
PREDICTED: Anguilla anguilla cadherin-related family member...	European eel	7936	32.2	32.2	80%	185	100.00	3591	XM_035394959.1

Anas platyrhynchos genome assembly, chromosome: 21	mallard	8839	32.2	32.2	80%	185	100.00	15673935	LS423631.1
Streptococcus pseudopneumoniae IS7493, complete genome	NA	1054460	32.2	32.2	80%	185	100.00	2190731	CP002925.1
Aerococcus urinae ACS-120-V-Col10a, complete genome	NA	866775	32.2	32.2	80%	185	100.00	2080974	CP002512.1
Arenicola marina lectin 1A mRNA, complete cds	lugworm	6344	32.2	32.2	100%	185	95.00	1013	HQ009860.1
Homo sapiens FOSMID clone ABC14-973614N14 from chromosome...	human	9606	32.2	32.2	80%	185	100.00	40375	AC241852.1
Homo sapiens FOSMID clone ABC11-48297800K14 from chromosome...	human	9606	32.2	64.4	80%	185	100.00	41740	AC235000.3
Homo sapiens FOSMID clone ABC11-49677400B19 from chromosome 15...	human	9606	32.2	64.4	80%	185	100.00	41473	AC216747.3
Vitis vinifera contig VV78X139398.8, whole genome shotgun...	wine grape	29760	32.2	32.2	80%	185	100.00	3702	AM485072.2
Pan troglodytes BAC clone CH251-655L15 from chromosome 7,...	chimpanzee	9598	32.2	32.2	80%	185	100.00	201596	AC193536.2
Prochlorococcus marinus str. MIT 9515, complete genome	NA	167542	32.2	32.2	80%	185	100.00	1704176	CP000552.1
Cenarchaeum symbiosum B clone C09B07, complete sequence	NA	414005	32.2	32.2	80%	185	100.00	40824	DQ397850.1
Mus musculus chromosome 1, clone RP24-499I2, complete sequence	house mouse	10090	32.2	32.2	80%	185	100.00	183516	AC120180.19
Arabidopsis thaliana type II inositol polyphosphate...	thale cress	3702	32.2	32.2	80%	185	100.00	3550	AY761186.1
Mus musculus BAC clone RP24-137B3 from chromosome 5, complete...	house mouse	10090	32.2	32.2	80%	185	100.00	157199	AC140492.3
Mus musculus BAC clone RP24-374E8 from 14, complete sequence	house mouse	10090	32.2	32.2	80%	185	100.00	160863	AC112795.6
Homo sapiens BAC clone RP11-518I12 from 7, complete sequence	human	9606	32.2	32.2	80%	185	100.00	205317	AC093856.3
Homo sapiens PAC clone RP4-782K24 from 7, complete sequence	human	9606	32.2	32.2	80%	185	100.00	123255	AC006003.4
Pan troglodytes BAC clone CH251-119B5 from chromosome 15,...	chimpanzee	9598	32.2	32.2	80%	185	100.00	150565	AC182398.3
Homo sapiens chromosome 5 clone CTD-2541N22, complete sequence	human	9606	32.2	32.2	80%	185	100.00	187032	AC114289.2
Homo sapiens BAC clone CTA-271G13 from 7, complete sequence	human	9606	32.2	32.2	80%	185	100.00	169739	AC005082.3
Arabidopsis thaliana clone RAFL16-01-I19 (R50205) unknown...	thale cress	3702	32.2	32.2	80%	185	100.00	3745	BT004211.1
Homo sapiens chromosome 15, clone RP11-817O13, complete sequence	human	9606	32.2	64.4	80%	185	100.00	174192	AC068338.14
Arabidopsis thaliana mRNA for inositol 1,4,5-trisphosphate...	thale cress	3702	32.2	32.2	80%	185	100.00	3506	AJ005682.1
Mus musculus chromosome 5, clone RP24-334E1, complete sequence	house mouse	10090	32.2	32.2	80%	185	100.00	163642	AC161499.2
Mus musculus BAC clone RP23-348K1 from 14, complete sequence	house mouse	10090	32.2	32.2	80%	185	100.00	250519	AC140288.5
Human chromosome 14 DNA sequence BAC R-179A9 of library RPCI-1...	human	9606	32.2	32.2	80%	185	100.00	180914	AL121612.5
Homo sapiens 12 BAC RP11-176O5 (Roswell Park Cancer Institute...	human	9606	32.2	32.2	80%	185	100.00	179350	AC026351.29
Erithacus rubecula genome assembly, chromosome: 6	European robin	37610	30.2	60.5	80%	730	100.00	60684490	LR812108.1
Erithacus rubecula genome assembly, chromosome: 23	European robin	37610	30.2	30.2	75%	730	100.00	7607207	LR812126.1
Erithacus rubecula genome assembly, chromosome: 15	European robin	37610	30.2	30.2	75%	730	100.00	19110993	LR812118.1

Erithacus rubecula genome assembly, chromosome: 10	European robin	37610	30.2	120	85%	730	100.00	29524214	LR812113.1
Bacillus anthracis strain FDAARGOS_702 chromosome	NA	1392	30.2	30.2	75%	730	100.00	5272559	**CP054800.1**
PREDICTED: Maniola hyperantus eukaryotic translation initiatio...	ringlet	2795564	30.2	30.2	95%	730	94.74	1853	XM_034985553.1
PREDICTED: Etheostoma cragini collagen type VII alpha 1-like...	Arkansas darter	417921	30.2	30.2	75%	730	100.00	9010	XM_034864121.1
Bacillus thuringiensis strain FDAARGOS_794 chromosome, complet...	NA	1428	30.2	30.2	75%	730	100.00	5214223	CP053934.1
Bacillus cereus strain FDAARGOS_797 chromosome, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5413450	CP053931.1
Bacillus cereus strain FDAARGOS_780 chromosome, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5271040	CP053997.1
Bacillus cereus strain FDAARGOS_802 chromosome, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5342923	CP053965.1
Bacillus tropicus strain FDAARGOS_782 chromosome, complete genome	NA	2026188	30.2	30.2	75%	730	100.00	5263142	CP053955.1
Felis catus Senzu DNA, chromosome: F2, American Shorthair breed	domestic cat	9685	30.2	30.2	75%	730	100.00	86116642	AP023169.1
Felis catus Senzu DNA, chromosome: E2, American Shorthair breed	domestic cat	9685	30.2	60.5	85%	730	100.00	64410938	AP023166.1
PREDICTED: Drosophila subobscura uncharacterized LOC117896312...	NA	7241	30.2	30.2	75%	730	100.00	5221	XM_034804539.1
PREDICTED: Drosophila subobscura uncharacterized LOC117896312...	NA	7241	30.2	30.2	75%	730	100.00	5264	XM_034804538.1
PREDICTED: Drosophila subobscura uncharacterized LOC117896312...	NA	7241	30.2	30.2	75%	730	100.00	5333	XM_034804537.1
PREDICTED: Trachemys scripta elegans ankyrin repeat domain 34A...	NA	31138	30.2	30.2	75%	730	100.00	4981	XM_034756968.1
Caenorhabditis elegans Papilin (mig-6), mRNA	NA	6239	30.2	30.2	75%	730	100.00	6739	NM_072616.7
PREDICTED: Ailuropoda melanoleuca uncharacterized LOC117795120...	giant panda	9646	30.2	30.2	75%	730	100.00	702	XR_004618948.1
PREDICTED: Setaria viridis uncharacterized LOC117846463...	NA	4556	30.2	30.2	75%	730	100.00	1542	XM_034727632.1
PREDICTED: Setaria viridis putative FBD-associated F-box prote...	NA	4556	30.2	30.2	75%	730	100.00	1944	XM_034723034.1
PREDICTED: Notolabrus celidotus complement C1q-like protein 4...	New Zealand ...	1203425	30.2	30.2	75%	730	100.00	518	XM_034701565.1
PREDICTED: Notolabrus celidotus ribonuclease H2, subunit C...	New Zealand ...	1203425	30.2	30.2	75%	730	100.00	714	XM_034689981.1
PREDICTED: Hippoglossus hippoglossus glucuronokinase with...	Atlantic hal...	8267	30.2	30.2	75%	730	100.00	2513	XM_034603980.1
PREDICTED: Hippoglossus hippoglossus POM121 transmembrane...	Atlantic hal...	8267	30.2	30.2	75%	730	100.00	4960	XM_034606908.1
Fusarium oxysporum Fo5176 chromosome 4	NA	660025	30.2	30.2	75%	730	100.00	5006977	CP053263.1
PREDICTED: Cyclopterus lumpus uncharacterized LOC117750388...	lumpfish	8103	30.2	30.2	75%	730	100.00	1653	XR_004611802.1
PREDICTED: Cyclopterus lumpus pleckstrin homology domain...	lumpfish	8103	30.2	30.2	75%	730	100.00	6330	XM_034547974.1

PREDICTED: Cyclopterus lumpus pleckstrin homology domain...	lumpfish	8103	30.2	30.2	75%	730	100.00	7705	XM_034547973.1
PREDICTED: Cyclopterus lumpus pleckstrin homology domain...	lumpfish	8103	30.2	30.2	75%	730	100.00	7711	XM_034547972.1
PREDICTED: Cyclopterus lumpus nuclear factor...	lumpfish	8103	30.2	30.2	75%	730	100.00	4550	XM_034540320.1
PREDICTED: Arvicanthis niloticus alpha-1,6-mannosylglycoprotei...	African gras...	61156	30.2	30.2	75%	730	100.00	8048	XM_034513055.1
PREDICTED: Arvicanthis niloticus alpha-1,6-mannosylglycoprotei...	African gras...	61156	30.2	30.2	75%	730	100.00	8342	XM_034513054.1
PREDICTED: Pantherophis guttatus uncharacterized LOC117658514...	NA	94885	30.2	30.2	75%	730	100.00	514	XR_004589290.1
PREDICTED: Gymnodraco acuticeps TERF1 (TRF1)-interacting nucle...	NA	8218	30.2	30.2	75%	730	100.00	2538	XM_034205301.1
PREDICTED: Gymnodraco acuticeps TERF1 (TRF1)-interacting nucle...	NA	8218	30.2	30.2	75%	730	100.00	2916	XM_034205300.1
PREDICTED: Gymnodraco acuticeps TERF1 (TRF1)-interacting nucle...	NA	8218	30.2	30.2	75%	730	100.00	2987	XM_034205299.1
PREDICTED: Trematomus bernacchii TERF1 (TRF1)-interacting...	emerald rockcod	40690	30.2	30.2	75%	730	100.00	2492	XM_034136913.1
PREDICTED: Trematomus bernacchii TERF1 (TRF1)-interacting...	emerald rockcod	40690	30.2	30.2	75%	730	100.00	2984	XM_034136912.1
PREDICTED: Trematomus bernacchii TERF1 (TRF1)-interacting...	emerald rockcod	40690	30.2	30.2	75%	730	100.00	3059	XM_034136911.1
PREDICTED: Periophthalmus magnuspinnatus BCL2 associated...	NA	409849	30.2	30.2	75%	730	100.00	4401	XM_033975114.1
PREDICTED: Periophthalmus magnuspinnatus TLE family member 2,...	NA	409849	30.2	30.2	75%	730	100.00	3679	XM_033964941.1
PREDICTED: Periophthalmus magnuspinnatus TLE family member 2,...	NA	409849	30.2	30.2	75%	730	100.00	3606	XM_033964940.1
Setaria viridis cultivar ME034v chromosome 2	NA	4556	30.2	60.5	75%	730	100.00	48726069	CP050796.1
PREDICTED: Tursiops truncatus ataxin 7 (ATXN7), mRNA	common bottl...	9739	30.2	30.2	75%	730	100.00	6819	XM_033865236.1
Trematosphaeria pertusa trichothecene 3-O-acetyltransferase...	NA	390896	30.2	30.2	75%	730	100.00	1945	XM_033830550.1
PREDICTED: Asterias rubens condensin-2 complex subunit D3-like...	European sta...	7604	30.2	30.2	75%	730	100.00	5538	XM_033782885.1
Digitaria exilis annotation	NA	1010633	30.2	30.2	95%	730	94.74	35142973	LR792821.1
Pseudovirgaria hyperparasitica uncharacterized protein...	NA	470096	30.2	30.2	75%	730	100.00	3579	XM_033745647.1
PREDICTED: Epinephelus lanceolatus collagen type VII alpha...	giant grouper	310571	30.2	30.2	75%	730	100.00	7444	XM_033615355.1
PREDICTED: Parus major regulator of G protein signaling 10...	Great Tit	9157	30.2	30.2	75%	730	100.00	647	XM_015633746.3
PREDICTED: Parus major regulator of G protein signaling 10...	Great Tit	9157	30.2	30.2	75%	730	100.00	3774	XM_015633744.2
PREDICTED: Parus major uncharacterized LOC107214162...	Great Tit	9157	30.2	30.2	75%	730	100.00	2075	XR_004500135.1
Digitaria exilis genome assembly, chromosome: 1B	NA	1010633	30.2	30.2	95%	730	94.74	35142973	LR761606.1
PREDICTED: Megalopta genalis uncharacterized LOC117223706...	NA	115081	30.2	30.2	75%	730	100.00	3545	XM_033476134.1
PREDICTED: Megalopta genalis filaggrin-like (LOC117222593),...	NA	115081	30.2	30.2	75%	730	100.00	3455	XM_033474365.1
PREDICTED: Megalopta genalis protein PRRC2C-like	NA	115081	30.2	30.2	75%	730	100.00	3903	XM_033484303.1

(LOC117228515...									
PREDICTED: Orcinus orca ataxin 7 (ATXN7), mRNA	killer whale	9733	30.2	30.2	75%	730	100.00	7089	XM_033424772.1
Bacillus anthracis strain FDAARGOS_699 chromosome	NA	1392	30.2	30.2	75%	730	100.00	5227345	**CP050973.1**
Bacillus anthracis strain FDAARGOS_697 chromosome	NA	1392	30.2	30.2	75%	730	100.00	5240765	**CP050972.1**
Pseudochaenichthys georgianus genome assembly, chromosome: 22	South Georgi...	52239	30.2	30.2	75%	730	100.00	35435734	LR792567.1
Pseudochaenichthys georgianus genome assembly, chromosome: 21	South Georgi...	52239	30.2	30.2	75%	730	100.00	39591329	LR792566.1
Pseudochaenichthys georgianus genome assembly, chromosome: 7	South Georgi...	52239	30.2	30.2	75%	730	100.00	45376657	LR792552.1
Yokenella regensburgei strain W13 chromosome, complete genome	NA	158877	30.2	30.2	75%	730	100.00	4962579	CP050811.1
Canis lupus familiaris breed Labrador retriever chromosome 11a	dog	9615	30.2	30.2	75%	730	100.00	73584800	CP050600.1
Canis lupus familiaris breed Labrador retriever chromosome 31a	dog	9615	30.2	30.2	75%	730	100.00	39430757	CP050592.1
Canis lupus familiaris breed Labrador retriever chromosome 14a	dog	9615	30.2	90.7	85%	730	100.00	62855878	CP050589.1
Canis lupus familiaris breed Labrador retriever chromosome 30a	dog	9615	30.2	30.2	75%	730	100.00	40385137	CP050583.1
Canis lupus familiaris breed Labrador retriever chromosome 19a	dog	9615	30.2	30.2	75%	730	100.00	56633346	CP050573.1
Canis lupus familiaris breed Labrador retriever chromosome 20a	dog	9615	30.2	30.2	95%	730	94.74	58324418	CP050571.1
Canis lupus familiaris breed Labrador retriever chromosome 20b	dog	9615	30.2	30.2	95%	730	94.74	58321546	CP050631.1
Canis lupus familiaris breed Labrador retriever chromosome 11b	dog	9615	30.2	30.2	75%	730	100.00	73564375	CP050630.1
Canis lupus familiaris breed Labrador retriever chromosome 14b	dog	9615	30.2	90.7	85%	730	100.00	62857718	CP050623.1
Canis lupus familiaris breed Labrador retriever chromosome 19b	dog	9615	30.2	30.2	75%	730	100.00	56576146	CP050621.1
Canis lupus familiaris breed Labrador retriever chromosome 31b	dog	9615	30.2	30.2	75%	730	100.00	39416698	CP050617.1
Canis lupus familiaris breed Labrador retriever chromosome 17b	dog	9615	30.2	60.5	80%	730	100.00	64169108	CP050614.1
Canis lupus familiaris breed Labrador retriever chromosome 30b	dog	9615	30.2	30.2	75%	730	100.00	40370200	CP050609.1
PREDICTED: Catharus ustulatus regulator of G protein signaling...	Swainson's t...	91951	30.2	30.2	75%	730	100.00	3777	XM_033066654.1
PREDICTED: Catharus ustulatus regulator of G protein signaling...	Swainson's t...	91951	30.2	30.2	75%	730	100.00	3695	XM_033066653.1
PREDICTED: Catharus ustulatus solute carrier family 35 member ...	Swainson's t...	91951	30.2	30.2	75%	730	100.00	2934	XM_033051704.1
PREDICTED: Catharus ustulatus uncharacterized LOC117011486...	Swainson's t...	91951	30.2	30.2	75%	730	100.00	783	XR_004420986.1
Rhizobium leguminosarum bv. trifolii strain 31B chromosome,...	NA	386	30.2	30.2	75%	730	100.00	5178457	CP050080.1
PREDICTED: Tyto alba alba alpha-2-macroglobulin (LOC104367175)...	NA	507980	30.2	30.2	75%	730	100.00	3397	XM_032983921.1
PREDICTED: Amblyraja radiata dedicator of cytokinesis protein...	thorny skate	386614	30.2	30.2	75%	730	100.00	2555	XM_033013874.1
PREDICTED: Rattus rattus alpha-1,6-mannosylglycoprotein...	black rat	10117	30.2	30.2	75%	730	100.00	4451	XM_032915150.1
PREDICTED: Lontra canadensis RFX family member 8, lacking RFX...	Northern Ame...	76717	30.2	30.2	75%	730	100.00	1170	XM_032840432.1
PREDICTED: Lontra canadensis RFX family member 8, lacking RFX...	Northern Ame...	76717	30.2	30.2	75%	730	100.00	1912	XM_032840431.1
PREDICTED: Lontra canadensis RFX family member 8, lacking RFX...	Northern Ame...	76717	30.2	30.2	75%	730	100.00	1996	XM_032840430.1

PREDICTED: Chelonoidis abingdonii Fas binding factor 1 (FBF1),...	Abingdon isl...	106734	30.2	30.2	75%	730	100.00	4720	XM_032792886.1
PREDICTED: Chelonoidis abingdonii Fas binding factor 1 (FBF1),...	Abingdon isl...	106734	30.2	30.2	75%	730	100.00	4928	XM_032792885.1
PREDICTED: Chelonoidis abingdonii Fas binding factor 1 (FBF1),...	Abingdon isl...	106734	30.2	30.2	75%	730	100.00	4940	XM_032792883.1
Raphanus sativus genome assembly, chromosome: 5	radish	3726	30.2	30.2	75%	730	100.00	43617977	LR778314.1
Coregonus sp. 'balchen' genome assembly, chromosome: 30	NA	861768	30.2	30.2	75%	730	100.00	48675208	LR778282.1
Jeotgalibaca arthritidis strain CECT 9157 chromosome, complete...	NA	1868794	30.2	30.2	75%	730	100.00	2348096	CP049740.1
Coregonus sp. 'balchen' genome assembly, chromosome: 28	NA	861768	30.2	30.2	75%	730	100.00	46671285	LR778280.1
Coregonus sp. 'balchen' genome assembly, chromosome: 21	NA	861768	30.2	30.2	75%	730	100.00	52945597	LR778273.1
Coregonus sp. 'balchen' genome assembly, chromosome: 17	NA	861768	30.2	30.2	75%	730	100.00	54216998	LR778269.1
Coregonus sp. 'balchen' genome assembly, chromosome: 8	NA	861768	30.2	30.2	75%	730	100.00	68138733	LR778260.1
PREDICTED: Phocoena sinus ataxin 7 (ATXN7), mRNA	vaquita	42100	30.2	30.2	75%	730	100.00	6809	XM_032649600.1
PREDICTED: Phocoena sinus alanine aminotransferase 1...	vaquita	42100	30.2	30.2	75%	730	100.00	6667	XM_032609681.1
PREDICTED: Phocoena sinus alanine aminotransferase 1...	vaquita	42100	30.2	30.2	75%	730	100.00	6672	XM_032609680.1
PREDICTED: Phocoena sinus alanine aminotransferase 1...	vaquita	42100	30.2	30.2	75%	730	100.00	6696	XM_032609679.1
PREDICTED: Phocoena sinus alanine aminotransferase 1...	vaquita	42100	30.2	30.2	75%	730	100.00	6449	XM_032609678.1
PREDICTED: Phocoena sinus alanine aminotransferase 1...	vaquita	42100	30.2	30.2	75%	730	100.00	5627	XM_032609677.1
PREDICTED: Phocoena sinus alanine aminotransferase 1...	vaquita	42100	30.2	30.2	75%	730	100.00	5817	XM_032609675.1
PREDICTED: Phocoena sinus alanine aminotransferase 1...	vaquita	42100	30.2	30.2	75%	730	100.00	6636	XM_032609674.1
PREDICTED: Phocoena sinus alanine aminotransferase 1...	vaquita	42100	30.2	30.2	75%	730	100.00	6750	XM_032609673.1
PREDICTED: Danaus plexippus plexippus dynein heavy chain 7,...	NA	278856	30.2	30.2	75%	730	100.00	12328	XM_032654679.1
PREDICTED: Danaus plexippus plexippus serine/threonine-protein...	NA	278856	30.2	30.2	95%	730	94.74	2085	XM_032667401.1
Crassostrea gigas strain QD chromosome 4	Pacific oyster	29159	30.2	30.2	75%	730	100.00	62642562	CP048842.1
PREDICTED: Etheostoma spectabile nuclear envelope pore membran...	orangethroat...	54343	30.2	30.2	75%	730	100.00	5169	XM_032533523.1
PREDICTED: Etheostoma spectabile nuclear envelope pore membran...	orangethroat...	54343	30.2	30.2	75%	730	100.00	5179	XM_032533522.1
Plectropomus leopardus DNA, chromosome 19, nearly complete...	leopard cora...	160734	30.2	60.5	75%	730	100.00	28624681	AP022718.1
Plectropomus leopardus DNA, chromosome 13, nearly complete...	leopard cora...	160734	30.2	30.2	75%	730	100.00	33579070	AP022712.1
Plectropomus leopardus DNA, chromosome 8, nearly complete...	leopard cora...	160734	30.2	30.2	75%	730	100.00	35874999	AP022707.1
Plectropomus leopardus DNA, chromosome 7, nearly complete...	leopard cora...	160734	30.2	60.5	75%	730	100.00	36063594	AP022706.1
Plectropomus leopardus DNA, chromosome 5, nearly complete...	leopard cora...	160734	30.2	60.5	75%	730	100.00	37020500	AP022704.1
Plectropomus leopardus DNA, chromosome 3, nearly complete...	leopard cora...	160734	30.2	30.2	75%	730	100.00	38158481	AP022702.1
Epinephelus fuscoguttatus DNA, LG23, complete sequence	brown-marble...	293821	30.2	30.2	75%	730	100.00	36946246	AP022697.1
Epinephelus fuscoguttatus DNA,	brown-	293821	30.2	90.7	75%	730	100.00	39642397	AP022695.1

LG21, complete sequence	marble...								
Epinephelus fuscoguttatus DNA, LG19, complete sequence	brown-marble...	293821	30.2	90.7	85%	730	100.00	41259535	AP022693.1
Epinephelus fuscoguttatus DNA, LG18, complete sequence	brown-marble...	293821	30.2	30.2	75%	730	100.00	41318902	AP022692.1
Epinephelus fuscoguttatus DNA, LG16, complete sequence	brown-marble...	293821	30.2	30.2	75%	730	100.00	42848118	AP022690.1
Epinephelus fuscoguttatus DNA, LG15, complete sequence	brown-marble...	293821	30.2	120	75%	730	100.00	43073509	AP022689.1
Epinephelus fuscoguttatus DNA, LG12, complete sequence	brown-marble...	293821	30.2	90.7	75%	730	100.00	44245273	AP022686.1
Epinephelus fuscoguttatus DNA, LG10, complete sequence	brown-marble...	293821	30.2	211	75%	730	100.00	45956267	AP022684.1
Epinephelus fuscoguttatus DNA, LG9, complete sequence	brown-marble...	293821	30.2	60.5	75%	730	100.00	46821238	AP022683.1
Epinephelus fuscoguttatus DNA, LG8, complete sequence	brown-marble...	293821	30.2	90.7	75%	730	100.00	47003518	AP022682.1
Epinephelus fuscoguttatus DNA, LG5, complete sequence	brown-marble...	293821	30.2	30.2	75%	730	100.00	47245075	AP022679.1
Epinephelus fuscoguttatus DNA, LG4, complete sequence	brown-marble...	293821	30.2	90.7	75%	730	100.00	47419940	AP022678.1
Epinephelus fuscoguttatus DNA, LG3, complete sequence	brown-marble...	293821	30.2	60.5	75%	730	100.00	48981850	AP022677.1
Epinephelus fuscoguttatus DNA, LG2, complete sequence	brown-marble...	293821	30.2	120	75%	730	100.00	52288159	AP022676.1
PREDICTED: Camelus ferus matrix metallopeptidase 15 (MMP15),...	Wild Bactria...	419612	30.2	30.2	75%	730	100.00	3801	XM_032486429.1
PREDICTED: Camelus ferus matrix metallopeptidase 15 (MMP15),...	Wild Bactria...	419612	30.2	30.2	75%	730	100.00	3554	XM_032486428.1
PREDICTED: Camelus ferus cell division cycle associated 3...	Wild Bactria...	419612	30.2	30.2	75%	730	100.00	1217	XM_032473445.1
PREDICTED: Camelus ferus cell division cycle associated 3...	Wild Bactria...	419612	30.2	30.2	75%	730	100.00	1162	XM_006176766.3
Bacillus paranthracis strain MN1F chromosome, complete genome	NA	2026186	30.2	30.2	75%	730	100.00	5687871	**CP048687.1**
Aphantopus hyperantus genome assembly, chromosome: 21	ringlet	2795564	30.2	30.2	75%	730	100.00	12342164	LR761668.1
Aphantopus hyperantus genome assembly, chromosome: 4	ringlet	2795564	30.2	30.2	95%	730	94.74	17319493	LR761651.1
Streptomyces sp. RLB1-8 chromosome, complete genome	NA	2594453	30.2	30.2	75%	730	100.00	11765395	CP041650.2
Streptomyces sp. S1A1-8 chromosome, complete genome	NA	2594460	30.2	30.2	75%	730	100.00	12037094	CP041612.2
Streptomyces sp. S1D4-14 chromosome, complete genome	NA	2594461	30.2	30.2	75%	730	100.00	11723552	CP041607.2
Streptomyces sp. S1D4-20 chromosome	NA	2594462	30.2	30.2	75%	730	100.00	11851273	CP041609.2
Streptomyces sp. S1D4-23 chromosome	NA	2594463	30.2	30.2	75%	730	100.00	12057750	CP041613.2
Streptomyces sp. S1A1-7 chromosome	NA	2594459	30.2	30.2	75%	730	100.00	11713216	CP041604.2
Streptomyces sp. RLB3-6 chromosome	NA	2594457	30.2	30.2	75%	730	100.00	12338170	CP041602.2
Streptomyces sp. RLB3-17 chromosome, complete genome	NA	2594455	30.2	30.2	75%	730	100.00	12022941	CP041610.2
PREDICTED: Mustela erminea RFX family member 8, lacking RFX DN...	ermine	36723	30.2	30.2	75%	730	100.00	2138	XM_032351765.1

PREDICTED: Mustela erminea RFX family member 8, lacking RFX DN...	ermine	36723	30.2	30.2	75%	730	100.00	4536	XM_032351764.1
PREDICTED: Sapajus apella uncharacterized LOC116542698...	tufted capuchin	9515	30.2	30.2	75%	730	100.00	1068	XR_004265326.1
Mycoplasma pneumoniae strain 16-734 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	818445	CP039761.1
Mycoplasma pneumoniae strain 16-710 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816537	CP039762.1
Mycoplasma pneumoniae strain 16-462 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816525	CP039763.1
Mycoplasma pneumoniae strain 16-118 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816467	CP039764.1
Mycoplasma pneumoniae strain 16-032 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816471	CP039765.1
Mycoplasma pneumoniae strain 16-004 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816561	CP039766.1
Mycoplasma pneumoniae strain 16-002 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816530	CP039767.1
Mycoplasma pneumoniae strain 15-982 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816495	CP039768.1
Mycoplasma pneumoniae strain 15-969 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816389	CP039769.1
Mycoplasma pneumoniae strain 15-885 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816420	CP039770.1
Mycoplasma pneumoniae strain 15-215 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816388	CP039771.1
Mycoplasma pneumoniae strain 14-637 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	818560	CP039772.1
Mycoplasma pneumoniae strain 12-091 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816510	CP039773.1
Mycoplasma pneumoniae strain 12-060 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816506	CP039774.1
Mycoplasma pneumoniae strain 11-1384 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	818669	CP039775.1
Mycoplasma pneumoniae strain 11-994 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816304	CP039776.1
Mycoplasma pneumoniae strain 11-949 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	817102	CP039777.1
Mycoplasma pneumoniae strain 11-634 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816551	CP039778.1
Mycoplasma pneumoniae strain 11-473 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816518	CP039779.1
Mycoplasma pneumoniae strain 11-212 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816503	CP039780.1
Mycoplasma pneumoniae strain 11-174 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	815686	CP039781.1
Mycoplasma pneumoniae strain 11-	NA	2104	30.2	30.2	75%	730	100.00	816432	CP039782.1

129 chromosome, complete genome									
Mycoplasma pneumoniae strain 11-107 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816346	CP039783.1
Mycoplasma pneumoniae strain 10-1385 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	817191	CP039784.1
Mycoplasma pneumoniae strain 10-1257 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816333	CP039785.1
Mycoplasma pneumoniae strain 10-1213 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816521	CP039786.1
Mycoplasma pneumoniae strain 10-1110 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816522	CP039787.1
Mycoplasma pneumoniae strain 10-1059 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816681	CP039788.1
Mycoplasma pneumoniae strain 10-1048 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816465	CP039789.1
Mycoplasma pneumoniae strain 10-980 chromosome, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816424	CP039790.1
PREDICTED: Corvus moneduloides myosin ID (MYO1D), mRNA	New Caledoni...	1196302	30.2	30.2	75%	730	100.00	5406	XM_032134297.1
PREDICTED: Corvus moneduloides uncharacterized LOC116453399...	New Caledoni...	1196302	30.2	30.2	75%	730	100.00	955	XR_004243794.1
PREDICTED: Corvus moneduloides regulator of G protein signalin...	New Caledoni...	1196302	30.2	30.2	75%	730	100.00	3952	XM_032116389.1
PREDICTED: Corvus moneduloides regulator of G protein signalin...	New Caledoni...	1196302	30.2	30.2	75%	730	100.00	3790	XM_032116388.1
PREDICTED: Corvus moneduloides regulator of G protein signalin...	New Caledoni...	1196302	30.2	30.2	75%	730	100.00	1944	XM_032116386.1
PREDICTED: Corvus moneduloides regulator of G protein signalin...	New Caledoni...	1196302	30.2	30.2	75%	730	100.00	2098	XM_032116385.1
PREDICTED: Corvus moneduloides regulator of G protein signalin...	New Caledoni...	1196302	30.2	30.2	75%	730	100.00	1144	XM_032116384.1
PREDICTED: Corvus moneduloides regulator of G protein signalin...	New Caledoni...	1196302	30.2	30.2	75%	730	100.00	961	XM_032116383.1
Lutra lutra genome assembly, chromosome: 14	Eurasian riv...	9657	30.2	60.5	85%	730	100.00	89080780	LR738416.1
Lutra lutra genome assembly, chromosome: 13	Eurasian riv...	9657	30.2	30.2	75%	730	100.00	95726014	LR738415.1
Lutra lutra genome assembly, chromosome: 12	Eurasian riv...	9657	30.2	60.5	80%	730	100.00	96445735	LR738414.1
PREDICTED: Sarcophilus harrisii uncharacterized LOC116419581...	Tasmanian devil	9305	30.2	30.2	75%	730	100.00	5148	XR_004229830.1
Bacillus anthracis strain FDAARGOS_704 chromosome, complete...	NA	1392	30.2	30.2	75%	730	100.00	5227450	**CP047111.1**
Bacillus anthracis strain FDAARGOS_705 chromosome, complete...	NA	1392	30.2	30.2	75%	730	100.00	5227452	**CP047107.1**
Bacillus anthracis strain FDAARGOS_701 chromosome, complete...	NA	1392	30.2	30.2	75%	730	100.00	5227419	**CP047098.1**
Micrococcus luteus strain NCCP 15687 chromosome, complete genome	NA	1270	30.2	30.2	75%	730	100.00	2445333	CP043849.1

PREDICTED: Anarrhichthys ocellatus protein FAM92B-like...	wolf-eel	433405	30.2	30.2	75%	730	100.00	1340	XM_031875996.1
PREDICTED: Anarrhichthys ocellatus synaptotagmin 14 (syt14),...	wolf-eel	433405	30.2	30.2	75%	730	100.00	10528	XM_031866733.1
PREDICTED: Anarrhichthys ocellatus synaptotagmin 14 (syt14),...	wolf-eel	433405	30.2	30.2	75%	730	100.00	10585	XM_031866732.1
PREDICTED: Anarrhichthys ocellatus synaptotagmin 14 (syt14),...	wolf-eel	433405	30.2	30.2	75%	730	100.00	10606	XM_031866731.1
PREDICTED: Anarrhichthys ocellatus eukaryotic translation...	wolf-eel	433405	30.2	30.2	75%	730	100.00	10504	XM_031860758.1
PREDICTED: Anarrhichthys ocellatus eukaryotic translation...	wolf-eel	433405	30.2	30.2	75%	730	100.00	11517	XM_031860756.1
PREDICTED: Anarrhichthys ocellatus collagen alpha-1(VII)...	wolf-eel	433405	30.2	30.2	75%	730	100.00	7093	XM_031859283.1
PREDICTED: Anarrhichthys ocellatus photoreceptor-specific...	wolf-eel	433405	30.2	30.2	75%	730	100.00	5990	XM_031865446.1
Bacillus luti strain FJ chromosome, complete genome	NA	2026191	30.2	30.2	75%	730	100.00	5202942	CP040336.1
PREDICTED: Oncorhynchus kisutch SPG11 vesicle trafficking...	coho salmon	8019	30.2	30.2	75%	730	100.00	7647	XM_020470019.2
PREDICTED: Oncorhynchus kisutch SPG11 vesicle trafficking...	coho salmon	8019	30.2	30.2	75%	730	100.00	7646	XM_020470018.2
PREDICTED: Oncorhynchus kisutch SPG11 vesicle trafficking...	coho salmon	8019	30.2	30.2	75%	730	100.00	7649	XM_020470017.2
PREDICTED: Oncorhynchus kisutch C-X-C chemokine receptor type...	coho salmon	8019	30.2	30.2	75%	730	100.00	2065	XM_020471105.2
PREDICTED: Oncorhynchus kisutch C-X-C chemokine receptor type...	coho salmon	8019	30.2	30.2	75%	730	100.00	2064	XM_020471104.2
PREDICTED: Vicugna pacos cell division cycle associated 3...	alpaca	30538	30.2	30.2	75%	730	100.00	1260	XM_031670725.1
PREDICTED: Vicugna pacos cell division cycle associated 3...	alpaca	30538	30.2	30.2	75%	730	100.00	1162	XM_006210874.3
Sciurus vulgaris genome assembly, chromosome: 15	Eurasian red...	55149	30.2	30.2	75%	730	100.00	90997183	LR738626.1
Sciurus carolinensis genome assembly, chromosome: 15	gray squirrel	30640	30.2	60.5	75%	730	100.00	83138899	LR738605.1
Sciurus carolinensis genome assembly, chromosome: 14	gray squirrel	30640	30.2	30.2	75%	730	100.00	88654151	LR738604.1
Neostethus bicornis genome assembly, chromosome: 22	NA	300306	30.2	30.2	75%	730	100.00	29119677	LR738552.1
Neostethus bicornis genome assembly, chromosome: 4	NA	300306	30.2	30.2	75%	730	100.00	31437157	LR738547.1
Neostethus bicornis genome assembly, chromosome: 9	NA	300306	30.2	30.2	75%	730	100.00	33440136	LR738545.1
Neostethus bicornis genome assembly, chromosome: 6	NA	300306	30.2	30.2	75%	730	100.00	33775925	LR738544.1
PREDICTED: Papio anubis solute carrier family 25 member 53...	olive baboon	9555	30.2	30.2	75%	730	100.00	1167	XR_004180639.1
Bacillus paranthracis strain CFSAN068816 chromosome, complete...	NA	2026186	30.2	30.2	75%	730	100.00	5351395	**CP045777.1**
PREDICTED: Lonchura striata domestica regulator of G protein...	Bengalese finch	299123	30.2	30.2	75%	730	100.00	1288	XM_021529272.2
PREDICTED: Lonchura striata domestica regulator of G protein...	Bengalese finch	299123	30.2	30.2	75%	730	100.00	1112	XM_021529271.2
PREDICTED: Camelus dromedarius matrix metallopeptidase 15...	Arabian camel	9838	30.2	30.2	75%	730	100.00	3550	XM_031458355.1
PREDICTED: Camelus dromedarius cell division cycle associated ...	Arabian camel	9838	30.2	30.2	75%	730	100.00	1162	XM_010990843.2
PREDICTED: Mastomys coucha alpha-1,6-mannosylglycoprotein...	southern mul...	35658	30.2	30.2	75%	730	100.00	8450	XM_031381010.1
PREDICTED: Mastomys coucha alpha-1,6-mannosylglycoprotein...	southern mul...	35658	30.2	30.2	75%	730	100.00	8111	XM_031381004.1
PREDICTED: Mastomys coucha	souther	35658	30.2	30.2	75%	730	100.00	8118	XM_031380999.1

alpha-1,6-mannosylglycoprotein...	n mul...								
PREDICTED: Mastomys coucha alpha-1,6-mannosylglycoprotein...	souther n mul...	35658	30.2	30.2	75%	730	100.00	8000	XM_031380990.1
PREDICTED: Mastomys coucha alpha-1,6-mannosylglycoprotein...	souther n mul...	35658	30.2	30.2	75%	730	100.00	8554	XM_031380981.1
PREDICTED: Mastomys coucha alpha-1,6-mannosylglycoprotein...	souther n mul...	35658	30.2	30.2	75%	730	100.00	8551	XM_031380977.1
PREDICTED: Mastomys coucha alpha-1,6-mannosylglycoprotein...	souther n mul...	35658	30.2	30.2	75%	730	100.00	8497	XM_031380974.1
PREDICTED: Mastomys coucha alpha-1,6-mannosylglycoprotein...	souther n mul...	35658	30.2	30.2	75%	730	100.00	8500	XM_031380967.1
Fusarium oxysporum NRRL 32931 uncharacterized protein...	NA	660029	30.2	30.2	75%	730	100.00	6194	XM_031172944.1
Fusarium oxysporum NRRL 32931 uncharacterized protein...	NA	660029	30.2	30.2	75%	730	100.00	6196	XM_031172943.1
Fusarium oxysporum NRRL 32931 uncharacterized protein...	NA	660029	30.2	30.2	75%	730	100.00	6251	XM_031172942.1
Fusarium oxysporum NRRL 32931 uncharacterized protein...	NA	660029	30.2	30.2	75%	730	100.00	6263	XM_031172941.1
Fusarium oxysporum NRRL 32931 uncharacterized protein...	NA	660029	30.2	30.2	75%	730	100.00	6265	XM_031172940.1
Fusarium oxysporum NRRL 32931 uncharacterized protein...	NA	660029	30.2	30.2	75%	730	100.00	6271	XM_031172939.1
Fusarium oxysporum NRRL 32931 uncharacterized protein...	NA	660029	30.2	30.2	75%	730	100.00	6328	XM_031172938.1
PREDICTED: Geospiza fortis complement C3b/C4b receptor 1 (Knop...	medium groun...	48883	30.2	30.2	75%	730	100.00	9253	XM_031063954.1
PREDICTED: Geospiza fortis regulator of G protein signaling 10...	medium groun...	48883	30.2	30.2	75%	730	100.00	3725	XM_031062573.1
Bradyrhizobium sp. TM102 DNA, complete genome	NA	2599819	30.2	30.2	75%	730	100.00	7363142	AP021855.1
Thalassophryne amazonica genome assembly, chromosome: 15	NA	390379	30.2	60.5	85%	730	100.00	97232431	LR722980.1
PREDICTED: Strongylocentrotus purpuratus sushi domain-containi...	purple sea u...	7668	30.2	30.2	75%	730	100.00	2909	XM_030977968.1
PREDICTED: Strongylocentrotus purpuratus sushi domain-containi...	purple sea u...	7668	30.2	30.2	75%	730	100.00	4359	XM_030977967.1
PREDICTED: Camarhynchus parvulus regulator of G protein...	NA	87175	30.2	30.2	75%	730	100.00	4011	XM_030951522.1
PREDICTED: Camarhynchus parvulus regulator of G protein...	NA	87175	30.2	30.2	75%	730	100.00	3811	XM_030951521.1
PREDICTED: Camarhynchus parvulus complement C3b/C4b receptor 1...	NA	87175	30.2	30.2	75%	730	100.00	9444	XM_030965559.1
PREDICTED: Globicephala melas ataxin 7 (ATXN7), mRNA	long-finned ...	9731	30.2	30.2	75%	730	100.00	7130	XM_030867630.1
PREDICTED: Archocentrus centrarchus protein kinase C alpha...	flier cichlid	63155	30.2	30.2	75%	730	100.00	7808	XM_030741718.1
PREDICTED: Syzygium oleosum uncharacterized LOC115686161...	NA	219896	30.2	30.2	75%	730	100.00	772	XM_030611370.1
PREDICTED: Gopherus evgoodei Fas binding factor 1 (FBF1),...	Goodes thorn...	1825980	30.2	30.2	75%	730	100.00	4009	XM_030534428.1
PREDICTED: Gopherus evgoodei Fas binding factor 1 (FBF1),...	Goodes thorn...	1825980	30.2	30.2	75%	730	100.00	4021	XM_030534427.1
PREDICTED: Gopherus evgoodei Fas binding factor 1 (FBF1),...	Goodes thorn...	1825980	30.2	30.2	75%	730	100.00	3880	XM_030534426.1
PREDICTED: Strigops habroptila alpha-2-macroglobulin-like...	Kakapo	2489341	30.2	30.2	75%	730	100.00	4790	XM_030480826.1
PREDICTED: Strigops habroptila alpha-2-macroglobulin-like...	Kakapo	2489341	30.2	30.2	75%	730	100.00	4793	XM_030480825.1
PREDICTED: Strigops habroptila alpha-2-macroglobulin-like...	Kakapo	2489341	30.2	30.2	75%	730	100.00	4793	XM_030480824.1
PREDICTED: Sparus aurata collagen alpha-1(VII) chain-like...	gilthead sea...	8175	30.2	30.2	75%	730	100.00	9659	XM_030439457.1
PREDICTED: Sparus aurata collagen alpha-1(VII) chain-like...	gilthead sea...	8175	30.2	30.2	75%	730	100.00	9686	XM_030439456.1

PREDICTED: Sparus aurata collagen alpha-1(VII) chain-like...	gilthead sea...	8175	30.2	30.2	75%	730	100.00	9492	XM_030439455.1
PREDICTED: Sparus aurata collagen alpha-1(VII) chain-like...	gilthead sea...	8175	30.2	30.2	75%	730	100.00	9447	XM_030439454.1
PREDICTED: Sparus aurata collagen alpha-1(VII) chain-like...	gilthead sea...	8175	30.2	30.2	75%	730	100.00	9704	XM_030439453.1
PREDICTED: Sparus aurata nuclear envelope pore membrane protei...	gilthead sea...	8175	30.2	30.2	75%	730	100.00	5049	XM_030438350.1
PREDICTED: Sparus aurata ribonuclease H2 subunit C (rnaseh2c),...	gilthead sea...	8175	30.2	30.2	75%	730	100.00	771	XM_030396374.1
Asterias rubens genome assembly, chromosome: 18	European sta...	7604	30.2	60.5	80%	730	100.00	12862124	LR699109.1
Asterias rubens genome assembly, chromosome: 8	European sta...	7604	30.2	30.2	75%	730	100.00	21693562	LR699099.1
PREDICTED: Gadus morhua Down syndrome cell adhesion...	Atlantic cod	8049	30.2	30.2	75%	730	100.00	1113	XM_030361122.1
Chanos chanos genome assembly, chromosome: 7	milkfish	29144	30.2	30.2	75%	730	100.00	49187548	LR697112.1
PREDICTED: Serinus canaria regulator of G protein signaling 10...	Common canary	9135	30.2	30.2	75%	730	100.00	3950	XM_030241358.1
PREDICTED: Serinus canaria regulator of G protein signaling 10...	Common canary	9135	30.2	30.2	75%	730	100.00	3754	XM_030241357.1
PREDICTED: Microcaecilia unicolor small integral membrane...	NA	1415580	30.2	30.2	75%	730	100.00	4399	XR_003943017.1
PREDICTED: Microcaecilia unicolor small integral membrane...	NA	1415580	30.2	30.2	75%	730	100.00	4816	XM_030211017.1
PREDICTED: Sphaeramia orbicularis immunoglobulin-like...	orbiculate c...	375764	30.2	30.2	75%	730	100.00	3167	XM_030123988.1
PREDICTED: Sphaeramia orbicularis immunoglobulin-like...	orbiculate c...	375764	30.2	30.2	75%	730	100.00	3009	XM_030123980.1
PREDICTED: Sphaeramia orbicularis metallophosphoesterase domai...	orbiculate c...	375764	30.2	30.2	75%	730	100.00	4963	XM_030148269.1
Phycisphaerae bacterium RAS2 chromosome, complete genome	NA	2528035	30.2	30.2	75%	730	100.00	4324589	CP036352.1
Planctomycetes bacterium K2D chromosome, complete genome	NA	2527962	30.2	90.7	75%	730	100.00	5769002	CP036350.1
Botrimarina mediterranea strain Spa11 chromosome	NA	2528022	30.2	90.7	75%	730	100.00	5871207	CP036349.1
Planctomycetes bacterium Pan216 chromosome, complete genome	NA	2527975	30.2	30.2	75%	730	100.00	7613473	CP036279.1
Thalassoglobus polymorphus strain Mal48 chromosome	NA	2527994	30.2	30.2	75%	730	100.00	6357355	CP036267.1
Sparus aurata genome assembly, chromosome: 23	gilthead sea...	8175	30.2	30.2	75%	730	100.00	30526999	LR537143.1
Sparus aurata genome assembly, chromosome: 21	gilthead sea...	8175	30.2	60.5	75%	730	100.00	35160130	LR537141.1
Sparus aurata genome assembly, chromosome: 16	gilthead sea...	8175	30.2	90.7	75%	730	100.00	30078578	LR537136.1
Sparus aurata genome assembly, chromosome: 14	gilthead sea...	8175	30.2	60.5	80%	730	100.00	25861820	LR537134.1
Sparus aurata genome assembly, chromosome: 13	gilthead sea...	8175	30.2	30.2	75%	730	100.00	35791275	LR537133.1
Sparus aurata genome assembly, chromosome: 12	gilthead sea...	8175	30.2	60.5	75%	730	100.00	30193437	LR537132.1
Sparus aurata genome assembly, chromosome: 11	gilthead sea...	8175	30.2	30.2	75%	730	100.00	35380617	LR537131.1
Sparus aurata genome assembly, chromosome: 8	gilthead sea...	8175	30.2	60.5	85%	730	100.00	36959192	LR537128.1
Sparus aurata genome assembly, chromosome: 7	gilthead sea...	8175	30.2	30.2	75%	730	100.00	35997798	LR537127.1
Sparus aurata genome assembly, chromosome: 5	gilthead sea...	8175	30.2	30.2	75%	730	100.00	38249111	LR537125.1
Sparus aurata genome assembly, chromosome: 4	gilthead sea...	8175	30.2	90.7	75%	730	100.00	41392777	LR537124.1
Sparus aurata genome assembly,	gilthead	8175	30.2	60.5	75%	730	100.00	36133474	LR537122.1

chromosome: 2	sea...								
Sparus aurata genome assembly, chromosome: 1	gilthead sea...	8175	30.2	90.7	90%	730	100.00	41035582	LR537121.1
Haemonchus contortus strain NZ_Hco_NP chromosome 4	barber pole ...	6289	30.2	30.2	75%	730	100.00	92053285	CP035804.1
PREDICTED: Salarias fasciatus eukaryotic translation initiatio...	jewelled blenny	181472	30.2	30.2	75%	730	100.00	1046	XM_030107926.1
PREDICTED: Salarias fasciatus lysophosphatidic acid receptor...	jewelled blenny	181472	30.2	30.2	75%	730	100.00	2691	XM_030109176.1
PREDICTED: Salarias fasciatus uncharacterized LOC115397348...	jewelled blenny	181472	30.2	30.2	75%	730	100.00	2856	XM_030103602.1
PREDICTED: Salarias fasciatus uncharacterized LOC115397348...	jewelled blenny	181472	30.2	30.2	75%	730	100.00	2886	XM_030103601.1
PREDICTED: Salarias fasciatus serine/arginine-rich splicing...	jewelled blenny	181472	30.2	30.2	75%	730	100.00	1080	XM_030093226.1
PREDICTED: Salarias fasciatus serine/arginine-rich splicing...	jewelled blenny	181472	30.2	30.2	75%	730	100.00	1080	XM_030092964.1
PREDICTED: Myripristis murdjan collagen alpha-1(VII) chain-lik...	pinecone sol...	586833	30.2	30.2	75%	730	100.00	9219	XM_030046429.1
Ornithinimicrobium sp. H23M54 chromosome, complete genome	NA	2594265	30.2	30.2	75%	730	100.00	4092907	CP041616.1
PREDICTED: Manacus vitellinus gap junction protein gamma 1...	golden-colla...	328815	30.2	30.2	75%	730	100.00	2970	XM_018087207.2
PREDICTED: Manacus vitellinus gap junction protein gamma 1...	golden-colla...	328815	30.2	30.2	75%	730	100.00	3037	XM_018087201.2
PREDICTED: Manacus vitellinus gap junction protein gamma 1...	golden-colla...	328815	30.2	30.2	75%	730	100.00	2967	XM_018087193.2
Streptomyces sp. RLB3-5 chromosome	NA	2594456	30.2	30.2	75%	730	100.00	11898970	CP041651.1
Streptomyces sp. S1A1-3 chromosome	NA	2594458	30.2	30.2	75%	730	100.00	12042091	CP041611.1
Streptomyces sp. RLB1-9 chromosome, complete genome	NA	2594454	30.2	30.2	75%	730	100.00	11940408	CP041654.1
Avian orthoreovirus strain T1600137 segment L1, partial sequence	NA	38170	30.2	30.2	75%	730	100.00	3873	MK562467.1
Avian orthoreovirus strain T1600260 segment L1, complete sequence	NA	38170	30.2	30.2	75%	730	100.00	3882	MK554704.1
Avian orthoreovirus strain K1600402 segment L1, complete sequence	NA	38170	30.2	30.2	75%	730	100.00	3882	MK551735.1
PREDICTED: Aedes albopictus GON-4-like protein (LOC109401056),...	Asian tiger ...	7160	30.2	30.2	95%	730	94.74	5577	XM_029879471.1
Avian orthoreovirus strain K1600600 lambdaA (L1) gene, complet...	NA	38170	30.2	30.2	75%	730	100.00	3926	MK416133.1
Gadus morhua genome assembly, chromosome: 14	Atlantic cod	8049	30.2	30.2	75%	730	100.00	29586942	LR633956.1
Gadus morhua genome assembly, chromosome: 12	Atlantic cod	8049	30.2	30.2	75%	730	100.00	30948897	LR633954.1
PREDICTED: Takifugu rubripes zinc finger CCHC-type containing ...	torafugu	31033	30.2	30.2	75%	730	100.00	1644	XM_011606476.2
PREDICTED: Takifugu rubripes mucin-17 (LOC105416723), transcri...	torafugu	31033	30.2	30.2	75%	730	100.00	2875	XM_029838632.1
PREDICTED: Takifugu rubripes mucin-17 (LOC105416723), transcri...	torafugu	31033	30.2	30.2	75%	730	100.00	3123	XM_011605841.2
PREDICTED: Takifugu rubripes mucin-17 (LOC105416723), transcri...	torafugu	31033	30.2	30.2	75%	730	100.00	3089	XM_011605842.2
PREDICTED: Takifugu rubripes mucin-17 (LOC105416723), transcri...	torafugu	31033	30.2	30.2	75%	730	100.00	3205	XM_029838631.1
PREDICTED: Takifugu rubripes mucin-17 (LOC105416723), transcri...	torafugu	31033	30.2	30.2	75%	730	100.00	3553	XM_029838630.1
PREDICTED: Takifugu rubripes collagen alpha-1(VII) chain-like...	torafugu	31033	30.2	30.2	75%	730	100.00	9056	XM_029825331.1
Aquila chrysaetos chrysaetos	NA	223781	30.2	30.2	75%	730	100.00	30976502	LR606195.1

genome assembly, chromosome: 15									
Aquila chrysaetos chrysaetos genome assembly, chromosome: 14	NA	223781	30.2	30.2	75%	730	100.00	34337559	LR606194.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 8	NA	223781	30.2	120	85%	730	100.00	46934974	LR606188.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 6	NA	223781	30.2	60.5	80%	730	100.00	54402963	LR606186.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 19	NA	223781	30.2	90.7	90%	730	100.00	27976474	LR606199.1
PREDICTED: Salmo trutta sorting nexin 11 (snx11), transcript...	river trout	8032	30.2	30.2	75%	730	100.00	3793	XM_029707753.1
PREDICTED: Salmo trutta sorting nexin 11 (snx11), transcript...	river trout	8032	30.2	30.2	75%	730	100.00	3368	XM_029707745.1
PREDICTED: Salmo trutta sorting nexin 11 (snx11), transcript...	river trout	8032	30.2	30.2	75%	730	100.00	3635	XM_029707735.1
PREDICTED: Salmo trutta sorting nexin 11 (snx11), transcript...	river trout	8032	30.2	30.2	75%	730	100.00	3460	XM_029707726.1
PREDICTED: Salmo trutta sorting nexin 11 (snx11), transcript...	river trout	8032	30.2	30.2	75%	730	100.00	3558	XM_029707716.1
PREDICTED: Salmo trutta SPG11 vesicle trafficking associated,...	river trout	8032	30.2	30.2	75%	730	100.00	7665	XM_029758366.1
PREDICTED: Salmo trutta SPG11 vesicle trafficking associated,...	river trout	8032	30.2	30.2	75%	730	100.00	7665	XM_029758365.1
PREDICTED: Salmo trutta SPG11 vesicle trafficking associated,...	river trout	8032	30.2	30.2	75%	730	100.00	7668	XM_029758364.1
PREDICTED: Salmo trutta C-X-C chemokine receptor type 3-like...	river trout	8032	30.2	30.2	75%	730	100.00	1747	XM_029737200.1
PREDICTED: Salmo trutta C-X-C chemokine receptor type 3-like...	river trout	8032	30.2	30.2	75%	730	100.00	1971	XM_029737199.1
PREDICTED: Salmo trutta C-X-C chemokine receptor type 3-like...	river trout	8032	30.2	30.2	75%	730	100.00	2220	XM_029744849.1
PREDICTED: Salmo trutta C-X-C chemokine receptor type 3-like...	river trout	8032	30.2	30.2	75%	730	100.00	2318	XM_029744843.1
PREDICTED: Oncorhynchus nerka SPG11 vesicle trafficking...	sockeye salmon	8023	30.2	30.2	75%	730	100.00	7620	XM_029668646.1
PREDICTED: Oncorhynchus nerka SPG11 vesicle trafficking...	sockeye salmon	8023	30.2	30.2	75%	730	100.00	7620	XM_029668645.1
PREDICTED: Oncorhynchus nerka SPG11 vesicle trafficking...	sockeye salmon	8023	30.2	30.2	75%	730	100.00	7619	XM_029668644.1
PREDICTED: Oncorhynchus nerka SPG11 vesicle trafficking...	sockeye salmon	8023	30.2	30.2	75%	730	100.00	7622	XM_029668643.1
PREDICTED: Oncorhynchus nerka C-X-C chemokine receptor type...	sockeye salmon	8023	30.2	30.2	75%	730	100.00	1702	XM_029620911.1
PREDICTED: Oncorhynchus nerka C-X-C chemokine receptor type...	sockeye salmon	8023	30.2	30.2	75%	730	100.00	1957	XM_029620903.1
PREDICTED: Oncorhynchus nerka C-X-C chemokine receptor type...	sockeye salmon	8023	30.2	30.2	75%	730	100.00	1728	XM_029647086.1
PREDICTED: Oncorhynchus nerka C-X-C chemokine receptor type...	sockeye salmon	8023	30.2	30.2	75%	730	100.00	1958	XM_029647085.1
Myripristis murdjan genome assembly, chromosome: 24	pinecone sol...	586833	30.2	60.5	100%	730	100.00	33539878	LR597573.1
Myripristis murdjan genome assembly, chromosome: 18	pinecone sol...	586833	30.2	30.2	75%	730	100.00	29228082	LR597567.1
Sphaeramia orbicularis genome assembly, chromosome: 13	orbiculate c...	375764	30.2	30.2	75%	730	100.00	53310899	LR597470.1
Salarias fasciatus genome assembly, chromosome: 19	jewelled blenny	181472	30.2	30.2	75%	730	100.00	26030347	LR597454.1
Salarias fasciatus genome assembly, chromosome: 4	jewelled blenny	181472	30.2	30.2	75%	730	100.00	27169852	LR597439.1
Salarias fasciatus genome assembly, chromosome: 2	jewelled blenny	181472	30.2	60.5	85%	730	100.00	35747288	LR597437.1
PREDICTED: Rhinatrema bivittatum septin 9 (SEPTIN9), transcrip...	two-lined	194408	30.2	30.2	75%	730	100.00	5590	XM_029600387.1

	ca...								
PREDICTED: Rhinatrema bivittatum septin 9 (SEPTIN9), transcrip...	two-lined ca...	194408	30.2	30.2	75%	730	100.00	5628	XM_029600386.1
PREDICTED: Rhinatrema bivittatum septin 9 (SEPTIN9), transcrip...	two-lined ca...	194408	30.2	30.2	75%	730	100.00	5697	XM_029600385.1
PREDICTED: Rhinatrema bivittatum septin 9 (SEPTIN9), transcrip...	two-lined ca...	194408	30.2	30.2	75%	730	100.00	5618	XM_029600384.1
PREDICTED: Rhinatrema bivittatum septin 9 (SEPTIN9), transcrip...	two-lined ca...	194408	30.2	30.2	75%	730	100.00	6242	XM_029600383.1
PREDICTED: Rhinatrema bivittatum septin 9 (SEPTIN9), transcrip...	two-lined ca...	194408	30.2	30.2	75%	730	100.00	6285	XM_029600382.1
PREDICTED: Rhinatrema bivittatum septin 9 (SEPTIN9), transcrip...	two-lined ca...	194408	30.2	30.2	75%	730	100.00	6562	XM_029600381.1
PREDICTED: Nannospalax galili tetratricopeptide repeat protein...	Upper Galile...	1026970	30.2	30.2	75%	730	100.00	4091	XM_008843158.3
Myxococcus xanthus strain MC3.3.5c16, complete genome	NA	34	30.2	30.2	75%	730	100.00	9316378	CP017173.1
Myxococcus xanthus strain MC3.5.9c15, complete genome	NA	34	30.2	30.2	75%	730	100.00	9316447	CP017174.1
PREDICTED: Echeneis naucrates glucuronokinase 1-like...	live sharksu...	173247	30.2	30.2	75%	730	100.00	2511	XM_029517883.1
Agaricus bisporus strain KMCC00540 chromosome 2	NA	5341	30.2	30.2	75%	730	100.00	3450904	CP039874.1
PREDICTED: Cottoperca gobio interleukin-12 receptor subunit...	NA	56716	30.2	30.2	75%	730	100.00	4739	XM_029429879.1
PREDICTED: Mus caroli alpha-1,6-mannosylglycoprotein...	Ryukyu mouse	10089	30.2	30.2	75%	730	100.00	6969	XM_029476569.1
PREDICTED: Mus caroli alpha-1,6-mannosylglycoprotein...	Ryukyu mouse	10089	30.2	30.2	75%	730	100.00	7087	XM_029476564.1
PREDICTED: Mus caroli alpha-1,6-mannosylglycoprotein...	Ryukyu mouse	10089	30.2	30.2	75%	730	100.00	6966	XM_021156497.2
PREDICTED: Mus caroli alpha-1,6-mannosylglycoprotein...	Ryukyu mouse	10089	30.2	30.2	75%	730	100.00	6968	XM_029476561.1
PREDICTED: Mus caroli alpha-1,6-mannosylglycoprotein...	Ryukyu mouse	10089	30.2	30.2	75%	730	100.00	7033	XM_021156489.2
PREDICTED: Mus caroli alpha-1,6-mannosylglycoprotein...	Ryukyu mouse	10089	30.2	30.2	75%	730	100.00	7386	XM_029476555.1
PREDICTED: Mus caroli alpha-1,6-mannosylglycoprotein...	Ryukyu mouse	10089	30.2	30.2	75%	730	100.00	7433	XM_021156480.2
PREDICTED: Mus caroli alpha-1,6-mannosylglycoprotein...	Ryukyu mouse	10089	30.2	30.2	75%	730	100.00	7436	XM_029476546.1
Streptopelia turtur genome assembly, chromosome: 10	NA	177155	30.2	30.2	75%	730	100.00	23073641	LR594562.1
Takifugu rubripes genome assembly, chromosome: 21	torafugu	31033	30.2	30.2	75%	730	100.00	20050447	LR584233.2
Takifugu rubripes genome assembly, chromosome: 9	torafugu	31033	30.2	30.2	75%	730	100.00	15473624	LR584246.2
Takifugu rubripes genome assembly, chromosome: 12	torafugu	31033	30.2	30.2	75%	730	100.00	13571579	LR584248.2
Trypanosoma conorhini mucin-associated surface protein (MASP)...	NA	83891	30.2	30.2	75%	730	100.00	1407	XM_029373879.1
Syngnathus acus genome assembly, chromosome: 15	greater pipe...	161584	30.2	30.2	75%	730	100.00	14382511	LR594600.1
Bacillus paranthracis strain PR1 chromosome, complete genome	NA	2026186	30.2	30.2	75%	730	100.00	5319903	**CP040515.1**
PREDICTED: Labrus bergylta semaphorin-4D (LOC109990786), mRNA	ballan wrasse	56723	30.2	30.2	75%	730	100.00	4917	XM_029279158.1
PREDICTED: Labrus bergylta ribonuclease H2 subunit C (rnaseh2c...	ballan wrasse	56723	30.2	30.2	75%	730	100.00	725	XM_020635746.2
PREDICTED: Labrus bergylta collagen alpha-1(VII) chain-like...	ballan wrasse	56723	30.2	30.2	75%	730	100.00	6633	XM_029280784.1

PREDICTED: Elaeis guineensis cytochrome P450 76M5...	African oil ...	51953	30.2	30.2	95%	730	94.74	1706	XM_010918967.3
PREDICTED: Monodon monoceros ataxin 7 (ATXN7), transcript...	narwhal	40151	30.2	30.2	75%	730	100.00	5703	XM_029243595.1
PREDICTED: Monodon monoceros ataxin 7 (ATXN7), transcript...	narwhal	40151	30.2	30.2	75%	730	100.00	5974	XM_029243592.1
Metallosphaera prunae strain Ron 12/II chromosome, complete...	NA	47304	30.2	30.2	75%	730	100.00	2202576	CP031156.1
Azospirillum sp. TSH100 chromosome 3, complete sequence	NA	652764	30.2	30.2	75%	730	100.00	917252	CP039636.1
PREDICTED: Ornithorhynchus anatinus cyclase associated actin...	platypus	9258	30.2	30.2	75%	730	100.00	3135	XM_007666436.3
PREDICTED: Macaca mulatta solute carrier family 25 member 53...	Rhesus monkey	9544	30.2	30.2	75%	730	100.00	1787	XR_001442067.2
PREDICTED: Podarcis muralis thrombospondin type 1 domain...	Common wall ...	64176	30.2	30.2	75%	730	100.00	5050	XM_028706826.1
PREDICTED: Podarcis muralis thrombospondin type 1 domain...	Common wall ...	64176	30.2	30.2	75%	730	100.00	5134	XM_028706825.1
PREDICTED: Podarcis muralis thrombospondin type 1 domain...	Common wall ...	64176	30.2	30.2	75%	730	100.00	6481	XM_028706824.1
PREDICTED: Podarcis muralis thrombospondin type 1 domain...	Common wall ...	64176	30.2	30.2	75%	730	100.00	6186	XM_028706823.1
PREDICTED: Podarcis muralis thrombospondin type 1 domain...	Common wall ...	64176	30.2	30.2	75%	730	100.00	6351	XM_028706822.1
PREDICTED: Podarcis muralis thrombospondin type 1 domain...	Common wall ...	64176	30.2	30.2	75%	730	100.00	6284	XM_028706820.1
PREDICTED: Erpetoichthys calabaricus nucleoporin 214 (nup214),...	reedfish	27687	30.2	30.2	75%	730	100.00	6176	XM_028793029.1
PREDICTED: Erpetoichthys calabaricus nucleoporin 214 (nup214),...	reedfish	27687	30.2	30.2	75%	730	100.00	8611	XM_028793028.1
PREDICTED: Erpetoichthys calabaricus nucleoporin 214 (nup214),...	reedfish	27687	30.2	30.2	75%	730	100.00	8614	XM_028793027.1
PREDICTED: Podarcis muralis purinergic receptor P2Y1 (P2RY1),...	Common wall ...	64176	30.2	30.2	75%	730	100.00	6934	XM_028731336.1
PREDICTED: Podarcis muralis purinergic receptor P2Y1 (P2RY1),...	Common wall ...	64176	30.2	30.2	75%	730	100.00	7037	XM_028731335.1
PREDICTED: Podarcis muralis purinergic receptor P2Y1 (P2RY1),...	Common wall ...	64176	30.2	30.2	75%	730	100.00	7392	XM_028731334.1
PREDICTED: Podarcis muralis purinergic	Common wall ...	64176	30.2	30.2	75%	730	100.00	7641	XM_028731333.1

receptor P2Y1 (P2RY1),...									
PREDICTED: Grammomys surdaster alpha-1,6-mannosylglycoprotein...	NA	491861	30.2	30.2	75%	730	100.00	6991	XM_028771515.1
Salmo trutta genome assembly, chromosome: 2	river trout	8032	30.2	30.2	75%	730	100.00	75345318	LR584445.1
Salmo trutta genome assembly, chromosome: 21	river trout	8032	30.2	60.5	75%	730	100.00	52728040	LR584437.1
Salmo trutta genome assembly, chromosome: 19	river trout	8032	30.2	30.2	75%	730	100.00	56583805	LR584427.1
Salmo trutta genome assembly, chromosome: 23	river trout	8032	30.2	30.2	75%	730	100.00	51488243	LR584421.1
Salmo trutta genome assembly, chromosome: 3	river trout	8032	30.2	30.2	75%	730	100.00	74753489	LR584416.1
Salmo trutta genome assembly, chromosome: 6	river trout	8032	30.2	30.2	75%	730	100.00	60103141	LR584406.1
Rhinatrema bivittatum genome assembly, chromosome: 16	two-lined ca...	194408	30.2	30.2	75%	730	100.00	74781573	LR584402.1
Rhinatrema bivittatum genome assembly, chromosome: 15	two-lined ca...	194408	30.2	60.5	75%	730	100.00	80992113	LR584401.1
Takifugu rubripes genome assembly, chromosome: 3	torafugu	31033	30.2	60.5	95%	730	100.00	17484280	LR584237.1
Scleropages formosus genome assembly, chromosome: 24	Asian bonyto...	113540	30.2	30.2	75%	730	100.00	21794140	LR584089.1
Scleropages formosus genome assembly, chromosome: 21	Asian bonyto...	113540	30.2	60.5	85%	730	100.00	25217654	LR584086.1
Scleropages formosus genome assembly, chromosome: 7	Asian bonyto...	113540	30.2	30.2	75%	730	100.00	33206717	LR584072.1
Echeneis naucrates genome assembly, chromosome: 20	live sharksu...	173247	30.2	30.2	75%	730	100.00	19088838	LR584061.1
Echeneis naucrates genome assembly, chromosome: 13	live sharksu...	173247	30.2	60.5	85%	730	100.00	25654854	LR584054.1
Echeneis naucrates genome assembly, chromosome: 7	live sharksu...	173247	30.2	30.2	75%	730	100.00	25443275	LR584048.1
Echeneis naucrates genome assembly, chromosome: 5	live sharksu...	173247	30.2	30.2	75%	730	100.00	26820162	LR584046.1
Apiotrichum porosum hypothetical protein (EHS24_001634), parti...	NA	105984	30.2	30.2	75%	730	100.00	2283	XM_028617419.1
PREDICTED: Perca flavescens collagen alpha-1(VII) chain-like...	yellow perch	8167	30.2	30.2	75%	730	100.00	2448	XM_028571298.1
Caenorhabditis elegans strain CB4856 chromosome V	NA	6239	30.2	30.2	75%	730	100.00	21389866	CP038191.1
PREDICTED: Dendronephthya gigantea hornerin-like (LOC114532570...	NA	151771	30.2	30.2	75%	730	100.00	3197	XM_028554105.1
PREDICTED: Dendronephthya gigantea hornerin-like (LOC114532570...	NA	151771	30.2	30.2	75%	730	100.00	3262	XM_028554104.1
PREDICTED: Dendronephthya gigantea hornerin-like (LOC114532570...	NA	151771	30.2	30.2	75%	730	100.00	3209	XM_028554103.1
Bacillus mycoides strain TH26 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5306036	CP037992.1
PREDICTED: Physeter catodon uncharacterized LOC114486219...	sperm whale	9755	30.2	30.2	75%	730	100.00	644	XR_003679573.1
PREDICTED: Physeter catodon uncharacterized LOC114486219...	sperm whale	9755	30.2	30.2	75%	730	100.00	783	XR_003679572.1
PREDICTED: Physeter catodon uncharacterized LOC114486219...	sperm whale	9755	30.2	30.2	75%	730	100.00	819	XR_003679571.1
PREDICTED: Physeter catodon	sperm whale	9755	30.2	30.2	75%	730	100.00	657	XR_003679570.1

uncharacterized LOC114486219...									
PREDICTED: Physeter catodon uncharacterized LOC114486219...	sperm whale	9755	30.2	30.2	75%	730	100.00	654	XR_003679569.1
PREDICTED: Physeter catodon ataxin 7 (ATXN7), mRNA	sperm whale	9755	30.2	30.2	75%	730	100.00	5955	XM_024123753.2
Erpetoichthys calabaricus genome assembly, chromosome: 18	reedfish	27687	30.2	30.2	75%	730	100.00	88365115	LR536449.1
Betta splendens genome assembly, chromosome: 8	Siamese figh...	158456	30.2	30.2	75%	730	100.00	16455974	LR132020.2
Betta splendens genome assembly, chromosome: 14	Siamese figh...	158456	30.2	30.2	75%	730	100.00	17358772	LR132016.2
Betta splendens genome assembly, chromosome: 16	Siamese figh...	158456	30.2	30.2	75%	730	100.00	21788636	LR132009.2
Mastacembelus armatus genome assembly, chromosome: 13	zig-zag eel	205130	30.2	30.2	75%	730	100.00	27498257	LR535845.1
Mastacembelus armatus genome assembly, chromosome: 1	zig-zag eel	205130	30.2	30.2	75%	730	100.00	26083871	LR535833.1
PREDICTED: Parambassis ranga collagen alpha-1(VII) chain-like...	Indian glass...	210632	30.2	30.2	75%	730	100.00	9002	XM_028419095.1
PREDICTED: Parambassis ranga POM121 transmembrane nucleoporin...	Indian glass...	210632	30.2	30.2	75%	730	100.00	4941	XM_028421535.1
PREDICTED: Parambassis ranga signal-induced...	Indian glass...	210632	30.2	30.2	75%	730	100.00	4501	XR_003671705.1
PREDICTED: Parambassis ranga signal-induced...	Indian glass...	210632	30.2	30.2	75%	730	100.00	4497	XM_028420900.1
PREDICTED: Parambassis ranga signal-induced...	Indian glass...	210632	30.2	30.2	75%	730	100.00	5766	XM_028420899.1
PREDICTED: Parambassis ranga signal-induced...	Indian glass...	210632	30.2	30.2	75%	730	100.00	4512	XR_003671704.1
PREDICTED: Parambassis ranga signal-induced...	Indian glass...	210632	30.2	30.2	75%	730	100.00	7155	XM_028420898.1
PREDICTED: Parambassis ranga signal-induced...	Indian glass...	210632	30.2	30.2	75%	730	100.00	7312	XM_028420895.1
PREDICTED: Parambassis ranga signal-induced...	Indian glass...	210632	30.2	30.2	75%	730	100.00	7132	XM_028420894.1
PREDICTED: Parambassis ranga signal-induced...	Indian glass...	210632	30.2	30.2	75%	730	100.00	7272	XM_028420893.1
PREDICTED: Parambassis ranga signal-induced...	Indian glass...	210632	30.2	30.2	75%	730	100.00	7491	XM_028420892.1
PREDICTED: Parambassis ranga signal-induced...	Indian glass...	210632	30.2	30.2	75%	730	100.00	7311	XM_028420891.1
Cercospora sojina strain RACE15 chromosome I, complete sequence	NA	438356	30.2	30.2	75%	730	100.00	2987846	CP036215.1
Anabas testudineus genome assembly, chromosome: 6	climbing perch	64144	30.2	30.2	75%	730	100.00	25063394	LR132047.1
Anabas testudineus genome assembly, chromosome: 23	climbing perch	64144	30.2	60.5	85%	730	100.00	15359112	LR132044.1
Gouania willdenowi genome assembly, chromosome: 12	blunt-snoute...	441366	30.2	60.5	75%	730	100.00	33478699	LR132004.1
Gouania willdenowi genome assembly, chromosome: 3	blunt-snoute...	441366	30.2	30.2	75%	730	100.00	46057556	LR132003.1
Gouania willdenowi genome assembly, chromosome: 6	blunt-snoute...	441366	30.2	30.2	75%	730	100.00	72451976	LR132000.1
Gouania willdenowi genome assembly, chromosome: 5	blunt-snoute...	441366	30.2	30.2	75%	730	100.00	42802790	LR131993.1
Gouania willdenowi genome assembly, chromosome: 8	blunt-snoute...	441366	30.2	151	75%	730	100.00	34658348	LR131991.1
Gouania willdenowi genome assembly, chromosome: 15	blunt-snoute...	441366	30.2	30.2	75%	730	100.00	37027010	LR131987.1
Gouania willdenowi genome assembly, chromosome: 7	blunt-snoute...	441366	30.2	60.5	75%	730	100.00	40544756	LR131985.1
Gouania willdenowi genome assembly, chromosome: 11	blunt-snoute..	441366	30.2	30.2	75%	730	100.00	32583565	LR131984.1

	.								
Jeotgalibaca ciconiae strain H21T32 chromosome, complete genome	NA	2496265	30.2	30.2	75%	730	100.00	2950593	CP034465.1
Parambassis ranga genome assembly, chromosome: 13	Indian glass...	210632	30.2	30.2	75%	730	100.00	24575694	LR131963.1
Cottoperca gobio genome assembly, chromosome: 5	NA	56716	30.2	60.5	75%	730	100.00	30479438	LR131935.1
Cottoperca gobio genome assembly, chromosome: 21	NA	56716	30.2	60.5	75%	730	100.00	24104793	LR131929.1
Cottoperca gobio genome assembly, chromosome: 20	NA	56716	30.2	90.7	75%	730	100.00	17599799	LR131928.1
Cottoperca gobio genome assembly, chromosome: 15	NA	56716	30.2	30.2	75%	730	100.00	24963210	LR131922.1
Cottoperca gobio genome assembly, chromosome: 13	NA	56716	30.2	30.2	75%	730	100.00	27742916	LR131920.1
PREDICTED: Larimichthys crocea nuclear envelope pore membrane...	large yellow...	215358	30.2	30.2	75%	730	100.00	5022	XM_010730862.3
PREDICTED: Tachysurus fulvidraco TATA-box binding protein...	yellow catfish	1234273	30.2	30.2	75%	730	100.00	3741	XM_027152836.1
Epichloe festucae Fl1 chromosome 2, complete sequence	NA	877507	30.2	30.2	95%	730	94.74	7605136	CP031386.1
Brassica oleracea HDEM genome, scaffold: C2	wild cabbage	3712	30.2	30.2	75%	730	100.00	63782621	LR031874.1
Brassica oleracea HDEM genome, scaffold: C3	wild cabbage	3712	30.2	30.2	75%	730	100.00	73711317	LR031872.1
PREDICTED: Lagenorhynchus obliquidens ataxin 7 (ATXN7), mRNA	Pacific whit...	90247	30.2	30.2	75%	730	100.00	7052	XM_027121307.1
PREDICTED: Acinonyx jubatus uncharacterized LOC113593382...	cheetah	32536	30.2	30.2	75%	730	100.00	825	XR_003413524.1
Leishmania donovani strain LdCL chromosome LdCL_32, complete...	NA	5661	30.2	30.2	75%	730	100.00	1561474	CP029531.1
PREDICTED: Athene cunicularia alpha-2-macroglobulin-like...	burrowing owl	194338	30.2	30.2	75%	730	100.00	4232	XM_026867704.1
PREDICTED: Athene cunicularia uncharacterized LOC113482430...	burrowing owl	194338	30.2	30.2	75%	730	100.00	659	XR_003398846.1
PREDICTED: Athene cunicularia LYR motif containing 9 (LYRM9),...	burrowing owl	194338	30.2	30.2	75%	730	100.00	1915	XM_026861637.1
PREDICTED: Zonotrichia albicollis regulator of G protein...	white-throat...	44394	30.2	30.2	75%	730	100.00	3794	XM_005489846.3
Streptomyces griseus subsp. griseus strain ATCC 13273...	NA	67263	30.2	60.5	90%	730	100.00	7238194	CP032543.1
Vibrio alfacsensis strain CAIM 1831 chromosome II, complete...	NA	1074311	30.2	30.2	75%	730	100.00	1596877	CP032094.1
PREDICTED: Anabas testudineus...	climbing perch	64144	30.2	30.2	75%	730	100.00	4903	XM_026362792.1
PREDICTED: Anabas testudineus...	climbing perch	64144	30.2	30.2	75%	730	100.00	4907	XM_026362791.1
PREDICTED: Anabas testudineus collagen type VII alpha 1-like...	climbing perch	64144	30.2	30.2	75%	730	100.00	8973	XM_026361089.1
PREDICTED: Mastacembelus armatus sulfated surface glycoprotein...	zig-zag eel	205130	30.2	30.2	75%	730	100.00	1771	XM_026303769.1
Haemonchus contortus, ISE/inbred ISE, WGS project CAVP01000000...	barber pole ...	6289	30.2	30.2	75%	730	100.00	51826579	LS997565.1
Haemonchus contortus, ISE/inbred ISE, WGS project CAVP01000000...	barber pole ...	6289	30.2	30.2	75%	730	100.00	47382676	LS997563.1
PREDICTED: Carassius auratus probable glutamate--tRNA ligase,...	goldfish	7957	30.2	30.2	75%	730	100.00	1649	XM_026246998.1
PREDICTED: Carassius auratus probable glutamate--tRNA ligase,...	goldfish	7957	30.2	30.2	75%	730	100.00	1787	XM_026246997.1
PREDICTED: Astatotilapia calliptera SAM and SH3 domain...	eastern happy	8154	30.2	30.2	75%	730	100.00	5347	XM_026143342.1
PREDICTED: Astatotilapia calliptera SAM and SH3 domain...	eastern happy	8154	30.2	30.2	75%	730	100.00	4638	XM_026143341.1
PREDICTED: Astatotilapia calliptera SAM and SH3 domain...	eastern happy	8154	30.2	30.2	75%	730	100.00	5220	XM_026143340.1

PREDICTED: Astatotilapia calliptera SAM and SH3 domain...	eastern happy	8154	30.2	30.2	75%	730	100.00	5772	XM_026143339.1
PREDICTED: Astatotilapia calliptera SAM and SH3 domain...	eastern happy	8154	30.2	30.2	75%	730	100.00	5196	XM_026143338.1
PREDICTED: Astatotilapia calliptera SAM and SH3 domain...	eastern happy	8154	30.2	30.2	75%	730	100.00	6233	XM_026143337.1
PREDICTED: Astatotilapia calliptera SAM and SH3 domain...	eastern happy	8154	30.2	30.2	75%	730	100.00	6186	XR_003269839.1
PREDICTED: Astatotilapia calliptera SAM and SH3 domain...	eastern happy	8154	30.2	30.2	75%	730	100.00	6332	XM_026143335.1
PREDICTED: Astatotilapia calliptera nuclear envelope pore...	eastern happy	8154	30.2	30.2	75%	730	100.00	4206	XM_026182600.1
Pseudonocardia autotrophica NBRC 12743 DNA, complete genome	NA	2074	30.2	30.2	75%	730	100.00	7246130	AP018920.1
Trachinotus ovatus Na-K-Cl cotransporter 1 alpha gene, complet...	derbio	173339	30.2	30.2	75%	730	100.00	69112	MG674400.1
PREDICTED: Balaenoptera acutorostrata scammoni ataxin 7 (ATXN7...	NA	310752	30.2	30.2	75%	730	100.00	6923	XM_028169136.1
PREDICTED: Vombatus ursinus RAB40C, member RAS oncogene family...	common wombat	29139	30.2	30.2	75%	730	100.00	1713	XM_027863171.1
PREDICTED: **Falco** cherrug protein kinase AMP-activated catalyti...	Saker falcon	345164	30.2	30.2	75%	730	100.00	13135	XM_027806960.1
PREDICTED: **Falco** cherrug protein kinase AMP-activated catalyti...	Saker falcon	345164	30.2	30.2	75%	730	100.00	7286	XM_027806959.1
PREDICTED: **Falco** peregrinus protein kinase AMP-activated...	peregrine fa...	8954	30.2	30.2	75%	730	100.00	12165	XM_027780447.1
PREDICTED: **Falco** peregrinus protein kinase AMP-activated...	peregrine fa...	8954	30.2	30.2	75%	730	100.00	7859	XM_027780446.1
Lateolabrax maculatus linkage group 10 sequence	spotted sea ...	315492	30.2	30.2	75%	730	100.00	25018904	CP032607.1
Lateolabrax maculatus linkage group 20 sequence	spotted sea ...	315492	30.2	30.2	75%	730	100.00	21427312	CP032594.1
Lateolabrax maculatus linkage group 19 sequence	spotted sea ...	315492	30.2	30.2	75%	730	100.00	22300342	CP032593.1
Lateolabrax maculatus linkage group 1 sequence	spotted sea ...	315492	30.2	30.2	75%	730	100.00	31475329	CP032584.1
Lateolabrax maculatus chromosome Lm12	spotted sea ...	315492	30.2	30.2	75%	730	100.00	23523986	CP027273.1
Lateolabrax maculatus chromosome Lm5	spotted sea ...	315492	30.2	30.2	75%	730	100.00	21471159	CP027266.1
Eukaryotic synthetic construct chromosome 19	NA	111789	30.2	30.2	75%	730	100.00	64242768	CP034522.1
Eukaryotic synthetic construct chromosome 20	NA	111789	30.2	90.7	100%	730	100.00	68480253	CP034499.1
Eukaryotic synthetic construct chromosome 19	NA	111789	30.2	30.2	75%	730	100.00	64242768	CP034497.1
Eukaryotic synthetic construct chromosome 17	NA	111789	30.2	120	75%	730	100.00	88299790	CP034495.1
Eukaryotic synthetic construct chromosome 16	NA	111789	30.2	90.7	80%	730	100.00	98200793	CP034494.1
Bacillus albus strain PFYN01 chromosome, complete genome	NA	2026189	30.2	30.2	75%	730	100.00	4939577	CP034548.1
PREDICTED: Dromaius novaehollandiae LYR motif containing 9...	emu	8790	30.2	30.2	75%	730	100.00	10195	XR_003260204.1
PREDICTED: Dromaius novaehollandiae LYR motif containing 9...	emu	8790	30.2	30.2	75%	730	100.00	10247	XR_003260203.1
PREDICTED: Dromaius novaehollandiae LYR motif containing 9...	emu	8790	30.2	30.2	75%	730	100.00	10422	XR_003260201.1
PREDICTED: Dromaius novaehollandiae LYR motif containing 9...	emu	8790	30.2	30.2	75%	730	100.00	10546	XR_003260199.1
PREDICTED: Dromaius novaehollandiae LYR motif	emu	8790	30.2	30.2	75%	730	100.00	10658	XR_003260197.1

containing 9...									
PREDICTED: Dromaius novaehollandiae LYR motif containing 9...	emu	8790	30.2	30.2	75%	730	100.00	9126	XR_003260195.1
PREDICTED: Apteryx rowi uncharacterized LOC112969108...	Okarito brow...	308060	30.2	30.2	75%	730	100.00	5891	XR_003254568.1
Bacillus sp. COPE52 chromosome	NA	2233998	30.2	30.2	75%	730	100.00	5806513	CP031292.1
PREDICTED: Oreochromis niloticus SAM and SH3 domain containing...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	6612	XM_013274206.3
PREDICTED: Oreochromis niloticus SAM and SH3 domain containing...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	7368	XM_013274205.3
PREDICTED: Oreochromis niloticus SAM and SH3 domain containing...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	6651	XM_025899210.1
PREDICTED: Oreochromis niloticus SAM and SH3 domain containing...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	7510	XM_013274203.3
PREDICTED: Oreochromis niloticus SAM and SH3 domain containing...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	7169	XM_025899209.1
PREDICTED: Oreochromis niloticus SAM and SH3 domain containing...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	7926	XM_025899208.1
PREDICTED: Oreochromis niloticus SAM and SH3 domain containing...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	7969	XM_025899207.1
PREDICTED: Oreochromis niloticus SAM and SH3 domain containing...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	7922	XR_003214303.1
PREDICTED: Oreochromis niloticus SAM and SH3 domain containing...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	8069	XM_025899206.1
PREDICTED: Oreochromis niloticus nuclear envelope pore membran...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	5182	XM_005456169.4
PREDICTED: Oreochromis niloticus protein kinase C alpha (prkca...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	7682	XM_019359706.2
PREDICTED: Oreochromis niloticus protein kinase C alpha (prkca...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	7710	XM_025907858.1
PREDICTED: Oreochromis niloticus protein kinase C alpha (prkca...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	7713	XM_019359705.2
PREDICTED: Arachis hypogaea uncharacterized LOC112730015...	peanut	3818	30.2	30.2	75%	730	100.00	1041	XM_025780136.1
Aspergillus heteromorphus CBS 117.55 tannase and feruloyl...	NA	1448321	30.2	30.2	75%	730	100.00	1834	XM_025547584.1
Corynebacterium jeikeium strain NCTC11914 genome assembly,...	NA	38289	30.2	30.2	75%	730	100.00	2414649	LS483459.1
Homo sapiens chromosome 1 clone CH17-128E4, complete sequence	human	9606	30.2	60.5	75%	730	100.00	237086	AC277989.1
Scophthalmus maximus chromosome 18	turbot	52904	30.2	30.2	75%	730	100.00	21356665	CP026260.1
Scophthalmus maximus chromosome 17	turbot	52904	30.2	30.2	75%	730	100.00	21403135	CP026259.1
Scophthalmus maximus chromosome 13	turbot	52904	30.2	30.2	75%	730	100.00	24512258	CP026255.1
Scophthalmus maximus chromosome 11	turbot	52904	30.2	30.2	75%	730	100.00	25101323	CP026253.1
Scophthalmus maximus chromosome 8	turbot	52904	30.2	60.5	75%	730	100.00	25790243	CP026250.1
Homo sapiens chromosome X clone CH17-114M3, complete sequence	human	9606	30.2	30.2	75%	730	100.00	203762	AC277893.1
PREDICTED: Pelodiscus sinensis heterogeneous nuclear...	Chinese soft...	13735	30.2	30.2	75%	730	100.00	1807	XM_014578606.2
PREDICTED: Pelodiscus sinensis heterogeneous nuclear...	Chinese soft...	13735	30.2	30.2	75%	730	100.00	1819	XM_006133122.3
PREDICTED: Cynoglossus semilaevis semaphorin 6D (sema6d),...	tongue sole	244447	30.2	30.2	75%	730	100.00	5012	XM_008310181.3
PREDICTED: Cynoglossus semilaevis semaphorin 6D (sema6d),...	tongue sole	244447	30.2	30.2	75%	730	100.00	5071	XM_008310180.3
PREDICTED: Cynoglossus semilaevis semaphorin 6D (sema6d),...	tongue sole	244447	30.2	30.2	75%	730	100.00	5200	XM_008310179.3
PREDICTED: Cynoglossus semilaevis semaphorin 6D	tongue sole	244447	30.2	30.2	75%	730	100.00	4459	XM_008310178.3

(sema6d),...									
PREDICTED: Cynoglossus semilaevis semaphorin 6D (sema6d),...	tongue sole	244447	30.2	30.2	75%	730	100.00	4187	XM_008310177.3
PREDICTED: Cynoglossus semilaevis semaphorin 6D (sema6d),...	tongue sole	244447	30.2	30.2	75%	730	100.00	5261	XM_008310175.3
PREDICTED: Cephus cinctus uncharacterized LOC107265957...	wheat stem s...	211228	30.2	30.2	75%	730	100.00	3951	XM_015735930.2
Anderseniella sp. Alg231_50 genome assembly, chromosome: V	NA	1922226	30.2	30.2	75%	730	100.00	365660	LT703007.1
Avian reovirus strain K738/14 segment L1, complete sequence	NA	38170	30.2	30.2	75%	730	100.00	3938	MF686695.1
Hyaloscypha bicolor E uncharacterized protein...	NA	1095630	30.2	30.2	75%	730	100.00	615	XM_024883435.1
Amorphotheca resinae ATCC 22711 hypothetical protein...	NA	857342	30.2	30.2	75%	730	100.00	1137	XM_024867595.1
PREDICTED: Macaca nemestrina solute carrier family 25 member 5...	pig-tailed m...	9545	30.2	30.2	75%	730	100.00	1085	XR_998301.2
PREDICTED: Maylandia zebra SAM and SH3 domain containing 1...	zebra mbuna	106582	30.2	30.2	75%	730	100.00	6062	XM_004541750.5
PREDICTED: Maylandia zebra SAM and SH3 domain containing 1...	zebra mbuna	106582	30.2	30.2	75%	730	100.00	6613	XM_004541749.4
PREDICTED: Maylandia zebra SAM and SH3 domain containing 1...	zebra mbuna	106582	30.2	30.2	75%	730	100.00	7436	XM_004541748.5
PREDICTED: Maylandia zebra SAM and SH3 domain containing 1...	zebra mbuna	106582	30.2	30.2	75%	730	100.00	7388	XR_190947.5
PREDICTED: Maylandia zebra SAM and SH3 domain containing 1...	zebra mbuna	106582	30.2	30.2	75%	730	100.00	7535	XM_004541747.5
PREDICTED: Maylandia zebra nuclear envelope pore membrane...	zebra mbuna	106582	30.2	30.2	75%	730	100.00	5171	XM_014409234.2
Zea mays putative elongation factor 1-gamma 2 (LOC100381466),...	NA	4577	30.2	30.2	75%	730	100.00	1588	NM_001361431.1
Leishmania infantum strain TR01 isolate Lin_TR01 chromosome 32...	NA	5671	30.2	30.2	75%	730	100.00	1551694	CP027832.1
PREDICTED: Oncorhynchus tshawytscha SPG11, spatacsin vesicle...	Chinook salmon	74940	30.2	30.2	75%	730	100.00	7657	XM_024378954.1
PREDICTED: Oncorhynchus tshawytscha SPG11, spatacsin vesicle...	Chinook salmon	74940	30.2	30.2	75%	730	100.00	7660	XM_024378953.1
PREDICTED: Oncorhynchus tshawytscha SPG11, spatacsin vesicle...	Chinook salmon	74940	30.2	30.2	75%	730	100.00	7672	XM_024378952.1
PREDICTED: Oncorhynchus tshawytscha SPG11, spatacsin vesicle...	Chinook salmon	74940	30.2	30.2	75%	730	100.00	7672	XM_024378951.1
PREDICTED: Oncorhynchus tshawytscha SPG11, spatacsin vesicle...	Chinook salmon	74940	30.2	30.2	75%	730	100.00	7675	XM_024378949.1
PREDICTED: Oncorhynchus tshawytscha C-X-C chemokine receptor...	Chinook salmon	74940	30.2	30.2	75%	730	100.00	2143	XM_024403435.1
PREDICTED: Oncorhynchus tshawytscha C-X-C chemokine receptor...	Chinook salmon	74940	30.2	30.2	75%	730	100.00	2367	XM_024403434.1
Bos mutus isolate yakQH1 chromosome 23	wild yak	72004	30.2	30.2	75%	730	100.00	45444811	CP027091.1
Bos mutus isolate yakQH1 chromosome 21	wild yak	72004	30.2	120	90%	730	100.00	67277862	CP027089.1
Bos mutus isolate yakQH1 chromosome 19	wild yak	72004	30.2	90.7	90%	730	100.00	60756558	CP027087.1
Bos mutus isolate yakQH1 chromosome 12	wild yak	72004	30.2	30.2	75%	730	100.00	78435519	CP027080.1
Bos mutus isolate yakQH1 chromosome 10	wild yak	72004	30.2	60.5	90%	730	100.00	33842169	CP027078.1
Watermelon chlorotic stunt virus	NA	35341	30.2	30.2	75%	730	100.00	2728	KY825716.1

isolate IR/Ker/TBa3/Tur:15...									
Bacillus sp. FDAARGOS_235 chromosome, complete genome	NA	1839798	30.2	30.2	75%	730	100.00	5287334	CP020437.2
PREDICTED: Lingula anatina uncharacterized LOC106179341...	NA	7574	30.2	30.2	75%	730	100.00	11084	XM_013562947.2
PREDICTED: Chrysemys picta bellii ankyrin repeat domain 34A...	western pain...	8478	30.2	30.2	75%	730	100.00	4961	XM_005293635.3
PREDICTED: Salvelinus alpinus C-X-C chemokine receptor type...	Arctic char	8036	30.2	30.2	75%	730	100.00	2488	XM_023980008.1
PREDICTED: Salvelinus alpinus C-X-C chemokine receptor type...	Arctic char	8036	30.2	30.2	75%	730	100.00	2740	XM_023980007.1
PREDICTED: Salvelinus alpinus sorting nexin 11 (snx11),...	Arctic char	8036	30.2	30.2	75%	730	100.00	1315	XM_024007270.1
PREDICTED: Salvelinus alpinus sorting nexin 11 (snx11),...	Arctic char	8036	30.2	30.2	75%	730	100.00	1888	XM_024007269.1
PREDICTED: Salvelinus alpinus sorting nexin 11 (snx11),...	Arctic char	8036	30.2	30.2	75%	730	100.00	1443	XM_024007268.1
PREDICTED: Salvelinus alpinus sorting nexin 11 (snx11),...	Arctic char	8036	30.2	30.2	75%	730	100.00	1614	XM_024007267.1
PREDICTED: Salvelinus alpinus sorting nexin 11 (snx11),...	Arctic char	8036	30.2	30.2	75%	730	100.00	1559	XM_024007266.1
PREDICTED: Salvelinus alpinus sorting nexin 11 (snx11),...	Arctic char	8036	30.2	30.2	75%	730	100.00	1755	XM_024007265.1
PREDICTED: Salvelinus alpinus sorting nexin 11 (snx11),...	Arctic char	8036	30.2	30.2	75%	730	100.00	1806	XM_024007264.1
PREDICTED: Salvelinus alpinus sorting nexin 11 (snx11),...	Arctic char	8036	30.2	30.2	75%	730	100.00	1885	XM_024007262.1
PREDICTED: Salvelinus alpinus C-X-C chemokine receptor type...	Arctic char	8036	30.2	30.2	75%	730	100.00	1336	XM_023988686.1
PREDICTED: Salvelinus alpinus SPG11, spatacsin vesicle...	Arctic char	8036	30.2	30.2	75%	730	100.00	7629	XM_023984904.1
PREDICTED: Salvelinus alpinus SPG11, spatacsin vesicle...	Arctic char	8036	30.2	30.2	75%	730	100.00	7632	XM_023984903.1
PREDICTED: Cyanistes caeruleus uncharacterized LOC111943229...	blue tit	156563	30.2	30.2	75%	730	100.00	370	XR_002870835.1
PREDICTED: Cyanistes caeruleus regulator of G protein signalin...	blue tit	156563	30.2	30.2	75%	730	100.00	3617	XM_023929956.1
PREDICTED: Cyanistes caeruleus regulator of G protein signalin...	blue tit	156563	30.2	30.2	75%	730	100.00	3897	XM_023929955.1
PREDICTED: Cyanistes caeruleus regulator of G protein signalin...	blue tit	156563	30.2	30.2	75%	730	100.00	4062	XM_023929954.1
Bacillus cereus strain G9241 chromosome	NA	1396	30.2	30.2	75%	730	100.00	4880708	CP026376.1
Aeromonas sp. ASNIH7 chromosome, complete genome	NA	1920107	30.2	30.2	75%	730	100.00	4817060	CP026226.1
PREDICTED: Myotis lucifugus ankyrin repeat domain-containing...	little brown...	59463	30.2	30.2	75%	730	100.00	5170	XM_014463861.2
PREDICTED: Myotis lucifugus ankyrin repeat domain-containing...	little brown...	59463	30.2	30.2	75%	730	100.00	4891	XM_023761971.1
PREDICTED: Myotis lucifugus ankyrin repeat domain-containing...	little brown...	59463	30.2	30.2	75%	730	100.00	4990	XM_023761970.1
PREDICTED: Myotis lucifugus ankyrin repeat domain-containing...	little brown...	59463	30.2	30.2	75%	730	100.00	5071	XM_023761968.1
PREDICTED: Myotis lucifugus ankyrin repeat domain-containing...	little brown...	59463	30.2	30.2	75%	730	100.00	5074	XM_023761967.1
PREDICTED: Myotis lucifugus ankyrin repeat domain-containing...	little brown...	59463	30.2	30.2	75%	730	100.00	5170	XM_023761966.1
PREDICTED: Myotis lucifugus ankyrin repeat domain-containing...	little brown...	59463	30.2	30.2	75%	730	100.00	5173	XM_014463860.2
PREDICTED: Myotis lucifugus ankyrin repeat domain-containing...	little brown...	59463	30.2	30.2	75%	730	100.00	5182	XM_023761965.1
PREDICTED: Equus caballus zinc finger protein 469 (ZNF469), mRNA	horse	9796	30.2	30.2	75%	730	100.00	16543	XM_023637473.1
PREDICTED: Equus caballus sosondowah ankyrin repeat domain...	horse	9796	30.2	30.2	75%	730	100.00	3533	XM_005615173.3
PREDICTED: Cavia porcellus diacylglycerol kinase theta (Dgkq),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	4359	XM_023562991.1

PREDICTED: Cavia porcellus diacylglycerol kinase theta (Dgkq),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	4379	XM_013147350.2
PREDICTED: Cavia porcellus diacylglycerol kinase theta (Dgkq),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	3350	XM_013147349.2
PREDICTED: Cavia porcellus diacylglycerol kinase theta (Dgkq),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	4414	XM_003465011.4
PREDICTED: Cavia porcellus transmembrane protein 94 (Tmem94),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	5126	XM_013146994.2
PREDICTED: Cavia porcellus transmembrane protein 94 (Tmem94),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	4822	XM_013146988.2
PREDICTED: Cavia porcellus transmembrane protein 94 (Tmem94),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	4945	XM_013146986.2
PREDICTED: Cavia porcellus transmembrane protein 94 (Tmem94),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	4954	XM_013146983.2
PREDICTED: Cavia porcellus transmembrane protein 94 (Tmem94),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	4966	XM_013146980.2
PREDICTED: Cavia porcellus transmembrane protein 94 (Tmem94),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	4989	XM_004999291.3
PREDICTED: Cavia porcellus transmembrane protein 94 (Tmem94),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	4929	XM_013146967.2
PREDICTED: Cavia porcellus transmembrane protein 94 (Tmem94),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	5004	XM_013146965.2
PREDICTED: Cavia porcellus transmembrane protein 94 (Tmem94),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	5001	XM_003460993.4
PREDICTED: Cavia porcellus transmembrane protein 94 (Tmem94),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	5020	XM_013146958.2
PREDICTED: Cavia porcellus transmembrane protein 94 (Tmem94),...	domestic gui...	10141	30.2	30.2	75%	730	100.00	5031	XM_013146955.2
Larimichthys crocea genome assembly, chromosome: XIX	large yellow...	215358	30.2	60.5	75%	730	100.00	20232972	LT972185.1
Larimichthys crocea genome assembly, chromosome: XV	large yellow...	215358	30.2	30.2	75%	730	100.00	16065804	LT972181.1
PREDICTED: Dasypus novemcinctus ankyrin repeat and SOCS box...	nine-banded ...	9361	30.2	30.2	75%	730	100.00	5549	XM_004465288.3
Vibrio owensii strain 051011B chromosome 2, complete sequence	NA	696485	30.2	30.2	75%	730	100.00	2367538	CP025797.1
PREDICTED: Loxodonta africana myosin XVB (MYO15B), mRNA	African sava...	9785	30.2	30.2	75%	730	100.00	8932	XM_023556733.1
PREDICTED: Otolemur garnettii DNA helicase B (HELB), transcrip...	small-eared ...	30611	30.2	30.2	75%	730	100.00	4241	XM_003798536.3
PREDICTED: Otolemur garnettii DNA helicase B (HELB), transcrip...	small-eared ...	30611	30.2	30.2	75%	730	100.00	3832	XM_023518410.1
PREDICTED: Seriola lalandi dorsalis p53-induced death...	NA	1841481	30.2	30.2	75%	730	100.00	4591	XM_023422522.1
PREDICTED: Seriola lalandi dorsalis coiled-coil...	NA	1841481	30.2	30.2	75%	730	100.00	3736	XM_023418536.1
PREDICTED: Seriola lalandi dorsalis coiled-coil...	NA	1841481	30.2	30.2	75%	730	100.00	3769	XM_023418535.1
PREDICTED: Seriola lalandi dorsalis coiled-coil...	NA	1841481	30.2	30.2	75%	730	100.00	3772	XM_023418534.1
PREDICTED: Seriola lalandi dorsalis zinc	NA	1841481	30.2	30.2	75%	730	100.00	3741	XM_023402509.1

finger protein 273-li...									
PREDICTED: Felis catus uncharacterized LOC109494577...	domestic cat	9685	30.2	30.2	75%	730	100.00	383	XR_002738648.1
Muscovy duck reovirus strain MW9710 segment L1, complete sequence	NA	77153	30.2	30.2	75%	730	100.00	3959	KY418032.1
PREDICTED: Maylandia zebra SAM and SH3 domain containing 1...	zebra mbuna	106582	30.2	30.2	75%	730	100.00	5953	XM_012916585.3
PREDICTED: Setaria italica putative FBD-associated F-box prote...	foxtail millet	4555	30.2	30.2	75%	730	100.00	1857	XM_012843899.2
PREDICTED: Seriola dumerili p53-induced death domain protein 1...	greater ambe...	41447	30.2	30.2	75%	730	100.00	3915	XM_022755966.1
PREDICTED: Seriola dumerili p53-induced death domain protein 1...	greater ambe...	41447	30.2	30.2	75%	730	100.00	4032	XM_022755965.1
Fonsecaea monophora alkylated DNA repair protein AlkB...	NA	254056	30.2	30.2	75%	730	100.00	1023	XM_022659761.1
Fonsecaea nubica alkylated DNA repair protein AlkB...	NA	856822	30.2	30.2	75%	730	100.00	1023	XM_022648142.1
PREDICTED: Delphinapterus leucas ataxin 7 (ATXN7), mRNA	beluga whale	9749	30.2	30.2	75%	730	100.00	6898	XM_022572646.1
PREDICTED: Enhydra lutris kenyoni RFX family member 8, lacking...	NA	391180	30.2	30.2	75%	730	100.00	1509	XM_022516431.1
Chitinophaga sp. MD30 chromosome	NA	2033437	30.2	30.2	75%	730	100.00	7661303	CP023254.1
Rhodococcus pyridinivorans strain GF3, complete genome	NA	103816	30.2	30.2	75%	730	100.00	5303895	CP022915.1
Leishmania donovani strain pasteur chromosome 32, complete...	NA	5661	30.2	30.2	75%	730	100.00	1593391	CP022647.1
PREDICTED: Spinacia oleracea uncharacterized protein At4g10930...	spinach	3562	30.2	30.2	75%	730	100.00	3621	XM_021990943.1
PREDICTED: Spinacia oleracea uncharacterized protein At4g10930...	spinach	3562	30.2	30.2	75%	730	100.00	4145	XM_021990942.1
Oryzias latipes strain HSOK chromosome 15	Japanese medaka	8090	30.2	60.5	90%	730	100.00	30564142	CP020635.1
Oryzias latipes strain HSOK chromosome 7	Japanese medaka	8090	30.2	30.2	75%	730	100.00	34886135	CP020627.1
Oryzias latipes strain HNI chromosome 15	Japanese medaka	8090	30.2	60.5	90%	730	100.00	28784337	CP020793.1
Oryzias latipes strain HNI chromosome 7	Japanese medaka	8090	30.2	30.2	75%	730	100.00	32810049	CP020785.1
Oryzias latipes strain HNI chromosome 4	Japanese medaka	8090	30.2	30.2	75%	730	100.00	31648822	CP020782.1
Oryzias latipes strain Hd-rR chromosome 15 sequence	Japanese medaka	8090	30.2	60.5	90%	730	100.00	30476034	CP020679.1
Oryzias latipes strain Hd-rR chromosome 7 sequence	Japanese medaka	8090	30.2	30.2	75%	730	100.00	34573382	CP020671.1
PREDICTED: Sorghum bicolor elongation factor 1-gamma 2...	sorghum	4558	30.2	30.2	75%	730	100.00	1661	XM_002451737.2
PREDICTED: Numida meleagris uncharacterized LOC110408316...	helmeted gui...	8996	30.2	30.2	75%	730	100.00	4422	XR_002444287.1
PREDICTED: Columba livia potassium calcium-activated channel...	rock pigeon	8932	30.2	30.2	75%	730	100.00	1860	XM_013370899.2
PREDICTED: Columba livia alpha-2-macroglobulin (LOC102097889),...	rock pigeon	8932	30.2	30.2	75%	730	100.00	3006	XM_021297595.1
PREDICTED: Heterocephalus glaber fibrillin 3 (Fbn3),	naked mole-rat	10181	30.2	30.2	75%	730	100.00	8289	XM_021245183.1

transcrip...

PREDICTED: Heterocephalus glaber fibrillin 3 (Fbn3), transcrip...	naked mole-rat	10181	30.2	30.2	75%	730	100.00	8302	XM_021245182.1
PREDICTED: Heterocephalus glaber fibrillin 3 (Fbn3), transcrip...	naked mole-rat	10181	30.2	30.2	75%	730	100.00	8403	XM_021245181.1
PREDICTED: Heterocephalus glaber fibrillin 3 (Fbn3), transcrip...	naked mole-rat	10181	30.2	30.2	75%	730	100.00	8400	XM_013065793.2
PREDICTED: Heterocephalus glaber fibrillin 3 (Fbn3), transcrip...	naked mole-rat	10181	30.2	30.2	75%	730	100.00	8400	XM_021245180.1
PREDICTED: Heterocephalus glaber fibrillin 3 (Fbn3), transcrip...	naked mole-rat	10181	30.2	30.2	75%	730	100.00	8408	XM_021245179.1
PREDICTED: Heterocephalus glaber fibrillin 3 (Fbn3), transcrip...	naked mole-rat	10181	30.2	30.2	75%	730	100.00	8409	XM_021245178.1
PREDICTED: Heterocephalus glaber fibrillin 3 (Fbn3), transcrip...	naked mole-rat	10181	30.2	30.2	75%	730	100.00	8407	XM_021245177.1
PREDICTED: Heterocephalus glaber fibrillin 3 (Fbn3), transcrip...	naked mole-rat	10181	30.2	30.2	75%	730	100.00	8465	XM_021245176.1
PREDICTED: Heterocephalus glaber fibrillin 3 (Fbn3), transcrip...	naked mole-rat	10181	30.2	30.2	75%	730	100.00	8514	XM_021245175.1
PREDICTED: Heterocephalus glaber fibrillin 3 (Fbn3), transcrip...	naked mole-rat	10181	30.2	30.2	75%	730	100.00	8528	XM_021245174.1
PREDICTED: Heterocephalus glaber actin-related protein 2/3...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	1744	XM_021260358.1
Mycoplasma pneumoniae strain M129 2002, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816528	CP017343.1
Mycoplasma pneumoniae strain CO3, complete genome	NA	2104	30.2	30.2	75%	730	100.00	818772	CP017342.1
Mycoplasma pneumoniae strain 1801, complete genome	NA	2104	30.2	30.2	75%	730	100.00	817171	CP017341.1
Mycoplasma pneumoniae strain RI3, complete genome	NA	2104	30.2	30.2	75%	730	100.00	817353	CP017340.1
Mycoplasma pneumoniae strain 519, complete genome	NA	2104	30.2	30.2	75%	730	100.00	818735	CP017339.1
Mycoplasma pneumoniae strain 1134, complete genome	NA	2104	30.2	30.2	75%	730	100.00	817126	CP017338.1
Mycoplasma pneumoniae strain 1006, complete genome	NA	2104	30.2	30.2	75%	730	100.00	817231	CP017337.1
Mycoplasma pneumoniae strain GA3, complete genome	NA	2104	30.2	30.2	75%	730	100.00	817252	CP017336.1
Mycoplasma pneumoniae strain CO103, complete genome	NA	2104	30.2	30.2	75%	730	100.00	817125	CP017335.1
Mycoplasma pneumoniae strain K27, complete genome	NA	2104	30.2	30.2	75%	730	100.00	817038	CP017334.1
Mycoplasma pneumoniae strain FL1, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816637	CP017333.1
Mycoplasma pneumoniae strain E16, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816459	CP017332.1
Mycoplasma pneumoniae strain FL8, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816491	CP017331.1
Mycoplasma pneumoniae strain 549, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816492	CP017330.1
Mycoplasma pneumoniae strain E57, complete genome	NA	2104	30.2	30.2	75%	730	100.00	818603	CP017329.1
Mycoplasma pneumoniae strain 685, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816292	CP017328.1
Rhizobium etli strain NXC12 chromosome, complete genome	NA	29449	30.2	30.2	75%	730	100.00	4297568	CP020906.1
PREDICTED: Drosophila serrata axonemal 84 kDa protein...	NA	7274	30.2	30.2	75%	730	100.00	3357	XM_020952784.1
PREDICTED: Drosophila serrata axonemal 84 kDa protein...	NA	7274	30.2	30.2	75%	730	100.00	3444	XM_020952783.1

PREDICTED: Odocoileus virginianus texanus kinesin light chain ...	NA	9880	30.2	30.2	75%	730	100.00	1682	XM_020911826.1
Mycoplasma pneumoniae strain S12-tet-R, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816430	CP020712.1
Mycoplasma pneumoniae strain S4-tet-R, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816433	CP020711.1
Mycoplasma pneumoniae strain S34-tet-R, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816433	CP020710.1
Mycoplasma pneumoniae strain S91-tet-R, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816429	CP020693.1
Mycoplasma pneumoniae strain S55-tet-R, complete genome	NA	2104	30.2	30.2	75%	730	100.00	815909	CP020692.1
Mycoplasma pneumoniae strain S68-tet-R, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816404	CP020691.1
Mycoplasma pneumoniae strain FH-tet-R, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816378	CP020690.1
Mycoplasma pneumoniae strain S63-tet-R, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816435	CP020689.1
PREDICTED: Pogona vitticeps glucagon receptor (GCGR), mRNA	central bear...	103695	30.2	30.2	75%	730	100.00	2367	XM_020814215.1
Streptomyces gilvosporeus strain F607, complete genome	NA	553510	30.2	30.2	75%	730	100.00	8482298	CP020569.1
Watermelon chlorotic stunt virus isolate WmCSV1 segment DNA-B,...	NA	35341	30.2	30.2	75%	730	100.00	2759	KY124281.1
PREDICTED: Amborella trichopoda putative U-box domain-containi...	NA	13333	30.2	30.2	75%	730	100.00	3492	XM_006844601.2
PREDICTED: Monopterus albus collagen alpha-1(VII) chain-like...	swamp eel	43700	30.2	30.2	75%	730	100.00	6836	XM_020599438.1
Nonomuraea sp. ATCC 55076, complete genome	NA	1909395	30.2	30.2	75%	730	100.00	13047416	CP017717.1
PREDICTED: Microcebus murinus uncharacterized LOC105862025...	gray mouse l...	30608	30.2	30.2	75%	730	100.00	2099	XR_002221554.1
PREDICTED: Microcebus murinus uncharacterized LOC105862025...	gray mouse l...	30608	30.2	30.2	75%	730	100.00	2845	XR_001149849.2
Trichoderma reesei QM6a chromosome II, complete sequence	NA	431241	30.2	30.2	75%	730	100.00	6234656	CP016233.1
Streptococcus phage IPP27, complete genome	NA	1916167	30.2	30.2	75%	730	100.00	32649	KY065468.1
Streptococcus phage IPP25, complete genome	NA	1916165	30.2	30.2	75%	730	100.00	33895	KY065466.1
Streptococcus phage IPP23, complete genome	NA	1916163	30.2	30.2	75%	730	100.00	33903	KY065464.1
Streptococcus phage IPP16, complete genome	NA	1916156	30.2	30.2	75%	730	100.00	34329	KY065457.1
Bacillus anthracis strain Sterne 34F2 genome	NA	1392	30.2	30.2	75%	730	100.00	5209112	**CP019726.1**
PREDICTED: Castor canadensis phosphorylase b kinase regulatory...	American beaver	51338	30.2	30.2	75%	730	100.00	5603	XM_020168704.1
PREDICTED: Castor canadensis E3 ubiquitin-protein ligase...	American beaver	51338	30.2	30.2	75%	730	100.00	1953	XM_020165128.1
PREDICTED: Paralichthys olivaceus semaphorin 4D (sema4d),...	Japanese flo...	8255	30.2	30.2	75%	730	100.00	1618	XM_020110430.1
PREDICTED: Paralichthys olivaceus nuclear envelope pore membra...	Japanese flo...	8255	30.2	30.2	75%	730	100.00	2003	XM_020085461.1
Leishmania donovani strain MHOM/IN/1983/AG83 isolate late...	NA	5661	30.2	30.2	75%	730	100.00	1559654	CP019541.1
Leishmania donovani strain MHOM/IN/1983/AG83 isolate early...	NA	5661	30.2	30.2	75%	730	100.00	1559743	CP018600.1
Companilactobacillus allii strain WiKim39, complete sequence	NA	1847728	30.2	30.2	75%	730	100.00	2506167	CP019323.1
Bacillus cereus strain JEM-2, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5229506	CP018935.1

Bacillus cereus strain ISSFR-3F, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5242668	CP018931.1
PREDICTED: Hippocampus comes nuclear envelope pore membrane...	tiger tail s...	109280	30.2	30.2	75%	730	100.00	4478	XM_019873428.1
PREDICTED: Branchiostoma belcheri probable ATP-dependent RNA...	Belcher's la...	7741	30.2	30.2	75%	730	100.00	2090	XM_019770773.1
Mycoplasma pneumoniae strain FH 2009, complete genome	NA	2104	30.2	30.2	75%	730	100.00	817275	CP017327.1
PREDICTED: Alligator mississippiensis uncharacterized...	American all...	8496	30.2	30.2	75%	730	100.00	1228	XR_002087932.1
PREDICTED: Alligator mississippiensis uncharacterized...	American all...	8496	30.2	30.2	75%	730	100.00	1319	XR_002087931.1
PREDICTED: Alligator mississippiensis integrator complex subun...	American all...	8496	30.2	30.2	75%	730	100.00	2747	XM_019484782.1
PREDICTED: Panthera pardus uncharacterized LOC109260457...	leopard	9691	30.2	30.2	75%	730	100.00	389	XR_002077050.1
PREDICTED: Aptenodytes forsteri alpha-2-macroglobulin (A2M), mRNA	emperor penguin	9233	30.2	30.2	75%	730	100.00	4525	XM_009280522.2
Avian orthoreovirus strain 3211-V-02 core shell gene, complete...	NA	38170	30.2	30.2	75%	730	100.00	3958	KX398272.1
Avian orthoreovirus strain 924-Bi-05 core shell gene, partial cds	NA	38170	30.2	30.2	75%	730	100.00	3863	KX398262.1
PREDICTED: Parus major regulator of G protein signaling 10...	Great Tit	9157	30.2	30.2	75%	730	100.00	3909	XM_015633745.2
Sclerotinia sclerotiorum chromosome 14, complete sequence	NA	665079	30.2	30.2	75%	730	100.00	1815632	CP017827.1
Actinomyces naeslundii DNA, complete genome	NA	1655	30.2	30.2	75%	730	100.00	3040449	AP017894.1
Toxoplasma gondii ME49 ICE family protease (caspase) p20...	NA	508771	30.2	30.2	75%	730	100.00	3885	XM_002367789.2
PREDICTED: Lates calcarifer nuclear envelope pore membrane...	barramundi p...	8187	30.2	30.2	75%	730	100.00	5037	XM_018692354.1
PREDICTED: Nanorana parkeri solute carrier family 17 member 9...	NA	125878	30.2	30.2	75%	730	100.00	1516	XM_018559848.1
Uncultured bacterium pAG2 genomic sequence	NA	1781152	30.2	30.2	75%	730	100.00	17965	KT982358.1
TPA: Oryzias latipes strain Hd-rR, complete genome assembly,...	Japanese medaka	8090	30.2	60.5	90%	730	100.00	30000224	HF933221.1
Pandoraea pnomenusa strain DSM 16536, complete genome	NA	93220	30.2	30.2	75%	730	100.00	5389285	CP009553.3
Paenibacillus sp. BIHB4019, complete genome	NA	1870819	30.2	30.2	75%	730	100.00	7246671	CP016808.1
PREDICTED: Corvus brachyrhynchos regulator of G-protein...	American crow	85066	30.2	30.2	75%	730	100.00	3958	XM_008643181.2
PREDICTED: Corvus brachyrhynchos regulator of G-protein...	American crow	85066	30.2	30.2	75%	730	100.00	4139	XM_017746863.1
PREDICTED: Corvus brachyrhynchos regulator of G-protein...	American crow	85066	30.2	30.2	75%	730	100.00	1312	XM_017746862.1
PREDICTED: Corvus brachyrhynchos regulator of G-protein...	American crow	85066	30.2	30.2	75%	730	100.00	2280	XM_017746861.1
PREDICTED: Corvus brachyrhynchos regulator of G-protein...	American crow	85066	30.2	30.2	75%	730	100.00	2289	XM_017746860.1
PREDICTED: Corvus brachyrhynchos regulator of G-protein...	American crow	85066	30.2	30.2	75%	730	100.00	2442	XM_017746859.1
Agaricus bisporus var. bisporus H97 chromosome 2 sequence	NA	936046	30.2	30.2	75%	730	100.00	3489786	CP015458.1
Agaricus bisporus var. bisporus strain H39 chromosome 2,...	NA	192523	30.2	30.2	75%	730	100.00	3241356	CP015471.1

Mycoplasma pneumoniae DNA, complete genome, strain: KCH-405	NA	2104	30.2	30.2	75%	730	100.00	817099	AP017319.1
Mycoplasma pneumoniae DNA, complete genome, strain: KCH-402	NA	2104	30.2	30.2	75%	730	100.00	817074	AP017318.1
Watermelon chlorotic stunt virus isolate Jizan101-SA segment B...	NA	35341	30.2	30.2	75%	730	100.00	2760	KU360595.1
Watermelon chlorotic stunt virus isolate Alahsaa02-SA segment ...	NA	35341	30.2	30.2	75%	730	100.00	2728	KU360594.1
PREDICTED: Drosophila ficusphila uncharacterized LOC108095436...	NA	30025	30.2	30.2	75%	730	100.00	5130	XM_017196546.1
PREDICTED: Drosophila rhopaloa protein Red (LOC108046603), mRNA	NA	1041015	30.2	30.2	75%	730	100.00	1953	XM_017126418.1
Homo sapiens chromosome 5 Treacher Collins syndrome (TCOF1)...	human	9606	30.2	30.2	75%	730	100.00	11832	AH004920.2
Cladophialophora bantiana CBS 173.52 hypothetical protein...	NA	1442370	30.2	30.2	75%	730	100.00	4284	XM_016763208.1
Exophiala mesophila hypothetical protein partial mRNA	NA	212818	30.2	30.2	75%	730	100.00	1949	XM_016372253.1
PREDICTED: Arachis ipaensis uncharacterized LOC107627233...	NA	130454	30.2	30.2	75%	730	100.00	1041	XM_016330086.1
PREDICTED: Ficedula albicollis regulator of G-protein signalin...	Collared fly...	59894	30.2	30.2	75%	730	100.00	1361	XM_005048714.2
PREDICTED: Ficedula albicollis zinc fingers and homeoboxes 2...	Collared fly...	59894	30.2	30.2	75%	730	100.00	4556	XM_016296865.1
Streptomyces sp. S10(2016), complete genome	NA	1783515	30.2	30.2	75%	730	100.00	9083372	CP015098.1
PREDICTED: Peromyscus maniculatus bairdii spectrin repeat...	prairie deer...	230844	30.2	30.2	75%	730	100.00	3630	XM_015992014.1
PREDICTED: Peromyscus maniculatus bairdii spectrin repeat...	prairie deer...	230844	30.2	30.2	75%	730	100.00	9426	XM_015992013.1
PREDICTED: Peromyscus maniculatus bairdii spectrin repeat...	prairie deer...	230844	30.2	30.2	75%	730	100.00	21731	XM_015992012.1
PREDICTED: Peromyscus maniculatus bairdii spectrin repeat...	prairie deer...	230844	30.2	30.2	75%	730	100.00	21800	XM_006973156.2
PREDICTED: Peromyscus maniculatus bairdii spectrin repeat...	prairie deer...	230844	30.2	30.2	75%	730	100.00	22481	XM_015992009.1
PREDICTED: Peromyscus maniculatus bairdii spectrin repeat...	prairie deer...	230844	30.2	30.2	75%	730	100.00	21784	XM_015992008.1
PREDICTED: Peromyscus maniculatus bairdii spectrin repeat...	prairie deer...	230844	30.2	30.2	75%	730	100.00	21803	XM_015992007.1
PREDICTED: Nothobranchius furzeri peptidoglycan recognition...	turquoise ki...	105023	30.2	30.2	75%	730	100.00	1504	XM_015976697.1
PREDICTED: Nothobranchius furzeri peptidoglycan recognition...	turquoise ki...	105023	30.2	30.2	75%	730	100.00	3597	XM_015976696.1
PREDICTED: Nothobranchius furzeri spermatogenesis associated...	turquoise ki...	105023	30.2	30.2	75%	730	100.00	4523	XM_015968434.1
PREDICTED: Nothobranchius furzeri spermatogenesis associated...	turquoise ki...	105023	30.2	30.2	75%	730	100.00	4589	XM_015968433.1
Watermelon chlorotic stunt virus DNA B complete sequence, clon...	NA	35341	30.2	30.2	75%	730	100.00	2727	HG969288.1
PREDICTED: Cephus cinctus uncharacterized LOC107265957...	wheat stem s...	211228	30.2	30.2	75%	730	100.00	4375	XM_015735931.1
PREDICTED: Parus major uncharacterized LOC107198915...	Great Tit	9157	30.2	30.2	75%	730	100.00	383	XR_001519137.1
Mycoplasma pneumoniae strain C267, complete genome	NA	2104	30.2	30.2	75%	730	100.00	816498	CP014267.1
Pseudomonas agarici strain NCPPB 2472 genome	NA	46677	30.2	30.2	75%	730	100.00	5502003	CP014135.1
Planococcus kocurii strain ATCC 43650, complete genome	NA	1374	30.2	30.2	75%	730	100.00	3472056	CP013661.2
PREDICTED: Macaca fascicularis solute carrier family 25 member...	crab-eating ...	9541	30.2	30.2	75%	730	100.00	1135	XR_001487902.1
PREDICTED: Macaca fascicularis	crab-	9541	30.2	30.2	75%	730	100.00	2096	XR_001489777.1

uncharacterized LOC107129346...	eating ...								
Microbacterium sp. XT11, complete genome	NA	367477	30.2	30.2	75%	730	100.00	3475315	CP013859.1
PREDICTED: Lepisosteus oculatus epithelial membrane protein 3...	spotted gar	7918	30.2	30.2	75%	730	100.00	2446	XM_015336755.1
PREDICTED: Lepisosteus oculatus epithelial membrane protein 3...	spotted gar	7918	30.2	30.2	75%	730	100.00	2383	XM_006641866.2
Mycoplasma pneumoniae strain S355, complete genome	NA	2104	30.2	30.2	75%	730	100.00	801203	CP013829.1
PREDICTED: Calidris pugnax V-set and transmembrane domain...	ruff	198806	30.2	30.2	75%	730	100.00	2928	XM_014958056.1
PREDICTED: Sturnus vulgaris regulator of G-protein signaling 1...	Common starling	9172	30.2	30.2	75%	730	100.00	3831	XM_014886821.1
PREDICTED: Sturnus vulgaris regulator of G-protein signaling 1...	Common starling	9172	30.2	30.2	75%	730	100.00	3720	XM_014886820.1
PREDICTED: Equus asinus zinc finger protein 469 (ZNF469), mRNA	ass	9793	30.2	30.2	75%	730	100.00	13093	XM_014836462.1
PREDICTED: Ceratotherium simum simum zinc finger protein 469...	southern whi...	73337	30.2	30.2	75%	730	100.00	12420	XM_014792599.1
Halomonas huangheensis strain BJGMM-B45, complete genome	NA	1178482	30.2	30.2	75%	730	100.00	4757486	CP013106.1
PREDICTED: Myotis brandtii ankyrin repeat domain 26 (ANKRD26),...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	5153	**XM_014547992.1**
PREDICTED: Myotis brandtii ankyrin repeat domain 26 (ANKRD26),...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	5156	**XM_014547991.1**
PREDICTED: Myotis brandtii ankyrin repeat domain 26 (ANKRD26),...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	5204	**XM_014547990.1**
PREDICTED: Myotis brandtii ankyrin repeat domain 26 (ANKRD26),...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	5207	**XM_014547989.1**
PREDICTED: Alligator sinensis integrator complex subunit 5...	Chinese alli...	38654	30.2	30.2	75%	730	100.00	1293	XM_014524458.1
Watermelon chlorotic stunt virus clone W-Kha-B9 segment DNA-B,...	NA	35341	30.2	30.2	75%	730	100.00	2730	KT272772.1
Watermelon chlorotic stunt virus clone W-Kh-B1 segment DNA-B,...	NA	35341	30.2	30.2	75%	730	100.00	2727	KT272770.1
Watermelon chlorotic stunt virus clone W-Da-B8 segment DNA-B,...	NA	35341	30.2	30.2	75%	730	100.00	2728	KT272766.1
Halanaeroarchaeum sulfurireducens strain M27-SA2, complete genome	NA	1604004	30.2	30.2	75%	730	100.00	2129244	CP011564.1
Oryza sativa Indica Group cultivar RP Bio-226 chromosome 11...	long-grained...	39946	30.2	30.2	75%	730	100.00	21418977	CP012619.1
PREDICTED: Haplochromis burtoni POM121 transmembrane nucleopor...	Burton's mou...	8153	30.2	30.2	75%	730	100.00	4998	XM_005923172.2
PREDICTED: Haplochromis burtoni SAM and SH3 domain containing ...	Burton's mou...	8153	30.2	30.2	75%	730	100.00	6604	XM_014338528.1
PREDICTED: Haplochromis burtoni SAM and SH3 domain containing ...	Burton's mou...	8153	30.2	30.2	75%	730	100.00	6648	XM_014338523.1
PREDICTED: Haplochromis burtoni SAM and SH3 domain containing ...	Burton's mou...	8153	30.2	30.2	75%	730	100.00	7520	XM_014338521.1
PREDICTED: Haplochromis burtoni SAM and SH3 domain containing ...	Burton's mou...	8153	30.2	30.2	75%	730	100.00	7162	XM_014338520.1
PREDICTED: Haplochromis burtoni SAM and SH3 domain containing ...	Burton's mou...	8153	30.2	30.2	75%	730	100.00	7978	XM_014338516.1
PREDICTED: Haplochromis burtoni SAM and SH3 domain containing ...	Burton's mou...	8153	30.2	30.2	75%	730	100.00	8077	XM_014338509.1
PREDICTED: Pseudopodoces humilis regulator of G-protein...	Tibetan grou...	181119	30.2	30.2	75%	730	100.00	3753	XM_014250539.1
PREDICTED: Salmo salar spastic paraplegia 11 (autosomal...	Atlantic salmon	8030	30.2	30.2	75%	730	100.00	7647	XM_014123972.1
PREDICTED: Salmo salar spastic paraplegia 11 (autosomal...	Atlantic salmon	8030	30.2	30.2	75%	730	100.00	7647	XM_014123971.1

PREDICTED: Salmo salar spastic paraplegia 11 (autosomal...	Atlantic salmon	8030	30.2	30.2	75%	730	100.00	7650	XM_014123970.1
PREDICTED: Salmo salar C-X-C chemokine receptor type 3-like...	Atlantic salmon	8030	30.2	30.2	75%	730	100.00	1926	XM_014201358.1
PREDICTED: Salmo salar C-X-C chemokine receptor type 3-like...	Atlantic salmon	8030	30.2	30.2	75%	730	100.00	1075	XM_014158224.1
PREDICTED: Salmo salar C-X-C chemokine receptor type 3-like...	Atlantic salmon	8030	30.2	30.2	75%	730	100.00	1279	XM_014158215.1
PREDICTED: Austrofundulus limnaeus NF-kappa-B inhibitor...	NA	52670	30.2	30.2	75%	730	100.00	2065	XM_014020450.1
PREDICTED: Austrofundulus limnaeus NF-kappa-B inhibitor...	NA	52670	30.2	30.2	75%	730	100.00	2067	XM_014020448.1
PREDICTED: Austrofundulus limnaeus NF-kappa-B inhibitor...	NA	52670	30.2	30.2	75%	730	100.00	2071	XM_014020447.1
PREDICTED: Apteryx australis mantelli uncharacterized...	NA	202946	30.2	30.2	75%	730	100.00	1417	XM_013948927.1
PREDICTED: Pundamilia nyererei POM121 transmembrane nucleopori...	NA	303518	30.2	30.2	75%	730	100.00	4685	XM_005748344.2
PREDICTED: Pundamilia nyererei SAM and SH3 domain containing 1...	NA	303518	30.2	30.2	75%	730	100.00	4592	XM_013911207.1
Mycoplasma pneumoniae PO1, complete genome	NA	1233262	30.2	30.2	75%	730	100.00	817216	CP010551.1
Mycoplasma pneumoniae MAC strain Mac, complete genome	NA	1263835	30.2	30.2	75%	730	100.00	817156	CP010550.1
Mycoplasma pneumoniae M2592, complete genome	NA	1280940	30.2	30.2	75%	730	100.00	817198	CP010549.1
Mycoplasma pneumoniae strain M2192, complete genome	NA	2104	30.2	30.2	75%	730	100.00	817169	CP010548.1
Mycoplasma pneumoniae M1139, complete genome	NA	1263763	30.2	30.2	75%	730	100.00	817045	CP010547.1
Mycoplasma pneumoniae FH, complete genome	NA	722438	30.2	30.2	75%	730	100.00	817207	CP010546.1
Mycoplasma pneumoniae 85138, complete genome	NA	1263760	30.2	30.2	75%	730	100.00	816402	CP010545.1
Mycoplasma pneumoniae 85084, complete genome	NA	1263762	30.2	30.2	75%	730	100.00	816404	CP010544.1
Mycoplasma pneumoniae 54524, complete genome	NA	1263757	30.2	30.2	75%	730	100.00	816583	CP010543.1
Mycoplasma pneumoniae 54089, complete genome	NA	1263756	30.2	30.2	75%	730	100.00	816565	CP010542.1
Mycoplasma pneumoniae 51494, complete genome	NA	1263758	30.2	30.2	75%	730	100.00	816404	CP010541.1
Mycoplasma pneumoniae 39443, complete genome	NA	1263761	30.2	30.2	75%	730	100.00	817184	CP010540.1
Mycoplasma pneumoniae 19294, complete genome	NA	1213463	30.2	30.2	75%	730	100.00	817313	CP010539.1
Mycoplasma pneumoniae PI 1428, complete genome	NA	1236904	30.2	30.2	75%	730	100.00	816496	CP010538.1
PREDICTED: Chinchilla lanigera actin related protein 2/3...	long-tailed ...	34839	30.2	30.2	95%	730	94.74	1967	XM_005413034.2
PREDICTED: Chinchilla lanigera lysophosphatidic acid receptor ...	long-tailed ...	34839	30.2	30.2	75%	730	100.00	3291	XM_005378798.2
Exophiala xenobiotica hypothetical protein mRNA	NA	348802	30.2	30.2	75%	730	100.00	4971	XM_013465671.1
Exophiala xenobiotica hypothetical protein, variant mRNA	NA	348802	30.2	30.2	75%	730	100.00	4870	XM_013465670.1
Rasamsonia emersonii CBS 393.64 Tyrosine--tRNA ligase mRNA	NA	1408163	30.2	30.2	75%	730	100.00	1842	XM_013473734.1
Rasamsonia emersonii CBS 393.64 hypothetical protein mRNA	NA	1408163	30.2	30.2	75%	730	100.00	1821	XM_013473290.1
Chondromyces crocatus strain Cm c5, complete genome	NA	52	30.2	30.2	75%	730	100.00	11388132	CP012159.1
Avian orthoreovirus isolate Reo/PA/Broiler/15511/13 segment L1...	NA	38170	30.2	30.2	75%	730	100.00	3958	KP731611.1
PREDICTED: Mustela putorius furo RFX family member 8, lacking...	domestic ferret	9669	30.2	30.2	75%	730	100.00	4068	XM_004753050.2

PREDICTED: Mustela putorius furo RFX family member 8, lacking...	domestic ferret	9669	30.2	30.2	75%	730	100.00	3879	XR_001179499.1
Ovis canadensis canadensis isolate 43U chromosome 17 sequence	NA	112262	30.2	30.2	75%	730	100.00	72372754	CP011902.1
Ovis canadensis canadensis isolate 43U chromosome 15 sequence	NA	112262	30.2	30.2	75%	730	100.00	81015546	CP011900.1
PREDICTED: Jaculus jaculus calmodulin regulated...	lesser Egypt...	51337	30.2	30.2	75%	730	100.00	2541	XM_012949474.1
PREDICTED: Jaculus jaculus calmodulin regulated...	lesser Egypt...	51337	30.2	30.2	75%	730	100.00	2556	XM_012949473.1
PREDICTED: Jaculus jaculus calmodulin regulated...	lesser Egypt...	51337	30.2	30.2	75%	730	100.00	2589	XM_012949472.1
PREDICTED: Jaculus jaculus calmodulin regulated...	lesser Egypt...	51337	30.2	30.2	75%	730	100.00	3780	XM_012949471.1
PREDICTED: Jaculus jaculus calmodulin regulated...	lesser Egypt...	51337	30.2	30.2	75%	730	100.00	3795	XM_012949470.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	95%	730	94.74	2527380	LK064903.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	90.7	95%	730	94.74	287077	LK067047.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	75%	730	100.00	348495	LK065335.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	75%	730	100.00	55736	LK093648.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	75%	730	100.00	1377843	LK064743.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	75%	730	100.00	8465949	LK064728.1
Watermelon chlorotic stunt virus isolate TMPWm-pro BC1-BV1...	NA	35341	30.2	30.2	75%	730	100.00	718	KP657700.1
PREDICTED: Propithecus coquereli transmembrane and coiled-coil...	Coquerel's s...	379532	30.2	30.2	75%	730	100.00	2381	XM_012656926.1
Halanaeroarchaeum sulfurireducens strain HSR2, complete genome	NA	1604004	30.2	30.2	75%	730	100.00	2085482	CP008874.1
Bacillus anthracis DNA, nearly complete genome, strain:...	NA	1392	30.2	30.2	75%	730	100.00	5228065	**AP014833.1**
TPA: Toxoplasma gondii VEG, chromosome chrVIIa, complete genome	NA	432359	30.2	30.2	75%	730	100.00	4532860	LN714496.1
TPA: Neospora caninum Liverpool, unplaced_1, complete genome	NA	572307	30.2	30.2	75%	730	100.00	3492925	LN714488.1
PREDICTED: Cercocebus atys solute carrier family 25, member 53...	sooty mangabey	9531	30.2	30.2	75%	730	100.00	1133	XR_001009763.1
PREDICTED: Colobus angolensis palliatus G protein-coupled...	NA	336983	30.2	30.2	75%	730	100.00	2538	XM_011946877.1
PREDICTED: Colobus angolensis palliatus G protein-coupled...	NA	336983	30.2	30.2	75%	730	100.00	2654	XM_011946876.1
PREDICTED: Mandrillus leucophaeus pleckstrin homology domain...	drill	9568	30.2	30.2	75%	730	100.00	3851	XM_011978330.1
PREDICTED: Wasmannia auropunctata cytoplasmic dynein 2 heavy...	little fire ant	64793	30.2	30.2	75%	730	100.00	13144	XM_011695665.1
Thermococcus guaymasensis DSM 11113, complete genome	NA	1432656	30.2	30.2	75%	730	100.00	1920914	CP007140.1
Mycoplasma pneumoniae M129-B7, complete genome	NA	1238993	30.2	30.2	75%	730	100.00	816451	CP003913.2
Bacillus cereus strain S2-8, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5271178	CP009605.1
PREDICTED: Fopius arisanus F-box/LRR-repeat protein 14...	NA	64838	30.2	30.2	75%	730	100.00	3933	XM_011317187.1
Bacillus thuringiensis strain 97-27, complete genome	NA	1428	30.2	30.2	75%	730	100.00	5235838	CP010088.1
Bacillus anthracis strain Ames, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5227467	**CP009981.1**
Bacillus cereus E33L, complete genome	NA	288681	30.2	30.2	75%	730	100.00	5305318	CP009968.1

Bacillus anthracis strain 2002013094, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5321900	**CP009902.1**
Bacillus thuringiensis strain HD682, complete genome	NA	1428	30.2	30.2	75%	730	100.00	5213295	CP009720.1
Bacillus cereus ATCC 4342, complete genome	NA	526977	30.2	30.2	75%	730	100.00	5269496	CP009628.1
Bacillus cereus G9241, complete genome	NA	269801	30.2	30.2	75%	730	100.00	5267792	CP009590.1
Bacillus anthracis str. V770-NP-1R, complete genome	NA	1449979	30.2	30.2	75%	730	100.00	5228687	**CP009598.1**
Bacillus cereus strain 3a, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5270991	CP009596.1
Bacillus anthracis strain BA1035, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5210596	**CP009700.1**
Bacillus anthracis strain BA1015, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5214671	**CP009544.1**
Bacillus anthracis str. Sterne, complete genome	NA	260799	30.2	30.2	75%	730	100.00	5227496	**CP009541.1**
Bacillus anthracis strain Pasteur, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5200082	**CP009476.1**
Bacillus anthracis strain SK-102, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5230088	**CP009464.1**
Bacillus mycoides strain ATCC 6462, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5255868	CP009692.1
Bacillus cereus strain FM1, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5295158	CP009369.1
Bacillus anthracis strain K3, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5228730	**CP009331.1**
Bacillus anthracis strain PAK-1, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5221627	**CP009325.1**
Bacillus cereus D17, complete genome	NA	1454382	30.2	30.2	75%	730	100.00	5379685	CP009300.1
Crocodylus porosus MHC class II antigen pseudogene, complete...	Australian s...	8502	30.2	30.2	75%	730	100.00	93741	KP118846.1
PREDICTED: Camelus bactrianus cell division cycle associated 3...	Bactrian camel	9837	30.2	30.2	75%	730	100.00	1116	XM_010957700.1
PREDICTED: Beta vulgaris subsp. vulgaris hypothetical protein...	NA	3555	30.2	30.2	75%	730	100.00	2109	XM_010691043.1
PREDICTED: Fukomys damarensis uncharacterized LOC104875628...	Damara mole-rat	885580	30.2	30.2	75%	730	100.00	1171	XM_010643316.1
Bacillus cereus strain 03BB87, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5457398	CP009941.1
PREDICTED: Balearica regulorum gibbericeps...	East African...	100784	30.2	30.2	75%	730	100.00	3499	XM_010298945.1
PREDICTED: Phaethon lepturus alpha-2-macroglobulin (A2M),...	White-tailed...	97097	30.2	30.2	75%	730	100.00	3547	XM_010292275.1
Bacillus weihenstephanensis strain WSBC 10204, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5608349	CP009746.1
PREDICTED: Colius striatus alpha-2-macroglobulin (A2M), partia...	speckled mou...	57412	30.2	30.2	75%	730	100.00	3541	XM_010200436.1
PREDICTED: Chlamydotis macqueenii ras-related C3 botulinum tox...	Macqueen's b...	187382	30.2	30.2	75%	730	100.00	1379	XM_010115552.1
PREDICTED: Mesitornis unicolor ladinin 1 (LAD1), mRNA	brown roatelo	54374	30.2	30.2	75%	730	100.00	1275	XM_010181770.1
PREDICTED: Chaetura pelagica ras-related C3 botulinum toxin...	chimney swift	8897	30.2	30.2	75%	730	100.00	1544	XM_010008644.1
PREDICTED: Nestor notabilis alpha-2-macroglobulin-like...	Kea	176057	30.2	30.2	75%	730	100.00	4209	XM_010016300.1
PREDICTED: Leptosomus discolor nucleoporin 214kDa (NUP214),...	cuckoo roller	188344	30.2	30.2	75%	730	100.00	6312	XM_009950985.1
PREDICTED: Leptosomus discolor ras-related C3 botulinum toxin...	cuckoo roller	188344	30.2	30.2	75%	730	100.00	1546	XM_009959565.1
PREDICTED: Leptosomus discolor alpha-2-macroglobulin-like...	cuckoo roller	188344	30.2	30.2	75%	730	100.00	1854	XM_009957031.1
PREDICTED: Picoides pubescens alpha-1-macroglobulin-like...	Downy woodpe...	118200	30.2	30.2	75%	730	100.00	4185	XM_009907912.1

PREDICTED: Charadrius vociferus alpha-2-macroglobulin (A2M), mRNA	killdeer	50402	30.2	30.2	75%	730	100.00	4042	XM_009894128.1
PREDICTED: Cariama cristata alpha-2-macroglobulin-like...	Red-legged s...	54380	30.2	30.2	75%	730	100.00	3435	XM_009698876.1
PREDICTED: Fulmarus glacialis alpha-2-macroglobulin-like...	Northern fulmar	30455	30.2	30.2	75%	730	100.00	3410	XM_009574404.1
Muscovy duck reovirus strain D1546 segment L1, complete sequence	NA	77153	30.2	30.2	75%	730	100.00	3958	KJ871017.1
Muscovy duck reovirus strain D2044 segment L1, complete sequence	NA	77153	30.2	30.2	75%	730	100.00	3958	KJ871007.1
PREDICTED: Phalacrocorax carbo alpha-2-macroglobulin-like...	great cormorant	9209	30.2	30.2	75%	730	100.00	2881	XM_009511456.1
PREDICTED: Nipponia nippon alpha-2-macroglobulin-like...	crested ibis	128390	30.2	30.2	75%	730	100.00	3852	XM_009467247.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	75%	730	100.00	931	LN318153.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	75%	730	100.00	3252	LN114804.1
PREDICTED: Pygoscelis adeliae alpha-2-macroglobulin (A2M), mRNA	Adelie penguin	9238	30.2	30.2	75%	730	100.00	4513	XM_009330277.1
Caenorhabditis elegans genome assembly...	NA	6239	30.2	30.2	75%	730	100.00	202805	LK927608.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common carp	7962	30.2	30.2	75%	730	100.00	5474	LN596439.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common carp	7962	30.2	30.2	75%	730	100.00	292345	LN592692.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common carp	7962	30.2	30.2	75%	730	100.00	563947	LN590970.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common carp	7962	30.2	30.2	75%	730	100.00	420562	LN590858.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common carp	7962	30.2	30.2	75%	730	100.00	1007695	LN590780.1
Cyprinus carpio genome assembly common carp genome, scaffold:...	common carp	7962	30.2	30.2	75%	730	100.00	19716050	LN590703.1
Pandoraea pnomenusa 3kgm, complete genome	NA	1416914	30.2	30.2	75%	730	100.00	5429298	CP006900.2
Bacillus anthracis strain delta Sterne genome	NA	1392	30.2	30.2	75%	730	100.00	5229650	**CP008752.1**
Bacillus anthracis strain 2000031021, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5236981	**CP007618.1**
Streptomyces lividans TK24, complete genome	NA	457428	30.2	30.2	75%	730	100.00	8345283	CP009124.1
Mycoplasma pneumoniae M29, complete genome	NA	1441379	30.2	60.5	75%	730	100.00	857799	CP008895.1
PREDICTED: Galeopterus variegatus uncharacterized LOC103598216...	Sunda flying...	482537	30.2	30.2	75%	730	100.00	618	XR_551183.1
PREDICTED: Equus przewalskii zinc finger protein 469 (ZNF469),...	Przewalski's...	9798	30.2	30.2	75%	730	100.00	12022	XM_008508853.1
PREDICTED: Equus przewalskii sosondowah ankyrin repeat domain...	Przewalski's...	9798	30.2	30.2	75%	730	100.00	2429	XM_008538692.1
Elopichthys bambusa microsatellite EBGT-80 sequence	yellowcheek ...	238031	30.2	30.2	75%	730	100.00	582	KJ507807.1
PREDICTED: Callorhinchus milii WDFY family member 4 (wdfy4), mRNA	elephant shark	7868	30.2	30.2	75%	730	100.00	10204	XM_007904626.1
Phanerochaete carnosa HHB-10118-sp uncharacterized protein...	NA	650164	30.2	30.2	95%	730	94.74	1563	XM_007402865.1
Agaricus bisporus var. burnettii JB137-S8 hypothetical protein...	NA	597362	30.2	30.2	75%	730	100.00	3469	XM_007334357.1
Fomitiporia mediterranea MF3/22 uncharacterized protein...	NA	694068	30.2	30.2	75%	730	100.00	2551	XM_007265243.1

Avian orthoreovirus strain D20/99 segment L1, complete sequence	NA	38170	30.2	30.2	75%	730	100.00	3958	KF809662.1
PREDICTED: Elephantulus edwardii nicotinate...	Cape elephan...	28737	30.2	30.2	75%	730	100.00	1596	XM_006879431.1
PREDICTED: Neolamprologus brichardi SAM and SH3 domain...	NA	32507	30.2	30.2	75%	730	100.00	6622	XM_006797048.1
PREDICTED: Neolamprologus brichardi SAM and SH3 domain...	NA	32507	30.2	30.2	75%	730	100.00	7177	XM_006797046.1
Chaetomium thermophilum var. thermophilum DSM 1495 putative...	NA	759272	30.2	30.2	75%	730	100.00	2124	XM_006691406.1
Agaricus bisporus var. bisporus H97 glycoside hydrolase family...	NA	936046	30.2	30.2	75%	730	100.00	3469	XM_006457278.1
Muscovy duck reovirus strain ZJ2000M segment L1, complete...	NA	77153	30.2	30.2	75%	730	100.00	3959	KF306082.1
Guillardia theta CCMP2712 hypothetical protein...	NA	905079	30.2	30.2	75%	730	100.00	2316	XM_005821634.1
PREDICTED: Pundamilia nyererei SAM and SH3 domain containing 1...	NA	303518	30.2	30.2	75%	730	100.00	5248	XM_005734461.1
PREDICTED: Pundamilia nyererei SAM and SH3 domain containing 1...	NA	303518	30.2	30.2	75%	730	100.00	4644	XM_005734460.1
PREDICTED: Pundamilia nyererei SAM and SH3 domain containing 1...	NA	303518	30.2	30.2	75%	730	100.00	5494	XM_005734459.1
PREDICTED: Pundamilia nyererei SAM and SH3 domain containing 1...	NA	303518	30.2	30.2	75%	730	100.00	5147	XM_005734458.1
PREDICTED: Pundamilia nyererei SAM and SH3 domain containing 1...	NA	303518	30.2	30.2	75%	730	100.00	5952	XM_005734457.1
PREDICTED: Pundamilia nyererei SAM and SH3 domain containing 1...	NA	303518	30.2	30.2	75%	730	100.00	6052	XM_005734456.1
Coccomyxa subellipsoidea C-169 hypothetical protein partial mRNA	NA	574566	30.2	30.2	75%	730	100.00	10335	XM_005645274.1
PREDICTED: Zonotrichia albicollis regulator of G protein...	white-throat...	44394	30.2	30.2	75%	730	100.00	3984	XM_005489847.1
Rhizobium etli bv. mimosae str. Mim1, complete genome	NA	1328306	30.2	30.2	75%	730	100.00	4284494	CP005950.1
PREDICTED: Ficedula albicollis ubiquitin specific peptidase 39...	Collared fly...	59894	30.2	30.2	75%	730	100.00	2299	XM_005057981.1
TPA_asm: Siphoviridae sp. isolate ctizJ1, partial genome	NA	0	30.2	60.5	95%	730	94.74	196040	BK024310.1
PREDICTED: Corvus kubaryi crystallin beta B3 (CRYBB3),...	Mariana crow	68294	30.2	30.2	75%	730	100.00	3472	XM_042035198.1
PREDICTED: Corvus kubaryi uncharacterized LOC121663408...	Mariana crow	68294	30.2	30.2	75%	730	100.00	953	XR_006015626.1
PREDICTED: Corvus kubaryi myosin ID (MYO1D), transcript varian...	Mariana crow	68294	30.2	30.2	75%	730	100.00	4888	XM_042021576.1
PREDICTED: Corvus kubaryi myosin ID (MYO1D), transcript varian...	Mariana crow	68294	30.2	30.2	75%	730	100.00	5362	XM_042021574.1
PREDICTED: Corvus kubaryi regulator of G protein signaling 10...	Mariana crow	68294	30.2	30.2	75%	730	100.00	3947	XM_042019451.1
PREDICTED: Corvus kubaryi regulator of G protein signaling 10...	Mariana crow	68294	30.2	30.2	75%	730	100.00	7964	XM_042019450.1
Bacillus mycoides strain BPN 08/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5281449	CP066847.1
Bacillus mycoides strain JAS12/5 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5233313	CP036085.1
Bacillus mycoides strain BPN37/2 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5490503	CP036004.1
Bacillus mycoides strain BPN37/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5322329	CP035999.1
Bacillus mycoides strain BPN36/3 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5215878	CP035997.1

PREDICTED: Chelmon rostratus collagen type VII alpha 1-like...	copperband b...	109905	30.2	30.2	75%	730	100.00	9107	XM_041964447.1
PREDICTED: Coregonus clupeaformis C-X-C chemokine receptor typ...	lake whitefish	59861	30.2	30.2	75%	730	100.00	1333	XM_041852455.1
PREDICTED: Coregonus clupeaformis C-X-C chemokine receptor typ...	lake whitefish	59861	30.2	30.2	75%	730	100.00	1720	XM_041852452.1
PREDICTED: Coregonus clupeaformis C-X-C chemokine receptor typ...	lake whitefish	59861	30.2	30.2	75%	730	100.00	1511	XM_041901829.1
PREDICTED: Coregonus clupeaformis C-X-C chemokine receptor typ...	lake whitefish	59861	30.2	30.2	75%	730	100.00	1351	XM_041901828.1
Streptomyces sp. MG62 chromosome, complete genome	NA	2838015	30.2	60.5	90%	730	100.00	8599513	CP075896.1
Streptomyces sp. JCM17656 chromosome, complete genome	NA	2768067	30.2	30.2	75%	730	100.00	10097084	CP075611.1
Bacillus paranthracis strain Colony502 chromosome	NA	2026186	30.2	30.2	75%	730	100.00	5269625	**CP075520.1**
PREDICTED: Cheilinus undulatus POM121 transmembrane nucleopori...	humphead wrasse	241271	30.2	30.2	75%	730	100.00	4250	XM_041800914.1
PREDICTED: Taeniopygia guttata regulator of G protein signalin...	zebra finch	59729	30.2	30.2	75%	730	100.00	1389	XM_030276541.3
PREDICTED: Taeniopygia guttata regulator of G protein signalin...	zebra finch	59729	30.2	30.2	75%	730	100.00	1256	XM_030276540.3
Aspergillus puulaauensis uncharacterized protein (APUU_22192A)...	NA	1220207	30.2	30.2	75%	730	100.00	1623	XM_041701027.1
PREDICTED: Drosophila elegans uncharacterized LOC108149732...	NA	30023	30.2	30.2	75%	730	100.00	677	XM_017277502.2
PREDICTED: Drosophila elegans titin (LOC108149734), mRNA	NA	30023	30.2	30.2	75%	730	100.00	13540	XM_017277504.2
Coccidioides posadasii str. Silveira chromosome 2	NA	443226	30.2	30.2	75%	730	100.00	8079863	CP075069.1
Idaea aversata genome assembly, chromosome: 17	NA	104447	30.2	30.2	75%	730	100.00	14423952	OU026100.1
Crocallis elinguaria genome assembly, chromosome: Z	NA	934829	30.2	30.2	75%	730	100.00	18277232	OU026077.1
Watermelon chlorotic stunt virus isolate LCM53_SP242H_WB segme...	NA	35341	30.2	30.2	75%	730	100.00	2759	MW588417.1
Watermelon chlorotic stunt virus isolate LCM51_SP242_WB segmen...	NA	35341	30.2	30.2	75%	730	100.00	2761	MW588416.1
Watermelon chlorotic stunt virus isolate LCM50_SP242_WB segmen...	NA	35341	30.2	30.2	75%	730	100.00	2759	MW588415.1
Watermelon chlorotic stunt virus isolate CUC-7 segment DNA B,...	NA	35341	30.2	30.2	75%	730	100.00	2728	MK649821.1
Watermelon chlorotic stunt virus isolate CUC-2 segment DNA B,...	NA	35341	30.2	30.2	75%	730	100.00	2728	MK649820.1
Watermelon chlorotic stunt virus clone Pum-4B segment DNA B,...	NA	35341	30.2	30.2	75%	730	100.00	2727	MH329675.1
Watermelon chlorotic stunt virus clone Pum-3B segment DNA B,...	NA	35341	30.2	30.2	75%	730	100.00	2727	MH329674.1
Watermelon chlorotic stunt virus clone Pum-2B segment DNA B,...	NA	35341	30.2	30.2	75%	730	100.00	2727	MH329673.1
Brachyptera putata genome assembly, chromosome: 6	NA	2065413	30.2	30.2	75%	730	100.00	32847393	OU015467.1
Hemaris fuciformis genome assembly, chromosome: 9	NA	987953	30.2	30.2	75%	730	100.00	16927926	OU015440.1
Fagus sylvatica genome assembly, chromosome: 9	European beech	28930	30.2	30.2	75%	730	100.00	39183504	OU015769.1
Zygaena filipendulae genome assembly, chromosome: 22	NA	287375	30.2	30.2	75%	730	100.00	10501088	OU015671.1
Caprimulgus europaeus genome	Eurasia	111811	30.2	30.2	75%	730	100.00	22349459	OU015538.1

assembly, chromosome: 14	n nig...								
Caprimulgus europaeus genome assembly, chromosome: 7	Eurasian nig...	111811	30.2	30.2	75%	730	100.00	60467248	OU015530.1
Muscovy duck reovirus strain 815-12 segment L1, complete sequence	NA	77153	30.2	30.2	75%	730	100.00	3958	KC508647.1
PREDICTED: Jaculus jaculus calmodulin regulated...	lesser Egypt...	51337	30.2	30.2	75%	730	100.00	3747	XM_004661740.1
PREDICTED: Jaculus jaculus calmodulin regulated...	lesser Egypt...	51337	30.2	30.2	75%	730	100.00	3828	XM_004661739.1
PREDICTED: Drosophila obscura uncharacterized LOC111075742...	NA	7282	30.2	30.2	75%	730	100.00	5241	XM_022369215.2
PREDICTED: Drosophila obscura ubiquitin fusion degradation...	NA	7282	30.2	30.2	95%	730	94.74	1181	XM_022362492.2
PREDICTED: Gigantopelta aegis triadin-like (LOC121391243), mRNA	NA	1735272	30.2	332	75%	730	100.00	1299	XM_041522935.1
Arvicola amphibius genome assembly, chromosome: 17	Eurasian wat...	1047088	30.2	30.2	75%	730	100.00	42645200	LR862397.2
Streptopelia turtur genome assembly, chromosome: Z	NA	177155	30.2	30.2	75%	730	100.00	77539467	LR594555.2
Homo sapiens isolate CHM13 chromosome 20	human	9606	30.2	60.5	100%	730	100.00	66210255	CP068258.2
Homo sapiens isolate CHM13 chromosome 19	human	9606	30.2	30.2	75%	730	100.00	61707364	CP068259.2
Homo sapiens isolate CHM13 chromosome 17	human	9606	30.2	90.7	75%	730	100.00	84276897	CP068261.2
Homo sapiens isolate CHM13 chromosome 16	human	9606	30.2	60.5	80%	730	100.00	96330374	CP068262.2
PREDICTED: Pyrgilauda ruficollis myosin ID (MYO1D), transcript...	rufous-necke...	221976	30.2	30.2	75%	730	100.00	5975	XM_041461977.1
PREDICTED: Pyrgilauda ruficollis regulator of G protein...	rufous-necke...	221976	30.2	30.2	75%	730	100.00	3784	XM_041461491.1
PREDICTED: Onychostruthus taczanowskii regulator of G protein...	white-rumped ...	356909	30.2	30.2	75%	730	100.00	1547	XM_041415549.1
PREDICTED: Betta splendens POM121 transmembrane nucleoporin...	Siamese figh...	158456	30.2	30.2	75%	730	100.00	4817	XM_029172923.2
Linderina pennispora uncharacterized protein (DL89DRAFT_213363...	NA	61395	30.2	30.2	75%	730	100.00	3228	XM_040884242.1
Penicillium solitum uncharacterized protein (PENSOL_c019G07383...	NA	60172	30.2	30.2	75%	730	100.00	1149	XM_040956617.1
Cucurbitaria berberidis CBS 394.84 uncharacterized protein...	NA	1168544	30.2	30.2	75%	730	100.00	4508	XM_040935744.1
Cryphonectria parasitica EP155 FMN-dependent 2-nitropropane...	NA	660469	30.2	30.2	75%	730	100.00	1158	XM_040917899.1
Synergistetes bacterium strain J.5.4.2-T.3.5.2 chromosome,...	NA	2268202	30.2	30.2	75%	730	100.00	3108337	CP072943.1
PREDICTED: Gallus gallus THAP domain containing 11 (THAP11), mRNA	chicken	9031	30.2	30.2	75%	730	100.00	2745	XM_040680884.1
PREDICTED: Gallus gallus THAP domain containing 11 (THAP11), mRNA	chicken	9031	30.2	30.2	75%	730	100.00	2742	XM_015279153.3
PREDICTED: Lepeophtheirus salmonis uncharacterized LOC12112216...	salmon louse	72036	30.2	30.2	75%	730	100.00	4532	XM_040717177.1
PREDICTED: Lepeophtheirus salmonis uncharacterized LOC12112216...	salmon louse	72036	30.2	30.2	75%	730	100.00	4616	XM_040717176.1
PREDICTED: **Falco** naumanni protein kinase AMP-activated catalyt...	lesser kestrel	148594	30.2	30.2	75%	730	100.00	8144	XM_040610672.1
PREDICTED: **Falco** naumanni nitric oxide synthase 2 (NOS2),...	lesser kestrel	148594	30.2	30.2	75%	730	100.00	21878	XM_040578509.1
PREDICTED: **Falco** naumanni nitric oxide synthase 2 (NOS2),...	lesser kestrel	148594	30.2	30.2	75%	730	100.00	21881	XM_040578500.1
Brevundimonas sp. AJA228-03	NA	2752515	30.2	30.2	95%	730	94.74	3038188	CP059297.1

chromosome, complete genome									
PREDICTED: Ixodes scapularis atypical protein kinase C...	black-legged...	6945	30.2	30.2	75%	730	100.00	4554	XM_029983194.3
PREDICTED: Puma yagouaroundi uncharacterized LOC121023428...	jaguarundi	1608482	30.2	30.2	75%	730	100.00	378	XR_005787383.1
Leptidea sinapis genome assembly, chromosome: 41	NA	189913	30.2	60.5	75%	730	100.00	9595617	FR990194.1
Leptidea sinapis genome assembly, chromosome: 36	NA	189913	30.2	30.2	75%	730	100.00	10558824	FR990189.1
Leptidea sinapis genome assembly, chromosome: 30	NA	189913	30.2	30.2	75%	730	100.00	12624251	FR990183.1
Leptidea sinapis genome assembly, chromosome: 20	NA	189913	30.2	60.5	75%	730	100.00	14099670	FR990173.1
Leptidea sinapis genome assembly, chromosome: 5	NA	189913	30.2	30.2	95%	730	94.74	16733303	FR990158.1
Leptidea sinapis genome assembly, chromosome: 4	NA	189913	30.2	30.2	75%	730	100.00	17197042	FR990157.1
Anthocharis cardamines genome assembly, chromosome: 1	orange tip	227532	30.2	30.2	75%	730	100.00	17367467	FR989950.1
Glaucopsyche alexis genome assembly, chromosome: 4	green-unders...	203781	30.2	30.2	75%	730	100.00	31458369	FR990046.1
Glaucopsyche alexis genome assembly, chromosome: Z	green-unders...	203781	30.2	30.2	75%	730	100.00	47686528	FR990042.1
PREDICTED: Aegilops tauschii subsp. strangulata uncharacterize...	NA	200361	30.2	30.2	75%	730	100.00	1631	XR_005754440.1
PREDICTED: Aegilops tauschii subsp. strangulata uncharacterize...	NA	200361	30.2	30.2	75%	730	100.00	1707	XM_040387185.1
PREDICTED: Aegilops tauschii subsp. strangulata uncharacterize...	NA	200361	30.2	30.2	75%	730	100.00	1702	XM_040387184.1
PREDICTED: Aegilops tauschii subsp. strangulata uncharacterize...	NA	200361	30.2	30.2	75%	730	100.00	1726	XM_040387183.1
PREDICTED: Aegilops tauschii subsp. strangulata uncharacterize...	NA	200361	30.2	30.2	75%	730	100.00	1658	XM_040387182.1
PREDICTED: Aegilops tauschii subsp. strangulata uncharacterize...	NA	200361	30.2	30.2	75%	730	100.00	1157	XM_040387181.1
PREDICTED: Aegilops tauschii subsp. strangulata uncharacterize...	NA	200361	30.2	30.2	75%	730	100.00	1052	XM_040387180.1
PREDICTED: Aegilops tauschii subsp. strangulata uncharacterize...	NA	200361	30.2	30.2	75%	730	100.00	1735	XM_040387179.1
Meleagris gallopavo genome assembly, chromosome: 15	turkey	9103	30.2	30.2	75%	730	100.00	17861904	HG999695.1
Meleagris gallopavo genome assembly, chromosome: 6	turkey	9103	30.2	60.5	80%	730	100.00	51422372	HG999686.1
Mutant Streptomyces lividans strain TK24-YQS040, complete genome	NA	1916	30.2	30.2	75%	730	100.00	8360641	CP071800.1
PREDICTED: Gasterosteus aculeatus aculeatus transmembrane...	three-spined...	481459	30.2	30.2	75%	730	100.00	1109	XM_040164825.1
PREDICTED: Gasterosteus aculeatus aculeatus transmembrane...	three-spined...	481459	30.2	30.2	75%	730	100.00	1082	XM_040164823.1
PREDICTED: Gasterosteus aculeatus aculeatus transmembrane...	three-spined...	481459	30.2	30.2	75%	730	100.00	1157	XM_040164822.1
PREDICTED: Simochromis diagramma SAM and SH3 domain containing...	NA	43689	30.2	30.2	75%	730	100.00	5616	XM_040017304.1
PREDICTED: Simochromis diagramma SAM and SH3 domain containing...	NA	43689	30.2	30.2	75%	730	100.00	6489	XM_040017303.1
PREDICTED: Simochromis diagramma SAM and SH3 domain containing...	NA	43689	30.2	30.2	75%	730	100.00	8282	XM_040017302.1
PREDICTED: Simochromis diagramma SAM and SH3 domain containing...	NA	43689	30.2	30.2	75%	730	100.00	6605	XM_040017301.1

PREDICTED: Simochromis diagramma SAM and SH3 domain containing...	NA	43689	30.2	30.2	75%	730	100.00	7374	XM_040017300.1
PREDICTED: Simochromis diagramma SAM and SH3 domain containing...	NA	43689	30.2	30.2	75%	730	100.00	7474	XM_040017299.1
PREDICTED: Simochromis diagramma POM121 transmembrane...	NA	43689	30.2	30.2	75%	730	100.00	5347	XM_040032393.1
Lysandra bellargus genome assembly, chromosome: 1	Adonis blue	138070	30.2	30.2	75%	730	100.00	18029887	HG995320.1
Mimas tiliae genome assembly, chromosome: 15	NA	522848	30.2	30.2	75%	730	100.00	17064915	HG995253.1
Duck reovirus strain TH11 segment L1, complete sequence	NA	1171667	30.2	30.2	75%	730	100.00	3958	KC493572.1
Watermelon chlorotic stunt virus isolate PAL segment DNA-B,...	NA	35341	30.2	30.2	75%	730	100.00	2760	KC462553.1
Muscovy duck reovirus strain J18 segment L1, complete sequence	NA	77153	30.2	30.2	75%	730	100.00	3959	JX478260.2
Duck reovirus NP03/CHN/2009 segment L1, complete sequence	NA	679727	30.2	30.2	75%	730	100.00	3959	KC312700.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	60.5	75%	730	100.00	22020185	HG994594.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	60.5	75%	730	100.00	59812117	HG994593.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	60.5	75%	730	100.00	31622076	HG994592.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	75%	730	100.00	22789392	HG994590.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	151	80%	730	100.00	72838482	HG994584.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	90.7	75%	730	100.00	51064559	HG994582.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	60.5	75%	730	100.00	39563600	HG994581.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	75%	730	100.00	53400701	HG994580.1
Histoplasma capsulatum G186AR chromosome 6	NA	447093	30.2	30.2	75%	730	100.00	6225384	CP069122.1
Histoplasma capsulatum strain WU24 chromosome 2	NA	5037	30.2	30.2	75%	730	100.00	6451018	CP069109.1
PREDICTED: Ornithorhynchus anatinus cyclase associated actin...	platypus	9258	30.2	30.2	75%	730	100.00	3248	XM_039910536.1
PREDICTED: Ornithorhynchus anatinus cyclase associated actin...	platypus	9258	30.2	30.2	75%	730	100.00	3138	XM_007666434.4
PREDICTED: Ornithorhynchus anatinus membrane...	platypus	9258	30.2	30.2	75%	730	100.00	3214	XM_029066812.2
Canis lupus genome assembly, chromosome: 37	gray wolf	9612	30.2	30.2	75%	730	100.00	31495737	HG994418.1
Canis lupus genome assembly, chromosome: 32	gray wolf	9612	30.2	60.5	75%	730	100.00	41774919	HG994414.1
Canis lupus genome assembly, chromosome: 28	gray wolf	9612	30.2	30.2	75%	730	100.00	42479636	HG994413.1
Canis lupus genome assembly, chromosome: 18	gray wolf	9612	30.2	60.5	100%	730	100.00	57593331	HG994402.1
Canis lupus genome assembly, chromosome: 14	gray wolf	9612	30.2	90.7	85%	730	100.00	62790595	HG994400.1
Canis lupus genome assembly, chromosome: 17	gray wolf	9612	30.2	60.5	80%	730	100.00	65956162	HG994396.1
Canis lupus genome assembly, chromosome: 11	gray wolf	9612	30.2	30.2	75%	730	100.00	75747776	HG994391.1
Brassica napus genome assembly, chromosome: C03	rape	3708	30.2	30.2	75%	730	100.00	73669886	HG994367.1
Mutant Streptomyces lividans strain TK24 DG2-P41, complete genome	NA	1916	30.2	30.2	75%	730	100.00	8380771	CP071123.1
PREDICTED: Perca fluviatilis collagen type VII alpha 1-like...	European perch	8168	30.2	30.2	75%	730	100.00	7666	XM_039791002.1
PREDICTED: Polypterus senegalus	gray	55291	30.2	30.2	75%	730	100.00	8846	XM_039764392.1

nucleoporin 214 (nup214),...	bichir								
PREDICTED: Polypterus senegalus nucleoporin 214 (nup214),...	gray bichir	55291	30.2	30.2	75%	730	100.00	8904	XM_039764391.1
PREDICTED: Polypterus senegalus nucleoporin 214 (nup214),...	gray bichir	55291	30.2	30.2	75%	730	100.00	8906	XM_039764390.1
PREDICTED: Passer montanus regulator of G protein signaling 10...	Eurasian tre...	9160	30.2	30.2	75%	730	100.00	3804	XM_039709377.1
Bacillus pacificus strain Colony7 chromosome	NA	2026187	30.2	30.2	75%	730	100.00	4543883	CP070478.1
Bacillus pacificus strain Colony 6 chromosome	NA	2026187	30.2	30.2	75%	730	100.00	4543883	CP070477.1
Bacillus pacificus strain Colony501 chromosome	NA	2026187	30.2	30.2	75%	730	100.00	4543883	CP070476.1
PREDICTED: Oreochromis aureus protein kinase C, alpha, a...	NA	47969	30.2	30.2	75%	730	100.00	7647	XM_031729013.2
PREDICTED: Oreochromis aureus SAM and SH3 domain containing 1a...	NA	47969	30.2	30.2	75%	730	100.00	6097	XM_039598739.1
PREDICTED: Oreochromis aureus SAM and SH3 domain containing 1a...	NA	47969	30.2	30.2	75%	730	100.00	6603	XM_031727634.2
PREDICTED: Oreochromis aureus SAM and SH3 domain containing 1a...	NA	47969	30.2	30.2	75%	730	100.00	7384	XM_039598738.1
PREDICTED: Oreochromis aureus SAM and SH3 domain containing 1a...	NA	47969	30.2	30.2	75%	730	100.00	7484	XM_039598737.1
PREDICTED: Oreochromis aureus POM121 transmembrane nucleoporin...	NA	47969	30.2	30.2	75%	730	100.00	4214	XM_031738263.2
Pyrenophora teres f. teres isolate W1-1 genome assembly,...	NA	97479	30.2	30.2	75%	730	100.00	3362090	HG992983.1
Spilosoma lubricipeda genome assembly, chromosome: 9	NA	875880	30.2	30.2	75%	730	100.00	21708008	HG992283.1
Lysandra coridon genome assembly, chromosome: 2	NA	268709	30.2	30.2	75%	730	100.00	9002119	HG992057.1
PREDICTED: Corvus cornix cornix uncharacterized LOC120410399...	NA	932674	30.2	30.2	75%	730	100.00	3665	XR_005602523.1
PREDICTED: Corvus cornix cornix uncharacterized LOC120410399...	NA	932674	30.2	30.2	75%	730	100.00	3737	XR_005602522.1
PREDICTED: Corvus cornix cornix uncharacterized LOC120410399...	NA	932674	30.2	30.2	75%	730	100.00	3760	XR_005602521.1
PREDICTED: Corvus cornix cornix uncharacterized LOC120410399...	NA	932674	30.2	30.2	75%	730	100.00	3832	XR_005602520.1
PREDICTED: Corvus cornix cornix uncharacterized LOC120410399...	NA	932674	30.2	30.2	75%	730	100.00	3824	XR_005602519.1
PREDICTED: Corvus cornix cornix uncharacterized LOC120410399...	NA	932674	30.2	30.2	75%	730	100.00	3906	XR_005602518.1
PREDICTED: Corvus cornix cornix regulator of G protein signali...	NA	932674	30.2	30.2	75%	730	100.00	3971	XM_010408288.4
PREDICTED: Corvus cornix cornix regulator of G protein signali...	NA	932674	30.2	30.2	75%	730	100.00	3809	XM_039554026.1
PREDICTED: Corvus cornix cornix regulator of G protein signali...	NA	932674	30.2	30.2	75%	730	100.00	2803	XM_019293907.3
PREDICTED: Corvus cornix cornix regulator of G protein signali...	NA	932674	30.2	30.2	75%	730	100.00	2471	XM_039554025.1
PREDICTED: Corvus cornix cornix regulator of G protein signali...	NA	932674	30.2	30.2	75%	730	100.00	2624	XM_039554024.1
PREDICTED: Corvus cornix cornix myosin ID (MYO1D), mRNA	NA	932674	30.2	30.2	75%	730	100.00	5402	XM_039565603.1
PREDICTED: Mauremys reevesii uncharacterized LOC120375059...	Reeves's turtle	260615	30.2	30.2	75%	730	100.00	1112	XR_005586417.1
Metabacillus sp. cB07 chromosome, complete genome	NA	2806989	30.2	30.2	75%	730	100.00	4148576	CP069296.1
Bacillus paranthracis strain BCCL1 chromosome	NA	2026186	30.2	30.2	75%	730	100.00	5687971	**CP069244.1**
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	60.5	75%	730	100.00	22020185	LR794198.1

Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	60.5	75%	730	100.00	59812117	LR794197.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	60.5	75%	730	100.00	31622076	LR794196.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	75%	730	100.00	22789392	LR794194.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	151	80%	730	100.00	72838482	LR794188.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	90.7	75%	730	100.00	51064559	LR794186.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	60.5	75%	730	100.00	39563600	LR794185.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	75%	730	100.00	53400701	LR794184.1
Trichoderma reesei strain QM6a x CBS999.97 isolate...	NA	51453	30.2	30.2	75%	730	100.00	6202018	CP021305.1
Trichoderma reesei strain QM6a x CBS999.97 isolate...	NA	51453	30.2	30.2	75%	730	100.00	6184402	CP021298.1
Caenorhabditis elegans Papilin (mig-6), mRNA	NA	6239	30.2	30.2	75%	730	100.00	7965	NM_001383344.2
Digitaria exilis genome assembly, chromosome: 1B	NA	1010633	30.2	30.2	95%	730	94.74	35142973	LR994605.1
Syritta pipiens genome assembly, chromosome: 4	NA	34682	30.2	30.2	75%	730	100.00	57582887	LR994574.1
Bacillus thuringiensis serovar andalousiensis strain NRRL...	NA	257985	30.2	30.2	75%	730	100.00	6039942	CP035727.2
2_Tcm_b3v08	California t...	61474	30.2	30.2	75%	730	100.00	333286	OE179356.1
2_Tcm_b3v08	California t...	61474	30.2	30.2	75%	730	100.00	15641	OE188084.1
2_Tcm_b3v08	California t...	61474	30.2	30.2	75%	730	100.00	19492	OE187212.1
2_Tcm_b3v08	California t...	61474	30.2	30.2	75%	730	100.00	61233	OE183203.1
Trachurus trachurus genome assembly, chromosome: 23	Atlantic hor...	36212	30.2	60.5	75%	730	100.00	25353499	LR991649.1
Trachurus trachurus genome assembly, chromosome: 20	Atlantic hor...	36212	30.2	90.7	80%	730	100.00	25462409	LR991648.1
Trachurus trachurus genome assembly, chromosome: 15	Atlantic hor...	36212	30.2	60.5	85%	730	100.00	31049438	LR991643.1
Trachurus trachurus genome assembly, chromosome: 7	Atlantic hor...	36212	30.2	30.2	75%	730	100.00	35447499	LR991638.1
Trachurus trachurus genome assembly, chromosome: 21	Atlantic hor...	36212	30.2	30.2	75%	730	100.00	35833567	LR991636.1
Trachurus trachurus genome assembly, chromosome: 4	Atlantic hor...	36212	30.2	120	85%	730	100.00	36093002	LR991635.1
Trachurus trachurus genome assembly, chromosome: 3	Atlantic hor...	36212	30.2	30.2	75%	730	100.00	40663798	LR991630.1
Trachurus trachurus genome assembly, chromosome: 1	Atlantic hor...	36212	30.2	90.7	80%	730	100.00	40754244	LR991628.1
Notocelia uddmanniana genome assembly, chromosome: 3	NA	1594315	30.2	30.2	75%	730	100.00	34895505	LR991055.1
Noctua fimbriata genome assembly, chromosome: 10	NA	753202	30.2	30.2	75%	730	100.00	19661042	LR990930.1
Thyatira batis genome assembly, chromosome: 8	NA	721163	30.2	30.2	75%	730	100.00	11676877	LR990493.1
Apotomis turbidana genome assembly, chromosome: 4	NA	1100916	30.2	181	75%	730	100.00	29684854	LR990284.1
Aricia agestis genome assembly, chromosome: 19	brown argus	91739	30.2	30.2	75%	730	100.00	14506835	LR990275.1
Caenorhabditis elegans Cosmid C37C3, complete sequence	NA	6239	30.2	30.2	75%	730	100.00	42522	FO080808.2
Goose orthoreovirus strain 03G segment L1, complete sequence	NA	1227559	30.2	30.2	75%	730	100.00	3958	JX145328.1
Watermelon chlorotic stunt virus segment DNA-B, complete sequence	NA	35341	30.2	30.2	75%	730	100.00	2772	JX131284.1
Bacillus cereus FRI-35, complete genome	NA	1217984	30.2	30.2	75%	730	100.00	5083176	CP003747.1

Neospora caninum Liverpool conserved hypothetical protein...	NA	572307	30.2	30.2	75%	730	100.00	11859	XM_003879896.1
Watermelon chlorotic stunt virus, isolate Als-2 segment B	NA	35341	30.2	30.2	75%	730	100.00	2726	HE800539.1
Euproctis similis genome assembly, chromosome: 2	NA	987935	30.2	30.2	95%	730	94.74	28426303	LR990104.1
Autographa gamma genome assembly, chromosome: 28	silver Y moth	254363	30.2	30.2	75%	730	100.00	6891251	LR989877.1
Streptomyces sp. KY70 isolate Streptomyces sp. KY70 genome...	NA	2772432	30.2	30.2	75%	730	100.00	7838151	LR881952.1
2_Tcm_b3v08	California t...	61474	30.2	30.2	75%	730	100.00	10626	OE189468.1
Nibea albiflora genome assembly, chromosome: 12	white flower...	240163	30.2	30.2	75%	730	100.00	24856270	LR699035.1
Nibea albiflora genome assembly, chromosome: 4	white flower...	240163	30.2	30.2	75%	730	100.00	26591590	LR699027.1
PREDICTED: Rattus norvegicus uncharacterized LOC120096622...	Norway rat	10116	30.2	30.2	75%	730	100.00	3336	XR_005493296.1
PREDICTED: Rattus norvegicus uncharacterized LOC120096622...	Norway rat	10116	30.2	30.2	75%	730	100.00	3352	XR_005493295.1
Phycisphaerales bacterium isolate...	NA	2052180	30.2	30.2	75%	730	100.00	3355795	CP064987.1
PREDICTED: Salvelinus namaycush C-X-C chemokine receptor type...	lake trout	8040	30.2	30.2	75%	730	100.00	1873	XM_038994775.1
PREDICTED: Salvelinus namaycush C-X-C chemokine receptor type...	lake trout	8040	30.2	30.2	75%	730	100.00	1185	XM_038992815.1
PREDICTED: Salvelinus namaycush uncharacterized LOC120046201...	lake trout	8040	30.2	30.2	75%	730	100.00	2072	XM_038991238.1
PREDICTED: Salvelinus namaycush uncharacterized LOC120046201...	lake trout	8040	30.2	30.2	75%	730	100.00	2544	XM_038991237.1
PREDICTED: Salvelinus namaycush uncharacterized LOC120046201...	lake trout	8040	30.2	30.2	75%	730	100.00	2468	XM_038991236.1
PREDICTED: Salvelinus namaycush uncharacterized LOC120046201...	lake trout	8040	30.2	30.2	75%	730	100.00	2575	XM_038991235.1
PREDICTED: Salvelinus namaycush uncharacterized LOC120046201...	lake trout	8040	30.2	30.2	75%	730	100.00	2655	XM_038991234.1
PREDICTED: Salvelinus namaycush SPG11 vesicle trafficking...	lake trout	8040	30.2	30.2	75%	730	100.00	7600	XM_039017181.1
PREDICTED: Salvelinus namaycush F-box protein 32 (fbxo32),...	lake trout	8040	30.2	211	75%	730	100.00	1751	XM_038985881.1
PREDICTED: Salvelinus namaycush F-box protein 32 (fbxo32),...	lake trout	8040	30.2	211	75%	730	100.00	1895	XM_038985880.1
Colletotrichum karsti uncharacterized protein (CkaCkLH20_07936...	NA	1095194	30.2	30.2	75%	730	100.00	2139	XM_038890652.1
Ascochyta rabiei uncharacterized protein (EKO05_006732), parti...	NA	5454	30.2	30.2	75%	730	100.00	2634	XM_038941191.1
Streptomyces sp. ZYC-3 chromosome, complete genome	NA	2797636	30.2	30.2	75%	730	100.00	11027222	CP066831.1
Micropterus salmoides LOW QUALITY PROTEIN: collagen alpha-1(VI...	largemouth bass	27706	30.2	30.2	75%	730	100.00	6518	XM_038695364.1
Micropterus salmoides LOW QUALITY PROTEIN: collagen alpha-1(VI...	largemouth bass	27706	30.2	30.2	75%	730	100.00	9813	XM_038739148.1
Micropterus salmoides tyrosine-protein kinase STYK1 (styk1a),...	largemouth bass	27706	30.2	30.2	75%	730	100.00	2976	XM_038725263.1
Dermochelys coriacea alpha-2-	leatherback ...	27794	30.2	30.2	75%	730	100.00	4578	XM_038414451.1

macroglobulin-like (LOC119860584)...									
4_Tbi_b3v08	NA	61472	30.2	30.2	75%	730	100.00	35513	OD570479.1
Bacillus cereus strain FDAARGOS_919 chromosome	NA	1396	30.2	30.2	75%	730	100.00	5307522	CP065881.1
1_Tps_b3v08	NA	170557	30.2	30.2	75%	730	100.00	326	OD387411.1
3_Tce_b3v08	NA	61476	30.2	30.2	75%	730	100.00	332801	OC316944.1
3_Tms_b3v08	NA	170555	30.2	30.2	75%	730	100.00	172677	OB794341.1
4_Tte_b3v08	NA	61484	30.2	30.2	75%	730	100.00	31537	OE007491.1
4_Tbi_b3v08	NA	61472	30.2	30.2	75%	730	100.00	309862	OD564690.1
1_Tps_b3v08	NA	170557	30.2	30.2	75%	730	100.00	20515	OD009155.1
PREDICTED: Patiria miniata dynein heavy chain 8, axonemal-like...	bat star	46514	30.2	30.2	75%	730	100.00	13412	XM_038209121.1
PREDICTED: Patiria miniata dynein heavy chain 8, axonemal-like...	bat star	46514	30.2	30.2	75%	730	100.00	15281	XM_038209120.1
Bacillus thuringiensis strain H3 chromosome, complete genome	NA	1428	30.2	30.2	75%	730	100.00	5466713	CP052061.1
PREDICTED: Motacilla alba alba regulator of G protein signalin...	NA	1094192	30.2	30.2	75%	730	100.00	3913	XM_038140389.1
PREDICTED: Motacilla alba alba regulator of G protein signalin...	NA	1094192	30.2	30.2	75%	730	100.00	3772	XM_038140388.1
PREDICTED: Chlorocebus sabaeus uncharacterized LOC119620926...	green monkey	60711	30.2	30.2	75%	730	100.00	688	XR_005237469.1
PREDICTED: Chlorocebus sabaeus small integral membrane protein...	green monkey	60711	30.2	30.2	75%	730	100.00	383	XM_038005960.1
2_Tsi_b3v08	NA	629360	30.2	30.2	75%	730	100.00	25708	OC008194.1
2_Tsi_b3v08	NA	629360	30.2	30.2	75%	730	100.00	397743	OC000198.1
1_Tdi_b3v08	NA	61478	30.2	30.2	75%	730	100.00	104921	OA566910.1
Darwinula stevensoni	NA	69355	30.2	30.2	75%	730	100.00	1788	LR914116.1
Darwinula stevensoni	NA	69355	30.2	30.2	75%	730	100.00	25337	LR903561.1
Darwinula stevensoni	NA	69355	30.2	30.2	75%	730	100.00	27869	LR903292.1
1_Tdi_b3v08	NA	61478	30.2	30.2	75%	730	100.00	258	OA862723.1
Darwinula stevensoni	NA	69355	30.2	30.2	75%	730	100.00	59061	LR901236.1
Darwinula stevensoni	NA	69355	30.2	30.2	75%	730	100.00	93988	LR900306.1
Corylus avellana genome assembly, chromosome: ca3	NA	13451	30.2	60.5	75%	730	100.00	39770678	LR899425.1
1_Tdi_b3v08	NA	61478	30.2	30.2	75%	730	100.00	9828	OA576132.1
Cyprideis torosa	NA	163714	30.2	30.2	75%	730	100.00	483	OB754470.1
Cyprideis torosa	NA	163714	30.2	30.2	75%	730	100.00	103041	OB660307.1
Macaca mulatta fosmid CH250-138B21 from chromosome X, complete...	Rhesus monkey	9544	30.2	30.2	75%	730	100.00	177671	AC280536.1
Pan troglodytes BAC CH251-550E20 from chromosome, complete...	chimpanzee	9598	30.2	30.2	75%	730	100.00	217778	AC280495.1
PREDICTED: Drosophila subpulchrella putative uncharacterized...	NA	1486046	30.2	30.2	75%	730	100.00	5272	XM_037862851.1
PREDICTED: Drosophila subpulchrella putative uncharacterized...	NA	1486046	30.2	30.2	75%	730	100.00	5284	XM_037862850.1
PREDICTED: Sebastes umbrosus uncharacterized LOC119495694...	honeycomb ro...	72105	30.2	30.2	75%	730	100.00	1197	XR_005208540.1
Avian orthoreovirus isolate ISR/5226/2007 lambda-1 gene, parti...	NA	38170	30.2	30.2	75%	730	100.00	380	MW057719.1
Avian orthoreovirus isolate ISR/2953/2020 lambda-1 gene, parti...	NA	38170	30.2	30.2	75%	730	100.00	380	MW057716.1
PREDICTED: Triticum dicoccoides uncharacterized LOC119287746...	NA	85692	30.2	30.2	75%	730	100.00	954	XR_005140932.1
PREDICTED: Triticum dicoccoides uncharacterized LOC119287746...	NA	85692	30.2	30.2	75%	730	100.00	2019	XR_005140931.1
PREDICTED: Triticum dicoccoides	NA	85692	30.2	30.2	75%	730	100.00	2319	XR_005140929.1

uncharacterized LOC119287746...									
PREDICTED: Triticum dicoccoides uncharacterized LOC119287746...	NA	85692	30.2	30.2	75%	730	100.00	2281	XR_005140928.1
PREDICTED: Triticum dicoccoides uncharacterized LOC119287746...	NA	85692	30.2	30.2	75%	730	100.00	2370	XR_005140927.1
PREDICTED: Triticum dicoccoides uncharacterized LOC119287746...	NA	85692	30.2	30.2	75%	730	100.00	1324	XR_005140926.1
PREDICTED: Triticum dicoccoides uncharacterized LOC119287746...	NA	85692	30.2	30.2	75%	730	100.00	1309	XR_005140925.1
PREDICTED: Triticum dicoccoides uncharacterized LOC119287746...	NA	85692	30.2	30.2	75%	730	100.00	2293	XR_005140924.1
PREDICTED: Triticum dicoccoides uncharacterized LOC119287746...	NA	85692	30.2	30.2	75%	730	100.00	1179	XM_037567350.1
PREDICTED: Triticum dicoccoides uncharacterized LOC119287746...	NA	85692	30.2	30.2	75%	730	100.00	1301	XM_037567349.1
PREDICTED: Triticum dicoccoides uncharacterized LOC119287746...	NA	85692	30.2	30.2	75%	730	100.00	1476	XM_037567348.1
PREDICTED: Triticum dicoccoides cytochrome P450 CYP99A1-like...	NA	85692	30.2	30.2	75%	730	100.00	1557	XM_037562353.1
PREDICTED: Triticum dicoccoides cytochrome P450 CYP99A1-like...	NA	85692	30.2	30.2	75%	730	100.00	1757	XM_037559487.1
PREDICTED: Triticum dicoccoides cytochrome P450 CYP99A1-like...	NA	85692	30.2	30.2	75%	730	100.00	1638	XM_037554109.1
PREDICTED: Talpa occidentalis PALM2 and AKAP2 fusion...	Iberian mole	50954	30.2	30.2	75%	730	100.00	4024	XM_037491605.1
PREDICTED: Talpa occidentalis PALM2 and AKAP2 fusion...	Iberian mole	50954	30.2	30.2	75%	730	100.00	4207	XM_037491604.1
PREDICTED: Talpa occidentalis PALM2 and AKAP2 fusion...	Iberian mole	50954	30.2	30.2	75%	730	100.00	4231	XM_037491603.1
PREDICTED: Talpa occidentalis PALM2 and AKAP2 fusion...	Iberian mole	50954	30.2	30.2	75%	730	100.00	4243	XM_037491602.1
PREDICTED: Talpa occidentalis PALM2 and AKAP2 fusion...	Iberian mole	50954	30.2	30.2	75%	730	100.00	4333	XM_037491601.1
PREDICTED: Talpa occidentalis PALM2 and AKAP2 fusion...	Iberian mole	50954	30.2	30.2	75%	730	100.00	4927	XM_037491600.1
PREDICTED: Talpa occidentalis PALM2 and AKAP2 fusion...	Iberian mole	50954	30.2	30.2	75%	730	100.00	3322	XM_037491598.1
PREDICTED: Talpa occidentalis PALM2 and AKAP2 fusion...	Iberian mole	50954	30.2	30.2	75%	730	100.00	4709	XM_037491597.1
PREDICTED: Pungitius pungitius podocalyxin-like 2 (podxl2),...	ninespine st...	134920	30.2	30.2	75%	730	100.00	3665	XM_037448395.1
PREDICTED: Pungitius pungitius podocalyxin-like 2 (podxl2),...	ninespine st...	134920	30.2	30.2	75%	730	100.00	3505	XM_037448394.1
PREDICTED: Pungitius pungitius podocalyxin-like 2 (podxl2),...	ninespine st...	134920	30.2	30.2	75%	730	100.00	3685	XM_037448393.1
PREDICTED: Pungitius pungitius podocalyxin-like 2 (podxl2),...	ninespine st...	134920	30.2	30.2	75%	730	100.00	3712	XM_037448392.1
PREDICTED: **Falco** rusticolus protein kinase AMP-activated...	gyrfalcon	120794	30.2	30.2	75%	730	100.00	5012	XM_037404327.1
PREDICTED: **Falco** rusticolus nitric oxide synthase 2 (NOS2),...	gyrfalcon	120794	30.2	30.2	75%	730	100.00	20389	XM_037411585.1
PREDICTED: **Falco** rusticolus nitric oxide synthase 2 (NOS2),...	gyrfalcon	120794	30.2	30.2	75%	730	100.00	20376	XM_037411576.1
PREDICTED: **Falco** rusticolus nitric oxide synthase 2 (NOS2),...	gyrfalcon	120794	30.2	30.2	75%	730	100.00	20379	XM_037411567.1
PREDICTED: Peromyscus leucopus spectrin repeat containing...	white-footed...	10041	30.2	30.2	75%	730	100.00	3663	XM_028876050.2
PREDICTED: Peromyscus leucopus spectrin repeat containing...	white-footed...	10041	30.2	30.2	75%	730	100.00	5362	XM_037210630.1
PREDICTED: Peromyscus leucopus spectrin repeat containing...	white-footed...	10041	30.2	30.2	75%	730	100.00	21687	XM_037210629.1
PREDICTED: Peromyscus leucopus spectrin repeat containing...	white-footed...	10041	30.2	30.2	75%	730	100.00	21686	XM_037210628.1
PREDICTED: Peromyscus leucopus spectrin repeat containing...	white-footed...	10041	30.2	30.2	75%	730	100.00	21690	XM_028876051.2
PREDICTED: Peromyscus leucopus spectrin repeat containing...	white-footed...	10041	30.2	30.2	75%	730	100.00	21752	XM_037210627.1
PREDICTED: Peromyscus leucopus	white-footed...	10041	30.2	30.2	75%	730	100.00	21756	XM_037210626.1

spectrin repeat containing...									
PREDICTED: Peromyscus leucopus spectrin repeat containing...	white-footed...	10041	30.2	30.2	75%	730	100.00	21756	XM_037210625.1
PREDICTED: Peromyscus leucopus spectrin repeat containing...	white-footed...	10041	30.2	30.2	75%	730	100.00	21911	XM_037210624.1
PREDICTED: Peromyscus leucopus spectrin repeat containing...	white-footed...	10041	30.2	30.2	75%	730	100.00	21744	XM_037210623.1
PREDICTED: Peromyscus leucopus spectrin repeat containing...	white-footed...	10041	30.2	30.2	75%	730	100.00	21760	XM_037210622.1
PREDICTED: Pollicipes pollicipes uncharacterized LOC119104666...	NA	41117	30.2	30.2	75%	730	100.00	2214	XM_037228387.1
PREDICTED: Pollicipes pollicipes cGMP-dependent protein kinase...	NA	41117	30.2	30.2	75%	730	100.00	3687	XM_037220697.1
Anaerobacillus isosaccharinicus strain NB2006 chromosome,...	NA	1532552	30.2	30.2	75%	730	100.00	5227144	CP063356.1
PREDICTED: Acanthopagrus latus ribonuclease H2, subunit C...	yellowfin se...	8177	30.2	30.2	75%	730	100.00	762	XM_037078168.1
PREDICTED: Acanthopagrus latus uncharacterized LOC119007563...	yellowfin se...	8177	30.2	30.2	75%	730	100.00	4128	XR_005071158.1
PREDICTED: Acanthopagrus latus collagen type VII alpha 1-like...	yellowfin se...	8177	30.2	30.2	75%	730	100.00	9424	XM_037121217.1
PREDICTED: Acanthopagrus latus POM121 transmembrane nucleopori...	yellowfin se...	8177	30.2	30.2	75%	730	100.00	5079	XM_037119117.1
PREDICTED: Acanthopagrus latus kelch-like family member 6...	yellowfin se...	8177	30.2	30.2	75%	730	100.00	2786	XR_005077170.1
PREDICTED: Acanthopagrus latus kelch-like family member 6...	yellowfin se...	8177	30.2	30.2	75%	730	100.00	3110	XM_037110954.1
PREDICTED: Acanthopagrus latus potassium voltage-gated channel...	yellowfin se...	8177	30.2	30.2	75%	730	100.00	5796	XM_037096847.1
PREDICTED: Acanthopagrus latus potassium voltage-gated channel...	yellowfin se...	8177	30.2	30.2	75%	730	100.00	5619	XM_037096846.1
PREDICTED: Sturnira hondurensis uncharacterized LOC118979773...	NA	192404	30.2	30.2	75%	730	100.00	2790	XR_005064989.1
PREDICTED: Manis javanica maestro heat like repeat family memb...	Malayan pang...	9974	30.2	30.2	75%	730	100.00	10081	**XR_005062615.1**
PREDICTED: Manis javanica maestro heat like repeat family memb...	Malayan pang...	9974	30.2	30.2	75%	730	100.00	10085	**XR_005062614.1**
PREDICTED: Manis javanica maestro heat like repeat family memb...	Malayan pang...	9974	30.2	30.2	75%	730	100.00	10231	**XM_037023171.1**
PREDICTED: Manis javanica maestro heat like repeat family memb...	Malayan pang...	9974	30.2	30.2	75%	730	100.00	11934	**XM_037023170.1**
PREDICTED: Manis javanica maestro heat like repeat family memb...	Malayan pang...	9974	30.2	30.2	75%	730	100.00	11907	**XR_005062613.1**
PREDICTED: Manis javanica maestro heat like repeat family memb...	Malayan pang...	9974	30.2	30.2	75%	730	100.00	12053	**XM_037023169.1**
PREDICTED: Oncorhynchus mykiss chemokine (C-X-C motif) recepto...	rainbow trout	8022	30.2	30.2	75%	730	100.00	1521	XM_021581457.2
PREDICTED: Oncorhynchus mykiss SPG11 vesicle trafficking...	rainbow trout	8022	30.2	30.2	75%	730	100.00	7647	XM_021565615.2
PREDICTED: Oncorhynchus mykiss SPG11 vesicle trafficking...	rainbow trout	8022	30.2	30.2	75%	730	100.00	7647	XM_021565607.2
PREDICTED: Oncorhynchus mykiss SPG11 vesicle trafficking...	rainbow trout	8022	30.2	30.2	75%	730	100.00	7650	XM_021565598.2
PREDICTED: Oncorhynchus mykiss C-X-C chemokine receptor type...	rainbow trout	8022	30.2	30.2	75%	730	100.00	2350	XM_036941837.1
PREDICTED: Oncorhynchus mykiss C-X-C chemokine receptor type...	rainbow trout	8022	30.2	30.2	75%	730	100.00	2626	XM_036941829.1
PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion...	Chinese pang...	143292	30.2	30.2	75%	730	100.00	6723	**XM_036903349.1**
PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion...	Chinese	143292	30.2	30.2	75%	730	100.00	6707	**XM_036903348.1**

	pang...								
PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion...	Chinese pang...	143292	30.2	30.2	75%	730	100.00	6866	**XM_036903346.1**
PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion...	Chinese pang...	143292	30.2	30.2	75%	730	100.00	7010	**XM_036903345.1**
PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion...	Chinese pang...	143292	30.2	30.2	75%	730	100.00	7049	**XM_036903344.1**
PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion...	Chinese pang...	143292	30.2	30.2	75%	730	100.00	7112	**XM_036903343.1**
PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion...	Chinese pang...	143292	30.2	30.2	75%	730	100.00	7151	**XM_036903342.1**
PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion...	Chinese pang...	143292	30.2	30.2	75%	730	100.00	3916	**XM_036903341.1**
PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion...	Chinese pang...	143292	30.2	30.2	75%	730	100.00	7745	**XM_036903340.1**
PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion...	Chinese pang...	143292	30.2	30.2	75%	730	100.00	7980	**XM_036903339.1**
PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion...	Chinese pang...	143292	30.2	30.2	75%	730	100.00	7919	**XM_036903338.1**
PREDICTED: Balaenoptera musculus ataxin 7 (ATXN7), mRNA	Blue whale	9771	30.2	30.2	75%	730	100.00	3610	XM_036868588.1
Homo sapiens BAC clone RP11-722G7 from chromosome x, complete...	human	9606	30.2	30.2	75%	730	100.00	189675	AC234783.5
Watermelon chlorotic stunt virus DNA A complete sequence, clon...	NA	35341	30.2	30.2	75%	730	100.00	2744	HG941655.1
Leishmania donovani BPK282A1 complete genome, chromosome 32	NA	5661	30.2	30.2	75%	730	100.00	1559911	FR799619.2
Mycoplasma pneumoniae 309 DNA, complete genome	NA	1112856	30.2	30.2	75%	730	100.00	817176	AP012303.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	7285	XM_036754310.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	7332	XM_036754309.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	7503	XM_036754308.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	7764	XM_036754307.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	7724	XM_036754306.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	2663	XM_036754305.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	2961	XM_036754304.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	3044	XM_036754303.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	8271	XM_036754302.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	8364	XM_036754301.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	2766	XM_036754299.1
PREDICTED: Trichosurus vulpecula microtubule associated protei...	common brush...	9337	30.2	30.2	75%	730	100.00	8472	XM_036754298.1

PREDICTED: Trichosurus vulpecula family with sequence similari...	common brush...	9337	30.2	30.2	75%	730	100.00	6129	XM_036750455.1
PREDICTED: Megalops cyprinoides dynein, axonemal, heavy chain ...	Indo-Pacific...	118141	30.2	30.2	75%	730	100.00	13913	XM_036538759.1
PREDICTED: Megalops cyprinoides dynein, axonemal, heavy chain ...	Indo-Pacific...	118141	30.2	30.2	75%	730	100.00	13925	XM_036538758.1
PREDICTED: Megalops cyprinoides DEXH (Asp-Glu-X-His) box...	Indo-Pacific...	118141	30.2	30.2	75%	730	100.00	2154	XM_036539926.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowfin se...	8177	30.2	30.2	75%	730	100.00	28391644	LR884480.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowfin se...	8177	30.2	60.5	75%	730	100.00	24955350	LR884478.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowfin se...	8177	30.2	60.5	75%	730	100.00	28960280	LR884474.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowfin se...	8177	30.2	60.5	80%	730	100.00	22160155	LR884473.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowfin se...	8177	30.2	60.5	75%	730	100.00	26679254	LR884471.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome: 8	yellowfin se...	8177	30.2	30.2	75%	730	100.00	31340161	LR884467.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome: 7	yellowfin se...	8177	30.2	30.2	75%	730	100.00	31194941	LR884466.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome: 2	yellowfin se...	8177	30.2	90.7	75%	730	100.00	32017321	LR884461.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome: 1	yellowfin se...	8177	30.2	60.5	75%	730	100.00	33527824	LR884460.1
Fusarium oxysporum f. sp. koae isolate 44 chromosome 4	NA	654392	30.2	30.2	75%	730	100.00	5152146	CP052899.1
PREDICTED: Pipistrellus kuhlii ankyrin repeat domain 26...	Kuhl's pipis...	59472	30.2	30.2	75%	730	100.00	4368	**XM_036453185.1**
PREDICTED: Pipistrellus kuhlii ankyrin repeat domain 26...	Kuhl's pipis...	59472	30.2	30.2	75%	730	100.00	4548	**XM_036453179.1**
PREDICTED: Pipistrellus kuhlii ankyrin repeat domain 26...	Kuhl's pipis...	59472	30.2	30.2	75%	730	100.00	5118	**XM_036453174.1**
PREDICTED: Pipistrellus kuhlii ankyrin repeat domain 26...	Kuhl's pipis...	59472	30.2	30.2	75%	730	100.00	5121	**XM_036453166.1**
PREDICTED: Pipistrellus kuhlii ankyrin repeat domain 26...	Kuhl's pipis...	59472	30.2	30.2	75%	730	100.00	5172	**XM_036453159.1**
PREDICTED: Molothrus ater complement receptor type 1-like...	NA	84834	30.2	30.2	75%	730	100.00	8117	XM_036398156.1
PREDICTED: Myotis myotis ankyrin repeat domain 26 (ANKRD26), mRNA	NA	51298	30.2	30.2	75%	730	100.00	5229	XM_036338112.1
PREDICTED: Molossus molossus ankyrin repeat domain-containing...	Pallas's mas...	27622	30.2	30.2	75%	730	100.00	4783	XM_036266485.1
PREDICTED: Oryzias melastigma ectopic P-granules autophagy...	Indian medaka	30732	30.2	30.2	75%	730	100.00	9652	XM_024275337.2
PREDICTED: Oryzias melastigma ectopic P-granules autophagy...	Indian medaka	30732	30.2	30.2	75%	730	100.00	9680	XM_024275336.2
PREDICTED: Oryzias melastigma ectopic P-granules autophagy...	Indian medaka	30732	30.2	30.2	75%	730	100.00	9680	XM_024275335.2
PREDICTED: Oryzias melastigma ectopic P-granules autophagy...	Indian medaka	30732	30.2	30.2	75%	730	100.00	9680	XM_024275333.2
PREDICTED: Oryzias melastigma ectopic P-granules autophagy...	Indian medaka	30732	30.2	30.2	75%	730	100.00	9583	XM_024275332.2
PREDICTED: Oryzias melastigma PI-PLC X domain-containing prote...	Indian medaka	30732	30.2	30.2	75%	730	100.00	1342	XM_024278831.2
Homo sapiens DNA, chromosome 20, nearly complete genome	human	9606	30.2	60.5	100%	730	100.00	62398354	AP023480.1
Homo sapiens DNA, chromosome 19, nearly complete genome	human	9606	30.2	30.2	75%	730	100.00	59105444	AP023479.1
Homo sapiens DNA, chromosome 17, nearly complete genome	human	9606	30.2	90.7	75%	730	100.00	80688777	AP023477.1
Homo sapiens DNA, chromosome 16, nearly complete genome	human	9606	30.2	60.5	80%	730	100.00	94690957	AP023476.1
PREDICTED: Onychomys torridus	souther	38674	30.2	30.2	75%	730	100.00	3531	XM_036205562.1

spectrin repeat containing nucle...	n gra...								
PREDICTED: Onychomys torridus spectrin repeat containing nucle...	southern gra...	38674	30.2	30.2	75%	730	100.00	21536	XM_036205561.1
PREDICTED: Mus musculus predicted gene, 31769 (Gm31769), ncRNA	house mouse	10090	30.2	30.2	75%	730	100.00	3838	XR_376632.3
PREDICTED: Mus musculus mannoside acetylglucosaminyltransferas...	house mouse	10090	30.2	30.2	75%	730	100.00	4840	XM_036166232.1
PREDICTED: Mus musculus mannoside acetylglucosaminyltransferas...	house mouse	10090	30.2	30.2	75%	730	100.00	5149	XM_006529057.5
PREDICTED: Mus musculus mannoside acetylglucosaminyltransferas...	house mouse	10090	30.2	30.2	75%	730	100.00	5253	XM_030255028.2
PREDICTED: Mus musculus mannoside acetylglucosaminyltransferas...	house mouse	10090	30.2	30.2	75%	730	100.00	5511	XM_006529056.5
PREDICTED: Mus musculus mannoside acetylglucosaminyltransferas...	house mouse	10090	30.2	30.2	75%	730	100.00	6170	XM_006529055.5
Poecilia reticulata genome assembly, chromosome: 17	guppy	8081	30.2	423	75%	730	100.00	28869038	LR880661.1
Poecilia reticulata genome assembly, chromosome: 14	guppy	8081	30.2	60.5	85%	730	100.00	27818384	LR880658.1
Poecilia reticulata genome assembly, chromosome: 9	guppy	8081	30.2	30.2	75%	730	100.00	33240922	LR880653.1
Leishmania chagasi strain MCER/BR/1981/M6445/Salvaterra isolat...	NA	44271	30.2	30.2	75%	730	100.00	1547487	CP048197.1
Leishmania chagasi strain MHOM/HD/2017/M32502/Amapala isolate...	NA	44271	30.2	30.2	75%	730	100.00	1547652	CP048161.1
PREDICTED: Sander lucioperca collagen type VII alpha 1-like...	pikeperch	283035	30.2	30.2	75%	730	100.00	9848	XM_035996213.1
PREDICTED: Sander lucioperca collagen type VII alpha 1-like...	pikeperch	283035	30.2	30.2	75%	730	100.00	9848	XM_035996212.1
PREDICTED: Sander lucioperca collagen type VII alpha 1-like...	pikeperch	283035	30.2	30.2	75%	730	100.00	9890	XM_035996211.1
PREDICTED: Sander lucioperca collagen type VII alpha 1-like...	pikeperch	283035	30.2	30.2	75%	730	100.00	9893	XM_035996210.1
Thermoanaerosceptrum fracticalcis strain DRI-13 chromosome,...	NA	1712410	30.2	30.2	75%	730	100.00	3805411	CP045798.1
Synechococcus sp. A15-24 chromosome, complete genome	NA	1050635	30.2	30.2	75%	730	100.00	2305373	CP047960.1
PREDICTED: Neolamprologus brichardi SAM and SH3 domain...	NA	32507	30.2	30.2	75%	730	100.00	5326	XM_006797049.2
PREDICTED: Neolamprologus brichardi SAM and SH3 domain...	NA	32507	30.2	30.2	75%	730	100.00	6629	XM_035910477.1
PREDICTED: Neolamprologus brichardi SAM and SH3 domain...	NA	32507	30.2	30.2	75%	730	100.00	7423	XM_006797047.2
PREDICTED: Neolamprologus brichardi SAM and SH3 domain...	NA	32507	30.2	30.2	75%	730	100.00	7880	XM_006797045.2
PREDICTED: Neolamprologus brichardi SAM and SH3 domain...	NA	32507	30.2	30.2	75%	730	100.00	7979	XM_006797044.2
PREDICTED: Neolamprologus brichardi POM121 transmembrane...	NA	32507	30.2	30.2	75%	730	100.00	5057	XM_006785208.2
Acomys russatus genome assembly, chromosome: 29	golden spiny...	60746	30.2	60.5	85%	730	100.00	47664281	LR877240.1
Acomys russatus genome assembly, chromosome: 26	golden spiny...	60746	30.2	120	90%	730	100.00	53312271	LR877237.1
Acomys russatus genome assembly, chromosome: 22	golden spiny...	60746	30.2	151	85%	730	100.00	59984821	LR877233.1
Acomys russatus genome assembly, chromosome: 21	golden spiny...	60746	30.2	30.2	75%	730	100.00	61132863	LR877232.1
Acomys russatus genome assembly, chromosome: 18	golden spiny...	60746	30.2	60.5	85%	730	100.00	64120505	LR877229.1
Acomys russatus genome	golden spiny...	60746	30.2	120	90%	730	100.00	67302882	LR877226.1

assembly, chromosome: 15									
Acomys russatus genome assembly, chromosome: 5	golden spiny...	60746	30.2	60.5	80%	730	100.00	79927262	LR877216.1
Onychomys torridus genome assembly, chromosome: 17	southern gra...	38674	30.2	90.7	90%	730	100.00	64256681	LR877204.1
Onychomys torridus genome assembly, chromosome: 16	southern gra...	38674	30.2	30.2	75%	730	100.00	68548656	LR877203.1
Onychomys torridus genome assembly, chromosome: 15	southern gra...	38674	30.2	90.7	90%	730	100.00	78039327	LR877202.1
Onychomys torridus genome assembly, chromosome: 14	southern gra...	38674	30.2	30.2	75%	730	100.00	84754330	LR877201.1
Onychomys torridus genome assembly, chromosome: 13	southern gra...	38674	30.2	30.2	75%	730	100.00	78371027	LR877200.1
Rhizobium leguminosarum bv. viciae strain RCAM2802 chromosome,...	NA	387	30.2	30.2	75%	730	100.00	5127347	CP050562.1
PREDICTED: Oncorhynchus keta chemokine (C-X-C motif) receptor ...	chum salmon	8018	30.2	30.2	75%	730	100.00	1720	XM_035751584.1
PREDICTED: Oncorhynchus keta chemokine (C-X-C motif) receptor ...	chum salmon	8018	30.2	30.2	75%	730	100.00	1954	XM_035751583.1
PREDICTED: Oncorhynchus keta chemokine (C-X-C motif) receptor ...	chum salmon	8018	30.2	30.2	75%	730	100.00	2243	XM_035751582.1
PREDICTED: Oncorhynchus keta SPG11 vesicle trafficking...	chum salmon	8018	30.2	30.2	75%	730	100.00	7639	XM_035790544.1
PREDICTED: Oncorhynchus keta SPG11 vesicle trafficking...	chum salmon	8018	30.2	30.2	75%	730	100.00	7639	XM_035790543.1
PREDICTED: Oncorhynchus keta SPG11 vesicle trafficking...	chum salmon	8018	30.2	30.2	75%	730	100.00	7642	XM_035790542.1
PREDICTED: Oncorhynchus keta C-X-C chemokine receptor type...	chum salmon	8018	30.2	30.2	75%	730	100.00	1918	XM_035756682.1
PREDICTED: Oncorhynchus keta C-X-C chemokine receptor type...	chum salmon	8018	30.2	30.2	75%	730	100.00	1937	XM_035756681.1
PREDICTED: Oncorhynchus keta C-X-C chemokine receptor type...	chum salmon	8018	30.2	30.2	75%	730	100.00	2165	XM_035756680.1
Streptacidiphilus sp. P02-A3a chromosome, complete genome	NA	2704468	30.2	30.2	75%	730	100.00	9330052	CP048289.1
Streptacidiphilus sp. PB12-B1b chromosome, complete genome	NA	2705012	30.2	30.2	75%	730	100.00	7672494	CP048405.1
PREDICTED: Zalophus californianus uncharacterized LOC113937729...	California s...	9704	30.2	30.2	75%	730	100.00	3420	XR_003524692.2
Pipistrellus pipistrellus genome assembly, chromosome: 17	common pipis...	59474	30.2	30.2	75%	730	100.00	45571527	**LR862373.1**
Pipistrellus pipistrellus genome assembly, chromosome: 16	common pipis...	59474	30.2	90.7	85%	730	100.00	46231460	**LR862372.1**
Pipistrellus pipistrellus genome assembly, chromosome: 11	common pipis...	59474	30.2	30.2	75%	730	100.00	69386144	**LR862367.1**
Pipistrellus pipistrellus genome assembly, chromosome: 7	common pipis...	59474	30.2	30.2	75%	730	100.00	84548104	**LR862363.1**
Pipistrellus pipistrellus genome assembly, chromosome: 6	common pipis...	59474	30.2	30.2	75%	730	100.00	85793147	**LR862362.1**
Pipistrellus pipistrellus genome assembly, chromosome: 5	common pipis...	59474	30.2	60.5	85%	730	100.00	94929986	**LR862361.1**
PREDICTED: Morone saxatilis sema domain, immunoglobulin domain...	striped sea-...	34816	30.2	30.2	75%	730	100.00	3765	XM_035667732.1
PREDICTED: Morone saxatilis sema domain, immunoglobulin domain...	striped sea-...	34816	30.2	30.2	75%	730	100.00	4210	XM_035667731.1
PREDICTED: Morone saxatilis nuclear envelope pore membrane...	striped sea-...	34816	30.2	30.2	75%	730	100.00	1584	XM_035663783.1
PREDICTED: Scophthalmus maximus uncharacterized LOC118313094...	turbot	52904	30.2	30.2	75%	730	100.00	5197	XR_004794377.1

PREDICTED: Scophthalmus maximus uncharacterized LOC118313094...	turbot	52904	30.2	30.2	75%	730	100.00	5314	XR_004794376.1
PREDICTED: Scophthalmus maximus POM121 transmembrane nucleopor...	turbot	52904	30.2	30.2	75%	730	100.00	5131	XM_035625486.1
Lactiplantibacillus plantarum strain BK-021 chromosome, comple...	NA	1590	30.2	30.2	75%	730	100.00	3351949	CP044233.1
PREDICTED: Cygnus atratus uncharacterized LOC118247781...	black swan	8868	30.2	30.2	75%	730	100.00	999	XM_035546042.1
Ananas comosus genome assembly, chromosome: 14	pineapple	4615	30.2	30.2	95%	730	94.74	11705491	LR828294.1
Methanomassiliicoccales archaeon isolate Ch47 chromosome	NA	1906667	30.2	30.2	75%	730	100.00	1818180	CP058896.1
PREDICTED: Cricetulus griseus stonin 1 (Ston1), transcript...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	3028	XM_027418004.2
PREDICTED: Cricetulus griseus stonin 1 (Ston1), transcript...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	2880	XM_027418003.2
PREDICTED: Cricetulus griseus stonin 1 (Ston1), transcript...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	3028	XM_007640305.4
PREDICTED: Cricetulus griseus stonin 1 (Ston1), transcript...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	2880	XM_003499539.5
PREDICTED: Hippoglossus stenolepis glucuronokinase with putati...	Pacific halibut	195615	30.2	30.2	75%	730	100.00	2527	XR_004695222.1
PREDICTED: Hippoglossus stenolepis glucuronokinase with putati...	Pacific halibut	195615	30.2	30.2	75%	730	100.00	2530	XM_035155220.1
PREDICTED: Hippoglossus stenolepis POM121 transmembrane...	Pacific halibut	195615	30.2	30.2	75%	730	100.00	4639	XM_035179139.1
Anas platyrhynchos genome assembly, chromosome: 27	mallard	8839	30.2	60.5	85%	730	100.00	6461411	LS423637.1
Anas platyrhynchos genome assembly, chromosome: 7	mallard	8839	30.2	60.5	80%	730	100.00	39267175	LS423617.1
Leishmania infantum genome assembly, chromosome: 32	NA	5671	30.2	30.2	75%	730	100.00	1544760	LR812965.1
Leishmania donovani genome assembly, chromosome: 32	NA	5661	30.2	30.2	75%	730	100.00	1564662	LR812652.1
Danio kyathit genome assembly, chromosome: 10	NA	242068	30.2	60.5	75%	730	100.00	54890799	LR812528.1
Danio aesculapii genome assembly, chromosome: 2	NA	1142201	30.2	30.2	75%	730	100.00	60050756	LR812511.1
Homo sapiens apoptosis associated tyrosine kinase (AATK),...	human	9606	30.2	30.2	75%	730	100.00	55778	NG_029981.1
Hordeum vulgare subsp. vulgare mRNA for predicted protein,...	domesticated...	112509	30.2	30.2	75%	730	100.00	1576	AK374186.1
Hordeum vulgare subsp. vulgare mRNA for predicted protein,...	domesticated...	112509	30.2	30.2	75%	730	100.00	1889	AK357998.1
Leishmania infantum JPCM5 genome chromosome 32	NA	435258	30.2	30.2	75%	730	100.00	1547509	FR796464.1
Fusarium vanettenii 77-13-4 uncharacterized protein...	NA	660122	30.2	30.2	75%	730	100.00	1383	XM_003043034.1
Mycoplasma pneumoniae FH, complete genome	NA	722438	30.2	30.2	75%	730	100.00	811088	CP002077.1
Watermelon chlorotic stunt virus isolate LB1 segment DNA-B,...	NA	35341	30.2	30.2	75%	730	100.00	2759	HM368372.1
Homo sapiens FOSMID clone ABC27-282D10 from chromosome 16,...	human	9606	30.2	30.2	75%	730	100.00	40440	AC240516.3
Chlorocebus aethiops BAC clone CH252-169K13 from chromosome 12...	grivet	9534	30.2	30.2	75%	730	100.00	185256	AC238856.3
Pig DNA sequence from clone CH242-151C9 on chromosome X,...	pig	9823	30.2	30.2	75%	730	100.00	171066	FP102814.4
Avian orthoreovirus strain 138 major	NA	38170	30.2	30.2	75%	730	100.00	3958	EU707933.1

core protein lambda A gen...									
Homo sapiens FOSMID clone ABC11-47211200N18 from chromosome...	human	9606	30.2	60.5	75%	730	100.00	41131	AC229659.3
Bacillus anthracis str. CDC 684, complete genome	NA	568206	30.2	30.2	75%	730	100.00	5230115	**CP001215.1**
Homo sapiens treacle ribosome biogenesis factor 1 (TCOF1),...	human	9606	30.2	30.2	75%	730	100.00	49670	NG_011341.1
Zea mays clone 278867 mRNA sequence	NA	4577	30.2	30.2	75%	730	100.00	1580	EU964428.1
Canis familiaris chromosome 14, clone XX-46G21, complete sequence	dog	9615	30.2	30.2	75%	730	100.00	222193	AC184816.5
Watermelon chlorotic stunt virus segment DNA-B, complete sequence	NA	35341	30.2	30.2	75%	730	100.00	2760	EU561236.1
Pongo abelii BAC clone CH276-514F18 from chromosome unknown,...	Sumatran ora...	9601	30.2	30.2	75%	730	100.00	195350	AC208196.4
Streptomyces eurythermus strain ATCC 23956 anglomycin...	NA	42237	30.2	30.2	75%	730	100.00	42960	EU220288.1
Pongo abelii BAC clone CH276-313P11 from chromosome unknown,...	Sumatran ora...	9601	30.2	30.2	75%	730	100.00	193477	AC206571.3
Canis familiaris, clone XX-92L16, complete sequence	dog	9615	30.2	30.2	75%	730	100.00	199653	AC198339.7
Histoplasma capsulatum NAm1 predicted protein partial mRNA	NA	339724	30.2	30.2	75%	730	100.00	507	XM_001536658.1
Oncorhynchus mykiss mRNA for c-x-c chemokine receptor type 3B,...	rainbow trout	8022	30.2	30.2	75%	730	100.00	1316	AJ888882.1
Oncorhynchus mykiss chemokine (C-X-C motif) receptor 3, tandem...	rainbow trout	8022	30.2	30.2	75%	730	100.00	1541	NM_001124423.1
Rhesus Macaque BAC CH250-411M2 () complete sequence	Rhesus monkey	9544	30.2	30.2	75%	730	100.00	150284	AC197618.5
Watermelon chlorotic stunt virus isolate IL segment DNA B,...	NA	35341	30.2	30.2	75%	730	100.00	2760	EF201810.1
Synthetic construct Bacillus anthracis clone FLH247526.01L rpl...	NA	32630	30.2	30.2	75%	730	100.00	345	**EF040156.1**
Canis Familiaris chromosome 14, clone XX-314I11, complete...	dog	9615	30.2	30.2	75%	730	100.00	210759	AC187022.6
Pan troglodytes BAC clone CH251-694H22 from chromosome 7,...	chimpanzee	9598	30.2	30.2	75%	730	100.00	181858	AC187516.3
Rhesus Macaque BAC CH250-243I15 () complete sequence	Rhesus monkey	9544	30.2	30.2	75%	730	100.00	174621	AC191882.4
Canis Familiaris chromosome 14, clone XX-66K24, complete sequence	dog	9615	30.2	30.2	75%	730	100.00	171196	AC187317.7
Pongo abelii chromosome UNK clone CH276-27H12, complete sequence	Sumatran ora...	9601	30.2	30.2	75%	730	100.00	204235	AC188097.1
Mus musculus chromosome 13, clone RP24-79G5, complete sequence	house mouse	10090	30.2	30.2	75%	730	100.00	209942	AC138401.9
Medicago truncatula chromosome 8 clone mth2-21h11, complete...	barrel medic	3880	30.2	30.2	75%	730	100.00	127696	AC138131.16
Dasypus novemcinctus clone VMRC5-10C22, complete sequence	nine-banded ...	9361	30.2	30.2	75%	730	100.00	123846	AC145506.1
Rhizobium etli CFN 42, complete genome	NA	347834	30.2	30.2	75%	730	100.00	4381608	CP000133.1
Mus musculus BAC clone RP24-207J5 from 13, complete sequence	house mouse	10090	30.2	30.2	75%	730	100.00	157713	AC121936.2
Pan troglodytes BAC clone RP43-32J19 from chromosome 7, comple...	chimpanzee	9598	30.2	30.2	75%	730	100.00	181835	AC146227.2
Homo sapiens PAC clone RP5-953F6 from 7, complete sequence	human	9606	30.2	30.2	75%	730	100.00	98935	AC004935.1

Mus musculus BAC clone RP23-273L18 from chromosome 13, complet...	house mouse	10090	30.2	30.2	75%	730	100.00	165475	AC159295.2
Tetraodon nigroviridis full-length cDNA	spotted gree...	99883	30.2	30.2	75%	730	100.00	343	CR677268.2
Tetraodon nigroviridis full-length cDNA	spotted gree...	99883	30.2	30.2	75%	730	100.00	341	CR679063.2
Tetraodon nigroviridis full-length cDNA	spotted gree...	99883	30.2	30.2	75%	730	100.00	343	CR669656.2
Tetraodon nigroviridis full-length cDNA	spotted gree...	99883	30.2	30.2	75%	730	100.00	343	CR655246.2
Tetraodon nigroviridis full-length cDNA	spotted gree...	99883	30.2	30.2	75%	730	100.00	343	CR638726.2
Homo sapiens chromosome 19 clone CTC-416D1, complete sequence	human	9606	30.2	30.2	75%	730	100.00	85297	AC011459.5
Homo sapiens chromosome 16 clone RP11-616M22, complete sequence	human	9606	30.2	30.2	75%	730	100.00	195680	AC120498.2
Human DNA sequence from clone RP5-930J4 on chromosome 1,...	human	9606	30.2	30.2	75%	730	100.00	85781	AL663074.13
Homo sapiens chromosome 16 clone RP11-331F4, complete sequence	human	9606	30.2	30.2	75%	730	100.00	176926	AC009078.6
Homo sapiens chromosome 8, clone RP11-313C15, complete sequence	human	9606	30.2	30.2	75%	730	100.00	188755	AC013562.6
Human DNA sequence from clone RP1-14N1 on chromosome...	human	9606	30.2	30.2	75%	730	100.00	83549	AL356504.5
Human DNA sequence from clone RP4-737E23 on chromosome...	human	9606	30.2	30.2	75%	730	100.00	123832	AL118508.27
Human DNA sequence from clone RP5-1172A22 on chromosome...	human	9606	30.2	30.2	75%	730	100.00	30758	AL034386.2
Pan troglodytes BAC clone CH251-149A3 from chromosome unknown,...	chimpanzee	9598	30.2	30.2	75%	730	100.00	174983	AC159040.2
Mus musculus cDNA clone IMAGE:6849527	house mouse	10090	30.2	30.2	75%	730	100.00	3447	BC094225.1
Medicago truncatula chromosome 5 clone mth2-115p22, COMPLETE...	barrel medic	3880	30.2	30.2	75%	730	100.00	133910	CR932963.2
Pan troglodytes BAC clone RP43-80G9 from chromosome 7, complet...	chimpanzee	9598	30.2	30.2	75%	730	100.00	184851	AC146055.4
Mouse DNA sequence from clone RP23-477F4 on chromosome 2,...	house mouse	10090	30.2	30.2	95%	730	94.74	163577	AL669896.7
Homo sapiens chromosome 17, clone RP11-667K14, complete sequence	human	9606	30.2	30.2	75%	730	100.00	204630	AC090617.16
Homo sapiens chromosome 5 clone CTB-108B20, complete sequence	human	9606	30.2	30.2	75%	730	100.00	183330	AC011372.7
Mouse DNA sequence from clone RP23-384C18 on chromosome 11,...	house mouse	10090	30.2	30.2	95%	730	94.74	205633	AL591496.13
Homo sapiens 3 BAC RP11-407B7 (Roswell Park Cancer Institute...	human	9606	30.2	30.2	75%	730	100.00	165016	AC024559.15
Homo sapiens BAC clone RP11-554H10 from 2, complete sequence	human	9606	30.2	60.5	75%	730	100.00	198694	AC012671.7
Dasypus novemcinctus clone VMRC5-254H15, complete sequence	nine-banded ...	9361	30.2	30.2	75%	730	100.00	114142	AC150475.2
Mus musculus BAC clone RP24-187F8 from 7, complete sequence	house mouse	10090	30.2	30.2	75%	730	100.00	163515	AC122432.4
Mus musculus chromosome 15, clone RP23-64J7, complete sequence	house mouse	10090	30.2	30.2	75%	730	100.00	243676	AC115763.10
Mus musculus mannoside acetylglucosaminyltransferase 5, mRNA...	house mouse	10090	30.2	30.2	75%	730	100.00	3294	BC053924.1

Mycoplasma pneumoniae M129, complete genome	NA	272634	30.2	30.2	75%	730	100.00	816394	U00089.2
Mouse DNA sequence from clone RP23-179F9 on chromosome 2,...	house mouse	10090	30.2	30.2	75%	730	100.00	198627	AL805958.8
Mouse DNA sequence from clone RP23-434B15 on chromosome X,...	house mouse	10090	30.2	30.2	75%	730	100.00	197111	AL732469.8
Mouse DNA sequence from clone RP23-38A10 on chromosome 11,...	house mouse	10090	30.2	30.2	75%	730	100.00	161787	AL645484.14
Homo sapiens genomic DNA, chromosome 11 clone:RP11-627G23,...	human	9606	30.2	30.2	75%	730	100.00	65900	AP004608.4
Homo sapiens genomic DNA, chromosome 11q, clone:CMB9-60D22,...	human	9606	30.2	30.2	75%	730	100.00	118465	AP004550.2
Homo sapiens genomic sequence surrounding NotI site, clone...	human	9606	30.2	30.2	75%	730	100.00	825	AJ327027.1
Homo sapiens chromosome 17 from PAC PAC RPCI-4 765O05 map...	human	9606	30.2	30.2	75%	730	100.00	120365	AL137038.5
Human DNA sequence from clone RP5-1102M4 on chromosome 1,...	human	9606	30.2	30.2	75%	730	100.00	150434	AL138784.30
watermelon chlorotic stunt virus DNA B, BC1 and BV1 genes	NA	35341	30.2	30.2	75%	730	100.00	2753	AJ012082.1
Watermelon chlorotic stunt virus-[IR] segment B, complete...	NA	223362	30.2	30.2	75%	730	100.00	2728	AJ245653.1
Watermelon chlorotic stunt virus-[SD] segment B, complete...	NA	223363	30.2	30.2	75%	730	100.00	2760	AJ245651.1
Erithacus rubecula genome assembly, chromosome: 7	European robin	37610	30.2	30.2	75%	730	100.00	46560559	LR812109.1
Erithacus rubecula genome assembly, chromosome: 28	European robin	37610	30.2	30.2	75%	730	100.00	5344592	LR812132.1
Erithacus rubecula genome assembly, chromosome: Z	European robin	37610	30.2	30.2	75%	730	100.00	31986675	LR812112.1
Bacillus anthracis strain FDAARGOS_695 chromosome	NA	1392	30.2	30.2	75%	730	100.00	5135792	**CP054816.1**
Bacillus anthracis strain FDAARGOS_703 chromosome	NA	1392	30.2	30.2	75%	730	100.00	5261520	**CP054797.1**
Bacillus thuringiensis strain FDAARGOS_791 chromosome, complet...	NA	1428	30.2	30.2	75%	730	100.00	5281841	CP054568.1
PREDICTED: Mirounga leonina SH3 and multiple ankyrin repeat...	Southern ele...	9715	30.2	30.2	75%	730	100.00	7710	XM_035013496.1
PREDICTED: Mirounga leonina SH3 and multiple ankyrin repeat...	Southern ele...	9715	30.2	30.2	75%	730	100.00	9341	XM_035013495.1
Streptomyces coelicolor strain M1154/pAMX4/pGP1416 chromosome,...	NA	1902	30.2	30.2	75%	730	100.00	8585093	CP050522.1
PREDICTED: Acipenser ruthenus major facilitator superfamily...	sterlet	7906	30.2	30.2	75%	730	100.00	3502	XM_034053851.2
PREDICTED: Pan paniscus BAR/IMD domain containing adaptor...	pygmy chimpa...	9597	30.2	30.2	75%	730	100.00	3350	XM_034943083.1
PREDICTED: Pan paniscus BAR/IMD domain containing adaptor...	pygmy chimpa...	9597	30.2	30.2	75%	730	100.00	3304	XM_034943079.1
PREDICTED: Etheostoma cragini collagen alpha-1(XVIII) chain-li...	Arkansas darter	417921	30.2	30.2	75%	730	100.00	5427	XM_034862238.1
PREDICTED: Etheostoma cragini collagen alpha-1(XVIII) chain-li...	Arkansas darter	417921	30.2	30.2	75%	730	100.00	5496	XM_034862237.1
PREDICTED: Etheostoma cragini matrix metallopeptidase 16b...	Arkansas darter	417921	30.2	30.2	75%	730	100.00	2279	XM_034887888.1
PREDICTED: Etheostoma cragini matrix metallopeptidase 16b...	Arkansas darter	417921	30.2	30.2	75%	730	100.00	3208	XM_034887887.1
Bacillus thuringiensis strain FDAARGOS_792 chromosome, complet...	NA	1428	30.2	30.2	75%	730	100.00	5251676	CP053938.1
Bacillus cereus strain	NA	1396	30.2	30.2	75%	730	100.00	5271029	CP053991.1

FDAARGOS_781 chromosome, complete genome									
Bacillus thuringiensis strain FDAARGOS_795 chromosome, complet...	NA	1428	30.2	30.2	75%	730	100.00	5228070	CP053980.1
Bacillus thuringiensis strain FDAARGOS_793 chromosome, complet...	NA	1428	30.2	30.2	75%	730	100.00	5256259	CP053981.1
Marchantia polymorpha subsp. ruderalis Tak-1 DNA, chromosome: 8	NA	1480154	30.2	30.2	75%	730	100.00	21314552	AP019873.1
Rhizobium leguminosarum bv. trifolii TA1 chromosome, complete...	NA	754521	30.2	30.2	75%	730	100.00	5036312	CP053205.2
PREDICTED: Cyclopterus lumpus megakaryocyte-associated tyrosin...	lumpfish	8103	30.2	30.2	75%	730	100.00	3236	XM_034529985.1
PREDICTED: Cyclopterus lumpus megakaryocyte-associated tyrosin...	lumpfish	8103	30.2	30.2	75%	730	100.00	3322	XM_034529984.1
PREDICTED: Cyclopterus lumpus megakaryocyte-associated tyrosin...	lumpfish	8103	30.2	30.2	75%	730	100.00	3258	XM_034529983.1
PREDICTED: Arvicanthis niloticus syntaxin 16 (Stx16), transcri...	African gras...	61156	30.2	30.2	95%	730	94.74	4290	XM_034494891.1
PREDICTED: Arvicanthis niloticus syntaxin 16 (Stx16), transcri...	African gras...	61156	30.2	30.2	95%	730	94.74	4302	XM_034494890.1
PREDICTED: Arvicanthis niloticus syntaxin 16 (Stx16), transcri...	African gras...	61156	30.2	30.2	95%	730	94.74	4351	XM_034494889.1
PREDICTED: Arvicanthis niloticus syntaxin 16 (Stx16), transcri...	African gras...	61156	30.2	30.2	95%	730	94.74	4363	XM_034494888.1
PREDICTED: Pantherophis guttatus tubulin gamma complex...	NA	94885	30.2	30.2	75%	730	100.00	3664	XM_034418925.1
PREDICTED: Pantherophis guttatus tubulin gamma complex...	NA	94885	30.2	30.2	75%	730	100.00	3868	XM_034418917.1
Fusarium oxysporum Fo47 chromosome II	NA	660027	30.2	30.2	75%	730	100.00	5611497	CP052039.1
PREDICTED: Pangasianodon hypophthalmus tubulin, gamma complex...	striped catfish	310915	30.2	30.2	75%	730	100.00	3874	XM_026932230.2
PREDICTED: Pangasianodon hypophthalmus chromodomain helicase D...	striped catfish	310915	30.2	30.2	75%	730	100.00	9297	XM_034299799.1
PREDICTED: Esox lucius kelch repeat and BTB (POZ) domain...	northern pike	8010	30.2	30.2	75%	730	100.00	3473	XM_010903171.3
PREDICTED: Esox lucius uncharacterized LOC105008131...	northern pike	8010	30.2	30.2	75%	730	100.00	959	XR_004574609.1
PREDICTED: Esox lucius SET domain containing 9 (setd9),...	northern pike	8010	30.2	30.2	75%	730	100.00	3810	XM_020044776.3
PREDICTED: Esox lucius paxillin b (pxnb), transcript variant X...	northern pike	8010	30.2	30.2	75%	730	100.00	4757	XM_029124779.2
PREDICTED: Esox lucius paxillin b (pxnb), transcript variant X...	northern pike	8010	30.2	30.2	75%	730	100.00	5148	XM_010876310.4
PREDICTED: Esox lucius paxillin b (pxnb), transcript variant X...	northern pike	8010	30.2	30.2	75%	730	100.00	5010	XM_010876309.4
PREDICTED: Esox lucius paxillin b (pxnb), transcript variant X...	northern pike	8010	30.2	30.2	75%	730	100.00	5124	XM_029124778.2
PREDICTED: Gymnodraco acuticeps tubulin, gamma complex...	NA	8218	30.2	30.2	75%	730	100.00	4491	XM_034217370.1
PREDICTED: Melopsittacus undulatus tubulin gamma complex...	budgerigar	13146	30.2	30.2	75%	730	100.00	3889	XM_034060034.1
PREDICTED: Trematomus bernacchii inhibin subunit beta Ab...	emerald rockcod	40690	30.2	30.2	75%	730	100.00	1205	XM_034113870.1
PREDICTED: Trematomus bernacchii tubulin, gamma complex...	emerald rockcod	40690	30.2	30.2	75%	730	100.00	4588	XM_034151078.1
PREDICTED: Pseudochaenichthys georgianus tubulin, gamma comple...	South Georgi...	52239	30.2	30.2	75%	730	100.00	4533	XM_034101384.1
Homo sapiens diphthamide biosynthesis 1 (DPH1), transcript...	human	9606	30.2	30.2	75%	730	100.00	2646	NM_001383.6
Phallusia mammillata mRNA for cathepsin D-like (Ctsd gene)	NA	59560	30.2	30.2	75%	730	100.00	1318	LR784234.1

PREDICTED: Fukomys damarensis triggering receptor expressed on...	Damara mole-rat	885580	30.2	30.2	75%	730	100.00	1066	XM_033766433.1
PREDICTED: Fukomys damarensis glutamate ionotropic receptor NM...	Damara mole-rat	885580	30.2	30.2	75%	730	100.00	16155	XM_010638438.3
Digitaria exilis annotation	NA	1010633	30.2	30.2	75%	730	100.00	42379666	LR792824.1
Aspergillus tanneri uncharacterized protein (ATNIH1004_010114)...	NA	1220188	30.2	30.2	75%	730	100.00	3003	XM_033574691.1
PREDICTED: Epinephelus lanceolatus ventricular zone expressed ...	giant grouper	310571	30.2	30.2	75%	730	100.00	4128	XM_033631873.1
PREDICTED: Epinephelus lanceolatus ventricular zone expressed ...	giant grouper	310571	30.2	30.2	75%	730	100.00	4305	XM_033631872.1
PREDICTED: Epinephelus lanceolatus ventricular zone expressed ...	giant grouper	310571	30.2	30.2	75%	730	100.00	4521	XM_033631871.1
PREDICTED: Epinephelus lanceolatus uncharacterized LOC11725179...	giant grouper	310571	30.2	30.2	75%	730	100.00	4227	XR_004501264.1
Digitaria exilis genome assembly, chromosome: 3A	NA	1010633	30.2	30.2	75%	730	100.00	42379666	LR761609.1
Bacillus anthracis strain FDAARGOS_696 chromosome	NA	1392	30.2	30.2	75%	730	100.00	5255974	**CP050971.1**
Bacillus anthracis strain FDAARGOS_694 chromosome	NA	1392	30.2	30.2	75%	730	100.00	5251490	**CP050970.1**
Pseudochaenichthys georgianus genome assembly, chromosome: 11	South Georgi...	52239	30.2	30.2	75%	730	100.00	33597571	LR792556.1
Canis lupus familiaris breed Labrador retriever chromosome 17a	dog	9615	30.2	30.2	75%	730	100.00	64150251	CP050603.1
Canis lupus familiaris breed Labrador retriever chromosome 18a	dog	9615	30.2	60.5	100%	730	100.00	55362250	CP050597.1
Canis lupus familiaris breed Labrador retriever chromosome 23a	dog	9615	30.2	30.2	75%	730	100.00	52268927	CP050590.1
Canis lupus familiaris breed Labrador retriever chromosome 35a	dog	9615	30.2	30.2	75%	730	100.00	26577597	CP050587.1
Canis lupus familiaris breed Labrador retriever chromosome 37a	dog	9615	30.2	30.2	75%	730	100.00	35123412	CP050579.1
Canis lupus familiaris breed Labrador retriever chromosome 16a	dog	9615	30.2	30.2	75%	730	100.00	54734298	CP050577.1
Canis lupus familiaris breed Labrador retriever chromosome 35b	dog	9615	30.2	30.2	75%	730	100.00	26531362	CP050645.1
Canis lupus familiaris breed Labrador retriever chromosome 37b	dog	9615	30.2	30.2	75%	730	100.00	35118724	CP050638.1
Canis lupus familiaris breed Labrador retriever chromosome 23b	dog	9615	30.2	30.2	75%	730	100.00	52281894	CP050632.1
Canis lupus familiaris breed Labrador retriever chromosome 18b	dog	9615	30.2	60.5	100%	730	100.00	55343242	CP050607.1
PREDICTED: Brassica rapa pyruvate, phosphate dikinase regulato...	field mustard	3711	30.2	30.2	75%	730	100.00	1460	XM_009136313.3
PREDICTED: Lacerta agilis mitogen-activated protein kinase 8...	NA	80427	30.2	30.2	75%	730	100.00	3754	XM_033162486.1
PREDICTED: Rhinolophus ferrumequinum MORN repeat containing 3...	greater hors...	59479	30.2	30.2	75%	730	100.00	4935	**XM_033097730.1**
PREDICTED: Rhinolophus ferrumequinum MORN repeat containing 3...	greater hors...	59479	30.2	30.2	75%	730	100.00	5030	**XM_033097729.1**
PREDICTED: Rhinolophus ferrumequinum MORN repeat containing 3...	greater hors...	59479	30.2	30.2	75%	730	100.00	4788	**XM_033097728.1**
PREDICTED: Rhinolophus ferrumequinum MORN repeat containing 3...	greater hors...	59479	30.2	30.2	75%	730	100.00	5204	**XM_033097727.1**
PREDICTED: Rhinolophus ferrumequinum tubulin gamma	greater hors...	59479	30.2	30.2	75%	730	100.00	3539	**XM_033104762.1**

complex...									
PREDICTED: Rhinolophus ferrumequinum tubulin gamma complex...	greater hors...	59479	30.2	30.2	75%	730	100.00	3935	**XM_033104761.1**
PREDICTED: Rhinolophus ferrumequinum ATPase phospholipid...	greater hors...	59479	30.2	30.2	75%	730	100.00	7899	**XM_033103990.1**
Rubrobacter sp. SCSIO 52909 chromosome, complete genome	NA	2653851	30.2	30.2	75%	730	100.00	4378772	CP045119.1
PREDICTED: Rattus rattus syntaxin 16 (Stx16), transcript varia...	black rat	10117	30.2	30.2	95%	730	94.74	2973	XM_032904703.1
PREDICTED: Rattus rattus syntaxin 16 (Stx16), transcript varia...	black rat	10117	30.2	30.2	95%	730	94.74	2985	XM_032904702.1
PREDICTED: Rattus rattus syntaxin 16 (Stx16), transcript varia...	black rat	10117	30.2	30.2	95%	730	94.74	3036	XM_032904701.1
PREDICTED: Rattus rattus inhibitory synaptic factor 2A...	black rat	10117	30.2	30.2	75%	730	100.00	6199	XM_032892396.1
Raphanus sativus genome assembly, chromosome: 1	radish	3726	30.2	30.2	75%	730	100.00	58898396	LR778310.1
Rhizobium leguminosarum strain A1 chromosome, complete genome	NA	384	30.2	30.2	75%	730	100.00	5067161	CP049730.1
Coregonus sp. 'balchen' genome assembly, chromosome: 36	NA	861768	30.2	30.2	75%	730	100.00	42009912	LR778288.1
Coregonus sp. 'balchen' genome assembly, chromosome: 33	NA	861768	30.2	30.2	75%	730	100.00	44662967	LR778285.1
Coregonus sp. 'balchen' genome assembly, chromosome: 25	NA	861768	30.2	30.2	75%	730	100.00	51033154	LR778277.1
Coregonus sp. 'balchen' genome assembly, chromosome: 22	NA	861768	30.2	30.2	75%	730	100.00	56862223	LR778274.1
Coregonus sp. 'balchen' genome assembly, chromosome: 14	NA	861768	30.2	30.2	75%	730	100.00	47256133	LR778266.1
Bacillus tropicus strain AOA-CPS1 chromosome	NA	2026188	30.2	30.2	75%	730	100.00	5246960	CP049019.1
PREDICTED: Lynx canadensis chromosome B4 C12orf4 homolog...	Canada lynx	61383	30.2	30.2	95%	730	94.74	6108	XM_030321663.2
PREDICTED: Etheostoma spectabile collagen alpha-1(XVIII)...	orangethroat...	54343	30.2	30.2	75%	730	100.00	5388	XM_032503423.1
PREDICTED: Etheostoma spectabile collagen alpha-1(XVIII)...	orangethroat...	54343	30.2	30.2	75%	730	100.00	5446	XM_032503422.1
PREDICTED: Etheostoma spectabile collagen alpha-1(XVIII)...	orangethroat...	54343	30.2	30.2	75%	730	100.00	5450	XM_032503421.1
PREDICTED: Etheostoma spectabile matrix...	orangethroat...	54343	30.2	30.2	75%	730	100.00	2276	XM_032531735.1
PREDICTED: Etheostoma spectabile matrix...	orangethroat...	54343	30.2	30.2	75%	730	100.00	3354	XR_004334397.1
PREDICTED: Etheostoma spectabile matrix...	orangethroat...	54343	30.2	30.2	75%	730	100.00	6983	XM_032531733.1
Plectropomus leopardus DNA, chromosome 18, nearly complete...	leopard cora...	160734	30.2	30.2	75%	730	100.00	29264940	AP022717.1
Plectropomus leopardus DNA, chromosome 15, nearly complete...	leopard cora...	160734	30.2	30.2	75%	730	100.00	32688519	AP022714.1
Plectropomus leopardus DNA, chromosome 14, nearly complete...	leopard cora...	160734	30.2	30.2	75%	730	100.00	33174000	AP022713.1
Plectropomus leopardus DNA, chromosome 9, nearly complete...	leopard cora...	160734	30.2	30.2	75%	730	100.00	35389916	AP022708.1
Plectropomus leopardus DNA, chromosome 4, nearly complete...	leopard cora...	160734	30.2	30.2	75%	730	100.00	37743081	AP022703.1
Plectropomus leopardus DNA, chromosome 2, nearly complete...	leopard cora...	160734	30.2	30.2	75%	730	100.00	42059005	AP022701.1
Epinephelus fuscoguttatus DNA, LG22, complete sequence	brown-marble...	293821	30.2	90.7	80%	730	100.00	37548733	AP022696.1
Epinephelus fuscoguttatus DNA, LG14, complete sequence	brown-marble...	293821	30.2	30.2	75%	730	100.00	43195012	AP022688.1
Epinephelus fuscoguttatus DNA, LG7, complete sequence	brown-marble...	293821	30.2	30.2	75%	730	100.00	47170333	AP022681.1
Epinephelus fuscoguttatus DNA,	brown-marble..	293821	30.2	30.2	75%	730	100.00	52788389	AP022675.1

LG1, complete sequence	.								
PREDICTED: Phoca vitulina SH3 and multiple ankyrin repeat...	harbor seal	9720	30.2	30.2	75%	730	100.00	8244	XM_032414570.1
PREDICTED: Mustela erminea SH3 and multiple ankyrin repeat...	ermine	36723	30.2	30.2	75%	730	100.00	10090	XM_032360193.1
PREDICTED: Mustela erminea SH3 and multiple ankyrin repeat...	ermine	36723	30.2	30.2	75%	730	100.00	11371	XM_032360192.1
PREDICTED: Sapajus apella IZUMO1 receptor, JUNO (IZUMO1R), mRNA	tufted capuchin	9515	30.2	30.2	75%	730	100.00	2006	XM_032295757.1
PREDICTED: Thamnophis elegans tubulin gamma complex associated...	Western terr...	35005	30.2	30.2	75%	730	100.00	3484	XM_032226661.1
PREDICTED: Aythya fuligula transmembrane protein 186 (TMEM186)...	tufted duck	219594	30.2	30.2	95%	730	94.74	929	XM_032197790.1
PREDICTED: Aythya fuligula uncharacterized LOC116494300...	tufted duck	219594	30.2	30.2	75%	730	100.00	4140	XR_004253850.1
PREDICTED: Aythya fuligula uncharacterized LOC116494300...	tufted duck	219594	30.2	30.2	75%	730	100.00	3889	XR_004253849.1
PREDICTED: Aythya fuligula uncharacterized LOC116494300...	tufted duck	219594	30.2	30.2	75%	730	100.00	3594	XR_004253848.1
PREDICTED: Aythya fuligula uncharacterized LOC116494300...	tufted duck	219594	30.2	30.2	75%	730	100.00	3552	XR_004253847.1
PREDICTED: Aythya fuligula uncharacterized LOC116494300...	tufted duck	219594	30.2	30.2	75%	730	100.00	3718	XR_004253846.1
PREDICTED: Aythya fuligula uncharacterized LOC116494300...	tufted duck	219594	30.2	30.2	75%	730	100.00	3576	XR_004253845.1
PREDICTED: Aythya fuligula uncharacterized LOC116494300...	tufted duck	219594	30.2	30.2	75%	730	100.00	3987	XR_004253844.1
PREDICTED: Aythya fuligula uncharacterized LOC116494300...	tufted duck	219594	30.2	30.2	75%	730	100.00	4126	XR_004253843.1
PREDICTED: Aythya fuligula uncharacterized LOC116494300...	tufted duck	219594	30.2	30.2	75%	730	100.00	3981	XR_004253842.1
PREDICTED: Aythya fuligula uncharacterized LOC116494300...	tufted duck	219594	30.2	30.2	75%	730	100.00	4642	XR_004253841.1
PREDICTED: Aythya fuligula uncharacterized LOC116494300...	tufted duck	219594	30.2	30.2	75%	730	100.00	4117	XR_004253840.1
PREDICTED: Corvus moneduloides AT-hook transcription factor...	New Caledoni...	1196302	30.2	30.2	75%	730	100.00	5919	XM_032130586.1
Bacillus pacificus strain NCCP 15909 chromosome, complete genome	NA	2026187	30.2	30.2	75%	730	100.00	5126903	CP041979.1
Bacillus paranthracis strain NCCP 15910 chromosome, complete...	NA	2026186	30.2	30.2	75%	730	100.00	5208566	**CP041981.1**
Bacillus paranthracis strain NCCP 14796 chromosome, complete...	NA	2026186	30.2	30.2	75%	730	100.00	5017580	**CP041750.1**
Streptomyces sp. HM190 chromosome, complete genome	NA	2695266	30.2	30.2	75%	730	100.00	7762826	CP047318.1
Lutra lutra genome assembly, chromosome: 18	Eurasian riv...	9657	30.2	30.2	75%	730	100.00	40428123	LR738420.1
Bacillus anthracis str. BF1 chromosome, complete genome	NA	1213182	30.2	30.2	75%	730	100.00	5213532	**CP047131.1**
Komagataeibacter xylinus strain CGMCC 17276 plasmid pA, comple...	NA	28448	30.2	30.2	75%	730	100.00	233861	CP041349.1
Bacillus anthracis strain FDAARGOS_706 chromosome, complete...	NA	1392	30.2	30.2	75%	730	100.00	5227454	**CP047104.1**
Bacillus anthracis strain FDAARGOS_700 chromosome, complete...	NA	1392	30.2	30.2	75%	730	100.00	5227419	**CP047099.1**
Bacillus anthracis strain FDAARGOS_698 chromosome, complete...	NA	1392	30.2	30.2	75%	730	100.00	5225746	**CP047097.1**

Bacillus paranthracis strain BC307 chromosome, complete genome	NA	2026186	30.2	30.2	75%	730	100.00	5248370	**CP047085.1**
Bacillus toyonensis strain BV-17 chromosome, complete genome	NA	155322	30.2	30.2	75%	730	100.00	5351266	CP047044.1
PREDICTED: Xenopus tropicalis gap junction beta-1 protein-like...	tropical cla...	8364	30.2	30.2	75%	730	100.00	1896	XM_004911015.4
PREDICTED: Anarrhichthys ocellatus megakaryocyte-associated...	wolf-eel	433405	30.2	30.2	75%	730	100.00	4390	XM_031863955.1
PREDICTED: Anarrhichthys ocellatus megakaryocyte-associated...	wolf-eel	433405	30.2	30.2	75%	730	100.00	4553	XM_031863954.1
PREDICTED: Anarrhichthys ocellatus megakaryocyte-associated...	wolf-eel	433405	30.2	30.2	75%	730	100.00	4531	XM_031863952.1
PREDICTED: Anarrhichthys ocellatus megakaryocyte-associated...	wolf-eel	433405	30.2	30.2	75%	730	100.00	4391	XM_031863951.1
PREDICTED: Anarrhichthys ocellatus megakaryocyte-associated...	wolf-eel	433405	30.2	30.2	75%	730	100.00	4394	XM_031863950.1
PREDICTED: Anarrhichthys ocellatus megakaryocyte-associated...	wolf-eel	433405	30.2	30.2	75%	730	100.00	4412	XM_031863949.1
PREDICTED: Anarrhichthys ocellatus neurobeachin like 2 (nbeal2...	wolf-eel	433405	30.2	30.2	75%	730	100.00	16525	XM_031853131.1
PREDICTED: Anarrhichthys ocellatus collagen alpha-1(XVIII)...	wolf-eel	433405	30.2	30.2	75%	730	100.00	6617	XM_031850165.1
PREDICTED: Anarrhichthys ocellatus collagen alpha-1(XVIII)...	wolf-eel	433405	30.2	30.2	75%	730	100.00	5322	XM_031850164.1
Bacillus albus strain DLOU-Yingkou chromosome, complete genome	NA	2026189	30.2	30.2	75%	730	100.00	5298275	CP040344.1
PREDICTED: Oncorhynchus kisutch EGF like, fibronectin type III...	coho salmon	8019	30.2	30.2	75%	730	100.00	1857	XM_031803144.1
PREDICTED: Oncorhynchus kisutch EGF like, fibronectin type III...	coho salmon	8019	30.2	30.2	75%	730	100.00	1886	XM_031803143.1
PREDICTED: Oncorhynchus kisutch EGF like, fibronectin type III...	coho salmon	8019	30.2	30.2	75%	730	100.00	3291	XM_031803142.1
PREDICTED: Oncorhynchus kisutch EGF like, fibronectin type III...	coho salmon	8019	30.2	30.2	75%	730	100.00	4340	XM_020458115.2
PREDICTED: Oncorhynchus kisutch EGF like, fibronectin type III...	coho salmon	8019	30.2	30.2	75%	730	100.00	4352	XM_031803141.1
Sciurus vulgaris genome assembly, chromosome: 16	Eurasian red...	55149	30.2	30.2	75%	730	100.00	79696672	LR738627.1
Sciurus vulgaris genome assembly, chromosome: 14	Eurasian red...	55149	30.2	30.2	75%	730	100.00	99237486	LR738625.1
Sciurus carolinensis genome assembly, chromosome: 17	gray squirrel	30640	30.2	30.2	75%	730	100.00	66045118	LR738607.1
Sciurus carolinensis genome assembly, chromosome: 16	gray squirrel	30640	30.2	30.2	75%	730	100.00	68567161	LR738606.1
Sciurus carolinensis genome assembly, chromosome: 13	gray squirrel	30640	30.2	30.2	75%	730	100.00	94684172	LR738603.1
Neostethus bicornis genome assembly, chromosome: 16	NA	300306	30.2	30.2	75%	730	100.00	41502881	LR738541.1
PREDICTED: Clupea harengus BTG anti-proliferation factor 1...	Atlantic her...	7950	30.2	30.2	75%	730	100.00	4761	XM_012824483.2
PREDICTED: Clupea harengus cellular communication network fact...	Atlantic her...	7950	30.2	30.2	75%	730	100.00	2176	XM_031573682.1
Fusarium fujikuroi strain Augusto2 chromosome VI	NA	5127	30.2	30.2	75%	730	100.00	4218434	CP023094.1
Fusarium fujikuroi strain I1.3 chromosome VI	NA	5127	30.2	30.2	75%	730	100.00	4426414	CP023106.1
Fusarium fujikuroi strain CSV1 chromosome VI	NA	5127	30.2	30.2	75%	730	100.00	4212448	CP023082.1
Caligus rogercresseyi isolate FCH chromosome 18	NA	217165	30.2	30.2	75%	730	100.00	14290352	CP045907.1

PREDICTED: Lonchura striata domestica protein Shroom1...	Bengalese finch	299123	30.2	30.2	75%	730	100.00	4845	XM_021549549.2
Streptomyces fagopyri strain QMT-28 chromosome, complete genome	NA	2662397	30.2	30.2	95%	730	94.74	8880330	CP045643.1
Bacillaceae bacterium C05 chromosome, complete genome	NA	2654326	30.2	30.2	75%	730	100.00	5258784	CP045537.1
Bacillaceae bacterium C02 chromosome, complete genome	NA	2654284	30.2	30.2	75%	730	100.00	5188692	CP045533.1
PREDICTED: Mastomys coucha syntaxin 16 (Stx16), transcript...	southern mul...	35658	30.2	30.2	95%	730	94.74	4262	XM_031372919.1
PREDICTED: Mastomys coucha syntaxin 16 (Stx16), transcript...	southern mul...	35658	30.2	30.2	95%	730	94.74	4274	XM_031372918.1
PREDICTED: Mastomys coucha syntaxin 16 (Stx16), transcript...	southern mul...	35658	30.2	30.2	95%	730	94.74	4313	XM_031372917.1
PREDICTED: Mastomys coucha syntaxin 16 (Stx16), transcript...	southern mul...	35658	30.2	30.2	95%	730	94.74	4322	XM_031372916.1
PREDICTED: Mastomys coucha syntaxin 16 (Stx16), transcript...	southern mul...	35658	30.2	30.2	95%	730	94.74	4325	XM_031372915.1
PREDICTED: Mastomys coucha syntaxin 16 (Stx16), transcript...	southern mul...	35658	30.2	30.2	95%	730	94.74	4352	XM_031372914.1
PREDICTED: Mastomys coucha glycerol kinase pseudogene...	southern mul...	35658	30.2	30.2	75%	730	100.00	1890	XR_004117543.1
Fusarium proliferatum ET1 related to ankyrin 1 (FPRO_13990),...	NA	1227346	30.2	30.2	95%	730	94.74	7773	XM_031218966.1
Fusarium proliferatum ET1 uncharacterized protein (FPRO_09124)...	NA	1227346	30.2	30.2	75%	730	100.00	1656	XM_031232482.1
PREDICTED: Ipomoea triloba probable leucine-rich repeat...	trilobed mor...	35885	30.2	30.2	75%	730	100.00	2694	XR_004099421.1
PREDICTED: Ipomoea triloba probable leucine-rich repeat...	trilobed mor...	35885	30.2	30.2	75%	730	100.00	3356	XM_031264786.1
Lachnellula hyalina Protein MSS51, mitochondrial (MSS51_1),...	NA	1316788	30.2	30.2	75%	730	100.00	1485	XM_031150408.1
Streptomyces coelicolor A3(2) strain CFB_NBC_0001 chromosome,...	NA	100226	30.2	30.2	75%	730	100.00	8667664	CP042324.1
Phialemoniopsis curvata uncharacterized protein (E0L32_008814)...	NA	1093900	30.2	30.2	75%	730	100.00	957	XM_031143710.1
Pyricularia grisea uncharacterized protein (PgNI_11188), mRNA	NA	148305	30.2	30.2	75%	730	100.00	2732	XM_031131161.1
Craseonycteris thonglongyai microsatellite Ct7 sequence	hog-nosed bat	208972	30.2	30.2	75%	730	100.00	410	**MK605526.1**
Bacillus wiedmannii strain SR52 chromosome, complete genome	NA	1890302	30.2	30.2	75%	730	100.00	5448361	CP032365.1
PREDICTED: Leptonychotes weddellii uncharacterized LOC11593798...	Weddell seal	9713	30.2	30.2	75%	730	100.00	2067	XR_004073192.1
PREDICTED: Leptonychotes weddellii SH3 and multiple ankyrin...	Weddell seal	9713	30.2	30.2	75%	730	100.00	8097	XM_031031776.1
PREDICTED: Gorilla gorilla gorilla uncharacterized LOC11593078...	western lowl...	9595	30.2	30.2	75%	730	100.00	1789	XR_004067374.1
Thalassophryne amazonica genome assembly, chromosome: 16	NA	390379	30.2	30.2	95%	730	94.74	92122960	LR722981.1
Streptomyces spectabilis strain ATCC 27465 chromosome, complet...	NA	68270	30.2	30.2	75%	730	100.00	9807160	CP023690.1
PREDICTED: Globicephala melas uncharacterized LOC115842690...	long-finned ...	9731	30.2	30.2	75%	730	100.00	3161	XR_004035430.1
PREDICTED: Nomascus leucogenys EGF like domain multiple 7...	northern whi...	61853	30.2	30.2	75%	730	100.00	1515	XM_030818213.1
PREDICTED: Nomascus leucogenys EGF like domain multiple 7...	northern whi...	61853	30.2	30.2	75%	730	100.00	2225	XR_004031477.1
PREDICTED: Nomascus leucogenys EGF like domain multiple 7...	northern whi...	61853	30.2	30.2	75%	730	100.00	2140	XR_004031476.1

Bacillus sp. BS98 chromosome, complete genome	NA	2608254	30.2	30.2	75%	730	100.00	5200216	CP043830.1
PREDICTED: Chanos chanos tubulin gamma complex associated...	milkfish	29144	30.2	30.2	75%	730	100.00	2803	XM_030780245.1
PREDICTED: Chanos chanos chromodomain helicase DNA binding...	milkfish	29144	30.2	30.2	75%	730	100.00	9153	XM_030765859.1
PREDICTED: Archocentrus centrarchus chromodomain helicase DNA...	flier cichlid	63155	30.2	30.2	75%	730	100.00	8057	XM_030751709.1
PREDICTED: Archocentrus centrarchus chromodomain helicase DNA...	flier cichlid	63155	30.2	30.2	75%	730	100.00	8028	XM_030751708.1
Bacillus mycoides strain BPN401 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5369163	CP031071.1
PREDICTED: Strigops habroptila uncharacterized LOC115605014...	Kakapo	2489341	30.2	30.2	75%	730	100.00	2785	XR_003990477.1
PREDICTED: Sparus aurata synaptoporin-like (LOC115582712), mRNA	gilthead sea...	8175	30.2	30.2	75%	730	100.00	3357	XM_030418846.1
Asterias rubens genome assembly, chromosome: 14	European sta...	7604	30.2	30.2	75%	730	100.00	14674731	LR699105.1
PREDICTED: Gadus morhua voltage-dependent calcium channel beta...	Atlantic cod	8049	30.2	30.2	75%	730	100.00	4146	XM_030363432.1
Chanos chanos genome assembly, chromosome: 8	milkfish	29144	30.2	30.2	75%	730	100.00	48343650	LR697113.1
Chanos chanos genome assembly, chromosome: 2	milkfish	29144	30.2	30.2	75%	730	100.00	59736555	LR697107.1
PREDICTED: Lynx canadensis rotatin (RTTN), transcript variant...	Canada lynx	61383	30.2	30.2	75%	730	100.00	7543	XM_030335855.1
PREDICTED: Lynx canadensis rotatin (RTTN), transcript variant...	Canada lynx	61383	30.2	30.2	75%	730	100.00	7245	XM_030335854.1
PREDICTED: Lynx canadensis trem-like transcript 2 protein...	Canada lynx	61383	30.2	30.2	75%	730	100.00	2295	XM_030315464.1
PREDICTED: Lynx canadensis trem-like transcript 2 protein...	Canada lynx	61383	30.2	30.2	75%	730	100.00	2466	XM_030315461.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	23671	XM_030223959.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	26270	XM_030223958.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	26276	XM_030223957.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	26912	XM_030223956.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27368	XM_030223955.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27371	XM_030223954.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27422	XM_030223953.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27431	XM_030223952.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27434	XM_030223951.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27635	XM_030223950.1

PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27674	XM_030223949.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27752	XM_030223948.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27755	XM_030223947.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27893	XM_030223946.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27902	XM_030223945.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27926	XM_030223944.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27959	XM_023307289.2
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27968	XM_030223943.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27977	XM_030223942.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	27998	XM_030223941.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	28001	XM_030223940.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	28004	XM_030223939.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	28019	XM_030223938.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	28037	XM_030223937.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	28040	XM_030223936.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	28067	XM_030223935.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	28073	XM_030223934.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	28073	XM_030223933.1
PREDICTED: Drosophila hydei twitchin (LOC111594130), transcrip...	NA	7224	30.2	30.2	95%	730	94.74	28076	XM_030223932.1
Pandoraea pnomenusa strain TF-18 chromosome, complete genome	NA	93220	30.2	30.2	75%	730	100.00	5499432	CP042219.1
Lacipirellula limnantheis strain I41 chromosome	NA	2528024	30.2	30.2	75%	730	100.00	6777282	CP036339.1
Caulifigura coniformis strain Pan44 chromosome	NA	2527983	30.2	30.2	75%	730	100.00	6761146	CP036271.1
Sparus aurata genome assembly, chromosome: 20	gilthead sea...	8175	30.2	30.2	75%	730	100.00	28386240	LR537140.1
Sparus aurata genome assembly, chromosome: 15	gilthead sea...	8175	30.2	30.2	75%	730	100.00	31859785	LR537135.1
Haemonchus contortus strain NZ_Hco_NP chromosome 5	barber pole ...	6289	30.2	30.2	75%	730	100.00	87242733	CP035803.1

PREDICTED: Salarias fasciatus ribosomal protein S6 kinase like...	jewelled blenny	181472	30.2	30.2	75%	730	100.00	2398	XM_030117458.1
PREDICTED: Salarias fasciatus BCL2 like 12 (bcl2l12), mRNA	jewelled blenny	181472	30.2	30.2	75%	730	100.00	2666	XM_030089927.1
PREDICTED: Salarias fasciatus nesprin-1-like (LOC115385427), mRNA	jewelled blenny	181472	30.2	30.2	75%	730	100.00	7225	XM_030087418.1
PREDICTED: Salarias fasciatus nesprin-1-like (LOC115385417), mRNA	jewelled blenny	181472	30.2	30.2	75%	730	100.00	6204	XM_030087408.1
Bacillus sp. BD59S chromosome, complete genome	NA	2499213	30.2	30.2	75%	730	100.00	5283933	CP034686.1
Gadus morhua genome assembly, chromosome: 22	Atlantic cod	8049	30.2	30.2	75%	730	100.00	23744039	LR633964.1
Gadus morhua genome assembly, chromosome: 17	Atlantic cod	8049	30.2	60.5	75%	730	100.00	21723002	LR633959.1
Gadus morhua genome assembly, chromosome: 16	Atlantic cod	8049	30.2	30.2	75%	730	100.00	34794352	LR633958.1
Gadus morhua genome assembly, chromosome: 8	Atlantic cod	8049	30.2	30.2	75%	730	100.00	29710654	LR633950.1
Gadus morhua genome assembly, chromosome: 7	Atlantic cod	8049	30.2	30.2	75%	730	100.00	34137969	LR633949.1
Gadus morhua genome assembly, chromosome: 6	Atlantic cod	8049	30.2	30.2	75%	730	100.00	27762770	LR633948.1
PREDICTED: Takifugu rubripes fibroblast growth factor 10-like...	torafugu	31033	30.2	30.2	75%	730	100.00	1498	XM_011604978.2
Aquila chrysaetos chrysaetos genome assembly, chromosome: 16	NA	223781	30.2	30.2	75%	730	100.00	30610376	LR606196.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 11	NA	223781	30.2	30.2	75%	730	100.00	43755789	LR606191.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 26	NA	223781	30.2	30.2	75%	730	100.00	17717355	LR606206.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 24	NA	223781	30.2	30.2	75%	730	100.00	20993271	LR606204.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 23	NA	223781	30.2	30.2	75%	730	100.00	21012167	LR606203.1
Pandoraea pnomenusa strain M202 chromosome, complete genome	NA	93220	30.2	30.2	75%	730	100.00	5389809	CP041237.1
PREDICTED: Salmo trutta EGF like, fibronectin type III and...	river trout	8032	30.2	30.2	75%	730	100.00	4151	XM_029709009.1
PREDICTED: Salmo trutta EGF like, fibronectin type III and...	river trout	8032	30.2	30.2	75%	730	100.00	3295	XM_029709008.1
PREDICTED: Salmo trutta EGF like, fibronectin type III and...	river trout	8032	30.2	30.2	75%	730	100.00	3436	XM_029709007.1
PREDICTED: Salmo trutta EGF like, fibronectin type III and...	river trout	8032	30.2	30.2	75%	730	100.00	3123	XR_003868879.1
PREDICTED: Salmo trutta EGF like, fibronectin type III and...	river trout	8032	30.2	30.2	75%	730	100.00	3044	XM_029709006.1
PREDICTED: Salmo trutta EGF like, fibronectin type III and...	river trout	8032	30.2	30.2	75%	730	100.00	3720	XM_029709005.1
PREDICTED: Oncorhynchus nerka EGF like, fibronectin type III a...	sockeye salmon	8023	30.2	30.2	75%	730	100.00	1752	XM_029654887.1
PREDICTED: Oncorhynchus nerka EGF like, fibronectin type III a...	sockeye salmon	8023	30.2	30.2	75%	730	100.00	4213	XM_029654881.1
PREDICTED: Oncorhynchus nerka EGF like, fibronectin type III a...	sockeye salmon	8023	30.2	30.2	75%	730	100.00	4237	XM_029654874.1
Myripristis murdjan genome assembly, chromosome: 23	pinecone sol...	586833	30.2	30.2	75%	730	100.00	28196746	LR597572.1
Myripristis murdjan genome assembly, chromosome: 9	pinecone sol...	586833	30.2	30.2	75%	730	100.00	38390726	LR597558.1
Myripristis murdjan genome assembly, chromosome: 8	pinecone sol...	586833	30.2	30.2	75%	730	100.00	36448408	LR597557.1
Sphaeramia orbicularis genome assembly, chromosome: 14	orbiculate c...	375764	30.2	30.2	75%	730	100.00	55997211	LR597471.1
Sphaeramia orbicularis genome assembly, chromosome: 3	orbiculate c...	375764	30.2	30.2	75%	730	100.00	63265450	LR597460.1

Salarias fasciatus genome assembly, chromosome: 20	jewelled blenny	181472	30.2	60.5	80%	730	100.00	34145682	LR597455.1
PREDICTED: Rhinatrema bivittatum aminoacylase 1 (ACY1),...	two-lined ca...	194408	30.2	30.2	75%	730	100.00	5547	XM_029599507.1
PREDICTED: Rhinatrema bivittatum aminoacylase 1 (ACY1),...	two-lined ca...	194408	30.2	30.2	75%	730	100.00	5551	XM_029599506.1
PREDICTED: Rhinatrema bivittatum aminoacylase 1 (ACY1),...	two-lined ca...	194408	30.2	30.2	75%	730	100.00	5380	XM_029599505.1
PREDICTED: Rhinatrema bivittatum aminoacylase 1 (ACY1),...	two-lined ca...	194408	30.2	30.2	75%	730	100.00	5657	XM_029599504.1
PREDICTED: Rhinatrema bivittatum V-set pre-B cell surrogate...	two-lined ca...	194408	30.2	30.2	75%	730	100.00	1766	XM_029571030.1
Azoarcus sp. DD4 chromosome, complete genome	NA	2027405	30.2	30.2	75%	730	100.00	5400077	CP022958.1
Bacillus tropicus strain LM1212-W3 chromosome, complete genome	NA	2026188	30.2	30.2	75%	730	100.00	5631167	CP041071.1
PREDICTED: Nannospalax galili dihydropyrimidinase like 4...	Upper Galile...	1026970	30.2	30.2	75%	730	100.00	3277	XM_008823149.3
Microcaecilia unicolor genome assembly, chromosome: 14	NA	1415580	30.2	30.2	75%	730	100.00	56647458	LR594645.1
PREDICTED: Mus pahari syntaxin 16 (Stx16), transcript variant...	shrew mouse	10093	30.2	30.2	95%	730	94.74	4389	XM_021193651.2
PREDICTED: Mus pahari syntaxin 16 (Stx16), transcript variant...	shrew mouse	10093	30.2	30.2	95%	730	94.74	4401	XM_021193650.2
Prunus dulcis DNA, pseudomolecule Pd06	almond	3755	30.2	30.2	75%	730	100.00	29142197	AP019302.1
Bacillus anthracis PCr DNA, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5209717	**AP019731.1**
PREDICTED: Mus caroli syntaxin 16 (Stx16), transcript variant...	Ryukyu mouse	10089	30.2	30.2	95%	730	94.74	4395	XM_021153540.2
PREDICTED: Mus caroli syntaxin 16 (Stx16), transcript variant...	Ryukyu mouse	10089	30.2	30.2	95%	730	94.74	4407	XM_021153534.2
PREDICTED: Mus caroli syntaxin 16 (Stx16), transcript variant...	Ryukyu mouse	10089	30.2	30.2	95%	730	94.74	4447	XM_021153525.2
PREDICTED: Mus caroli syntaxin 16 (Stx16), transcript variant...	Ryukyu mouse	10089	30.2	30.2	95%	730	94.74	4459	XM_021153517.2
Bacillus anthracis strain 17OD930 chromosome, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5213297	**CP029323.1**
Rhodococcus pyridinivorans strain YF3 chromosome, complete genome	NA	103816	30.2	30.2	75%	730	100.00	5257019	CP040719.1
Gossypium raimondii isolate D5-4 chromosome D5_03	NA	29730	30.2	30.2	75%	730	100.00	63031283	CP032555.1
Homo sapiens BAR/IMD domain containing adaptor protein 2...	human	9606	30.2	30.2	75%	730	100.00	2892	NM_017451.3
Homo sapiens BAR/IMD domain containing adaptor protein 2...	human	9606	30.2	30.2	75%	730	100.00	3304	NM_001144888.2
Homo sapiens BAR/IMD domain containing adaptor protein 2...	human	9606	30.2	30.2	75%	730	100.00	3350	NM_006340.3
Takifugu rubripes genome assembly, chromosome: 18	torafugu	31033	30.2	30.2	75%	730	100.00	10237708	LR584252.2
Syngnathus acus genome assembly, chromosome: 22	greater pipe...	161584	30.2	30.2	75%	730	100.00	11039312	LR594606.1
Syngnathus acus genome assembly, chromosome: 21	greater pipe...	161584	30.2	30.2	75%	730	100.00	14974571	LR594605.1
Syngnathus acus genome assembly, chromosome: 19	greater pipe...	161584	30.2	30.2	75%	730	100.00	8952397	LR594603.1
PREDICTED: Labrus bergylta uncharacterized LOC114920755...	ballan wrasse	56723	30.2	30.2	75%	730	100.00	829	XR_003809051.1
PREDICTED: Labrus bergylta PHD finger protein 19 (phf19),...	ballan wrasse	56723	30.2	30.2	75%	730	100.00	4515	XM_020640742.2
PREDICTED: Labrus bergylta PHD finger protein 19 (phf19),...	ballan wrasse	56723	30.2	30.2	75%	730	100.00	4518	XM_020640741.2
Alkalihalobacillus halodurans isolate LB-1 chromosome, complet...	NA	86665	30.2	30.2	75%	730	100.00	4315604	CP040441.1

PREDICTED: Scleropages formosus tubulin tyrosine ligase like 1...	Asian bonyto...	113540	30.2	30.2	75%	730	100.00	3418	XM_029253083.1
PREDICTED: Scleropages formosus G-protein coupled receptor...	Asian bonyto...	113540	30.2	30.2	75%	730	100.00	3245	XM_018746897.2
Leishmania amazonensis strain UA301 chromosome 21	NA	5659	30.2	30.2	75%	730	100.00	735541	CP040149.1
PREDICTED: Podarcis muralis mitogen-activated protein kinase 8...	Common wall ...	64176	30.2	30.2	75%	730	100.00	6037	XM_028746670.1
PREDICTED: Dendrobium catenatum uncharacterized LOC110097660...	NA	906689	30.2	30.2	75%	730	100.00	3447	XM_020824168.2
PREDICTED: Grammomys surdaster syntaxin 16 (Stx16), transcript...	NA	491861	30.2	30.2	95%	730	94.74	4044	XM_028769548.1
PREDICTED: Grammomys surdaster syntaxin 16 (Stx16), transcript...	NA	491861	30.2	30.2	95%	730	94.74	4056	XM_028769547.1
PREDICTED: Grammomys surdaster syntaxin 16 (Stx16), transcript...	NA	491861	30.2	30.2	95%	730	94.74	4095	XM_028769546.1
PREDICTED: Grammomys surdaster syntaxin 16 (Stx16), transcript...	NA	491861	30.2	30.2	95%	730	94.74	4107	XM_028769545.1
Bacillus cereus strain MH19 chromosome, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5247580	CP039269.1
Plasmodium gonderi hypothetical protein, conserved (PGO_131840...	NA	77519	30.2	30.2	75%	730	100.00	4374	XM_028689700.1
Salmo trutta genome assembly, chromosome: 12	river trout	8032	30.2	30.2	75%	730	100.00	97529106	LR584441.1
Salmo trutta genome assembly, chromosome: 7	river trout	8032	30.2	30.2	75%	730	100.00	59837330	LR584430.1
Salmo trutta genome assembly, chromosome: 31	river trout	8032	30.2	30.2	75%	730	100.00	45589842	LR584423.1
Salmo trutta genome assembly, chromosome: 29	river trout	8032	30.2	30.2	75%	730	100.00	46063367	LR584418.1
Salmo trutta genome assembly, chromosome: 37	river trout	8032	30.2	30.2	75%	730	100.00	35205783	LR584417.1
Salmo trutta genome assembly, chromosome: 33	river trout	8032	30.2	30.2	75%	730	100.00	44893998	LR584414.1
Salmo trutta genome assembly, chromosome: 9	river trout	8032	30.2	30.2	75%	730	100.00	49359203	LR584409.1
Takifugu rubripes genome assembly, chromosome: 7	torafugu	31033	30.2	60.5	85%	730	100.00	17515293	LR584238.1
Scleropages formosus genome assembly, chromosome: 25	Asian bonyto...	113540	30.2	30.2	75%	730	100.00	19076140	LR584090.1
Scleropages formosus genome assembly, chromosome: 18	Asian bonyto...	113540	30.2	30.2	75%	730	100.00	26243056	LR584083.1
Scleropages formosus genome assembly, chromosome: 11	Asian bonyto...	113540	30.2	30.2	75%	730	100.00	31084684	LR584076.1
Scleropages formosus genome assembly, chromosome: 2	Asian bonyto...	113540	30.2	30.2	75%	730	100.00	43577283	LR584067.1
Scleropages formosus genome assembly, chromosome: 1	Asian bonyto...	113540	30.2	30.2	75%	730	100.00	54115380	LR584066.1
Echeneis naucrates genome assembly, chromosome: 21	live sharksu...	173247	30.2	90.7	85%	730	100.00	23068250	LR584062.1
Echeneis naucrates genome assembly, chromosome: 18	live sharksu...	173247	30.2	30.2	75%	730	100.00	15424226	LR584059.1
Echeneis naucrates genome assembly, chromosome: 9	live sharksu...	173247	30.2	30.2	75%	730	100.00	24718712	LR584050.1
Caenorhabditis elegans strain CB4856 chromosome I	NA	6239	30.2	30.2	75%	730	100.00	15528896	CP038187.1

PREDICTED: Gouania willdenowi DNA topoisomerase III alpha...	blunt-snoute...	441366	30.2	30.2	75%	730	100.00	3642	XM_028454412.1
Betta splendens genome assembly, chromosome: 2	Siamese figh...	158456	30.2	30.2	75%	730	100.00	29498272	LR132025.2
Denticeps clupeoides genome assembly, chromosome: 17	denticle her...	299321	30.2	30.2	75%	730	100.00	20348767	LR535829.1
Denticeps clupeoides genome assembly, chromosome: 14	denticle her...	299321	30.2	60.5	75%	730	100.00	21670620	LR535826.1
Denticeps clupeoides genome assembly, chromosome: 10	denticle her...	299321	30.2	30.2	75%	730	100.00	22713814	LR535822.1
Bacillus anthracis strain HDZK-BYSB7 chromosome, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5294779	**CP026608.1**
Bacillus sp. SYJ chromosome, complete genome	NA	2529386	30.2	30.2	75%	730	100.00	5296886	CP036356.1
Anabas testudineus genome assembly, chromosome: 1	climbing perch	64144	30.2	30.2	75%	730	100.00	27357120	LR132051.1
Anabas testudineus genome assembly, chromosome: 9	climbing perch	64144	30.2	30.2	75%	730	100.00	28519589	LR132038.1
Gouania willdenowi genome assembly, chromosome: 20	blunt-snoute...	441366	30.2	30.2	75%	730	100.00	28787763	LR131990.1
Gouania willdenowi genome assembly, chromosome: 18	blunt-snoute...	441366	30.2	30.2	75%	730	100.00	28478336	LR131982.1
Mesorhizobium sp. M7D.F.Ca.US.005.01.1.1 chromosome	NA	2493678	30.2	30.2	75%	730	100.00	7168230	CP034453.1
Parambassis ranga genome assembly, chromosome: 14	Indian glass...	210632	30.2	60.5	90%	730	100.00	21894654	LR131964.1
Cottoperca gobio genome assembly, chromosome: 6	NA	56716	30.2	30.2	75%	730	100.00	27680345	LR131936.1
Cottoperca gobio genome assembly, chromosome: 3	NA	56716	30.2	30.2	75%	730	100.00	30028995	LR131933.1
Cottoperca gobio genome assembly, chromosome: 23	NA	56716	30.2	30.2	75%	730	100.00	15932363	LR131931.1
Cottoperca gobio genome assembly, chromosome: 16	NA	56716	30.2	30.2	75%	730	100.00	26581398	LR131923.1
PREDICTED: Coffea eugenioides small glutamine-rich...	NA	49369	30.2	30.2	75%	730	100.00	1597	XM_027294241.1
PREDICTED: Coffea eugenioides small glutamine-rich...	NA	49369	30.2	30.2	75%	730	100.00	1639	XM_027294213.1
Bacillus wiedmannii bv. thuringiensis strain FCC41 chromosome,...	NA	2494319	30.2	30.2	75%	730	100.00	5513449	CP024684.1
PREDICTED: Coffea arabica small glutamine-rich tetratricopepti...	coffee	13443	30.2	30.2	75%	730	100.00	1691	XM_027236078.1
PREDICTED: Coffea arabica small glutamine-rich tetratricopepti...	coffee	13443	30.2	30.2	75%	730	100.00	1733	XM_027238876.1
Bacillus sp. FDAARGOS_527 chromosome, complete genome	NA	2576356	30.2	30.2	75%	730	100.00	5277296	CP033795.1
Brassica oleracea HDEM genome, scaffold: C1	wild cabbage	3712	30.2	30.2	75%	730	100.00	52030199	LR031878.1
Brassica rapa genome, scaffold: A03	field mustard	3711	30.2	30.2	75%	730	100.00	34481995	LR031572.1
Brassica rapa genome, scaffold: A01	field mustard	3711	30.2	30.2	75%	730	100.00	37915545	LR031571.1
PREDICTED: Lagenorhynchus obliquidens uncharacterized...	Pacific whit...	90247	30.2	30.2	75%	730	100.00	2426	XM_027080869.1
PREDICTED: Acinonyx jubatus rotatin (RTTN), transcript variant...	cheetah	32536	30.2	30.2	75%	730	100.00	6394	XM_027069162.1
PREDICTED: Acinonyx jubatus rotatin (RTTN), transcript variant...	cheetah	32536	30.2	30.2	75%	730	100.00	7275	XM_027069161.1
PREDICTED: Acinonyx jubatus rotatin (RTTN), transcript variant...	cheetah	32536	30.2	30.2	75%	730	100.00	7278	XM_027069160.1
PREDICTED: Acinonyx jubatus rotatin (RTTN), transcript variant...	cheetah	32536	30.2	30.2	75%	730	100.00	7339	XM_027069159.1
Vibrio owensii strain V180403	NA	696485	30.2	30.2	75%	730	100.00	2486946	CP033145.1

chromosome 2, complete sequence									
PREDICTED: Athene cunicularia cryptochrome-2-like...	burrowing owl	194338	30.2	30.2	75%	730	100.00	1641	XM_026864369.1
PREDICTED: Microtus ochrogaster cullin 4B (Cul4b), mRNA	prairie vole	79684	30.2	30.2	75%	730	100.00	5057	XM_013350462.2
PREDICTED: Zonotrichia albicollis cadherin-13 (LOC102060476),...	white-throat...	44394	30.2	30.2	75%	730	100.00	7597	XM_005496117.3
PREDICTED: Pseudonaja textilis tubulin gamma complex associate...	NA	8673	30.2	30.2	75%	730	100.00	3322	XM_026708377.1
PREDICTED: Notechis scutatus tubulin gamma complex associated...	mainland tig...	8663	30.2	30.2	75%	730	100.00	3313	XM_026668888.1
Bacillus mobilis strain ML-A2C4 chromosome, complete genome	NA	2026190	30.2	30.2	75%	730	100.00	5468285	CP031443.1
PREDICTED: Ursus arctos horribilis SH3 and multiple ankyrin...	NA	116960	30.2	30.2	75%	730	100.00	9491	XM_026482962.1
PREDICTED: Ursus arctos horribilis SH3 and multiple ankyrin...	NA	116960	30.2	30.2	75%	730	100.00	10053	XM_026482961.1
PREDICTED: Ursus arctos horribilis SH3 and multiple ankyrin...	NA	116960	30.2	30.2	75%	730	100.00	9360	XM_026482959.1
PREDICTED: Ursus arctos horribilis SH3 and multiple ankyrin...	NA	116960	30.2	30.2	75%	730	100.00	10047	XM_026482958.1
PREDICTED: Ursus arctos horribilis SH3 and multiple ankyrin...	NA	116960	30.2	30.2	75%	730	100.00	9575	XM_026482957.1
PREDICTED: Ursus arctos horribilis SH3 and multiple ankyrin...	NA	116960	30.2	30.2	75%	730	100.00	9518	XM_026482956.1
PREDICTED: Piliocolobus tephrosceles spermine oxidase (SMOX),...	Ugandan red ...	591936	30.2	30.2	75%	730	100.00	4610	XM_023217936.2
PREDICTED: Piliocolobus tephrosceles spermine oxidase (SMOX),...	Ugandan red ...	591936	30.2	30.2	75%	730	100.00	4700	XM_023217935.2
Ipomoea triloba cultivar NCNSP0323 chromosome 1	trilobed mor...	35885	30.2	30.2	75%	730	100.00	38093535	CP025660.1
Ipomoea trifida cultivar NCNSP0306 chromosome 1	NA	35884	30.2	30.2	75%	730	100.00	32247286	CP025644.1
Bacillus thuringiensis LM1212 chromosome, complete genome	NA	1417985	30.2	30.2	75%	730	100.00	5705934	CP024771.1
PREDICTED: Anabas testudineus chromosome 9 C5orf34 homolog...	climbing perch	64144	30.2	30.2	75%	730	100.00	1762	XM_026342558.1
PREDICTED: Anabas testudineus chromosome 9 C5orf34 homolog...	climbing perch	64144	30.2	30.2	75%	730	100.00	1813	XM_026342557.1
PREDICTED: Mastacembelus armatus tubulin gamma complex...	zig-zag eel	205130	30.2	30.2	75%	730	100.00	5097	XM_026301552.1
PREDICTED: Carassius auratus chromodomain-helicase-DNA-binding...	goldfish	7957	30.2	30.2	75%	730	100.00	9188	XM_026205056.1
PREDICTED: Carassius auratus chromodomain-helicase-DNA-binding...	goldfish	7957	30.2	30.2	75%	730	100.00	9096	XM_026205055.1
PREDICTED: Carassius auratus chromodomain-helicase-DNA-binding...	goldfish	7957	30.2	30.2	75%	730	100.00	9191	XM_026205054.1
PREDICTED: Carassius auratus TBC1 domain family member 5-like...	goldfish	7957	30.2	30.2	75%	730	100.00	3572	XM_026289961.1
PREDICTED: Carassius auratus TBC1 domain family member 5-like...	goldfish	7957	30.2	30.2	75%	730	100.00	2776	XM_026289960.1
PREDICTED: Carassius auratus TBC1 domain family member 5-like...	goldfish	7957	30.2	30.2	75%	730	100.00	3645	XM_026289959.1
PREDICTED: Carassius auratus TBC1 domain family member 5-like...	goldfish	7957	30.2	30.2	75%	730	100.00	3707	XM_026289957.1
Auritidibacter sp. NML130574 chromosome, complete genome	NA	2170745	30.2	30.2	75%	730	100.00	2656163	CP031746.1
Bacillus anthracis CZC5 DNA,	NA	1392	30.2	30.2	75%	730	100.00	5219278	**AP018443.1**

complete genome									
Bacillus anthracis strain MCCC 1A02161 chromosome, complete...	NA	1392	30.2	30.2	75%	730	100.00	5231857	**CP031642.1**
Bacillus anthracis strain MCCC 1A01412 chromosome, complete...	NA	1392	30.2	30.2	75%	730	100.00	5291783	**CP031643.1**
PREDICTED: Eptesicus fuscus TRPM8 channel associated factor 1...	big brown bat	29078	30.2	30.2	75%	730	100.00	2959	**XM_028128984.1**
PREDICTED: Eptesicus fuscus TRPM8 channel associated factor 1...	big brown bat	29078	30.2	30.2	75%	730	100.00	3701	**XM_028128983.1**
PREDICTED: Eptesicus fuscus TRPM8 channel associated factor 1...	big brown bat	29078	30.2	30.2	75%	730	100.00	3740	**XM_028128982.1**
PREDICTED: Eptesicus fuscus TRPM8 channel associated factor 1...	big brown bat	29078	30.2	30.2	75%	730	100.00	3747	**XM_028128981.1**
PREDICTED: Eptesicus fuscus KRAB-A domain containing 1 (KRBA1)...	big brown bat	29078	30.2	30.2	95%	730	94.74	4892	**XM_028128946.1**
PREDICTED: Eptesicus fuscus KRAB-A domain containing 1 (KRBA1)...	big brown bat	29078	30.2	30.2	95%	730	94.74	5157	**XM_028128945.1**
PREDICTED: Eptesicus fuscus KRAB-A domain containing 1 (KRBA1)...	big brown bat	29078	30.2	30.2	95%	730	94.74	5295	**XM_028128944.1**
PREDICTED: Eptesicus fuscus KRAB-A domain containing 1 (KRBA1)...	big brown bat	29078	30.2	30.2	95%	730	94.74	5338	**XM_028128943.1**
PREDICTED: Eptesicus fuscus tubulin gamma complex associated...	big brown bat	29078	30.2	30.2	75%	730	100.00	3156	**XM_028148815.1**
PREDICTED: Eptesicus fuscus tubulin gamma complex associated...	big brown bat	29078	30.2	30.2	75%	730	100.00	3900	**XM_008143924.2**
Mycoplasma pneumoniae strain NCTC10119 genome assembly,...	NA	2104	30.2	30.2	75%	730	100.00	817125	LR214945.1
Bradyrhizobium guangxiense strain CCBAU 53363 chromosome,...	NA	1325115	30.2	30.2	75%	730	100.00	7220948	CP022219.1
PREDICTED: Empidonax traillii CD7 molecule (CD7), mRNA	willow flyca...	164674	30.2	30.2	75%	730	100.00	2938	XM_027886117.1
Corallococcus coralloides strain B035 chromosome, complete genome	NA	184914	30.2	60.5	75%	730	100.00	9587888	CP034669.1
PREDICTED: Falco cherrug cancer susceptibility 1 (CASC1),...	Saker falcon	345164	30.2	30.2	75%	730	100.00	5389	XM_027797425.1
PREDICTED: Falco cherrug cancer susceptibility 1 (CASC1),...	Saker falcon	345164	30.2	30.2	75%	730	100.00	5534	XM_027797424.1
PREDICTED: Falco cherrug cancer susceptibility 1 (CASC1),...	Saker falcon	345164	30.2	30.2	75%	730	100.00	3561	XM_027797422.1
PREDICTED: Falco cherrug cancer susceptibility 1 (CASC1),...	Saker falcon	345164	30.2	30.2	75%	730	100.00	4379	XM_027797421.1
PREDICTED: Falco cherrug cancer susceptibility 1 (CASC1),...	Saker falcon	345164	30.2	30.2	75%	730	100.00	3774	XM_014287046.2
PREDICTED: Falco peregrinus cancer susceptibility 1 (CASC1),...	peregrine fa...	8954	30.2	30.2	75%	730	100.00	6448	XM_027790469.1
PREDICTED: Falco peregrinus cancer susceptibility 1 (CASC1),...	peregrine fa...	8954	30.2	30.2	75%	730	100.00	6593	XM_027790468.1
PREDICTED: Falco peregrinus cancer susceptibility 1 (CASC1),...	peregrine fa...	8954	30.2	30.2	75%	730	100.00	4621	XM_027790467.1
PREDICTED: Falco peregrinus cancer susceptibility 1 (CASC1),...	peregrine fa...	8954	30.2	30.2	75%	730	100.00	5439	XM_027790466.1
PREDICTED: Falco peregrinus cancer susceptibility 1 (CASC1),...	peregrine fa...	8954	30.2	30.2	75%	730	100.00	4834	XM_027790465.1
Lateolabrax maculatus linkage group 23 sequence	spotted sea ...	315492	30.2	30.2	75%	730	100.00	16923262	CP032598.1

Lateolabrax maculatus linkage group 15 sequence	spotted sea ...	315492	30.2	30.2	75%	730	100.00	23369250	CP032589.1
Lateolabrax maculatus linkage group 12 sequence	spotted sea ...	315492	30.2	30.2	75%	730	100.00	24885600	CP032586.1
Lateolabrax maculatus chromosome Lm16	spotted sea ...	315492	30.2	30.2	75%	730	100.00	22793363	CP027277.1
Lateolabrax maculatus chromosome Lm13	spotted sea ...	315492	30.2	30.2	75%	730	100.00	21871954	CP027274.1
Lateolabrax maculatus chromosome Lm10	spotted sea ...	315492	30.2	30.2	75%	730	100.00	17765475	CP027271.1
Lateolabrax maculatus chromosome Lm4	spotted sea ...	315492	30.2	30.2	75%	730	100.00	19156603	CP027265.1
Eukaryotic synthetic construct chromosome 13	NA	111789	30.2	60.5	80%	730	100.00	96089878	CP034516.1
Eukaryotic synthetic construct chromosome 18	NA	111789	30.2	30.2	75%	730	100.00	84899006	CP034496.1
Eukaryotic synthetic construct chromosome 13	NA	111789	30.2	60.5	80%	730	100.00	96089878	CP034491.1
Homo sapiens PDS5 cohesin associated factor B (PDS5B),...	human	9606	30.2	30.2	75%	730	100.00	198594	NG_021308.2
Homo sapiens BAR/IMD domain containing adaptor protein 2...	human	9606	30.2	30.2	75%	730	100.00	89286	NG_029486.2
Homo sapiens NAD(P) dependent steroid dehydrogenase-like...	human	9606	30.2	30.2	75%	730	100.00	45397	NG_009163.2
PREDICTED: Bos indicus x Bos taurus delta 4-desaturase,...	hybrid cattle	30522	30.2	30.2	75%	730	100.00	3712	XM_027520724.1
PREDICTED: Bos indicus x Bos taurus delta 4-desaturase,...	hybrid cattle	30522	30.2	30.2	75%	730	100.00	4480	XM_027520723.1
PREDICTED: Bos indicus x Bos taurus delta 4-desaturase,...	hybrid cattle	30522	30.2	30.2	75%	730	100.00	4491	XM_027520722.1
PREDICTED: Bos indicus x Bos taurus delta 4-desaturase,...	hybrid cattle	30522	30.2	30.2	75%	730	100.00	4444	XM_027520721.1
PREDICTED: Bos indicus x Bos taurus delta 4-desaturase,...	hybrid cattle	30522	30.2	30.2	75%	730	100.00	3585	XM_027520720.1
PREDICTED: Bos indicus x Bos taurus delta 4-desaturase,...	hybrid cattle	30522	30.2	30.2	75%	730	100.00	3836	XM_027520719.1
PREDICTED: Dromaius novaehollandiae sacsin-like (LOC112983176)...	emu	8790	30.2	30.2	75%	730	100.00	13160	XM_026100112.1
PREDICTED: Nothoprocta perdicaria tubulin gamma complex...	NA	30464	30.2	30.2	75%	730	100.00	3385	XM_026044295.1
PREDICTED: Nothoprocta perdicaria tubulin gamma complex...	NA	30464	30.2	30.2	75%	730	100.00	3255	XM_026044294.1
Lactobacillus zeae isolate CECT 9104 genome assembly,...	NA	57037	30.2	30.2	75%	730	100.00	3045762	LS991421.1
PREDICTED: Vulpes vulpes menin 1 (MEN1), transcript variant X7...	red fox	9627	30.2	30.2	75%	730	100.00	2644	XM_026004514.1
PREDICTED: Vulpes vulpes menin 1 (MEN1), transcript variant X6...	red fox	9627	30.2	30.2	75%	730	100.00	2682	XM_026004513.1
PREDICTED: Vulpes vulpes menin 1 (MEN1), transcript variant X5...	red fox	9627	30.2	30.2	75%	730	100.00	2705	XM_026004512.1
PREDICTED: Vulpes vulpes menin 1 (MEN1), transcript variant X4...	red fox	9627	30.2	30.2	75%	730	100.00	2536	XM_026004510.1
PREDICTED: Vulpes vulpes menin 1 (MEN1), transcript variant X3...	red fox	9627	30.2	30.2	75%	730	100.00	2546	XM_026004509.1
PREDICTED: Vulpes vulpes menin 1 (MEN1), transcript variant X2...	red fox	9627	30.2	30.2	75%	730	100.00	2747	XM_026004508.1
PREDICTED: Vulpes vulpes menin 1 (MEN1), transcript variant X1...	red fox	9627	30.2	30.2	75%	730	100.00	2741	XM_026004507.1
PREDICTED: Vulpes vulpes SH3 and multiple ankyrin repeat domai...	red fox	9627	30.2	30.2	75%	730	100.00	9085	XM_026004205.1
PREDICTED: Puma concolor rotatin (RTTN), mRNA	puma	9696	30.2	30.2	75%	730	100.00	6693	XM_025931071.1
PREDICTED: Oreochromis niloticus prostaglandin D2 receptor...	Nile tilapia	8128	30.2	30.2	75%	730	100.00	5671	XM_005470029.4
Rhodococcus biphenylivorans strain TG9 chromosome, complete...	NA	1500843	30.2	30.2	75%	730	100.00	5034221	CP022208.1
Homo sapiens chromosome 16 clone CH17-437M17, complete	human	9606	30.2	30.2	75%	730	100.00	209009	AC277753.2

sequence									
PREDICTED: Bubalus bubalis transmembrane protein 173 (TMEM173)...	water buffalo	89462	30.2	30.2	75%	730	100.00	1918	XM_006070800.2
Bacillus anthracis strain London_499 chromosome, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5228599	**CP029805.1**
PREDICTED: Pomacea canaliculata scavenger receptor class F...	NA	400727	30.2	30.2	75%	730	100.00	3304	XM_025259968.1
Scophthalmus maximus chromosome 20	turbot	52904	30.2	30.2	75%	730	100.00	19912231	CP026262.1
Scophthalmus maximus chromosome 19	turbot	52904	30.2	30.2	75%	730	100.00	20258455	CP026261.1
Scophthalmus maximus chromosome 16	turbot	52904	30.2	30.2	75%	730	100.00	21452505	CP026258.1
Scophthalmus maximus chromosome 14	turbot	52904	30.2	30.2	75%	730	100.00	22753422	CP026256.1
Scophthalmus maximus chromosome 12	turbot	52904	30.2	30.2	75%	730	100.00	24811384	CP026254.1
Scophthalmus maximus chromosome 10	turbot	52904	30.2	30.2	75%	730	100.00	25207873	CP026252.1
Scophthalmus maximus chromosome 9	turbot	52904	30.2	30.2	75%	730	100.00	25242470	CP026251.1
Scophthalmus maximus chromosome 4	turbot	52904	30.2	90.7	75%	730	100.00	30934145	CP026246.1
Scophthalmus maximus chromosome 2	turbot	52904	30.2	60.5	80%	730	100.00	23836697	CP026244.1
PREDICTED: Alligator sinensis tripartite motif-containing...	Chinese alli...	38654	30.2	30.2	75%	730	100.00	2308	XR_003091842.1
PREDICTED: Alligator sinensis tripartite motif-containing...	Chinese alli...	38654	30.2	30.2	75%	730	100.00	3818	XM_025192037.1
PREDICTED: Python bivittatus tubulin gamma complex associated...	Burmese python	176946	30.2	30.2	75%	730	100.00	3858	XM_007427529.3
PREDICTED: Cynoglossus semilaevis chromodomain helicase DNA...	tongue sole	244447	30.2	30.2	75%	730	100.00	8654	XM_025055726.1
PREDICTED: Cynoglossus semilaevis chromodomain helicase DNA...	tongue sole	244447	30.2	30.2	75%	730	100.00	9690	XM_025055725.1
PREDICTED: Cynoglossus semilaevis chromodomain helicase DNA...	tongue sole	244447	30.2	30.2	75%	730	100.00	9694	XM_025055724.1
PREDICTED: Cynoglossus semilaevis chromodomain helicase DNA...	tongue sole	244447	30.2	30.2	75%	730	100.00	10198	XM_025055723.1
PREDICTED: Cynoglossus semilaevis chromodomain helicase DNA...	tongue sole	244447	30.2	30.2	75%	730	100.00	11576	XM_025055722.1
PREDICTED: Cynoglossus semilaevis chromodomain helicase DNA...	tongue sole	244447	30.2	30.2	75%	730	100.00	11610	XM_008310455.3
PREDICTED: Cynoglossus semilaevis chromodomain helicase DNA...	tongue sole	244447	30.2	30.2	75%	730	100.00	11626	XM_025055721.1
PREDICTED: Cynoglossus semilaevis transcription factor...	tongue sole	244447	30.2	30.2	75%	730	100.00	4028	XM_008331249.3
PREDICTED: Pteropus alecto tubulin gamma complex associated...	black flying...	9402	30.2	30.2	75%	730	100.00	3862	**XM_025044972.1**
PREDICTED: Pteropus alecto tubulin gamma complex associated...	black flying...	9402	30.2	30.2	75%	730	100.00	3909	**XM_006909358.3**
PREDICTED: Pteropus alecto inhibitor of nuclear factor kappa B...	black flying...	9402	30.2	30.2	75%	730	100.00	5645	**XM_006904795.3**
PREDICTED: Pteropus alecto inhibitor of nuclear factor kappa	black flying...	9402	30.2	30.2	75%	730	100.00	5662	**XM_006904794.3**

B...									
Streptomyces lunaelactis strain MM109 chromosome, complete genome	NA	1535768	30.2	30.2	75%	730	100.00	8396100	CP026304.1
Sordaria macrospora k-hell uncharacterized protein (SMAC_06743...	NA	771870	30.2	30.2	75%	730	100.00	3021	XM_024655213.1
PREDICTED: Desmodus rotundus tubulin gamma complex associated...	common vampi...	9430	30.2	30.2	75%	730	100.00	3712	XM_024578966.1
PREDICTED: Desmodus rotundus DEAD-box helicase 51 (DDX51), mRNA	common vampi...	9430	30.2	30.2	75%	730	100.00	2009	XM_024566654.1
Postia placenta MAD-698-R-SB12 hypothetical protein...	NA	670580	30.2	30.2	75%	730	100.00	2580	XM_024484097.1
PREDICTED: Oncorhynchus tshawytscha EGF like, fibronectin type...	Chinook salmon	74940	30.2	30.2	75%	730	100.00	1750	XM_024380778.1
PREDICTED: Oncorhynchus tshawytscha EGF like, fibronectin type...	Chinook salmon	74940	30.2	30.2	75%	730	100.00	4147	XM_024380777.1
PREDICTED: Oncorhynchus tshawytscha EGF like, fibronectin type...	Chinook salmon	74940	30.2	30.2	75%	730	100.00	4172	XM_024380775.1
PREDICTED: Pan troglodytes zinc finger and SCAN...	chimpanzee	9598	30.2	30.2	75%	730	100.00	9108	XM_003318896.5
PREDICTED: Pan troglodytes zinc finger and SCAN...	chimpanzee	9598	30.2	30.2	75%	730	100.00	9232	XM_009454539.3
PREDICTED: Pan troglodytes zinc finger and SCAN...	chimpanzee	9598	30.2	30.2	75%	730	100.00	9695	XM_009454535.3
PREDICTED: Pan troglodytes zinc finger and SCAN...	chimpanzee	9598	30.2	30.2	75%	730	100.00	10885	XM_009454538.3
Bacillus anthracis strain FDAARGOS_341 chromosome, complete...	NA	1392	30.2	30.2	75%	730	100.00	5228806	**CP022044.2**
Bos mutus isolate yakQH1 chromosome 24	wild yak	72004	30.2	30.2	75%	730	100.00	61837517	CP027092.1
Bos mutus isolate yakQH1 chromosome 22	wild yak	72004	30.2	30.2	75%	730	100.00	59497618	CP027090.1
Bos mutus isolate yakQH1 chromosome 18	wild yak	72004	30.2	30.2	75%	730	100.00	57350394	CP027086.1
PREDICTED: Pongo abelii BAI1 associated protein 2 (BAIAP2),...	Sumatran ora...	9601	30.2	30.2	75%	730	100.00	2999	XM_024234720.1
PREDICTED: Eutrema salsugineum S-locus-specific glycoprotein...	NA	72664	30.2	30.2	75%	730	100.00	1332	XM_006407319.2
PREDICTED: Physeter catodon free fatty acid receptor 4 (FFAR4)...	sperm whale	9755	30.2	30.2	75%	730	100.00	838	XM_024121567.1
Alternaria solani isolate NL03003 chromosome 1, complete sequence	NA	48100	30.2	30.2	75%	730	100.00	6940169	CP022024.1
PREDICTED: Salvelinus alpinus pikachurin (LOC111961439), mRNA	Arctic char	8036	30.2	30.2	75%	730	100.00	3786	XM_023983708.1
PREDICTED: Cyanistes caeruleus collagen alpha-1(VII) chain-lik...	blue tit	156563	30.2	30.2	75%	730	100.00	3914	XM_023918828.1
PREDICTED: Cyanistes caeruleus collagen alpha-1(VII) chain-lik...	blue tit	156563	30.2	30.2	75%	730	100.00	3985	XM_023918827.1
Bacillus cereus ATCC 10987 chromosome	NA	222523	30.2	30.2	75%	730	100.00	4871269	CP026375.1
PREDICTED: Paramormyrops kingsleyae nudix hydrolase 17 (nudt17...	NA	1676925	30.2	30.2	75%	730	100.00	3225	XM_023801189.1
PREDICTED: Paramormyrops kingsleyae nudix hydrolase 17 (nudt17...	NA	1676925	30.2	30.2	75%	730	100.00	3322	XM_023801188.1
PREDICTED: Paramormyrops kingsleyae Janus kinase 1 (jak1), mRNA	NA	1676925	30.2	30.2	75%	730	100.00	4475	XM_023794591.1
PREDICTED: Myotis lucifugus TRPM8 channel associated factor	little brown...	59463	30.2	30.2	75%	730	100.00	2533	XM_006108619.3

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PREDICTED: Myotis lucifugus tubulin gamma complex associated...	little brown...	59463	30.2	30.2	75%	730	100.00	3620	XM_023752456.1
PREDICTED: Myotis lucifugus tubulin gamma complex associated...	little brown...	59463	30.2	30.2	75%	730	100.00	3698	XM_023752455.1
PREDICTED: Myotis lucifugus tubulin gamma complex associated...	little brown...	59463	30.2	30.2	75%	730	100.00	3927	XM_023752454.1
PREDICTED: Myotis lucifugus tubulin gamma complex associated...	little brown...	59463	30.2	30.2	75%	730	100.00	3941	XM_023752453.1
PREDICTED: Myotis lucifugus tubulin gamma complex associated...	little brown...	59463	30.2	30.2	75%	730	100.00	3965	XM_023752452.1
PREDICTED: Myotis lucifugus tubulin gamma complex associated...	little brown...	59463	30.2	30.2	75%	730	100.00	3986	XM_023752450.1
PREDICTED: Myotis lucifugus tubulin gamma complex associated...	little brown...	59463	30.2	30.2	75%	730	100.00	3996	XM_006086892.3
PREDICTED: Myotis lucifugus tubulin gamma complex associated...	little brown...	59463	30.2	30.2	75%	730	100.00	4040	XM_006086891.3
PREDICTED: Trichechus manatus latirostris YKT6 v-SNARE homolog...	Florida manatee	127582	30.2	30.2	75%	730	100.00	2902	XM_004386093.2
Nostoc sp. CENA543 chromosome, complete genome	NA	1869241	30.2	30.2	75%	730	100.00	6990729	CP023278.1
PREDICTED: Equus caballus NOP14 nucleolar protein (NOP14),...	horse	9796	30.2	30.2	75%	730	100.00	2668	XM_005608934.3
PREDICTED: Equus caballus NOP14 nucleolar protein (NOP14),...	horse	9796	30.2	30.2	75%	730	100.00	2720	XM_001489809.4
PREDICTED: Equus caballus tubulin gamma complex associated...	horse	9796	30.2	30.2	75%	730	100.00	3849	XM_023621859.1
PREDICTED: Pteropus vampyrus tubulin gamma complex associated...	large flying...	132908	30.2	30.2	75%	730	100.00	3483	**XM_023522907.1**
PREDICTED: Pteropus vampyrus inhibitor of nuclear factor kappa...	large flying...	132908	30.2	30.2	75%	730	100.00	4872	**XM_023520638.1**
PREDICTED: Cavia porcellus uncharacterized LOC106025513...	domestic gui...	10141	30.2	30.2	75%	730	100.00	1453	XR_002788999.1
PREDICTED: Cavia porcellus uncharacterized LOC106025513...	domestic gui...	10141	30.2	30.2	75%	730	100.00	1540	XR_002788998.1
PREDICTED: Cavia porcellus uncharacterized LOC106025513...	domestic gui...	10141	30.2	30.2	75%	730	100.00	1460	XR_001199088.2
Larimichthys crocea genome assembly, chromosome: VI	large yellow...	215358	30.2	30.2	75%	730	100.00	24582047	LT972195.1
PREDICTED: Loxodonta africana YKT6 v-SNARE homolog (YKT6),...	African sava...	9785	30.2	30.2	75%	730	100.00	2869	XM_010598269.2
PREDICTED: Loxodonta africana FLYWCH-type zinc finger-containi...	African sava...	9785	30.2	30.2	75%	730	100.00	2989	XM_010597387.2
PREDICTED: Loxodonta africana FLYWCH-type zinc finger-containi...	African sava...	9785	30.2	30.2	75%	730	100.00	3276	XR_002787606.1
PREDICTED: Loxodonta africana FLYWCH-type zinc finger-containi...	African sava...	9785	30.2	30.2	75%	730	100.00	4163	XM_023557487.1
PREDICTED: Loxodonta africana FLYWCH-type zinc finger-containi...	African sava...	9785	30.2	30.2	75%	730	100.00	3175	XM_023557486.1
PREDICTED: Loxodonta africana FLYWCH-type zinc finger-containi...	African sava...	9785	30.2	30.2	75%	730	100.00	3191	XM_023557485.1
PREDICTED: Loxodonta africana FLYWCH-type zinc finger-containi...	African sava...	9785	30.2	30.2	75%	730	100.00	3363	XM_023557484.1
PREDICTED: Loxodonta africana FLYWCH-type zinc finger-containi...	African sava...	9785	30.2	30.2	75%	730	100.00	3424	XM_010597381.2

PREDICTED: Loxodonta africana FLYWCH-type zinc finger-containi...	African sava...	9785	30.2	30.2	75%	730	100.00	3155	XR_002787605.1
PREDICTED: Loxodonta africana FLYWCH-type zinc finger-containi...	African sava...	9785	30.2	30.2	75%	730	100.00	3449	XM_023557483.1
Fusarium fujikuroi IMI 58289 uncharacterized protein...	NA	1279085	30.2	30.2	75%	730	100.00	1656	XM_023578879.1
PREDICTED: Otolemur garnettii menin 1 (MEN1), mRNA	small-eared ...	30611	30.2	30.2	75%	730	100.00	2890	XM_012810735.2
PREDICTED: Seriola lalandi dorsalis SWI/SNF-related...	NA	1841481	30.2	30.2	75%	730	100.00	2782	XM_023397865.1
PREDICTED: Centruroides sculpturatus uncharacterized...	bark scorpion	218467	30.2	30.2	75%	730	100.00	1155	XM_023365373.1
PREDICTED: Felis catus rotatin (RTTN), transcript variant X4,...	domestic cat	9685	30.2	30.2	75%	730	100.00	4802	XM_019815424.2
PREDICTED: Felis catus rotatin (RTTN), transcript variant X3,...	domestic cat	9685	30.2	30.2	75%	730	100.00	6348	XM_023242095.1
PREDICTED: Felis catus rotatin (RTTN), transcript variant X2,...	domestic cat	9685	30.2	30.2	75%	730	100.00	7227	XM_019815422.2
PREDICTED: Felis catus rotatin (RTTN), transcript variant X1,...	domestic cat	9685	30.2	30.2	75%	730	100.00	7293	XM_011288133.3
Bacillus sp. HBCD-sjtu chromosome, complete genome	NA	2053832	30.2	30.2	75%	730	100.00	5230501	CP025122.1
PREDICTED: Leptinotarsa decemlineata exocyst complex component...	Colorado pot...	7539	30.2	30.2	75%	730	100.00	2608	XM_023166666.1
PREDICTED: Spodoptera litura tripartite motif-containing prote...	NA	69820	30.2	30.2	75%	730	100.00	1966	XM_022964845.1
PREDICTED: Spodoptera litura tripartite motif-containing prote...	NA	69820	30.2	30.2	75%	730	100.00	2099	XM_022964844.1
PREDICTED: Spodoptera litura tripartite motif-containing prote...	NA	69820	30.2	30.2	75%	730	100.00	2143	XM_022964843.1
Mycobacterium phage Kumao, complete genome	NA	2041344	30.2	30.2	75%	730	100.00	70373	NC_053512.1
Bacillus cereus strain BHU2 chromosome	NA	1396	30.2	30.2	75%	730	100.00	5186653	CP023726.1
PREDICTED: Brassica napus pyruvate, phosphate dikinase...	rape	3708	30.2	30.2	75%	730	100.00	1430	XM_013879457.2
PREDICTED: Brassica napus pyruvate, phosphate dikinase...	rape	3708	30.2	30.2	75%	730	100.00	1405	XM_013881933.2
PREDICTED: Brassica napus pyruvate, phosphate dikinase...	rape	3708	30.2	30.2	75%	730	100.00	1546	XM_013847087.2
PREDICTED: Astyanax mexicanus tubulin gamma complex associated...	Mexican tetra	7994	30.2	30.2	75%	730	100.00	3793	XM_007253111.3
PREDICTED: Enhydra lutris kenyoni SH3 and multiple ankyrin...	NA	391180	30.2	30.2	75%	730	100.00	7271	XM_022507316.1
Bacillus cereus strain CC-1 chromosome, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5279524	CP023179.1
Bacillus anthracis strain 14RA5914, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5245242	**CP023001.1**
PREDICTED: Acanthochromis polyacanthus collagen alpha-1(XVIII)...	spiny chromis	80966	30.2	30.2	75%	730	100.00	5396	XM_022208438.1
PREDICTED: Acanthochromis polyacanthus collagen alpha-1(XVIII)...	spiny chromis	80966	30.2	30.2	75%	730	100.00	5399	XM_022208437.1
PREDICTED: Acanthochromis polyacanthus...	spiny chromis	80966	30.2	30.2	75%	730	100.00	8046	XM_022197165.1
PREDICTED: Acanthochromis polyacanthus...	spiny chromis	80966	30.2	30.2	75%	730	100.00	8049	XM_022197164.1
PREDICTED: Acanthochromis polyacanthus...	spiny chromis	80966	30.2	30.2	75%	730	100.00	8127	XM_022197163.1
PREDICTED: Acanthochromis polyacanthus...	spiny chromis	80966	30.2	30.2	75%	730	100.00	8130	XM_022197162.1
PREDICTED: Zootermopsis nevadensis upstream stimulatory factor...	NA	136037	30.2	30.2	75%	730	100.00	3824	XM_022083074.1

Labrenzia sp. VG12 chromosome, complete genome	NA	2021862	30.2	30.2	75%	730	100.00	5977548	CP022529.1
Oryzias latipes strain HSOK chromosome 19	Japanese medaka	8090	30.2	30.2	75%	730	100.00	24983015	CP020639.1
Oryzias latipes strain HSOK chromosome 5	Japanese medaka	8090	30.2	30.2	75%	730	100.00	34406696	CP020625.1
Oryzias latipes strain HNI chromosome 5	Japanese medaka	8090	30.2	30.2	75%	730	100.00	31424114	CP020783.1
Oryzias latipes strain Hd-rR chromosome 5 sequence	Japanese medaka	8090	30.2	30.2	75%	730	100.00	33205099	CP020669.1
Oryzias latipes strain Hd-rR chromosome 1 sequence	Japanese medaka	8090	30.2	30.2	75%	730	100.00	37713152	CP020665.1
Bosea sp. AS-1 chromosome, complete genome	NA	2015316	30.2	30.2	75%	730	100.00	5536255	CP022372.1
Bacillus cereus strain M3, complete sequence	NA	1396	30.2	30.2	75%	730	100.00	5218997	CP016316.1
Streptomyces sp. 1H-SSA4 genome	NA	2014920	30.2	30.2	75%	730	100.00	10989391	CP022161.1
PREDICTED: Aotus nancymaae solute carrier family 40 member 1...	Ma's night m...	37293	30.2	30.2	75%	730	100.00	3186	XM_012464106.2
PREDICTED: Neomonachus schauinslandi SH3 and multiple ankyrin...	Hawaiian mon...	29088	30.2	30.2	75%	730	100.00	9068	XM_021685282.1
PREDICTED: Meriones unguiculatus syntaxin 16 (Stx16), transcri...	Mongolian ge...	10047	30.2	30.2	95%	730	94.74	4323	XM_021644407.1
PREDICTED: Meriones unguiculatus syntaxin 16 (Stx16), transcri...	Mongolian ge...	10047	30.2	30.2	95%	730	94.74	4335	XM_021644406.1
PREDICTED: Meriones unguiculatus syntaxin 16 (Stx16), transcri...	Mongolian ge...	10047	30.2	30.2	95%	730	94.74	4374	XM_021644405.1
PREDICTED: Meriones unguiculatus syntaxin 16 (Stx16), transcri...	Mongolian ge...	10047	30.2	30.2	95%	730	94.74	4386	XM_021644404.1
Caenorhabditis sp. 34 TK-2017 DNA. chromosome 2, nearly comple...	NA	1978547	30.2	30.2	75%	730	100.00	20116996	AP018152.1
Bacillus thuringiensis strain BM-BT15426, complete genome	NA	1428	30.2	30.2	75%	730	100.00	5246329	CP020723.1
PREDICTED: Columba livia tsukushi, small leucine rich...	rock pigeon	8932	30.2	30.2	75%	730	100.00	3472	XM_021285083.1
PREDICTED: Columba livia tsukushi, small leucine rich...	rock pigeon	8932	30.2	30.2	75%	730	100.00	3870	XM_021285082.1
PREDICTED: Columba livia tsukushi, small leucine rich...	rock pigeon	8932	30.2	30.2	75%	730	100.00	3563	XM_005500593.2
PREDICTED: Columba livia tsukushi, small leucine rich...	rock pigeon	8932	30.2	30.2	75%	730	100.00	3597	XM_005500592.2
PREDICTED: Heterocephalus glaber triggering receptor expressed...	naked mole-rat	10181	30.2	30.2	75%	730	100.00	3352	XM_004846606.2
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16), transcri...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	2010	XM_021255167.1
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16), transcri...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	2061	XM_021255166.1
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16), transcri...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	2220	XM_013070790.2
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16), transcri...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	2406	XM_004840951.3
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16),	naked mole-	10181	30.2	30.2	95%	730	94.74	4578	XM_004840949.3

transcri...	rat								
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16), transcri...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	4590	XM_004840948.3
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16), transcri...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	1881	XM_004840947.3
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16), transcri...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	1893	XM_004840946.3
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16), transcri...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	4631	XM_004840944.3
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16), transcri...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	4643	XM_004840943.3
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16), transcri...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	1938	XM_004840942.3
PREDICTED: Heterocephalus glaber syntaxin 16 (Stx16), transcri...	naked mole-rat	10181	30.2	30.2	95%	730	94.74	1948	XM_004840941.3
PREDICTED: Mus pahari WD repeat domain 81 (Wdr81), mRNA	shrew mouse	10093	30.2	30.2	95%	730	94.74	6909	XM_021212472.1
Oryza sativa Indica Group cultivar Shuhui498 chromosome 11...	long-grained...	39946	30.2	30.2	75%	730	100.00	31778392	CP018167.1
Bacillus cereus strain BC-AK genomic sequence	NA	1396	30.2	30.2	75%	730	100.00	5231712	CP020937.1
PREDICTED: Athalia rosae neuronal calcium sensor 2...	coleseed sawfly	37344	30.2	30.2	75%	730	100.00	1297	XM_012413665.2
PREDICTED: Athalia rosae neuronal calcium sensor 2...	coleseed sawfly	37344	30.2	30.2	75%	730	100.00	1298	XM_012413664.2
PREDICTED: Athalia rosae neuronal calcium sensor 2...	coleseed sawfly	37344	30.2	30.2	75%	730	100.00	1332	XM_012413663.2
Bacillus mycoides strain Gnyt1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5597907	CP020743.1
PREDICTED: Pogona vitticeps solute carrier family 22 member...	central bear...	103695	30.2	30.2	95%	730	94.74	2396	XM_020777476.1
PREDICTED: Rhincodon typus carboxypeptidase A6-like...	whale shark	259920	30.2	30.2	75%	730	100.00	724	XM_020522354.1
Planococcus faecalis strain AJ003 chromosome, complete genome	NA	1598147	30.2	30.2	75%	730	100.00	3495892	CP019401.1
PREDICTED: Microcebus murinus menin 1 (MEN1), transcript varia...	gray mouse l...	30608	30.2	30.2	75%	730	100.00	2454	XM_012777998.2
PREDICTED: Microcebus murinus menin 1 (MEN1), transcript varia...	gray mouse l...	30608	30.2	30.2	75%	730	100.00	2383	XM_012777997.2
PREDICTED: Microcebus murinus menin 1 (MEN1), transcript varia...	gray mouse l...	30608	30.2	30.2	75%	730	100.00	2407	XM_012777996.2
PREDICTED: Microcebus murinus chloride voltage-gated channel K...	gray mouse l...	30608	30.2	30.2	75%	730	100.00	2707	XM_020281564.1
PREDICTED: Microcebus murinus chloride voltage-gated channel K...	gray mouse l...	30608	30.2	30.2	75%	730	100.00	4163	XM_020281563.1
PREDICTED: Microcebus murinus chloride voltage-gated channel K...	gray mouse l...	30608	30.2	30.2	75%	730	100.00	3413	XM_020281562.1
PREDICTED: Ananas comosus tetraspanin-8-like (LOC109720558), mRNA	pineapple	4615	30.2	30.2	95%	730	94.74	1171	XM_020247764.1
PREDICTED: Castor canadensis NACHT, LRR and PYD...	American beaver	51338	30.2	30.2	75%	730	100.00	2133	XM_020162150.1
Labrenzia aggregata strain RMAR6-6 chromosome, complete genome	NA	187304	30.2	30.2	75%	730	100.00	6149397	CP019630.1
PREDICTED: Paralichthys olivaceus tubulin gamma complex...	Japanese flo...	8255	30.2	30.2	75%	730	100.00	4468	XM_020103923.1

PREDICTED: Paralichthys olivaceus family with sequence...	Japanese flo...	8255	30.2	30.2	75%	730	100.00	4054	XM_020099314.1
PREDICTED: Paralichthys olivaceus family with sequence...	Japanese flo...	8255	30.2	30.2	75%	730	100.00	3910	XM_020099313.1
PREDICTED: Paralichthys olivaceus family with sequence...	Japanese flo...	8255	30.2	30.2	75%	730	100.00	3870	XM_020099312.1
PREDICTED: Paralichthys olivaceus flotillin 2 (flot2),...	Japanese flo...	8255	30.2	30.2	75%	730	100.00	4679	XM_020085718.1
PREDICTED: Paralichthys olivaceus flotillin 2 (flot2),...	Japanese flo...	8255	30.2	30.2	75%	730	100.00	4677	XM_020085717.1
Bacillus anthracis strain SPV842_15, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5228667	**CP019588.1**
Jeotgalibaca sp. PTS2502, complete genome	NA	1903686	30.2	30.2	75%	730	100.00	2300992	CP019433.1
Bacillus cereus strain ISSFR-9F, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5243376	CP018933.1
Bacillus anthracis strain Tyrol 4675, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5227565	**CP018903.1**
PREDICTED: Felis catus uncharacterized LOC109498882...	domestic cat	9685	30.2	30.2	75%	730	100.00	1694	XR_002155865.1
PREDICTED: Felis catus uncharacterized LOC109498882...	domestic cat	9685	30.2	30.2	75%	730	100.00	1980	XR_002155864.1
PREDICTED: Hipposideros armiger keratin-associated protein 11-...	great roundl...	186990	30.2	30.2	75%	730	100.00	495	XM_019662813.1
PREDICTED: Hipposideros armiger tubulin gamma complex associat...	great roundl...	186990	30.2	30.2	75%	730	100.00	3849	XM_019644832.1
PREDICTED: Hipposideros armiger tubulin gamma complex associat...	great roundl...	186990	30.2	30.2	75%	730	100.00	3933	XM_019644831.1
PREDICTED: Panthera pardus rotatin (RTTN), transcript variant...	leopard	9691	30.2	30.2	75%	730	100.00	4815	XM_019432563.1
PREDICTED: Panthera pardus rotatin (RTTN), transcript variant...	leopard	9691	30.2	30.2	75%	730	100.00	4459	XM_019432562.1
PREDICTED: Panthera pardus rotatin (RTTN), transcript variant...	leopard	9691	30.2	30.2	75%	730	100.00	7126	XM_019432561.1
PREDICTED: Panthera pardus rotatin (RTTN), transcript variant...	leopard	9691	30.2	30.2	75%	730	100.00	7196	XM_019432560.1
PREDICTED: Ipomoea nil probable leucine-rich repeat...	Japanese mor...	35883	30.2	30.2	75%	730	100.00	3437	XM_019334628.1
PREDICTED: Fukomys damarensis retrotransposon Gag like 6 (Rtl6...	Damara mole-rat	885580	30.2	30.2	75%	730	100.00	3749	XM_010634348.2
Pandoraea pnomenusa strain RB-44, complete genome	NA	93220	30.2	30.2	75%	730	100.00	5385946	CP006938.2
Bacillus cereus strain AR156, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5160326	CP015589.1
PREDICTED: Cyprinus carpio chromodomain helicase DNA binding...	common carp	7962	30.2	30.2	75%	730	100.00	8736	XM_019113328.1
Bacillus anthracis str. A16R, complete genome	NA	673518	30.2	30.2	75%	730	100.00	5228828	**CP001974.2**
Planococcus donghaensis strain DSM 22276, complete genome	NA	414778	30.2	30.2	75%	730	100.00	3305371	CP016543.2
Planococcus halocryophilus strain DSM 24743, complete genome	NA	1215089	30.2	30.2	75%	730	100.00	3424893	CP016537.2
Planococcus antarcticus DSM 14505, complete genome	NA	1185653	30.2	30.2	75%	730	100.00	3765545	CP016534.2
Bacillus anthracis str. A16, complete genome	NA	743835	30.2	30.2	75%	730	100.00	5228842	**CP001970.2**
Bacillus sp. ABP14, complete genome	NA	1892404	30.2	30.2	75%	730	100.00	5141367	CP017016.1
Homo sapiens diphthamide biosynthesis 1 (DPH1), RefSeqGene on...	human	9606	30.2	30.2	75%	730	100.00	20320	NG_051946.1
Streptomyces sp. 2114.2 genome assembly, chromosome: I	NA	1881022	30.2	30.2	75%	730	100.00	8620263	LT629768.1
Toxoplasma gondii ME49 hypothetical protein partial mRNA	NA	508771	30.2	30.2	75%	730	100.00	26069	XM_018779513.1
PREDICTED: Lates calcarifer	barram	8187	30.2	30.2	75%	730	100.00	952	XM_018680036.1

nuclear factor 7, ovary-like...	undi p...								
PREDICTED: Raphanus sativus ABC transporter F family member...	radish	3726	30.2	30.2	75%	730	100.00	2398	XM_018602675.1
PREDICTED: Raphanus sativus fimbrin-2 (LOC108828099), mRNA	radish	3726	30.2	30.2	75%	730	100.00	2239	XM_018601665.1
PREDICTED: Raphanus sativus pyruvate, phosphate dikinase...	radish	3726	30.2	30.2	75%	730	100.00	1600	XM_018616230.1
PREDICTED: Nanorana parkeri sterile alpha and TIR motif...	NA	125878	30.2	30.2	75%	730	100.00	2571	XM_018557134.1
PREDICTED: Capra hircus transmembrane protein 173 (TMEM173),...	goat	9925	30.2	30.2	75%	730	100.00	2731	XM_018049970.1
PREDICTED: Capra hircus glutamate ionotropic receptor NMDA typ...	goat	9925	30.2	30.2	75%	730	100.00	6316	XM_018048456.1
TPA: Oryzias latipes strain Hd-rR, complete genome assembly,...	Japanese medaka	8090	30.2	30.2	75%	730	100.00	33792114	HF933211.1
Rhodococcus sp. p52, complete genome	NA	935199	30.2	30.2	75%	730	100.00	4893347	CP016819.1
Micromonospora echinofusca strain DSM 43913 genome assembly,...	NA	47858	30.2	30.2	75%	730	100.00	7002627	LT607733.1
PREDICTED: Corvus brachyrhynchos uncharacterized LOC108446849...	American crow	85066	30.2	30.2	95%	730	94.74	1142	XM_017734743.1
PREDICTED: Corvus brachyrhynchos uncharacterized LOC108445281...	American crow	85066	30.2	30.2	75%	730	100.00	9304	XR_001860087.1
Homo sapiens sidekick cell adhesion molecule 1 (SDK1),...	human	9606	30.2	30.2	75%	730	100.00	974553	NG_051298.1
Bacillus anthracis strain PR10-4, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5227079	**CP012728.1**
Bacillus anthracis strain PR09-4, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5227090	**CP012727.1**
Bacillus anthracis strain PR09-1, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5227060	**CP012726.1**
Bacillus anthracis strain PR08, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5227091	**CP012725.1**
Bacillus anthracis strain PR07, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5227094	**CP012724.1**
Bacillus anthracis strain PR06, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5228656	**CP012723.1**
Bacillus anthracis strain PR05, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5228658	**CP012722.1**
Bacillus anthracis strain PR02, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5228657	**CP012721.1**
Bacillus anthracis strain PR01, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5228656	**CP012720.1**
Bacillus anthracis strain Parent1, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5228660	**CP012730.1**
Bacillus anthracis strain Parent2, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5227092	**CP012729.1**
PREDICTED: Ictalurus punctatus chromodomain helicase DNA bindi...	channel catfish	7998	30.2	30.2	75%	730	100.00	10970	XM_017458583.1
PREDICTED: Ictalurus punctatus chromodomain helicase DNA bindi...	channel catfish	7998	30.2	30.2	75%	730	100.00	9374	XM_017458582.1
PREDICTED: Ictalurus punctatus chromodomain helicase DNA bindi...	channel catfish	7998	30.2	30.2	75%	730	100.00	12175	XM_017458581.1
PREDICTED: Ictalurus punctatus chromodomain helicase DNA bindi...	channel catfish	7998	30.2	30.2	75%	730	100.00	12178	XM_017458579.1
PREDICTED: Ictalurus punctatus chromodomain helicase DNA bindi...	channel catfish	7998	30.2	30.2	75%	730	100.00	12229	XM_017458578.1
PREDICTED: Ictalurus punctatus chromodomain helicase DNA bindi...	channel catfish	7998	30.2	30.2	75%	730	100.00	12229	XM_017458577.1
PREDICTED: Ictalurus punctatus chromodomain helicase DNA bindi...	channel catfish	7998	30.2	30.2	75%	730	100.00	12397	XM_017458576.1
PREDICTED: Ictalurus punctatus chromodomain helicase DNA bindi...	channel catfish	7998	30.2	30.2	75%	730	100.00	12232	XM_017458575.1

PREDICTED: Ictalurus punctatus tubulin gamma complex associate...	channel catfish	7998	30.2	30.2	75%	730	100.00	3020	XM_017458128.1
PREDICTED: Oryctolagus cuniculus G protein subunit gamma...	rabbit	9986	30.2	30.2	75%	730	100.00	922	XM_017349160.1
PREDICTED: Poecilia reticulata myelin transcription factor...	guppy	8081	30.2	30.2	75%	730	100.00	6072	XM_017302137.1
PREDICTED: Drosophila biarmipes uncharacterized LOC108033437...	NA	125945	30.2	30.2	75%	730	100.00	1562	XM_017107762.1
Bacillus anthracis strain Tangail-1, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5227292	**CP015779.1**
PREDICTED: Anolis carolinensis inverted formin, FH2 and WH2...	green anole	28377	30.2	30.2	75%	730	100.00	11003	XM_016990632.1
PREDICTED: Anolis carolinensis inverted formin, FH2 and WH2...	green anole	28377	30.2	30.2	75%	730	100.00	1065	XM_016990631.1
Pongo abelii chromosome 10 clone CH276-147H8, complete sequence	Sumatran ora...	9601	30.2	30.2	75%	730	100.00	184302	AC270636.1
PREDICTED: Poecilia formosa myelin transcription factor 1-like...	Amazon molly	48698	30.2	30.2	75%	730	100.00	5977	XR_001659688.1
PREDICTED: Sinocyclocheilus rhinocerous...	NA	307959	30.2	30.2	75%	730	100.00	8725	XM_016549843.1
PREDICTED: Sinocyclocheilus rhinocerous...	NA	307959	30.2	30.2	75%	730	100.00	8546	XM_016549842.1
PREDICTED: Sinocyclocheilus rhinocerous...	NA	307959	30.2	30.2	75%	730	100.00	8728	XM_016549841.1
Pandoraea pnomenusa strain MCB032, complete genome	NA	93220	30.2	30.2	75%	730	100.00	5584076	CP015371.1
PREDICTED: Sinocyclocheilus anshuiensis PHD finger protein...	NA	1608454	30.2	30.2	75%	730	100.00	3660	XM_016443911.1
PREDICTED: Sinocyclocheilus anshuiensis PHD finger protein...	NA	1608454	30.2	30.2	75%	730	100.00	3678	XM_016443909.1
PREDICTED: Sinocyclocheilus anshuiensis PHD finger protein...	NA	1608454	30.2	30.2	75%	730	100.00	3744	XM_016443908.1
PREDICTED: Monodelphis domestica mas-related G-protein coupled...	gray short-t...	13616	30.2	30.2	75%	730	100.00	1113	XM_007490047.2
PREDICTED: Monodelphis domestica plakophilin-3-like...	gray short-t...	13616	30.2	30.2	75%	730	100.00	1103	XM_007506596.2
Canis lupus familiaris isolate 501-0946_1405 multiple endocrin...	dog	9615	30.2	30.2	75%	730	100.00	366	KF027367.1
PREDICTED: Ficedula albicollis ankyrin repeat and SOCS box...	Collared fly...	59894	30.2	30.2	75%	730	100.00	1850	XM_016298372.1
PREDICTED: Sinocyclocheilus grahami PHD finger protein 21A-lik...	NA	75366	30.2	30.2	75%	730	100.00	4925	XM_016244191.1
PREDICTED: Sinocyclocheilus grahami PHD finger protein 21A-lik...	NA	75366	30.2	30.2	75%	730	100.00	5006	XM_016244190.1
PREDICTED: Sinocyclocheilus grahami PHD finger protein 21A-lik...	NA	75366	30.2	30.2	75%	730	100.00	5108	XM_016244189.1
PREDICTED: Sinocyclocheilus grahami PHD finger protein 21A-lik...	NA	75366	30.2	30.2	75%	730	100.00	5126	XM_016244188.1
PREDICTED: Sinocyclocheilus grahami PHD finger protein 21A-lik...	NA	75366	30.2	30.2	75%	730	100.00	5192	XM_016244187.1
PREDICTED: Sinocyclocheilus grahami...	NA	75366	30.2	30.2	75%	730	100.00	8192	XM_016280534.1
PREDICTED: Sinocyclocheilus grahami...	NA	75366	30.2	30.2	75%	730	100.00	8016	XM_016280533.1
PREDICTED: Sinocyclocheilus grahami...	NA	75366	30.2	30.2	75%	730	100.00	8120	XM_016280532.1
PREDICTED: Sinocyclocheilus grahami...	NA	75366	30.2	30.2	75%	730	100.00	8195	XM_016280530.1
PREDICTED: Miniopterus natalensis tubulin gamma complex...	NA	291302	30.2	30.2	75%	730	100.00	3834	XM_016212868.1
PREDICTED: Peromyscus	prairie	230844	30.2	30.2	75%	730	100.00	4733	XM_016007712.1

maniculatus bairdii scribbled planar cel...	deer...								
PREDICTED: Peromyscus maniculatus bairdii scribbled planar cel...	prairie deer...	230844	30.2	30.2	75%	730	100.00	5183	XM_006989309.2
PREDICTED: Peromyscus maniculatus bairdii scribbled planar cel...	prairie deer...	230844	30.2	30.2	75%	730	100.00	5219	XM_016007711.1
PREDICTED: Peromyscus maniculatus bairdii scribbled planar cel...	prairie deer...	230844	30.2	30.2	75%	730	100.00	5255	XM_006989308.2
PREDICTED: Peromyscus maniculatus bairdii tubulin gamma comple...	prairie deer...	230844	30.2	30.2	75%	730	100.00	3703	XM_006981314.2
PREDICTED: Peromyscus maniculatus bairdii WD repeat domain 81...	prairie deer...	230844	30.2	30.2	95%	730	94.74	5604	XR_001578019.1
PREDICTED: Peromyscus maniculatus bairdii WD repeat domain 81...	prairie deer...	230844	30.2	30.2	95%	730	94.74	5635	XR_001578018.1
PREDICTED: Peromyscus maniculatus bairdii WD repeat domain 81...	prairie deer...	230844	30.2	30.2	95%	730	94.74	5653	XM_015996178.1
PREDICTED: Peromyscus maniculatus bairdii WD repeat domain 81...	prairie deer...	230844	30.2	30.2	95%	730	94.74	6702	XM_015996177.1
PREDICTED: Peromyscus maniculatus bairdii WD repeat domain 81...	prairie deer...	230844	30.2	30.2	95%	730	94.74	6650	XM_015996176.1
PREDICTED: Peromyscus maniculatus bairdii WD repeat domain 81...	prairie deer...	230844	30.2	30.2	95%	730	94.74	6905	XM_006977387.2
PREDICTED: Tribolium castaneum neuferricin (LOC659028), mRNA	red flour be...	7070	30.2	30.2	75%	730	100.00	961	XM_965367.3
Pandoraea pnomenusa strain RB38, complete genome	NA	93220	30.2	30.2	75%	730	100.00	5378916	CP007506.3
Labrenzia sp. CP4, complete genome	NA	1674922	30.2	30.2	75%	730	100.00	5952682	CP011927.1
PREDICTED: Protobothrops mucrosquamatus tubulin gamma complex...	NA	103944	30.2	30.2	75%	730	100.00	3657	XM_015827349.1
PREDICTED: Myotis davidii KRAB-A domain containing 1 (KRBA1),...	NA	225400	30.2	30.2	95%	730	94.74	4753	XM_015572711.1
PREDICTED: Myotis davidii KRAB-A domain containing 1 (KRBA1),...	NA	225400	30.2	30.2	95%	730	94.74	4888	XM_006777151.2
PREDICTED: Myotis davidii KRAB-A domain containing 1 (KRBA1),...	NA	225400	30.2	30.2	95%	730	94.74	4891	XM_006777150.2
PREDICTED: Myotis davidii KRAB-A domain containing 1 (KRBA1),...	NA	225400	30.2	30.2	95%	730	94.74	4918	XM_006777149.2
PREDICTED: Myotis davidii KRAB-A domain containing 1 (KRBA1),...	NA	225400	30.2	30.2	95%	730	94.74	4918	XM_015572710.1
PREDICTED: Myotis davidii KRAB-A domain containing 1 (KRBA1),...	NA	225400	30.2	30.2	95%	730	94.74	4921	XM_015572709.1
PREDICTED: Myotis davidii TRPM8 channel-associated factor 1...	NA	225400	30.2	30.2	75%	730	100.00	3059	XM_006774518.2
PREDICTED: Myotis davidii TRPM8 channel-associated factor 1...	NA	225400	30.2	30.2	75%	730	100.00	4412	XM_006774516.2
PREDICTED: Myotis davidii TRPM8 channel-associated factor 1...	NA	225400	30.2	30.2	75%	730	100.00	4365	XM_006774517.2
PREDICTED: Myotis davidii TRPM8 channel-associated factor 1...	NA	225400	30.2	30.2	75%	730	100.00	4510	XM_006774515.2
PREDICTED: Myotis davidii tubulin gamma complex associated...	NA	225400	30.2	30.2	75%	730	100.00	3591	XM_015568430.1
PREDICTED: Myotis davidii tubulin gamma complex associated...	NA	225400	30.2	30.2	75%	730	100.00	3636	XM_015568429.1
PREDICTED: Myotis davidii tubulin gamma complex associated...	NA	225400	30.2	30.2	75%	730	100.00	3636	XM_015568428.1
PREDICTED: Panthera tigris altaica	Amur	74533	30.2	30.2	75%	730	100.00	7582	XM_007084766.2

rotatin (RTTN), mRNA	tiger								
Bacillus anthracis strain Stendal, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5226939	**CP014179.1**
PREDICTED: Gekko japonicus ADAM metallopeptidase domain 15...	NA	146911	30.2	30.2	75%	730	100.00	3439	XM_015419105.1
PREDICTED: Poecilia latipinna uncharacterized LOC106935566...	sailfin molly	48699	30.2	30.2	75%	730	100.00	1077	XR_001421921.1
PREDICTED: Sturnus vulgaris phosphatidylinositol glycan anchor...	Common starling	9172	30.2	30.2	75%	730	100.00	1469	XM_014880677.1
PREDICTED: Sturnus vulgaris uncharacterized LOC106853845...	Common starling	9172	30.2	30.2	75%	730	100.00	3240	XM_014877324.1
PREDICTED: Equus asinus NOP14 nucleolar protein (NOP14), mRNA	ass	9793	30.2	30.2	75%	730	100.00	2926	XM_014832814.1
PREDICTED: Equus asinus tubulin, gamma complex associated...	ass	9793	30.2	30.2	75%	730	100.00	3629	XM_014854920.1
PREDICTED: Equus asinus leukotriene A4 hydrolase (LTA4H),...	ass	9793	30.2	30.2	75%	730	100.00	5142	XM_014850706.1
Bacillus thuringiensis strain CTC, complete genome	NA	1428	30.2	30.2	75%	730	100.00	5327397	CP013274.1
PREDICTED: Polistes canadensis MFS-type transporter SLC18B1-li...	NA	91411	30.2	30.2	75%	730	100.00	2741	XM_014752222.1
Tokudaia muenninki WDR81 gene for WD repeat domain 81, complet...	Okinawa isla...	742503	30.2	30.2	95%	730	94.74	13842	AB984700.1
PREDICTED: Myotis brandtii tubulin, gamma complex associated...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	3633	**XM_005884450.2**
PREDICTED: Myotis brandtii tubulin, gamma complex associated...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	3642	**XM_005884449.2**
PREDICTED: Myotis brandtii tubulin, gamma complex associated...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	3687	**XM_005884448.2**
PREDICTED: Myotis brandtii chemokine (C motif) receptor 1...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	2384	**XM_014548402.1**
PREDICTED: Myotis brandtii TRPM8 channel-associated factor 1...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	3114	**XM_005862810.2**
PREDICTED: Myotis brandtii TRPM8 channel-associated factor 1...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	3944	**XM_005862809.2**
PREDICTED: Myotis brandtii TRPM8 channel-associated factor 1...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	3994	**XM_005862807.2**
PREDICTED: Myotis brandtii TRPM8 channel-associated factor 1...	Brandt's bat	109478	30.2	30.2	75%	730	100.00	4142	**XM_005862805.2**
PREDICTED: Papilio machaon neuronal calcium sensor 2...	common yello...	76193	30.2	30.2	75%	730	100.00	2245	XM_014510791.1
PREDICTED: Papilio machaon neuronal calcium sensor 2...	common yello...	76193	30.2	30.2	75%	730	100.00	2413	XM_014510790.1
Bacillus thuringiensis strain XL6, complete genome	NA	1428	30.2	30.2	75%	730	100.00	5308217	CP013000.1
Oryza sativa Japonica Group DNA, chromosome 11, cultivar:...	Japanese rice	39947	30.2	30.2	75%	730	100.00	29021106	AP014967.1
PREDICTED: Salmo salar vasopressin V2 receptor-like...	Atlantic salmon	8030	30.2	30.2	75%	730	100.00	3143	XM_014135794.1
PREDICTED: Salmo salar vasopressin V2 receptor-like...	Atlantic salmon	8030	30.2	30.2	75%	730	100.00	3181	XM_014135793.1
PREDICTED: Salmo salar vasopressin V2 receptor-like...	Atlantic salmon	8030	30.2	30.2	75%	730	100.00	3184	XM_014135792.1
PREDICTED: Salmo salar pikachurin-like (LOC106564097), mRNA	Atlantic salmon	8030	30.2	30.2	75%	730	100.00	1188	XM_014130093.1
PREDICTED: Thamnophis sirtalis tubulin, gamma complex associat...	NA	35019	30.2	30.2	75%	730	100.00	3951	XM_014059037.1

Bacillus anthracis strain Larissa, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5226878	**CP012519.1**
Canis lupus familiaris menin 1 (MEN1), mRNA	dog	9615	30.2	30.2	75%	730	100.00	1848	NM_001081508.2
Thecamonas trahens ATCC 50062 hypothetical protein partial mRNA	NA	461836	30.2	30.2	75%	730	100.00	9435	XM_013901219.1
PREDICTED: Brassica oleracea var. oleracea pyruvate, phosphate...	NA	109376	30.2	30.2	75%	730	100.00	1368	XM_013732967.1
PREDICTED: Chinchilla lanigera poliovirus receptor...	long-tailed ...	34839	30.2	30.2	75%	730	100.00	2126	XM_005412471.2
PREDICTED: Chinchilla lanigera pleckstrin homology domain...	long-tailed ...	34839	30.2	30.2	75%	730	100.00	2844	XR_001234621.1
PREDICTED: Chinchilla lanigera pleckstrin homology domain...	long-tailed ...	34839	30.2	30.2	75%	730	100.00	2884	XR_001234620.1
PREDICTED: Chinchilla lanigera pleckstrin homology domain...	long-tailed ...	34839	30.2	30.2	75%	730	100.00	2958	XR_001234619.1
PREDICTED: Chinchilla lanigera pleckstrin homology domain...	long-tailed ...	34839	30.2	30.2	75%	730	100.00	2980	XR_001234618.1
Rasamsonia emersonii CBS 393.64 Carbon catabolite repression...	NA	1408163	30.2	30.2	75%	730	100.00	1860	XM_013476963.1
Rhinocladiella mackenziei CBS 650.93 hypothetical protein...	NA	1442369	30.2	30.2	75%	730	100.00	873	XM_013419985.1
Eimeria acervulina Midasin, related partial mRNA	NA	5801	30.2	30.2	75%	730	100.00	24813	XM_013396939.1
Eimeria acervulina protein phosphatase 2C, putative partial mRNA	NA	5801	30.2	30.2	75%	730	100.00	6693	XM_013396477.1
Tilletiaria anomala UBC 951 glycoside hydrolase family 3 prote...	NA	1037660	30.2	30.2	75%	730	100.00	2557	XM_013386467.1
Metallosphaera sedula strain SARC-M1, complete genome	NA	43687	30.2	30.2	75%	730	100.00	2191533	CP012176.1
Metallosphaera sedula strain ARS120-2, complete genome	NA	43687	30.2	30.2	75%	730	100.00	2191533	CP012175.1
Metallosphaera sedula strain ARS120-1, complete genome	NA	43687	30.2	30.2	75%	730	100.00	2191531	CP012174.1
Metallosphaera sedula strain ARS50-2, complete genome	NA	43687	30.2	30.2	75%	730	100.00	2191529	CP012173.1
Metallosphaera sedula strain ARS50-1, complete genome	NA	43687	30.2	30.2	75%	730	100.00	2191533	CP012172.1
PREDICTED: Cavia porcellus triggering receptor expressed on...	domestic gui...	10141	30.2	30.2	75%	730	100.00	2703	XM_013156546.1
PREDICTED: Mustela putorius furo SH3 and multiple ankyrin repe...	domestic ferret	9669	30.2	30.2	75%	730	100.00	12294	XM_013059879.1
PREDICTED: Mustela putorius furo uncharacterized LOC106005549...	domestic ferret	9669	30.2	30.2	75%	730	100.00	7576	XR_001178978.1
Ovis canadensis canadensis isolate 43U chromosome 24 sequence	NA	112262	30.2	30.2	75%	730	100.00	42086755	CP011909.1
Ovis canadensis canadensis isolate 43U chromosome 19 sequence	NA	112262	30.2	30.2	75%	730	100.00	60532937	CP011904.1
Ovis canadensis canadensis isolate 43U chromosome 11 sequence	NA	112262	30.2	30.2	75%	730	100.00	62327148	CP011896.1
Ovis canadensis canadensis isolate 43U chromosome 10 sequence	NA	112262	30.2	30.2	75%	730	100.00	86551329	CP011895.1
Ovis canadensis canadensis isolate 43U chromosome 8 sequence	NA	112262	30.2	30.2	75%	730	100.00	90795278	CP011893.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	75%	730	100.00	20460901	LK064963.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	75%	730	100.00	1261513	LK067639.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	60.5	75%	730	100.00	596415	LK065459.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	75%	730	100.00	59088	LK070831.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	75%	730	100.00	2335339	LK065183.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	95%	730	94.74	1698452	LK064756.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	75%	730	100.00	9561987	LK064687.1

PREDICTED: Microcebus murinus menin 1 (MEN1), transcript varia...	gray mouse l...	30608	30.2	30.2	75%	730	100.00	2439	XM_012777995.1
PREDICTED: Microcebus murinus menin 1 (MEN1), transcript varia...	gray mouse l...	30608	30.2	30.2	75%	730	100.00	2439	XM_012777994.1
PREDICTED: Propithecus coquereli chloride channel protein...	Coquerel's s...	379532	30.2	30.2	75%	730	100.00	1589	XM_012662476.1
PREDICTED: Odobenus rosmarus divergens KRAB-A domain containin...	Pacific walrus	9708	30.2	30.2	95%	730	94.74	3514	XM_012565393.1
TPA: Toxoplasma gondii VEG, chromosome chrIV, complete genome	NA	432359	30.2	30.2	75%	730	100.00	2662467	LN714493.1
TPA: Neospora caninum Liverpool, chromosome chrII, complete...	NA	572307	30.2	30.2	75%	730	100.00	2174329	LN714476.1
TPA: Neospora caninum Liverpool, chromosome chrIb, complete...	NA	572307	30.2	30.2	75%	730	100.00	1909405	LN714475.1
Calothrix sp. 336/3, complete genome	NA	1337936	30.2	30.2	75%	730	100.00	6283267	CP011382.1
PREDICTED: Aotus nancymaae uncharacterized LOC105719292...	Ma's night m...	37293	30.2	30.2	75%	730	100.00	1666	XR_001107947.1
Coccidioides immitis RS TBC domain-containing protein...	NA	246410	30.2	30.2	75%	730	100.00	2203	XM_001244506.2
PREDICTED: Macaca nemestrina uncharacterized LOC105490566...	pig-tailed m...	9545	30.2	30.2	75%	730	100.00	1797	XR_992943.1
PREDICTED: Cercocebus atys uncharacterized LOC105596489...	sooty mangabey	9531	30.2	30.2	75%	730	100.00	3937	XR_001018652.1
Paenibacillus sp. IHBB 10380, complete genome	NA	1566358	30.2	30.2	75%	730	100.00	5770242	CP010976.1
Bacillus anthracis strain A1144, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5200257	**CP010852.1**
PREDICTED: Fopius arisanus uncharacterized LOC105266759...	NA	64838	30.2	30.2	75%	730	100.00	2096	XM_011305157.1
Bacillus anthracis strain Canadian_bison, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5229224	**CP010322.1**
Bacillus cereus 03BB108, complete genome	NA	451709	30.2	30.2	75%	730	100.00	5342933	CP009641.1
Bacillus thuringiensis strain HD571, complete genome	NA	1428	30.2	30.2	75%	730	100.00	5256240	CP009600.1
Bacillus anthracis strain RA3, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5213209	**CP009697.1**
Bacillus anthracis strain Ohio ACB, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5222171	**CP009341.1**
Bacillus anthracis strain Vollum 1B, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5229969	**CP009328.1**
Bacillus thuringiensis strain HD1011, complete genome	NA	1428	30.2	30.2	75%	730	100.00	5232696	CP009335.1
Bacillus cereus 03BB102, complete genome	NA	572264	30.2	30.2	75%	730	100.00	5268427	CP009318.1
Bacillus anthracis str. Turkey32, complete genome	NA	1452727	30.2	30.2	75%	730	100.00	5228731	**CP009315.1**
Bacillus anthracis strain Pollino sequence	NA	1392	30.2	30.2	75%	730	100.00	5227410	**CP010813.1**
PREDICTED: Notothenia coriiceps gamma-tubulin complex componen...	black rockcod	8208	30.2	30.2	75%	730	100.00	3103	XM_010794432.1
PREDICTED: Loxodonta africana YKT6 v-SNARE homolog (YKT6),...	African sava...	9785	30.2	30.2	75%	730	100.00	2850	XM_003418607.2
PREDICTED: Tinamus guttatus tubulin, gamma complex associated...	white-throat...	94827	30.2	30.2	75%	730	100.00	1929	XM_010211696.1
PREDICTED: Colius striatus ankyrin repeat domain 16 (ANKRD16),...	speckled mou...	57412	30.2	30.2	75%	730	100.00	952	XM_010207757.1
PREDICTED: Tauraco erythrolophus SMAD specific E3	red-crested ...	121530	30.2	30.2	75%	730	100.00	2376	XM_009980498.1

ubiquitin...									
PREDICTED: Picoides pubescens CSRP2 binding protein (CSRP2BP),...	Downy woodpe ...	118200	30.2	30.2	75%	730	100.00	2362	XM_009905952.1
Aphanomyces astaci hypothetical protein mRNA	NA	112090	30.2	30.2	75%	730	100.00	1430	XM_009843759.1
PREDICTED: Struthio camelus australis **Fanconi anemia,...**	NA	441894	30.2	30.2	75%	730	100.00	2250	**XM_009685403.1**
PREDICTED: Fulmarus glacialis **Fanconi anemia, complementation...**	Northern fulmar	30455	30.2	30.2	75%	730	100.00	1769	**XM_009586677.1**
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	75%	730	100.00	2699	LN139148.1
Caenorhabditis elegans genome assembly...	NA	6239	30.2	30.2	75%	730	100.00	169569	LK927641.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common carp	7962	30.2	30.2	75%	730	100.00	379135	LN593647.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common carp	7962	30.2	60.5	75%	730	100.00	183361	LN590810.1
Cyprinus carpio genome assembly common carp genome, scaffold:...	common carp	7962	30.2	30.2	75%	730	100.00	27918166	LN590683.1
Human DNA sequence from clone ABC10-44052000G22 on chromosome...	human	9606	30.2	30.2	75%	730	100.00	41189	FO681525.1
Metallosphaera sedula strain CuR1 genome	NA	43687	30.2	30.2	75%	730	100.00	2191492	CP008822.1
Bacillus anthracis strain Han, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5225433	**CP008854.1**
Bacillus anthracis strain Cvac02, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5227170	**CP008853.1**
Phytophthora parasitica INRA-310 hypothetical protein, variant...	NA	761204	30.2	30.2	75%	730	100.00	1545	XM_008902712.1
Phytophthora parasitica INRA-310 hypothetical protein mRNA	NA	761204	30.2	30.2	75%	730	100.00	1548	XM_008902711.1
Bacillus anthracis str. Vollum, complete genome	NA	261591	30.2	30.2	75%	730	100.00	5229469	**CP007666.1**
Bacillus anthracis strain BFV genome	NA	1392	30.2	30.2	75%	730	100.00	5230053	**CP007704.1**
Aphanomyces invadans hypothetical protein mRNA	NA	157072	30.2	30.2	75%	730	100.00	1805	XM_008882044.1
Aphanomyces invadans hypothetical protein, variant mRNA	NA	157072	30.2	30.2	75%	730	100.00	1830	XM_008882043.1
Bacillus anthracis strain HYU01, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5213498	**CP008846.1**
PREDICTED: Equus przewalskii tubulin, gamma complex associated...	Przewalski's...	9798	30.2	30.2	75%	730	100.00	3769	XM_008542230.1
PREDICTED: Equus przewalskii NOP14 nucleolar protein (NOP14),...	Przewalski's...	9798	30.2	30.2	75%	730	100.00	2924	XM_008532388.1
PREDICTED: Equus przewalskii NOP14 nucleolar protein (NOP14),...	Przewalski's...	9798	30.2	30.2	75%	730	100.00	3029	XM_008532386.1
Solanum lycopersicum chromosome ch04, complete genome	tomato	4081	30.2	30.2	75%	730	100.00	64069666	HG975516.1
Bacillus cereus strain FT9, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5223665	CP008712.1
PREDICTED: Stegastes partitus collagen alpha-1(XVIII) chain-li...	bicolor dams...	144197	30.2	30.2	75%	730	100.00	5190	XM_008292708.1
PREDICTED: Stegastes partitus collagen alpha-1(XVIII) chain-li...	bicolor dams...	144197	30.2	30.2	75%	730	100.00	5232	XM_008292707.1
Phaseolus vulgaris hypothetical protein (PHAVU_009G139100g)...	NA	3885	30.2	30.2	75%	730	100.00	2671	XM_007137528.1
PREDICTED: Peromyscus maniculatus bairdii scribbled planar cel...	prairie deer...	230844	30.2	30.2	75%	730	100.00	5099	XM_006989311.1
PREDICTED: Peromyscus	prairie deer...	230844	30.2	30.2	75%	730	100.00	5174	XM_006989310.1

maniculatus bairdii scribbled planar cel...									
PREDICTED: Peromyscus maniculatus bairdii scribbled planar cel...	prairie deer...	230844	30.2	30.2	75%	730	100.00	5258	XM_006989307.1
Bacillus anthracis str. SVA11, complete genome	NA	1392837	30.2	30.2	75%	730	100.00	5210966	**CP006742.1**
PREDICTED: Chrysochloris asiatica spen family transcriptional...	Cape golden ...	185453	30.2	30.2	75%	730	100.00	10890	XM_006866416.1
PREDICTED: Chrysochloris asiatica multiple endocrine neoplasia...	Cape golden ...	185453	30.2	30.2	75%	730	100.00	1882	XM_006860959.1
PREDICTED: Chrysochloris asiatica multiple endocrine neoplasia...	Cape golden ...	185453	30.2	30.2	75%	730	100.00	1897	XM_006860958.1
PREDICTED: Elephantulus edwardii ankyrin repeat and MYND domai...	Cape elephan ...	28737	30.2	30.2	75%	730	100.00	3390	XM_006893500.1
Homo sapiens SCO cytochrome c oxidase assembly protein 1 (SCO1...	human	9606	30.2	30.2	75%	730	100.00	24237	NG_008228.2
Chaetomium thermophilum var. thermophilum DSM 1495 hypothetica...	NA	759272	30.2	30.2	75%	730	100.00	2529	XM_006696138.1
Bacillus toyonensis BCT-7112, complete genome	NA	1415784	30.2	30.2	75%	730	100.00	4940474	CP006863.1
PREDICTED: Microtus ochrogaster keratin 2 (Krt2), mRNA	prairie vole	79684	30.2	60.5	75%	730	100.00	2070	XM_005353841.1
Streptomyces ansochromogenes clone pks1 metabolite biosyntheti...	NA	115647	30.2	30.2	75%	730	100.00	94167	KF170321.1
PREDICTED: Arvicola amphibius scribble planar cell polarity...	NA	0	30.2	30.2	75%	730	100.00	5283	XM_038342578.2
PREDICTED: Corvus kubaryi microtubule organization protein...	Mariana crow	68294	30.2	30.2	75%	730	100.00	5815	XM_042044903.1
PREDICTED: Corvus kubaryi microtubule organization protein...	Mariana crow	68294	30.2	30.2	75%	730	100.00	5817	XM_042044900.1
PREDICTED: Melanotaenia boesemani chromodomain helicase DNA...	Boeseman's r...	1250792	30.2	30.2	75%	730	100.00	9767	XM_041991309.1
Bacillus mycoides strain BPN29/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5243016	CP072065.1
Bacillus mycoides strain JAS06/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5352400	CP072061.1
Bacillus mycoides strain JAS12/5 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5265397	CP072057.1
Bacillus mycoides strain JAS85/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5339421	CP072055.1
Bacillus mycoides strain JAS94/5 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5275222	CP036145.1
Bacillus mycoides strain JAS85/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5202602	CP036137.1
Bacillus mycoides strain JAS823 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5114971	CP036132.1
Bacillus mycoides strain JAS635 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5473381	CP036121.1
Bacillus mycoides strain JAS481 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5296574	CP036117.1
Bacillus toyonensis strain JAS411 chromosome, complete genome	NA	155322	30.2	30.2	75%	730	100.00	5361187	CP036111.1
Bacillus mycoides strain JAS391 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5235951	CP036102.1
Bacillus wiedmannii strain JAS28/2 chromosome, complete genome	NA	1890302	30.2	30.2	75%	730	100.00	5534165	CP036101.1
Bacillus mycoides strain JAS23/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5313017	CP036099.1
Bacillus toyonensis strain JAS22/1 chromosome, complete genome	NA	155322	30.2	30.2	75%	730	100.00	5307379	CP036094.1
Bacillus mycoides strain JAS15/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5291025	CP071811.1

Bacillus toyonensis strain JAS13/1 chromosome, complete genome	NA	155322	30.2	30.2	75%	730	100.00	5360709	CP036090.1
Bacillus mycoides strain JAS1004 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5407642	CP036084.1
Bacillus wiedmannii strain JAS08/1 chromosome, complete genome	NA	1890302	30.2	30.2	75%	730	100.00	5513922	CP036073.1
Bacillus wiedmannii strain JAS07/5 chromosome, complete genome	NA	1890302	30.2	30.2	75%	730	100.00	5239489	CP036070.1
Bacillus mycoides strain JAS06/3 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5348830	CP036064.1
Bacillus mycoides strain JAS06/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5361170	CP036057.1
Bacillus toyonensis strain JAS03/3 chromosome, complete genome	NA	155322	30.2	30.2	75%	730	100.00	5281277	CP036052.1
Bacillus mycoides strain JAS014 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5146518	CP071808.1
Bacillus mycoides strain BPN601 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5245175	CP036046.1
Bacillus mycoides strain BPN58/4 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5248764	CP036043.1
Bacillus mycoides strain BPN573 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5281925	CP036040.1
Bacillus mycoides strain BPN57/2 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5067631	CP036034.1
Bacillus mycoides strain BPN54/2 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5208286	CP036026.1
Bacillus mycoides strain BPN52/2 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5266779	CP036023.1
Bacillus mycoides strain BPN51/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5281951	CP036017.1
Bacillus toyonensis strain BPN45/4 chromosome, complete genome	NA	155322	30.2	30.2	75%	730	100.00	5446351	CP036014.1
Bacillus mycoides strain BPN43/2 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5205885	CP036009.1
Bacillus mycoides strain BPN36/2 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5347123	CP035994.1
Bacillus mycoides strain BPN29/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5642477	CP035987.1
Bacillus mycoides strain BPN211 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5265340	CP035984.1
Bacillus mycoides strain BPN121 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5243491	CP035978.1
Bacillus mycoides strain BPN102 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5093759	CP035974.1
Bacillus mycoides strain BPN09/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5340691	CP035965.1
Bacillus mycoides strain BPN07/3 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5145716	CP035962.1
Bacillus mycoides strain BPN03/1 chromosome, complete genome	NA	1405	30.2	30.2	75%	730	100.00	5010935	CP035953.1
PREDICTED: Chelmon rostratus Ras suppressor protein 1 (rsu1),...	copperband b...	109905	30.2	30.2	75%	730	100.00	3080	XM_041961404.1
PREDICTED: Coregonus clupeaformis vasopressin V2 receptor-like...	lake whitefish	59861	30.2	30.2	75%	730	100.00	1843	XM_041857992.1
Fusarium mangiferae uncharacterized protein (FMAN_08655),...	NA	192010	30.2	30.2	75%	730	100.00	1656	XM_041829410.1
PREDICTED: Cheilinus undulatus collagen alpha-1(XVIII)...	humphead wrasse	241271	30.2	30.2	75%	730	100.00	6563	XM_041814073.1
PREDICTED: Vulpes lagopus menin 1 (MEN1), transcript variant X...	Arctic fox	494514	30.2	30.2	75%	730	100.00	3304	XM_041723541.1
PREDICTED: Vulpes lagopus menin 1 (MEN1), transcript variant X...	Arctic fox	494514	30.2	30.2	75%	730	100.00	2778	XM_041723540.1
PREDICTED: Vulpes lagopus menin 1 (MEN1), transcript variant X...	Arctic fox	494514	30.2	30.2	75%	730	100.00	3343	XM_041723539.1
PREDICTED: Vulpes lagopus menin 1 (MEN1), transcript variant X...	Arctic fox	494514	30.2	30.2	75%	730	100.00	3331	XM_041723538.1

PREDICTED: Vulpes lagopus SH3 and multiple ankyrin repeat...	Arctic fox	494514	30.2	30.2	75%	730	100.00	9526	XM_041774026.1
PREDICTED: Vulpes lagopus SH3 and multiple ankyrin repeat...	Arctic fox	494514	30.2	30.2	75%	730	100.00	9543	XM_041774025.1
PREDICTED: Vulpes lagopus SH3 and multiple ankyrin repeat...	Arctic fox	494514	30.2	30.2	75%	730	100.00	9548	XM_041774024.1
PREDICTED: Vulpes lagopus SH3 and multiple ankyrin repeat...	Arctic fox	494514	30.2	30.2	75%	730	100.00	9552	XM_041774023.1
PREDICTED: Vulpes lagopus SH3 and multiple ankyrin repeat...	Arctic fox	494514	30.2	30.2	75%	730	100.00	9711	XM_041774022.1
PREDICTED: Vulpes lagopus SH3 and multiple ankyrin repeat...	Arctic fox	494514	30.2	30.2	75%	730	100.00	9575	XM_041774021.1
Aspergillus puulaauensis uncharacterized protein (APUU_81027S)...	NA	1220207	30.2	30.2	75%	730	100.00	2208	XM_041697373.1
Blastobasis adustella genome assembly, chromosome: 16	NA	1869501	30.2	30.2	95%	730	94.74	17489016	OU026130.1
Synergistetes bacterium strain L-13 chromosome, complete genome	NA	2268202	30.2	30.2	75%	730	100.00	3196753	CP074691.1
Pseudomonas qingdaonensis strain S-1 chromosome, complete genome	NA	2056231	30.2	30.2	75%	730	100.00	5938989	CP074676.1
Habrosyne pyritoides genome assembly, chromosome: 9	NA	721137	30.2	30.2	75%	730	100.00	14359141	OU015594.1
Habrosyne pyritoides genome assembly, chromosome: 6	NA	721137	30.2	30.2	75%	730	100.00	15105336	OU015591.1
Caprimulgus europaeus genome assembly, chromosome: 18	Eurasian nig...	111811	30.2	30.2	75%	730	100.00	15699869	OU015542.1
Caprimulgus europaeus genome assembly, chromosome: 24	Eurasian nig...	111811	30.2	30.2	75%	730	100.00	7570459	OU015548.1
Caprimulgus europaeus genome assembly, chromosome: 23	Eurasian nig...	111811	30.2	30.2	75%	730	100.00	8187400	OU015547.1
Caprimulgus europaeus genome assembly, chromosome: 6	Eurasian nig...	111811	30.2	30.2	75%	730	100.00	65352188	OU015529.1
Fusarium fujikuroi IMI 58289 draft genome, chromosome FFUJ_chr06	NA	1279085	30.2	30.2	75%	730	100.00	4234805	HF679028.1
Saccharomycetaceae sp. 'Ashbya aceri' chromosome II, complete...	NA	566037	30.2	30.2	75%	730	100.00	1019532	CP006021.1
Lacticaseibacillus zeae strain FBL8 chromosome, complete genome	NA	57037	30.2	30.2	75%	730	100.00	3132522	CP074379.1
PREDICTED: Microtus oregoni scribble planar cell polarity...	creeping vole	111838	30.2	30.2	75%	730	100.00	5426	XM_041672161.1
PREDICTED: Microtus oregoni scribble planar cell polarity...	creeping vole	111838	30.2	30.2	75%	730	100.00	5432	XM_041672160.1
PREDICTED: Microtus oregoni scribble planar cell polarity...	creeping vole	111838	30.2	30.2	75%	730	100.00	5438	XM_041672159.1
PREDICTED: Microtus oregoni scribble planar cell polarity...	creeping vole	111838	30.2	30.2	75%	730	100.00	5501	XM_041672158.1
PREDICTED: Microtus oregoni scribble planar cell polarity...	creeping vole	111838	30.2	30.2	75%	730	100.00	5510	XM_041672157.1
PREDICTED: Microtus oregoni scribble planar cell polarity...	creeping vole	111838	30.2	30.2	75%	730	100.00	5522	XM_041672156.1
PREDICTED: Microtus oregoni scribble planar cell polarity...	creeping vole	111838	30.2	30.2	75%	730	100.00	5582	XM_041672155.1
PREDICTED: Microtus oregoni scribble planar cell polarity...	creeping vole	111838	30.2	30.2	75%	730	100.00	5582	XM_041672154.1
PREDICTED: Microtus oregoni scribble planar cell polarity...	creeping vole	111838	30.2	30.2	75%	730	100.00	5585	XM_041672152.1
Bacillus cereus strain BC07 chromosome, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5206228	CP072769.1
Bacillus cereus strain BC06 chromosome, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5211756	CP072766.1
Homo sapiens isolate CHM13 chromosome 18	human	9606	30.2	30.2	75%	730	100.00	80542538	CP068260.2
Suillus discolor uncharacterized protein (F5147DRAFT_822294),...	NA	1912936	30.2	30.2	75%	730	100.00	2570	XM_041443728.1
Suillus discolor uncharacterized protein (F5147DRAFT_785151),...	NA	1912936	30.2	30.2	75%	730	100.00	2577	XM_041442908.1
PREDICTED: Pyrgilauda ruficollis tripartite motif containing 2...	rufous-necke...	221976	30.2	30.2	75%	730	100.00	1439	XM_041487563.1

PREDICTED: Pyrgilauda ruficollis collagen alpha-3(IV) chain-li...	rufous-necke...	221976	30.2	60.5	75%	730	100.00	1894	XM_041471373.1
PREDICTED: Onychostruthus taczanowskii tripartite motif...	white-rumped ...	356909	30.2	30.2	75%	730	100.00	3245	XM_041409630.1
PREDICTED: Aquila chrysaetos chrysaetos serine active site...	NA	223781	30.2	30.2	75%	730	100.00	6112	XM_030022863.2
Bacillus tropicus strain LM1212-DB chromosome, complete genome	NA	2026188	30.2	30.2	75%	730	100.00	5631499	CP051013.1
Bacillus nitratireducens strain BM02 chromosome, complete genome	NA	2026193	30.2	30.2	75%	730	100.00	5138923	CP047366.1
PREDICTED: Toxotes jaculatrix methyltransferase like 25...	banded arche...	941984	30.2	30.2	75%	730	100.00	2970	XM_041029704.1
Homo sapiens lncRNA for PREDICTED lncRNA (TCONS_00007772)	human	9606	30.2	30.2	75%	730	100.00	2060	OA985529.1
Aspergillus sydowii CBS 593.65 uncharacterized protein...	NA	1036612	30.2	30.2	75%	730	100.00	2208	XM_040842684.1
Aspergillus versicolor CBS 583.65 uncharacterized protein...	NA	1036611	30.2	30.2	75%	730	100.00	2208	XM_040818170.1
Aureobasidium melanogenum strain TN3-1 chromosome 17	NA	46634	30.2	30.2	75%	730	100.00	2190916	CP061996.1
PREDICTED: Mesocricetus auratus scribble planar cell polarity...	golden hamster	10036	30.2	30.2	75%	730	100.00	5405	XM_040736428.1
PREDICTED: Mesocricetus auratus scribble planar cell polarity...	golden hamster	10036	30.2	30.2	75%	730	100.00	5419	XM_040736427.1
PREDICTED: Mesocricetus auratus scribble planar cell polarity...	golden hamster	10036	30.2	30.2	75%	730	100.00	5481	XM_040736426.1
PREDICTED: Mesocricetus auratus scribble planar cell polarity...	golden hamster	10036	30.2	30.2	75%	730	100.00	5490	XM_040736425.1
PREDICTED: Mesocricetus auratus scribble planar cell polarity...	golden hamster	10036	30.2	30.2	75%	730	100.00	5503	XM_040736424.1
PREDICTED: Mesocricetus auratus scribble planar cell polarity...	golden hamster	10036	30.2	30.2	75%	730	100.00	5563	XM_040736423.1
PREDICTED: Mesocricetus auratus scribble planar cell polarity...	golden hamster	10036	30.2	30.2	75%	730	100.00	5566	XM_040736422.1
PREDICTED: Mesocricetus auratus syntaxin 16 (Stx16), transcrip...	golden hamster	10036	30.2	30.2	95%	730	94.74	4396	XM_005074480.4
PREDICTED: Mesocricetus auratus syntaxin 16 (Stx16), transcrip...	golden hamster	10036	30.2	30.2	95%	730	94.74	4408	XM_005074479.4
PREDICTED: Mesocricetus auratus syntaxin 16 (Stx16), transcrip...	golden hamster	10036	30.2	30.2	95%	730	94.74	4448	XM_005074478.4
PREDICTED: Mesocricetus auratus syntaxin 16 (Stx16), transcrip...	golden hamster	10036	30.2	30.2	95%	730	94.74	4459	XM_005074477.4
Sus scrofa breed NS chromosome 12	NA	415978	30.2	30.2	75%	730	100.00	63073457	CP071563.1
Sus scrofa breed NS chromosome 10	NA	415978	30.2	30.2	75%	730	100.00	71502813	CP071561.1
PREDICTED: Falco naumanni dynein axonemal intermediate chain 7...	lesser kestrel	148594	30.2	30.2	75%	730	100.00	6468	XM_040594673.1
PREDICTED: Falco naumanni dynein axonemal intermediate chain 7...	lesser kestrel	148594	30.2	30.2	75%	730	100.00	6613	XM_040594672.1
PREDICTED: Falco naumanni dynein axonemal intermediate chain 7...	lesser kestrel	148594	30.2	30.2	75%	730	100.00	4858	XM_040594670.1
PREDICTED: Rosa chinensis ABC transporter F family member 2...	NA	74649	30.2	30.2	75%	730	100.00	4244	XM_040513735.1
PREDICTED: Rosa chinensis ABC transporter F family member 5...	NA	74649	30.2	30.2	75%	730	100.00	2598	XM_040513734.1
PREDICTED: Rosa chinensis ABC transporter F family member 5...	NA	74649	30.2	30.2	75%	730	100.00	2584	XM_040513733.1
PREDICTED: Rosa chinensis ABC transporter F family member 5...	NA	74649	30.2	30.2	75%	730	100.00	2726	XM_040513732.1
PREDICTED: Rosa chinensis ABC transporter F family member 5...	NA	74649	30.2	30.2	75%	730	100.00	2711	XM_024325807.2
PREDICTED: Rosa chinensis ABC transporter F family member 2...	NA	74649	30.2	30.2	75%	730	100.00	1033	XR_005805633.1

PREDICTED: Rosa chinensis ABC transporter F family member 2...	NA	74649	30.2	30.2	75%	730	100.00	1188	XM_040513731.1
PREDICTED: Rosa chinensis ABC transporter F family member 2...	NA	74649	30.2	30.2	75%	730	100.00	1205	XR_005805632.1
PREDICTED: Rosa chinensis ABC transporter F family member 2...	NA	74649	30.2	30.2	75%	730	100.00	1205	XR_005805631.1
PREDICTED: Ixodes scapularis protein transport protein Sec31A...	black-legged...	6945	30.2	30.2	75%	730	100.00	3937	XM_029969169.3
PREDICTED: Ixodes scapularis protein transport protein Sec31A...	black-legged...	6945	30.2	30.2	75%	730	100.00	4546	XM_029969168.3
PREDICTED: Puma yagouaroundi neuroligin 3 (NLGN3), transcript...	jaguarundi	1608482	30.2	30.2	75%	730	100.00	2259	XM_040467767.1
PREDICTED: Puma yagouaroundi chromosome unknown C12orf4 homolo...	jaguarundi	1608482	30.2	30.2	95%	730	94.74	1395	XM_040462992.1
PREDICTED: Puma yagouaroundi chromosome unknown C12orf4 homolo...	jaguarundi	1608482	30.2	30.2	95%	730	94.74	1515	XM_040462991.1
PREDICTED: Puma yagouaroundi chromosome unknown C12orf4 homolo...	jaguarundi	1608482	30.2	30.2	95%	730	94.74	1410	XM_040462990.1
PREDICTED: Puma yagouaroundi chromosome unknown C12orf4 homolo...	jaguarundi	1608482	30.2	30.2	95%	730	94.74	2225	XM_040462989.1
PREDICTED: Puma yagouaroundi chromosome unknown C12orf4 homolo...	jaguarundi	1608482	30.2	30.2	95%	730	94.74	2245	XM_040462988.1
PREDICTED: Puma yagouaroundi rotatin (RTTN), transcript varian...	jaguarundi	1608482	30.2	30.2	75%	730	100.00	4797	XM_040478590.1
PREDICTED: Puma yagouaroundi rotatin (RTTN), transcript varian...	jaguarundi	1608482	30.2	30.2	75%	730	100.00	4815	XM_040478589.1
PREDICTED: Puma yagouaroundi rotatin (RTTN), transcript varian...	jaguarundi	1608482	30.2	30.2	75%	730	100.00	6062	XM_040478588.1
PREDICTED: Puma yagouaroundi rotatin (RTTN), transcript varian...	jaguarundi	1608482	30.2	30.2	75%	730	100.00	6947	XM_040478587.1
PREDICTED: Puma yagouaroundi rotatin (RTTN), transcript varian...	jaguarundi	1608482	30.2	30.2	75%	730	100.00	7280	XM_040478586.1
Leptidea sinapis genome assembly, chromosome: 47	NA	189913	30.2	30.2	75%	730	100.00	8352274	FR990200.1
Leptidea sinapis genome assembly, chromosome: 28	NA	189913	30.2	30.2	75%	730	100.00	12898090	FR990181.1
Leptidea sinapis genome assembly, chromosome: 22	NA	189913	30.2	30.2	75%	730	100.00	13724482	FR990175.1
Leptidea sinapis genome assembly, chromosome: 19	NA	189913	30.2	30.2	75%	730	100.00	14266499	FR990172.1
Leptidea sinapis genome assembly, chromosome: 1	NA	189913	30.2	30.2	75%	730	100.00	34332082	FR990154.1
Ochlodes sylvanus genome assembly, chromosome: 16	NA	876063	30.2	30.2	75%	730	100.00	12618286	FR990139.1
Meleagris gallopavo genome assembly, chromosome: 22	turkey	9103	30.2	30.2	75%	730	100.00	14137791	HG999697.1
PREDICTED: Oryx dammah glutamate ionotropic receptor NMDA type...	scimitar-hor...	59534	30.2	30.2	75%	730	100.00	15573	XM_040235229.1
PREDICTED: Oryx dammah olfactory receptor 1L8-like...	scimitar-hor...	59534	30.2	30.2	75%	730	100.00	960	XM_040225052.1
PREDICTED: Oryx dammah stimulator of interferon response cGAMP...	scimitar-hor...	59534	30.2	30.2	75%	730	100.00	2059	XM_040239958.1
PREDICTED: Oryx dammah stimulator of interferon response cGAMP...	scimitar-hor...	59534	30.2	30.2	75%	730	100.00	3026	XM_040239957.1
PREDICTED: Gasterosteus aculeatus aculeatus LHFPL tetraspan...	three-spined...	481459	30.2	30.2	75%	730	100.00	2420	XM_040175292.1
PREDICTED: Gasterosteus aculeatus aculeatus LHFPL	three-spined...	481459	30.2	30.2	75%	730	100.00	2718	XM_040175291.1

tetraspan...									
PREDICTED: Xiphias gladius chloride channel, voltage-sensitive...	swordfish	8245	30.2	30.2	75%	730	100.00	7207	XM_040142792.1
PREDICTED: Xiphias gladius chloride channel, voltage-sensitive...	swordfish	8245	30.2	30.2	75%	730	100.00	6913	XM_040142791.1
Monilinia vaccinii-corymbosi strain RL-1 chromosome 4	NA	61207	30.2	30.2	75%	730	100.00	3929668	CP063408.1
Rhizobium ruizarguesonis strain NZLR24 chromosome, complete...	NA	2081791	30.2	30.2	75%	730	100.00	5043164	CP071678.1
Rhizobium binae strain BLR195 plasmid p1, complete sequence	NA	1138190	30.2	30.2	75%	730	100.00	529274	CP071605.1
Atethmia centrago genome assembly, chromosome: 6	NA	988071	30.2	30.2	75%	730	100.00	34201488	HG995372.1
Hecatera dysodea genome assembly, chromosome: 12	NA	988125	30.2	30.2	75%	730	100.00	21999099	HG995298.1
Maniola jurtina genome assembly, chromosome: 22	meadow brown	191418	30.2	30.2	75%	730	100.00	12131722	HG995229.1
Maniola jurtina genome assembly, chromosome: 18	meadow brown	191418	30.2	30.2	75%	730	100.00	13539626	HG995225.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	75%	730	100.00	24042410	HG994589.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	75%	730	100.00	36024245	HG994587.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	75%	730	100.00	43017027	HG994586.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	90.7	75%	730	100.00	51920379	HG994583.1
Histoplasma capsulatum H88 chromosome 3	NA	544711	30.2	30.2	75%	730	100.00	7000705	CP069104.1
Canis lupus genome assembly, chromosome: 24	gray wolf	9612	30.2	60.5	75%	730	100.00	49877449	HG994407.1
Canis lupus genome assembly, chromosome: 23	gray wolf	9612	30.2	30.2	75%	730	100.00	52955009	HG994406.1
Canis lupus genome assembly, chromosome: 19	gray wolf	9612	30.2	30.2	75%	730	100.00	56745407	HG994403.1
Canis lupus genome assembly, chromosome: 20	gray wolf	9612	30.2	30.2	95%	730	94.74	59774210	HG994401.1
Canis lupus genome assembly, chromosome: 8	gray wolf	9612	30.2	30.2	75%	730	100.00	77585995	HG994390.1
Canis lupus genome assembly, chromosome: 6	gray wolf	9612	30.2	30.2	75%	730	100.00	78385505	HG994389.1
Canis lupus genome assembly, chromosome: 7	gray wolf	9612	30.2	30.2	75%	730	100.00	82288100	HG994388.1
Brassica napus genome assembly, chromosome: C01	rape	3708	30.2	30.2	75%	730	100.00	48239358	HG994365.1
Brassica napus genome assembly, chromosome: A03	rape	3708	30.2	30.2	75%	730	100.00	39685748	HG994357.1
Brassica napus genome assembly, chromosome: A01	rape	3708	30.2	30.2	75%	730	100.00	32958928	HG994355.1
PREDICTED: Pteropus giganteus MORN repeat containing 3 (MORN3)...	Indian flyin...	143291	30.2	30.2	75%	730	100.00	2725	**XM_039879388.1**
PREDICTED: Pteropus giganteus tubulin gamma complex associated...	Indian flyin...	143291	30.2	30.2	75%	730	100.00	3198	**XM_039878806.1**
PREDICTED: Pteropus giganteus tubulin gamma complex associated...	Indian flyin...	143291	30.2	30.2	75%	730	100.00	3907	**XM_039878805.1**
PREDICTED: Pteropus giganteus uncharacterized LOC120584563...	Indian flyin...	143291	30.2	30.2	75%	730	100.00	3030	**XR_005648070.1**
PREDICTED: Pteropus giganteus uncharacterized LOC120584563...	Indian flyin...	143291	30.2	30.2	75%	730	100.00	3482	**XR_005648069.1**
PREDICTED: Perca fluviatilis matrix metallopeptidase 16b...	European perch	8168	30.2	30.2	75%	730	100.00	2351	XM_039816478.1
PREDICTED: Perca fluviatilis matrix metallopeptidase 16b...	European perch	8168	30.2	30.2	75%	730	100.00	6487	XM_039816477.1

PREDICTED: Pimephales promelas chromodomain helicase DNA bindi...	fathead minnow	90988	30.2	30.2	75%	730	100.00	8995	XM_039654639.1
PREDICTED: Pimephales promelas chromodomain helicase DNA bindi...	fathead minnow	90988	30.2	30.2	75%	730	100.00	8998	XM_039654638.1
PREDICTED: Pimephales promelas chromodomain helicase DNA bindi...	fathead minnow	90988	30.2	30.2	75%	730	100.00	9022	XM_039654637.1
PREDICTED: Pimephales promelas chromodomain helicase DNA bindi...	fathead minnow	90988	30.2	30.2	75%	730	100.00	9025	XM_039654636.1
PREDICTED: Oreochromis aureus prostaglandin D2 receptor 2...	NA	47969	30.2	30.2	75%	730	100.00	1666	XM_031756473.2
PREDICTED: Oreochromis aureus prostaglandin D2 receptor 2...	NA	47969	30.2	30.2	75%	730	100.00	2905	XM_031756465.2
Deilephila porcellus genome assembly, chromosome: 15	NA	644661	30.2	30.2	75%	730	100.00	14251341	LR999985.1
Melitaea cinxia genome assembly, chromosome: 3	Glanville fr...	113334	30.2	30.2	75%	730	100.00	20523172	HG992212.1
Mellicta athalia genome assembly, chromosome: 14	NA	113330	30.2	30.2	75%	730	100.00	20209291	HG992190.1
Mellicta athalia genome assembly, chromosome: 3	NA	113330	30.2	30.2	75%	730	100.00	23648884	HG992179.1
PREDICTED: Corvus cornix cornix uncharacterized LOC109144413...	NA	932674	30.2	30.2	95%	730	94.74	850	XR_002045180.3
PREDICTED: Mauremys reevesii low density lipoprotein receptor...	Reeves's turtle	260615	30.2	30.2	75%	730	100.00	4912	XM_039514386.1
PREDICTED: Mauremys reevesii low density lipoprotein receptor...	Reeves's turtle	260615	30.2	30.2	75%	730	100.00	4878	XM_039514385.1
Microvirga sp. VF16 chromosome, complete genome	NA	2807101	30.2	30.2	75%	730	100.00	5422403	CP069354.1
Archangium violaceum strain SDU34 chromosome, complete genome	NA	83451	30.2	30.2	75%	730	100.00	12677854	CP069338.1
PREDICTED: Crotalus tigris tubulin gamma complex associated...	Tiger rattle...	88082	30.2	30.2	75%	730	100.00	3872	XM_039359740.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	75%	730	100.00	24042410	LR794193.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	75%	730	100.00	36024245	LR794191.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	30.2	75%	730	100.00	43017027	LR794190.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon louse	72036	30.2	90.7	75%	730	100.00	51920379	LR794187.1
Digitaria exilis genome assembly, chromosome: 3A	NA	1010633	30.2	30.2	75%	730	100.00	42379666	LR994608.1
Celastrina argiolus genome assembly, chromosome: 11	holly blue	203782	30.2	30.2	75%	730	100.00	19022155	LR994588.1
Cyaniris semiargus genome assembly, chromosome: Z	NA	988025	30.2	30.2	75%	730	100.00	24709970	LR994547.1
Aspergillus puulaauensis MK2 DNA, chromosome 8, nearly complet...	NA	1220207	30.2	30.2	75%	730	100.00	2824896	AP024450.1
Aspergillus puulaauensis MK2 DNA, chromosome 2, nearly complet...	NA	1220207	30.2	30.2	75%	730	100.00	5431972	AP024444.1
PREDICTED: Hyaena hyaena mucin 1, cell surface associated...	striped hyena	95912	30.2	30.2	75%	730	100.00	1396	XM_039251282.1
5_Tge_b3v08	NA	629358	30.2	30.2	75%	730	100.00	182310	OE840448.1
Trachurus trachurus genome assembly, chromosome: 18	Atlantic hor...	36212	30.2	60.5	75%	730	100.00	29245829	LR991646.1
Trachurus trachurus genome assembly, chromosome: 8	Atlantic hor...	36212	30.2	30.2	75%	730	100.00	33049929	LR991642.1
Trachurus trachurus genome assembly, chromosome: 16	Atlantic hor...	36212	30.2	30.2	75%	730	100.00	35009248	LR991639.1
Trachurus trachurus genome assembly, chromosome: 6	Atlantic hor...	36212	30.2	30.2	75%	730	100.00	36283071	LR991634.1
Trachurus trachurus genome assembly, chromosome: 5	Atlantic hor...	36212	30.2	30.2	75%	730	100.00	36888734	LR991633.1
Apotomis turbidana genome assembly, chromosome: 3	NA	1100916	30.2	30.2	75%	730	100.00	30528616	LR990283.1
Aricia agestis genome assembly, chromosome: Z	brown argus	91739	30.2	30.2	75%	730	100.00	42150342	LR990256.1

Hypena proboscidalis genome assembly, chromosome: 17	NA	753189	30.2	30.2	75%	730	100.00	20496581	LR990143.1
Dactylococcopsis salina PCC 8305, complete genome	NA	13035	30.2	30.2	75%	730	100.00	3781008	CP003944.1
Bacillus thuringiensis MC28, complete genome	NA	1195464	30.2	30.2	75%	730	100.00	5414494	CP003687.1
Euproctis similis genome assembly, chromosome: 4	NA	987935	30.2	30.2	75%	730	100.00	26396858	LR990106.1
Erynnis tages genome assembly, chromosome: 17	NA	520884	30.2	30.2	75%	730	100.00	10807718	LR990088.1
Streptomyces sp. KY75 isolate Streptomyces sp. KY75 genome...	NA	2772433	30.2	30.2	75%	730	100.00	7837660	LR881953.1
PREDICTED: Rattus norvegicus integrin subunit alpha 9 (Itga9),...	Norway rat	10116	30.2	30.2	75%	730	100.00	5193	XM_039082700.1
PREDICTED: Rattus norvegicus syntaxin 16 (Stx16), transcript...	Norway rat	10116	30.2	30.2	95%	730	94.74	1550	XR_005501944.1
PREDICTED: Rattus norvegicus syntaxin 16 (Stx16), transcript...	Norway rat	10116	30.2	30.2	95%	730	94.74	4291	XM_006235696.4
PREDICTED: Rattus norvegicus syntaxin 16 (Stx16), transcript...	Norway rat	10116	30.2	30.2	95%	730	94.74	4303	XM_006235695.4
PREDICTED: Rattus norvegicus syntaxin 16 (Stx16), transcript...	Norway rat	10116	30.2	30.2	95%	730	94.74	4343	XM_006235694.4
PREDICTED: Rattus norvegicus syntaxin 16 (Stx16), transcript...	Norway rat	10116	30.2	30.2	95%	730	94.74	4354	XM_006235693.4
PREDICTED: Salvelinus namaycush pikachurin-like (LOC120025571)...	lake trout	8040	30.2	30.2	75%	730	100.00	2316	XM_038970126.1
PREDICTED: Salvelinus namaycush vasopressin V2 receptor-like...	lake trout	8040	30.2	30.2	75%	730	100.00	1239	XM_039007542.1
Breznakiella homolactica strain RmG30 chromosome, complete genome	NA	2798577	30.2	30.2	75%	730	100.00	4673019	CP067089.1
Bacillus toyonensis strain P18 chromosome, complete genome	NA	155322	30.2	30.2	75%	730	100.00	5250895	CP064875.1
Rhodococcus biphenylivorans strain B403 chromosome, complete...	NA	1500843	30.2	30.2	75%	730	100.00	4944495	CP066853.1
PREDICTED: Canis lupus familiaris zinc finger and BTB domain...	dog	9615	30.2	30.2	75%	730	100.00	6382	XM_038664164.1
PREDICTED: Canis lupus familiaris SH3 and multiple ankyrin...	dog	9615	30.2	30.2	75%	730	100.00	8578	XM_038424630.1
PREDICTED: Canis lupus familiaris SH3 and multiple ankyrin...	dog	9615	30.2	30.2	75%	730	100.00	9119	XM_038424629.1
PREDICTED: Canis lupus familiaris SH3 and multiple ankyrin...	dog	9615	30.2	30.2	75%	730	100.00	9287	XM_038424628.1
PREDICTED: Canis lupus familiaris menin 1 (MEN1), transcript...	dog	9615	30.2	30.2	75%	730	100.00	2597	XM_038423453.1
PREDICTED: Canis lupus familiaris menin 1 (MEN1), transcript...	dog	9615	30.2	30.2	75%	730	100.00	2570	XM_038423452.1
PREDICTED: Canis lupus familiaris menin 1 (MEN1), transcript...	dog	9615	30.2	30.2	75%	730	100.00	2587	XM_038423451.1
PREDICTED: Canis lupus familiaris menin 1 (MEN1), transcript...	dog	9615	30.2	30.2	75%	730	100.00	2637	XM_038423450.1
PREDICTED: Canis lupus familiaris menin 1 (MEN1), transcript...	dog	9615	30.2	30.2	75%	730	100.00	2626	XM_038423449.1
PREDICTED: Canis lupus familiaris SH3 and multiple ankyrin...	dog	9615	30.2	30.2	75%	730	100.00	8576	XM_038454507.1
PREDICTED: Canis lupus familiaris SH3 and multiple ankyrin...	dog	9615	30.2	30.2	75%	730	100.00	9122	XM_038454506.1
PREDICTED: Canis lupus familiaris SH3 and multiple ankyrin...	dog	9615	30.2	30.2	75%	730	100.00	9152	XM_038454505.1
Xanthomonas citri strain UnB-XtecTG02-2 chromosome, complete...	NA	346	30.2	30.2	75%	730	100.00	5153348	CP048712.1
Aspergillus felis strain FM324 chromosome 2	NA	1287682	30.2	30.2	75%	730	100.00	5009416	CP066504.1
Arvicola amphibius cullin-4B (Cul4b), mRNA	Eurasian wat...	1047088	30.2	30.2	75%	730	100.00	3028	XM_038316469.1

Arvicola amphibius protein scribble homolog transcript variant...	Eurasian wat...	1047088	30.2	30.2	75%	730	100.00	5370	XM_038342582.1
Arvicola amphibius protein scribble homolog transcript variant...	Eurasian wat...	1047088	30.2	30.2	75%	730	100.00	5206	XM_038342581.1
Arvicola amphibius protein scribble homolog transcript variant...	Eurasian wat...	1047088	30.2	30.2	75%	730	100.00	5222	XM_038342580.1
Arvicola amphibius protein scribble homolog transcript variant...	Eurasian wat...	1047088	30.2	30.2	75%	730	100.00	5282	XM_038342579.1
Bacillus anthracis strain STI1 chromosome, complete genome	NA	1392	30.2	30.2	75%	730	100.00	5229731	**CP066168.1**
Oryza sativa Indica Group cultivar Zhenshan 97 chromosome 11	long-grained...	39946	30.2	30.2	75%	730	100.00	32624309	CP056062.1
Oryza sativa Indica Group cultivar Minghui 63 chromosome 11	long-grained...	39946	30.2	30.2	75%	730	100.00	34100580	CP054686.1
Actinomyces naeslundii strain FDAARGOS_1037 chromosome, comple...	NA	1655	30.2	30.2	75%	730	100.00	3152123	CP066049.1
4_Tte_b3v08	NA	61484	30.2	30.2	75%	730	100.00	42977	OE006330.1
4_Tte_b3v08	NA	61484	30.2	30.2	75%	730	100.00	80026	OE003866.1
4_Tbi_b3v08	NA	61472	30.2	30.2	75%	730	100.00	61095	OD568610.1
Bacillus mycoides strain FDAARGOS_924 chromosome	NA	1405	30.2	30.2	75%	730	100.00	5274331	CP065877.1
1_Tps_b3v08	NA	170557	30.2	30.2	75%	730	100.00	3725	OD029144.1
Scyliorhinus canicula chromosome 23	smaller spot...	7830	30.2	30.2	75%	730	100.00	27685257	LR744052.1
Scyliorhinus canicula chromosome 21	smaller spot...	7830	30.2	30.2	75%	730	100.00	71046048	LR744050.1
Scyliorhinus canicula chromosome 20	smaller spot...	7830	30.2	30.2	75%	730	100.00	98274498	LR744049.1
Bacillus tropicus strain FDAARGOS_897 chromosome, complete genome	NA	2026188	30.2	30.2	75%	730	100.00	5264567	CP065743.1
Streptococcus oralis strain FDAARGOS_885 chromosome, complete...	NA	1303	30.2	30.2	75%	730	100.00	2024323	CP065707.1
Bacillus cereus strain FDAARGOS_918 chromosome, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5270035	CP065650.1
Bacillus tropicus strain FDAARGOS_920 chromosome, complete genome	NA	2026188	30.2	30.2	75%	730	100.00	5298747	CP065739.1
Candidatus Atribacteria bacterium strain RT761 chromosome,...	NA	2053509	30.2	30.2	75%	730	100.00	3101225	CP065383.1
PREDICTED: Chlorocebus sabaeus zinc finger and SCAN...	green monkey	60711	30.2	30.2	75%	730	100.00	10052	XM_037990950.1
PREDICTED: Chlorocebus sabaeus uncharacterized LOC119620509...	green monkey	60711	30.2	30.2	75%	730	100.00	5018	XR_005237000.1
Bacillus paranthracis strain Gxun-30 chromosome, complete genome	NA	2026186	30.2	30.2	75%	730	100.00	5149464	**CP065149.1**
PREDICTED: Kryptolebias marmoratus 23 kDa integral membrane...	mangrove riv...	37003	30.2	30.2	75%	730	100.00	3570	XM_037981224.1
2_Tsi_b3v08	NA	629360	30.2	30.2	75%	730	100.00	46475	OC005816.1
1_Tdi_b3v08	NA	61478	30.2	30.2	75%	730	100.00	48584	OA569843.1
Darwinula stevensoni	NA	69355	30.2	30.2	75%	730	100.00	11230	LR905701.1
Darwinula stevensoni	NA	69355	30.2	30.2	75%	730	100.00	21639	LR904021.1
Darwinula stevensoni	NA	69355	30.2	30.2	75%	730	100.00	83324	LR900498.1
Pan troglodytes BAC CH251-542D16 from chromosome, complete...	chimpanzee	9598	30.2	30.2	75%	730	100.00	187951	AC280579.1
PREDICTED: Cebus imitator IZUMO1 receptor, JUNO (IZUMO1R),...	Panamanian w...	2715852	30.2	30.2	75%	730	100.00	1598	XM_037727836.1
PREDICTED: Cebus imitator	Panamanian	2715852	30.2	30.2	75%	730	100.00	1435	XM_017498441.2

IZUMO1 receptor, JUNO (IZUMO1R),...	w...								
PREDICTED: Nematolebias whitei chromodomain helicase DNA bindi...	Rio pearlfish	451745	30.2	30.2	75%	730	100.00	8651	XM_037682106.1
PREDICTED: Pygocentrus nattereri tubulin, gamma complex...	red-bellied ...	42514	30.2	30.2	75%	730	100.00	4808	XM_017699054.2
Bacillus cereus strain EFR-1 chromosome	NA	1396	30.2	30.2	75%	730	100.00	5315863	CP064072.1
Bacillus paranthracis strain EFR-4 chromosome	NA	2026186	30.2	30.2	75%	730	100.00	5315901	**CP064079.1**
PREDICTED: **Falco** rusticolus cilia and flagella associated...	gyrfalcon	120794	30.2	30.2	75%	730	100.00	5393	XM_037388107.1
PREDICTED: **Falco** rusticolus cilia and flagella associated...	gyrfalcon	120794	30.2	30.2	75%	730	100.00	5538	XM_037388106.1
PREDICTED: **Falco** rusticolus cilia and flagella associated...	gyrfalcon	120794	30.2	30.2	75%	730	100.00	4385	XM_037388105.1
Microbacterium sp. WY121 chromosome, complete genome	NA	2782168	30.2	30.2	75%	730	100.00	3712988	CP063813.1
PREDICTED: Peromyscus leucopus WD repeat domain 81 (Wdr81), mRNA	white-footed...	10041	30.2	30.2	95%	730	94.74	6891	XM_028866748.2
PREDICTED: Peromyscus leucopus chromosome 22 C2orf16 homolog...	white-footed...	10041	30.2	30.2	75%	730	100.00	16799	XM_037198074.1
PREDICTED: Peromyscus leucopus tubulin gamma complex associate...	white-footed...	10041	30.2	30.2	75%	730	100.00	3715	XM_028881296.2
Xanthomonas citri strain UnB-Xtec2D chromosome, complete genome	NA	346	30.2	30.2	75%	730	100.00	5153268	CP048044.1
Streptomyces olivaceus strain SCSIO T05 chromosome, complete...	NA	47716	30.2	30.2	75%	730	100.00	8458055	CP043317.1
Bacillus cereus strain 39 chromosome	NA	1396	30.2	30.2	75%	730	100.00	4894731	CP063651.1
Rhodococcus pyridinivorans strain 5Ap chromosome, complete genome	NA	103816	30.2	30.2	75%	730	100.00	5220735	CP063450.1
PREDICTED: Artibeus jamaicensis tubulin gamma complex associat...	Jamaican fru...	9417	30.2	30.2	75%	730	100.00	3906	XM_037140984.1
Streptomyces ferrugineus strain CCTCC AA2014009 chromosome,...	NA	1413221	30.2	30.2	75%	730	100.00	9959088	CP063373.1
PREDICTED: Sturnira hondurensis tubulin gamma complex associat...	NA	192404	30.2	30.2	75%	730	100.00	3892	XM_037042042.1
PREDICTED: Manis javanica uncharacterized LOC108399514...	Malayan pang...	9974	30.2	30.2	75%	730	100.00	2450	**XR_005053859.1**
PREDICTED: Manis javanica uncharacterized LOC108399514...	Malayan pang...	9974	30.2	30.2	75%	730	100.00	2505	**XR_005053858.1**
PREDICTED: Manis javanica uncharacterized LOC108399514...	Malayan pang...	9974	30.2	30.2	75%	730	100.00	1153	**XR_005053857.1**
PREDICTED: Manis javanica uncharacterized LOC108399514...	Malayan pang...	9974	30.2	30.2	75%	730	100.00	963	**XR_005053855.1**
PREDICTED: Oncorhynchus mykiss pikachurin (LOC110523766),...	rainbow trout	8022	30.2	30.2	75%	730	100.00	2107	XM_036977444.1
PREDICTED: Oncorhynchus mykiss pikachurin (LOC110523766),...	rainbow trout	8022	30.2	30.2	75%	730	100.00	4521	XM_021602759.2
PREDICTED: Oncorhynchus mykiss pikachurin (LOC110523766),...	rainbow trout	8022	30.2	30.2	75%	730	100.00	4545	XM_036977443.1
Macrobrachium nipponense isolate FS-2020 chromosome 26	NA	159736	30.2	30.2	95%	730	94.74	78463671	CP062012.1
Macrobrachium nipponense isolate FS-2020 chromosome 19	NA	159736	30.2	30.2	75%	730	100.00	86821439	CP062040.1
Penstemon cyananthus clone PS051 microsatellite sequence	NA	388136	30.2	30.2	75%	730	100.00	493	JQ967019.1
PREDICTED: Metaseiulus occidentalis E3 ubiquitin-protein ligas...	western pred...	34638	30.2	30.2	75%	730	100.00	2487	XM_003744271.1

Bacillus anthracis str. H9401, complete genome	NA	768494	30.2	30.2	75%	730	100.00	5218947	**CP002091.1**
Seriola quinqueradiata DNA, microsatellite locus Sequ0869TUF	Japanese amb...	8161	30.2	30.2	75%	730	100.00	180	AB644109.1
Corallococcus coralloides DSM 2259, complete genome	NA	1144275	30.2	30.2	75%	730	100.00	10080619	CP003389.1
Methanocella conradii HZ254, complete genome	NA	1041930	30.2	30.2	75%	730	100.00	2378438	CP003243.1
Homo sapiens contactin 1 (CNTN1), RefSeqGene on chromosome 12	human	9606	30.2	30.2	75%	730	100.00	386857	NG_012058.2
Bacillus cereus F837/76, complete genome	NA	347495	30.2	30.2	75%	730	100.00	5222906	CP003187.1
Bacillus cereus NC7401 genomic DNA, complete genome	NA	334406	30.2	30.2	75%	730	100.00	5221581	AP007209.1
Mus musculus targeted non-conditional, lacZ-tagged mutant alle...	house mouse	10090	30.2	30.2	75%	730	100.00	39924	JN960305.1
PREDICTED: Trichosurus vulpecula 5'-nucleotidase, cytosolic II...	common brush...	9337	30.2	30.2	75%	730	100.00	4672	XM_036738782.1
PREDICTED: Colossoma macropomum tubulin, gamma complex...	tambaqui	42526	30.2	30.2	75%	730	100.00	4054	XM_036563423.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowfin se...	8177	30.2	60.5	75%	730	100.00	28107325	LR884472.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome: 3	yellowfin se...	8177	30.2	30.2	75%	730	100.00	26361780	LR884462.1
Bacillus cereus strain CTMA_1571 chromosome, complete genome	NA	1396	30.2	30.2	75%	730	100.00	5182254	CP053656.2
PREDICTED: Pipistrellus kuhlii tubulin gamma complex associate...	Kuhl's pipis...	59472	30.2	30.2	75%	730	100.00	3856	**XM_036456104.1**
PREDICTED: Pipistrellus kuhlii tubulin gamma complex associate...	Kuhl's pipis...	59472	30.2	30.2	75%	730	100.00	3901	**XM_036456103.1**
PREDICTED: Pipistrellus kuhlii lysophosphatidylglycerol...	Kuhl's pipis...	59472	30.2	30.2	75%	730	100.00	7001	**XM_036442652.1**
PREDICTED: Pipistrellus kuhlii lysophosphatidylglycerol...	Kuhl's pipis...	59472	30.2	30.2	75%	730	100.00	7031	**XM_036442651.1**
PREDICTED: Pipistrellus kuhlii lysophosphatidylglycerol...	Kuhl's pipis...	59472	30.2	30.2	75%	730	100.00	7102	**XM_036442650.1**
PREDICTED: Pipistrellus kuhlii KRAB-A domain containing 1...	Kuhl's pipis...	59472	30.2	30.2	95%	730	94.74	3902	**XM_036429839.1**
PREDICTED: Pipistrellus kuhlii KRAB-A domain containing 1...	Kuhl's pipis...	59472	30.2	30.2	95%	730	94.74	3802	**XM_036429837.1**
PREDICTED: Molothrus ater shroom family member 1 (SHROOM1), mRNA	NA	84834	30.2	30.2	75%	730	100.00	2163	XM_036391881.1
PREDICTED: Myotis myotis tubulin gamma complex associated...	NA	51298	30.2	30.2	75%	730	100.00	2969	XM_036297521.1
PREDICTED: Myotis myotis tubulin gamma complex associated...	NA	51298	30.2	30.2	75%	730	100.00	3840	XM_036297520.1
PREDICTED: Myotis myotis tubulin gamma complex associated...	NA	51298	30.2	30.2	75%	730	100.00	3885	XM_036297519.1
PREDICTED: Myotis myotis lysophosphatidylglycerol...	NA	51298	30.2	30.2	75%	730	100.00	7511	XM_036342576.1
PREDICTED: Myotis myotis lysophosphatidylglycerol...	NA	51298	30.2	30.2	75%	730	100.00	7321	XM_036342575.1
PREDICTED: Myotis myotis lysophosphatidylglycerol...	NA	51298	30.2	30.2	75%	730	100.00	7415	XM_036342574.1
PREDICTED: Myotis myotis lysophosphatidylglycerol...	NA	51298	30.2	30.2	75%	730	100.00	7527	XM_036342573.1
PREDICTED: Myotis myotis TRPM8 channel associated factor 1...	NA	51298	30.2	30.2	75%	730	100.00	2945	XM_036328455.1
PREDICTED: Myotis myotis TRPM8 channel associated factor 1...	NA	51298	30.2	30.2	75%	730	100.00	5909	XM_036328454.1
PREDICTED: Myotis myotis TRPM8 channel associated factor 1...	NA	51298	30.2	30.2	75%	730	100.00	5926	XM_036328453.1

PREDICTED: Myotis myotis TRPM8 channel associated factor 1...	NA	51298	30.2	30.2	75%	730	100.00	5986	XM_036328452.1
PREDICTED: Myotis myotis TRPM8 channel associated factor 1...	NA	51298	30.2	30.2	75%	730	100.00	5948	XM_036328451.1
PREDICTED: Myotis myotis KRAB-A domain containing 1 (KRBA1),...	NA	51298	30.2	30.2	95%	730	94.74	4808	XM_036328380.1
PREDICTED: Myotis myotis KRAB-A domain containing 1 (KRBA1),...	NA	51298	30.2	30.2	95%	730	94.74	5011	XM_036328379.1
PREDICTED: Myotis myotis KRAB-A domain containing 1 (KRBA1),...	NA	51298	30.2	30.2	95%	730	94.74	4923	XM_036328377.1
PREDICTED: Myotis myotis KRAB-A domain containing 1 (KRBA1),...	NA	51298	30.2	30.2	95%	730	94.74	5084	XM_036328376.1
PREDICTED: Myotis myotis KRAB-A domain containing 1 (KRBA1),...	NA	51298	30.2	30.2	95%	730	94.74	5106	XM_036328375.1
PREDICTED: Myotis myotis KRAB-A domain containing 1 (KRBA1),...	NA	51298	30.2	30.2	95%	730	94.74	5109	XM_036328374.1
PREDICTED: Myotis myotis KRAB-A domain containing 1 (KRBA1),...	NA	51298	30.2	30.2	95%	730	94.74	5186	XM_036328373.1
PREDICTED: Myotis myotis KRAB-A domain containing 1 (KRBA1),...	NA	51298	30.2	30.2	95%	730	94.74	5288	XM_036328372.1
PREDICTED: Myotis myotis KRAB-A domain containing 1 (KRBA1),...	NA	51298	30.2	30.2	95%	730	94.74	5288	XM_036328371.1
PREDICTED: Myotis myotis KRAB-A domain containing 1 (KRBA1),...	NA	51298	30.2	30.2	95%	730	94.74	5291	XM_036328370.1
PREDICTED: Molossus molossus tRNA splicing endonuclease subuni...	Pallas's mas...	27622	30.2	30.2	75%	730	100.00	1605	XM_036273700.1
PREDICTED: Rousettus aegyptiacus tubulin gamma complex...	Egyptian rou...	9407	30.2	30.2	75%	730	100.00	3906	**XM_016151905.2**
PREDICTED: Rousettus aegyptiacus tubulin gamma complex...	Egyptian rou...	9407	30.2	30.2	75%	730	100.00	4612	**XM_036228799.1**
PREDICTED: Rousettus aegyptiacus tubulin gamma complex...	Egyptian rou...	9407	30.2	30.2	75%	730	100.00	4636	**XM_016151902.2**
PREDICTED: Rousettus aegyptiacus tubulin gamma complex...	Egyptian rou...	9407	30.2	30.2	75%	730	100.00	4000	**XM_016151901.2**
Homo sapiens DNA, chromosome 18, nearly complete genome	human	9606	30.2	30.2	75%	730	100.00	77846715	AP023478.1
Alternaria alternata strain Z7 chromosome 10, complete sequence	NA	5599	30.2	30.2	75%	730	100.00	1841737	CP061884.1
PREDICTED: Onychomys torridus syntaxin 16 (Stx16), transcript...	southern gra...	38674	30.2	30.2	95%	730	94.74	1693	XM_036184077.1
PREDICTED: Onychomys torridus syntaxin 16 (Stx16), transcript...	southern gra...	38674	30.2	30.2	95%	730	94.74	1705	XM_036184076.1
PREDICTED: Onychomys torridus syntaxin 16 (Stx16), transcript...	southern gra...	38674	30.2	30.2	95%	730	94.74	1756	XM_036184074.1
PREDICTED: Onychomys torridus tubulin gamma complex associated...	southern gra...	38674	30.2	30.2	75%	730	100.00	3701	XM_036209465.1
PREDICTED: Mus musculus WD repeat domain 81 (Wdr81), transcrip...	house mouse	10090	30.2	30.2	95%	730	94.74	8693	XR_388372.5
PREDICTED: Mus musculus WD repeat domain 81 (Wdr81), transcrip...	house mouse	10090	30.2	30.2	95%	730	94.74	6855	XR_388371.5
PREDICTED: Mus musculus WD repeat domain 81 (Wdr81), transcrip...	house mouse	10090	30.2	30.2	95%	730	94.74	5091	XM_036156441.1
PREDICTED: Mus musculus WD repeat domain 81 (Wdr81), transcrip...	house mouse	10090	30.2	30.2	95%	730	94.74	6951	XR_879536.4
PREDICTED: Mus musculus WD repeat domain 81 (Wdr81), transcrip...	house mouse	10090	30.2	30.2	95%	730	94.74	6724	XM_006532548.5

PREDICTED: Mus musculus WD repeat domain 81 (Wdr81), transcrip...	house mouse	10090	30.2	30.2	95%	730	94.74	6757	XM_006532547.5
PREDICTED: Mus musculus WD repeat domain 81 (Wdr81), transcrip...	house mouse	10090	30.2	30.2	95%	730	94.74	6937	XM_006532546.5
PREDICTED: Fundulus heteroclitus serine/arginine repetitive...	mummichog	8078	30.2	30.2	75%	730	100.00	1966	XR_002428290.2
PREDICTED: Fundulus heteroclitus serine/arginine repetitive...	mummichog	8078	30.2	30.2	75%	730	100.00	3681	XM_036134033.1
PREDICTED: Fundulus heteroclitus serine/arginine repetitive...	mummichog	8078	30.2	30.2	75%	730	100.00	3684	XM_012865033.3
PREDICTED: Halichoerus grypus SH3 and multiple ankyrin repeat...	gray seal	9711	30.2	30.2	75%	730	100.00	8918	XM_036077865.1
PREDICTED: Halichoerus grypus SH3 and multiple ankyrin repeat...	gray seal	9711	30.2	30.2	75%	730	100.00	8921	XM_036077864.1
PREDICTED: Halichoerus grypus SH3 and multiple ankyrin repeat...	gray seal	9711	30.2	30.2	75%	730	100.00	8948	XM_036077863.1
PREDICTED: Halichoerus grypus SH3 and multiple ankyrin repeat...	gray seal	9711	30.2	30.2	75%	730	100.00	8960	XM_036077862.1
PREDICTED: Phyllostomus discolor G protein-coupled receptor 14...	pale spear-n...	89673	30.2	30.2	75%	730	100.00	1685	XM_028521466.2
PREDICTED: Phyllostomus discolor chloride channel protein ClC-...	pale spear-n...	89673	30.2	30.2	75%	730	100.00	2155	XM_036025357.1
PREDICTED: Phyllostomus discolor chloride channel protein ClC-...	pale spear-n...	89673	30.2	30.2	75%	730	100.00	2329	XM_028512896.2
PREDICTED: Phyllostomus discolor mitogen-activated protein...	pale spear-n...	89673	30.2	30.2	75%	730	100.00	2093	XM_036014698.1
PREDICTED: Phyllostomus discolor tubulin gamma complex...	pale spear-n...	89673	30.2	30.2	75%	730	100.00	3893	XM_028526403.2
PREDICTED: Sander lucioperca matrix metallopeptidase 16b...	pikeperch	283035	30.2	30.2	75%	730	100.00	2334	XM_031294473.2
PREDICTED: Sander lucioperca matrix metallopeptidase 16b...	pikeperch	283035	30.2	30.2	75%	730	100.00	6424	XM_031294472.2
PREDICTED: Aplysia californica histone deacetylase 6...	California s...	6500	30.2	30.2	75%	730	100.00	2376	XM_035972959.1
PREDICTED: Aplysia californica histone deacetylase 6...	California s...	6500	30.2	30.2	75%	730	100.00	5443	XM_005098636.3
Pyrenophora teres f. maculata isolate P-A14 chromosome 7	NA	97480	30.2	60.5	95%	730	100.00	3491396	CP060574.1
Pyrenophora teres f. maculata isolate FGOB10Ptm-1 chromosome 7	NA	97480	30.2	60.5	95%	730	100.00	3032745	CP060562.1
Pyrenophora teres f. maculata isolate NZKF2 chromosome 7	NA	97480	30.2	60.5	95%	730	100.00	3534726	CP060553.1
Pyrenophora teres f. maculata isolate DEN2.6 chromosome 7	NA	97480	30.2	60.5	95%	730	100.00	3282016	CP060541.1
PREDICTED: Amphiprion ocellaris chromodomain helicase DNA...	clown anemon...	80972	30.2	30.2	75%	730	100.00	8800	XM_023284521.2
PREDICTED: Amphiprion ocellaris chromodomain helicase DNA...	clown anemon...	80972	30.2	30.2	75%	730	100.00	8803	XM_023284520.2
PREDICTED: Amphiprion ocellaris chromodomain helicase DNA...	clown anemon...	80972	30.2	30.2	75%	730	100.00	8881	XM_023284519.2
PREDICTED: Amphiprion ocellaris chromodomain helicase DNA...	clown anemon...	80972	30.2	30.2	75%	730	100.00	8884	XM_023284518.2
Acomys russatus genome assembly, chromosome: 30	golden spiny...	60746	30.2	30.2	75%	730	100.00	40934070	LR877241.1
Acomys russatus genome assembly, chromosome: 28	golden spiny...	60746	30.2	60.5	85%	730	100.00	43538471	LR877239.1
Acomys russatus genome assembly, chromosome: 20	golden spiny...	60746	30.2	30.2	75%	730	100.00	74893780	LR877231.1
Onychomys torridus genome assembly, chromosome: 22	southern gra...	38674	30.2	30.2	75%	730	100.00	42861602	LR877209.1

Onychomys torridus genome assembly, chromosome: 20	southern gra...	38674	30.2	30.2	75%	730	100.00	48895294	LR877207.1
Onychomys torridus genome assembly, chromosome: 19	southern gra...	38674	30.2	60.5	75%	730	100.00	66005817	LR877206.1
Bacillus anthracis strain Kanchipuram chromosome	NA	1392	30.2	30.2	75%	730	100.00	5227419	**CP060194.1**
Bacillus sp. PAMC26568 chromosome, complete genome	NA	2760090	30.2	30.2	75%	730	100.00	3899947	CP060137.1
Kribbella qitaiheensis strain SPB151 chromosome, complete genome	NA	1544730	30.2	30.2	75%	730	100.00	8156807	CP043661.1
Homo sapiens diphthamide biosynthesis 1 (DPH1), transcript...	human	9606	30.2	30.2	75%	730	100.00	3028	NR_144476.2
Homo sapiens diphthamide biosynthesis 1 (DPH1), transcript...	human	9606	30.2	30.2	75%	730	100.00	2969	NR_144475.2
Homo sapiens diphthamide biosynthesis 1 (DPH1), transcript...	human	9606	30.2	30.2	75%	730	100.00	3002	NR_144474.2
Homo sapiens diphthamide biosynthesis 1 (DPH1), transcript...	human	9606	30.2	30.2	75%	730	100.00	2524	NM_001346576.2
PREDICTED: Oncorhynchus keta riboflavin-binding protein-like...	chum salmon	8018	30.2	30.2	75%	730	100.00	2332	XM_035747871.1
PREDICTED: Oncorhynchus keta pikachurin-like (LOC118387713),...	chum salmon	8018	30.2	30.2	75%	730	100.00	1808	XM_035776361.1
PREDICTED: Oncorhynchus keta pikachurin-like (LOC118387713),...	chum salmon	8018	30.2	30.2	75%	730	100.00	4754	XM_035776360.1
PREDICTED: Oncorhynchus keta pikachurin-like (LOC118387713),...	chum salmon	8018	30.2	30.2	75%	730	100.00	3213	XR_004826447.1
PREDICTED: Oncorhynchus keta pikachurin-like (LOC118387713),...	chum salmon	8018	30.2	30.2	75%	730	100.00	4206	XM_035776359.1
PREDICTED: Oncorhynchus keta pikachurin-like (LOC118387713),...	chum salmon	8018	30.2	30.2	75%	730	100.00	4232	XM_035776358.1
PREDICTED: Canis lupus dingo menin 1 (MEN1), transcript varian...	dingo	286419	30.2	30.2	75%	730	100.00	2610	XM_035701663.1
PREDICTED: Canis lupus dingo menin 1 (MEN1), transcript varian...	dingo	286419	30.2	30.2	75%	730	100.00	2599	XM_025446153.2
PREDICTED: Canis lupus dingo menin 1 (MEN1), transcript varian...	dingo	286419	30.2	30.2	75%	730	100.00	2572	XM_025446152.2
PREDICTED: Canis lupus dingo menin 1 (MEN1), transcript varian...	dingo	286419	30.2	30.2	75%	730	100.00	2590	XM_025446154.2
PREDICTED: Canis lupus dingo menin 1 (MEN1), transcript varian...	dingo	286419	30.2	30.2	75%	730	100.00	2639	XM_025446151.2
PREDICTED: Canis lupus dingo menin 1 (MEN1), transcript varian...	dingo	286419	30.2	30.2	75%	730	100.00	2628	XM_025446150.2
PREDICTED: Canis lupus dingo SH3 and multiple ankyrin repeat...	dingo	286419	30.2	30.2	75%	730	100.00	8582	XM_025451800.2
PREDICTED: Canis lupus dingo SH3 and multiple ankyrin repeat...	dingo	286419	30.2	30.2	75%	730	100.00	9124	XM_035701273.1
PREDICTED: Canis lupus dingo SH3 and multiple ankyrin repeat...	dingo	286419	30.2	30.2	75%	730	100.00	9206	XM_025451799.2
PREDICTED: Zalophus californianus SH3 and multiple ankyrin...	California s...	9704	30.2	30.2	75%	730	100.00	7421	XM_027580403.2
Arvicola amphibius genome assembly, chromosome: 14	Eurasian wat...	1047088	30.2	30.2	75%	730	100.00	63161238	LR862394.1
Pipistrellus pipistrellus genome assembly, chromosome: 20	common pipis...	59474	30.2	30.2	75%	730	100.00	15565596	**LR862376.1**
Pipistrellus pipistrellus genome assembly, chromosome: 18	common pipis...	59474	30.2	30.2	75%	730	100.00	39450869	**LR862374.1**
Pipistrellus pipistrellus genome assembly, chromosome: 9	common pipis...	59474	30.2	90.7	80%	730	100.00	72542072	**LR862365.1**
Comamonas testosteroni strain R5-28 chromosome, complete genome	NA	285	30.2	30.2	75%	730	100.00	5726362	CP043573.1
Comamonas testosteroni strain T5-67 chromosome, complete genome	NA	285	30.2	30.2	75%	730	100.00	5943463	CP043568.1
Ananas comosus var. bracteatus genome assembly, chromosome: 6	NA	296719	30.2	60.5	95%	730	94.74	18486390	LR862134.1
PREDICTED: Morone saxatilis RAB3 GTPase activating protein...	striped sea-...	34816	30.2	30.2	75%	730	100.00	5742	XM_035661762.1

PREDICTED: Scophthalmus maximus ubiquitin domain containing 1b...	turbot	52904	30.2	30.2	75%	730	100.00	5348	XM_035612914.1
PREDICTED: Scophthalmus maximus sorting nexin-18-like...	turbot	52904	30.2	30.2	75%	730	100.00	4843	XM_035607720.1
PREDICTED: Electrophorus electricus chromodomain helicase DNA...	electric eel	8005	30.2	30.2	75%	730	100.00	8669	XM_035536070.1
PREDICTED: Electrophorus electricus chromodomain helicase DNA...	electric eel	8005	30.2	30.2	75%	730	100.00	8767	XM_035536069.1
PREDICTED: Electrophorus electricus chromodomain helicase DNA...	electric eel	8005	30.2	30.2	75%	730	100.00	8749	XM_035536068.1
PREDICTED: Electrophorus electricus chromodomain helicase DNA...	electric eel	8005	30.2	30.2	75%	730	100.00	8770	XM_035536067.1
Geosmithia morbida beta-glucosidase (GMORB2_4275), partial mRNA	NA	1094350	30.2	30.2	75%	730	100.00	2133	XM_035466250.1
PREDICTED: Cricetulus griseus scribble planar cell polarity...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	5490	XM_027404162.2
PREDICTED: Cricetulus griseus scribble planar cell polarity...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	5575	XM_027404158.2
PREDICTED: Cricetulus griseus scribble planar cell polarity...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	5352	XM_035440684.1
PREDICTED: Cricetulus griseus scribble planar cell polarity...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	5414	XM_027404164.2
PREDICTED: Cricetulus griseus scribble planar cell polarity...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	5436	XM_035440683.1
PREDICTED: Cricetulus griseus scribble planar cell polarity...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	5496	XM_035440682.1
PREDICTED: Cricetulus griseus scribble planar cell polarity...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	5499	XM_027404161.2
PREDICTED: Cricetulus griseus scribble planar cell polarity...	Chinese hamster	10029	30.2	30.2	75%	730	100.00	5279	XM_035459313.1
Homo sapiens BAR/IMD domain containing adaptor protein 2...	human	9606	30.2	30.2	75%	730	100.00	2547	NM_001385129.1
Homo sapiens BAR/IMD domain containing adaptor protein 2...	human	9606	30.2	30.2	75%	730	100.00	2448	NM_001385127.1
Streptococcus sp. oral taxon 061 strain F0704 chromosome,...	NA	712623	30.2	30.2	75%	730	100.00	1765730	CP058258.1
PREDICTED: Anguilla anguilla cyclic GMP-AMP synthase...	European eel	7936	30.2	30.2	75%	730	100.00	2791	XM_035428108.1
PREDICTED: Anguilla anguilla uncharacterized LOC118220079...	European eel	7936	30.2	30.2	75%	730	100.00	229	XR_004763908.1
PREDICTED: Anguilla anguilla D-aspartate oxidase (ddo),...	European eel	7936	30.2	30.2	75%	730	100.00	3069	XM_035430233.1
PREDICTED: Anguilla anguilla D-aspartate oxidase (ddo),...	European eel	7936	30.2	30.2	75%	730	100.00	3188	XM_035430224.1
PREDICTED: Anguilla anguilla D-aspartate oxidase (ddo),...	European eel	7936	30.2	30.2	75%	730	100.00	3024	XM_035430220.1
PREDICTED: Anguilla anguilla D-aspartate oxidase (ddo),...	European eel	7936	30.2	30.2	75%	730	100.00	2988	XM_035430211.1
PREDICTED: Anguilla anguilla D-aspartate oxidase (ddo),...	European eel	7936	30.2	30.2	75%	730	100.00	3107	XM_035430203.1
Helicoverpa zea clone Hz_Scaffold_38 SNP Hz6_38 genomic sequence	corn earworm	7113	30.2	30.2	75%	730	100.00	753145	MT702895.1
PREDICTED: Callithrix jacchus uncharacterized LOC118153537...	white-tufted...	9483	30.2	30.2	75%	730	100.00	5564	XR_004742740.1
Anas platyrhynchos genome assembly, chromosome: 9	mallard	8839	30.2	30.2	75%	730	100.00	26142558	LS423619.1

Anas platyrhynchos genome assembly, chromosome: 4	mallard	8839	30.2	30.2	75%	730	100.00	74522197	LS423614.1
Danio rerio strain Nadia (NA) genome assembly, chromosome: 15	zebrafish	7955	30.2	30.2	75%	730	100.00	46203510	LR812583.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged...	house mouse	10090	30.2	30.2	75%	730	100.00	39901	JN955992.1
Mus musculus targeted non-conditional, lacZ-tagged mutant alle...	house mouse	10090	30.2	30.2	95%	730	94.74	38653	JN952247.1
Chlorocebus aethiops BAC clone CH252-28B14 from chromosome 6,...	grivet	9534	30.2	30.2	75%	730	100.00	164477	AC241604.1
Candidatus Frankia datiscae strain Dg1 chromosome, complete...	NA	2716812	30.2	30.2	75%	730	100.00	5323186	CP002801.1
Pig DNA sequence from clone CH242-40K22 on chromosome X,...	pig	9823	30.2	30.2	75%	730	100.00	173663	CU862063.11
Hordeum vulgare subsp. vulgare mRNA for predicted protein,...	domesticated...	112509	30.2	30.2	75%	730	100.00	4070	AK377061.1
Hordeum vulgare subsp. vulgare mRNA for predicted protein,...	domesticated...	112509	30.2	30.2	75%	730	100.00	1524	AK365840.1
Neospora caninum Liverpool complete genome, chromosome II	NA	572307	30.2	30.2	75%	730	100.00	2170133	FR823382.1
Neospora caninum Liverpool complete genome, chromosome Ib	NA	572307	30.2	30.2	75%	730	100.00	1908326	FR823381.1
Bacillus thuringiensis serovar finitimus YBT-020 chromosome,...	NA	930170	30.2	30.2	75%	730	100.00	5355490	CP002508.1
Leishmania mexicana MHOM/GT/2001/U1103 complete genome,...	NA	929439	30.2	30.2	75%	730	100.00	736625	FR799574.1
Nannizzia gypsea CBS 118893 TBC1 domain family member 5...	NA	535722	30.2	30.2	75%	730	100.00	2253	XM_003176966.1
Stigmatella aurantiaca DW4/3-1, complete genome	NA	378806	30.2	60.5	100%	730	100.00	10260756	CP002271.1
Caenorhabditis remanei hypothetical protein (CRE_14731) mRNA,...	NA	31234	30.2	30.2	75%	730	100.00	1008	XM_003107042.1
Coccidioides posadasii C735 delta SOWgp TBC domain containing...	NA	222929	30.2	30.2	75%	730	100.00	2345	XM_003068338.1
Volvox carteri f. nagariensis NimA-related protein kinase 6...	NA	3068	30.2	30.2	75%	730	100.00	3285	XM_002947858.1
Bacillus cereus biovar anthracis str. CI, complete genome	NA	637380	30.2	30.2	75%	730	100.00	5196054	**CP001746.1**
Pirellula staleyi DSM 6068 chromosome, complete genome	NA	530564	30.2	30.2	75%	730	100.00	6196199	CP001848.1
Homo sapiens FOSMID clone ABC11-49393400H22 from chromosome 1,...	human	9606	30.2	30.2	75%	730	100.00	40810	AC216817.3
Rattus norvegicus CH230-239B9 (Children's Hospital Oakland...	Norway rat	10116	30.2	30.2	75%	730	100.00	214704	AC118841.6
Mus musculus WD repeat domain 81 (Wdr81), mRNA	house mouse	10090	30.2	30.2	95%	730	94.74	6976	NM_138950.2
Bacillus anthracis str. A0248, complete genome	NA	592021	30.2	30.2	75%	730	100.00	5227419	**CP001598.1**
Homo sapiens FOSMID clone ABC11-47395500N10 from chromosome...	human	9606	30.2	30.2	75%	730	100.00	39571	AC231539.2
Carassius auratus gibelio Dazl (Dazl) gene, complete cds	silver cruci...	101364	30.2	30.2	75%	730	100.00	129464	FJ774071.1
Bacillus cereus 03BB102, complete genome	NA	572264	30.2	30.2	75%	730	100.00	5269628	CP001407.1
Bacillus cereus Q1, complete genome	NA	361100	30.2	30.2	75%	730	100.00	5214195	CP000227.1
Homo sapiens BAC clone RP11-168D15 from chromosome x, complete...	human	9606	30.2	60.5	75%	730	100.00	175277	AC233283.3
Bacillus cereus AH820, complete genome	NA	405535	30.2	30.2	75%	730	100.00	5302683	CP001283.1
Bacillus cereus AH187, complete genome	NA	405534	30.2	30.2	75%	730	100.00	5269030	CP001177.1

Canis familiaris chromosome 28, clone XX-448I5, complete sequence	dog	9615	30.2	30.2	75%	730	100.00	168243	AC194584.12
Bacillus weihenstephanensis KBAB4, complete genome	NA	315730	30.2	30.2	75%	730	100.00	5262775	CP000903.1
Pan troglodytes BAC clone CH251-52P5 from chromosome x, comple...	chimpanzee	9598	30.2	30.2	75%	730	100.00	163048	AC193242.3
MACACA MULATTA BAC clone CH250-521P20 from chromosome 2,...	Rhesus monkey	9544	30.2	30.2	75%	730	100.00	176707	AC200644.3
Macaca mulatta BAC CH250-37P11 (Children's Hospital Oakland...	Rhesus monkey	9544	30.2	30.2	75%	730	100.00	171032	AC202623.8
Pan troglodytes BAC clone CH251-261H24 from chromosome 7,...	chimpanzee	9598	30.2	30.2	75%	730	100.00	161016	AC197407.4
Sclerotinia sclerotiorum 1980 UF-70 hypothetical protein parti...	NA	665079	30.2	30.2	75%	730	100.00	2184	XM_001589963.1
Metallosphaera sedula DSM 5348, complete genome	NA	399549	30.2	30.2	75%	730	100.00	2191517	CP000682.1
Canis familiaris multiple endocrine neoplasia protein (MEN1)...	dog	9615	30.2	30.2	75%	730	100.00	1848	DQ366289.1
Canis Familiaris chromosome 18, clone XX-334C1, complete sequence	dog	9615	30.2	30.2	75%	730	100.00	190076	AC190106.10
Bacillus thuringiensis str. Al Hakam, complete genome	NA	412694	30.2	30.2	75%	730	100.00	5257091	CP000485.1
Gallus gallus BAC clone CH261-17N11 from chromosome z, complet...	chicken	9031	30.2	30.2	75%	730	100.00	227257	AC189120.2
Gallus gallus BAC clone CH261-84J8 from chromosome z, complete...	chicken	9031	30.2	30.2	75%	730	100.00	176080	AC189660.2
Aspergillus terreus NIH2624 predicted protein (ATEG_08842)...	NA	341663	30.2	30.2	75%	730	100.00	2268	XM_001217427.1
Mus musculus chromosome 15, clone RP24-252G18, complete sequence	house mouse	10090	30.2	30.2	75%	730	100.00	170539	AC158974.8
Mus musculus chromosome 3, clone RP24-389G6, complete sequence	house mouse	10090	30.2	30.2	75%	730	100.00	184243	AC102296.6
Pan troglodytes chromosome X clone RP43-007H19 map human...	chimpanzee	9598	30.2	30.2	75%	730	100.00	200796	AC151667.1
Mus musculus chromosome 5, clone RP23-415E17, complete sequence	house mouse	10090	30.2	30.2	75%	730	100.00	229028	AC111030.11
Caenorhabditis elegans Cosmid C32F10, complete sequence	NA	6239	30.2	30.2	75%	730	100.00	30102	FO080198.1
Bacillus thuringiensis serovar konkukian str. 97-27, complete...	NA	281309	30.2	30.2	75%	730	100.00	5237682	AE017355.1
Mus musculus BAC clone RP24-344D20 from chromosome 9, complete...	house mouse	10090	30.2	30.2	75%	730	100.00	180602	AC134429.3
Bacillus anthracis str. 'Ames Ancestor', complete genome	NA	261594	30.2	30.2	75%	730	100.00	5227419	**AE017334.2**
Mus musculus chromosome 3, clone RP23-166M8, complete sequence	house mouse	10090	30.2	30.2	75%	730	100.00	215166	AC117586.10
Bacillus anthracis str. Sterne, complete genome	NA	260799	30.2	30.2	75%	730	100.00	5228663	**AE017225.1**
Pan troglodytes BAC clone CH251-184I22 from X, complete sequence	chimpanzee	9598	30.2	30.2	75%	730	100.00	181915	AC145689.4
Mus musculus BAC clone RP24-132F22 from chromosome 9, complete...	house mouse	10090	30.2	30.2	75%	730	100.00	174426	AC142504.2
Oryza sativa (japonica cultivar-group) chromosome 11 BAC clone...	Japanese rice	39947	30.2	30.2	75%	730	100.00	156331	AC144700.2
Mus musculus BAC clone RP24-499E13 from chromosome 1, complete...	house mouse	10090	30.2	30.2	75%	730	100.00	173781	AC163636.5
Mus musculus BAC clone RP24-79E2 from chromosome 3,	house mouse	10090	30.2	30.2	75%	730	100.00	180558	AC121840.3

complete...									
Mus musculus BAC clone RP23-171M24 from 3, complete sequence	house mouse	10090	30.2	30.2	75%	730	100.00	198281	AC122254.4
Homo sapiens chromosome 17, clone RP13-1277B16, complete sequence	human	9606	30.2	30.2	75%	730	100.00	182735	AC129919.9
Homo sapiens BAC clone RP11-511P7 from 7, complete sequence	human	9606	30.2	30.2	75%	730	100.00	115003	AC073111.8
Homo sapiens chromosome 18, clone RP11-111H3, complete sequence	human	9606	30.2	30.2	75%	730	100.00	167954	AC034110.13
Caenorhabditis elegans Cosmid B0414, complete sequence	NA	6239	30.2	30.2	75%	730	100.00	38525	FO080197.1
Bacillus cereus E33L, complete genome	NA	288681	30.2	30.2	75%	730	100.00	5300915	CP000001.1
Homo sapiens chromosome 17, clone RP11-149I9, complete sequence	human	9606	30.2	30.2	75%	730	100.00	161156	AC115099.6
Homo sapiens cDNA FLJ45353 fis, clone BRHIP3012289	human	9606	30.2	30.2	75%	730	100.00	4034	AK127286.1
Mus musculus 6 days neonate spleen cDNA, RIKEN full-length...	house mouse	10090	30.2	30.2	95%	730	94.74	2989	AK143628.1
Mus musculus 6 BAC RP23-333F8 (Roswell Park Cancer Institute...	house mouse	10090	30.2	30.2	75%	730	100.00	233589	AC163199.8
Mus musculus activated spleen cDNA, RIKEN full-length enriched...	house mouse	10090	30.2	30.2	95%	730	94.74	3090	AK172019.1
Mus musculus adult male hippocampus cDNA, RIKEN full-length...	house mouse	10090	30.2	30.2	95%	730	94.74	949	AK160663.1
Mus musculus 13 days embryo liver cDNA, RIKEN full-length...	house mouse	10090	30.2	30.2	95%	730	94.74	2942	AK160585.1
Mus musculus BAC clone RP24-495F22 from chromosome 6, complete...	house mouse	10090	30.2	30.2	75%	730	100.00	171057	AC135355.3
Mus musculus BAC clone RP23-56C10 from chromosome 1, complete...	house mouse	10090	30.2	30.2	75%	730	100.00	233538	AC130527.4
Homo sapiens ovca1-like gene, partial sequence; and ovca2 gene...	human	9606	30.2	30.2	75%	730	100.00	17200	AF335321.1
Homo sapiens chromosome 17, clone RP11-648P8, complete sequence	human	9606	30.2	30.2	75%	730	100.00	157850	AC034303.14
Human DNA sequence from clone RP11-555C22 on chromosome 1,...	human	9606	30.2	30.2	75%	730	100.00	39004	AL627110.21
Homo sapiens BAC clone RP11-367J11 from 4, complete sequence	human	9606	30.2	30.2	75%	730	100.00	210515	AC097382.3
Human DNA sequence from clone RP1-233G16 on chromosome...	human	9606	30.2	30.2	75%	730	100.00	67343	AL135959.2
Human DNA sequence from clone RP11-214O11 on chromosome 13,...	human	9606	30.2	30.2	75%	730	100.00	168790	AL138959.20
Homo sapiens BAC clone CTB-161C1 from 7, complete sequence	human	9606	30.2	30.2	75%	730	100.00	196416	AC006483.3
Human DNA sequence from clone RP4-779E11 on chromosome 20,...	human	9606	30.2	30.2	75%	730	100.00	113168	AL121675.36
Human DNA sequence from clone RP1-26H23 on chromosome 13...	human	9606	30.2	30.2	75%	730	100.00	91835	Z84467.1
Methylococcus capsulatus str. Bath, complete genome	NA	243233	30.2	30.2	75%	730	100.00	3304561	AE017282.2
Mus musculus premature mRNA for mFLJ00182 protein	house mouse	10090	30.2	30.2	95%	730	94.74	3446	AK131146.1
Bacillus halodurans C-125 DNA, complete genome	NA	272558	30.2	30.2	75%	730	100.00	4202352	BA000004.3
Homo sapiens IRSp53 gene for insulin receptor substrate p53...	human	9606	30.2	30.2	75%	730	100.00	82262	AB104726.1
Homo sapiens chromosome X multiple clones map q28, complete...	human	9606	30.2	30.2	75%	730	100.00	324604	U82671.5

Homo sapiens chromosome 17, clone CTC-297N7, complete sequence	human	9606	30.2	30.2	75%	730	100.00	134706	AC002347.3
Streptomyces coelicolor A3(2) complete genome; segment 13/29	NA	100226	30.2	30.2	75%	730	100.00	293050	AL939116.1
Homo sapiens BAC clone RP11-141B14 from 2, complete sequence	human	9606	30.2	30.2	75%	730	100.00	135317	AC110769.2
Takifugu rubripes clone 264E2, complete sequence	torafugu	31033	30.2	30.2	75%	730	100.00	88203	AC097628.2
Homo sapiens BAC clone RP11-31G7 from 2, complete sequence	human	9606	30.2	30.2	75%	730	100.00	157285	AC068483.6
Homo sapiens, Similar to hypothetical protein FLJ11736, clone...	human	9606	30.2	30.2	75%	730	100.00	1828	BC014333.1
Homo sapiens 12 BAC RP11-367O10 (Roswell Park Cancer Institute...	human	9606	30.2	30.2	75%	730	100.00	178453	AC016144.13
Comamonas testosteroni strain YZW-D isophthalate degradation...	NA	285	30.2	30.2	75%	730	100.00	12190	AY923836.1
Medicago truncatula chromosome 8 clone mth2-28c12, complete...	barrel medic	3880	30.2	30.2	75%	730	100.00	112461	AC152347.14
Mus musculus BAC clone RP23-278A22 from 6, complete sequence	house mouse	10090	30.2	30.2	75%	730	100.00	187115	AC144778.3
Bacillus cereus ATCC 10987, complete genome	NA	222523	30.2	30.2	75%	730	100.00	5224283	AE017194.1
Mouse DNA sequence from clone RP23-324J22 on chromosome 7,...	house mouse	10090	30.2	30.2	75%	730	100.00	157941	BX649462.9
Bacillus anthracis str. Ames, complete genome	NA	198094	30.2	30.2	75%	730	100.00	5227293	**AE016879.1**
Mouse DNA sequence from clone RP23-227P19 on chromosome 4,...	house mouse	10090	30.2	30.2	75%	730	100.00	131275	AL669860.8
Homo sapiens chromosome X sequence from BAC CEPHB160J21, map...	human	9606	30.2	60.5	75%	730	100.00	150966	AL627244.1
Human chromosome 14 DNA sequence BAC C-3104H21 of library...	human	9606	30.2	30.2	75%	730	100.00	231893	AL162151.5
Homo sapiens chromosome X sequence from 4 cosmids, map Xp21.1...	human	9606	30.2	60.5	75%	730	100.00	106604	AJ239329.2
Homo sapiens mRNA for insulin receptor substrate protein of 53...	human	9606	30.2	30.2	75%	730	100.00	2877	AB017119.1

SELEZIONE DI ALLINEAMENTI SIGNIFICATIVI

PREDICTED: Dromaius novaehollandiae FA complementation group G (FANCG), transcript variant X2, mRNA

Sequence ID: XM_026108231.1Length: 2420Number of Matches: 1

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Range 1: 1383 to 1400 GenBank Graphics

```
Score          Expect  Identities       Gaps        Strand


36.2 bits(18)  12     18/18(100%)  0/18(0%)  Plus/Minus


CDS: Putative 1        5          D  Q  L  C  R

Query                  1      CCGTCCTGGAGACACCTC  18

                              ||||||||||||||||||

Sbjct                  1400   CCGTCCTGGAGACACCTC  1383

CDS:Fanconi anemia g   283    G  D  Q  L  C  R
```

/prodotto=" Fanconi anemia group G protein"

Fanconi anemia group G protein

La **Poteina del gruppo G dell’Anemia di Fanconi** (codificata dal **gene FANCG**) è una **proteina di riparazione del DNA** che può operare in una riparazione post-replicazione o in una funzione di checkpoint del ciclo cellulare. Può essere implicata nella riparazione dei legami incrociati tra i filamenti di DNA e nel mantenimento della normale stabilità dei cromosomi. ***Gene candidato come soppressore del tumore*** (https://www.uniprot.org/uniprot/O15287). L’**Anemia di Fanconi** è una **malattia autosomica recessiva** con diversi sintomi clinici, tra cui ***anomalie dello sviluppo, insufficienza midollare e insorgenza precoce di tumori maligni***. Sono stati identificati un minimo di **8 geni FA** (https://en.wikipedia.org/wiki/FANCG). Il **gene FANCG è responsabile del gruppo di complementazione G**. Le proteine FA interagiscono attraverso una via multiproteica. I legami incrociati tra i filamenti del DNA sono danni altamente deleteri che vengono riparati dalla ricombinazione omologa che coinvolge il coordinamento delle proteine FA e ***il gene 1 di suscettibilità al cancro al seno (BRCA1)***, ma l’esatto ruolo biochimico di queste proteine è attualmente poco chiaro (https://en.wikipedia.org/wiki/FANCG). La **perdita di FANCG** provoca l’**apoptosi dei progenitori neurali** durante lo sviluppo del proencefalo, probabilmente correlata alla riparazione difettosa del DNA. **Questo effetto persiste nell’età adulta** portando all’esaurimento del pool di cellule staminali neurali con l’**invecchiamento**. Il fenotipo FA può essere interpretato come un *invecchiamento prematuro delle cellule staminali*, i danni al DNA sono la forza trainante dell'invecchiamento (https://en.wikipedia.org/wiki/FANCG). La **malattia** è causata da varianti che interessano il gene FANCG ed è un disordine che colpisce tutti gli elementi del **midollo osseo** e provoca **anemia**, **leucopenia** e **trombopenia**. Si associa a **malformazioni cardiache**, **renali** e degli **arti**, ad **alterazioni pigmentarie dermiche** e ad una **predisposizione allo sviluppo di tumori maligni**. A livello cellulare è associata a **ipersensibilità agli agenti dannosi per il DNA, instabilità cromosomica (aumento della rottura dei cromosomi) e riparazione difettosa del DNA** (https://www.uniprot.org/uniprot/O15287). I topi mutanti FANCG maschi e femmine hanno **gametogenesi difettosa, ipogonadismo** e **fertilità ridotta**, coerenti con il fenotipo dei pazienti con **AF**. Nel topo non mutante, la proteina FANCG è espressa negli spermatogoni, negli spermatociti preleptotene e negli spermatociti negli stadi di meiosi leptotene, zigotene e pachitene (https://en.wikipedia.org/wiki/FANCG; https://www.nextprot.org/entry/NX_O15287/).

PREDICTED: Pteropus alecto immunoglobulin superfamily member 9 (IGSF9), transcript variant X5, mRNA

Sequence ID: XM_015597873.2Length: 4122Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 859 to 875 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
CDS: Putative 1        1       L  E  T  P  P
Query                  4     TCCTGGAGACACCTCCC   20
                             |||||||||||||||||
Sbjct                  859   TCCTGGAGACACCTCCC   875
CDS:protein turtle h   138   F  L  E  T  P  P
```

/prodotto="protein turtle homolog A isoform X4"

Protein Turtle Homolog A è membro della **superfamiglia delle immunoglobuline 9 (IGSF9A)** ed è un gene che codifica per proteine. Le malattie associate a IGSF9 includono il **Labbro Leporino Isolato**. Le annotazioni di Gene Ontology (GO) relative a questo gene includono l'**attività del mediatore dell'adesione cellula-cellula**. Svolge funzioni nella crescita dei dendriti e nella maturazione delle sinapsi Un importante paralogo di questo gene è **IGSF9B** (https://www.genecards.org/cgi-bin/carddisp.pl?gene=IGSF9; https://www.uniprot.org/uniprot/Q9P2J2). **IGSF9B** (**Immunoglobulin Superfamily Member 9B**) è un gene che codifica per proteine. Le malattie associate a IGSF9B includono il **Cancro Ovarico**. Le annotazioni di Gene Ontology (GO) relative a questo gene includono il **legame della chinasi**. IGSF9B è una *proteina transmembrana* che è abbondantemente espressa negli *interneuroni*, dove può regolare lo sviluppo di *sinapsi inibitorie*. Può mediare l'*adesione cellulare omofila* (https://www.genecards.org/cgi-bin/carddisp.pl?gene=IGSF9B).

PREDICTED: Pteropus vampyrus immunoglobulin superfamily member 9 (IGSF9), transcript variant X6, mRNA

Sequence ID: XM_023538320.1Length: 3916Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 437 to 453GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
Query  4     TCCTGGAGACACCTCCC   20
             |||||||||||||||||
Sbjct  437   TCCTGGAGACACCTCCC   453
```

Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), RefSeqGene on chromosome 22

Sequence ID: NG_052986.1Length: 102256Number of Matches: 1

Range 1: 88133 to 88149 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
Query  4      TCCTGGAGACACCTCCC  20
              |||||||||||||||||
Sbjct  88133  TCCTGGAGACACCTCCC  88149
```

Kringle containing transmembrane protein 1 (KREMEN1)

Questo gene codifica per un **recettore transmembrana omologo 1 dickkopf ad alta affinità (DKK1) che coopera funzionalmente con DKK1 per bloccare la segnalazione senza ali (WNT)/beta-catenina.** La proteina codificata è un componente di un complesso di membrana che modula la segnalazione WNT canonica attraverso la proteina 6 correlata al recettore della lipoproteina (LRP6). Contiene *domini extracellulari kringle, WSC e CUB*. Per questo gene sono state osservate varianti di trascritto splicing alternativo che codificano isoforme distinte (https://www.genecards.org/cgi-bin/carddisp.pl?gene=KREMEN1). **KREMEN1** coopera con DKK1/2 per inibire la segnalazione Wnt/beta-catenina promuovendo l'endocitosi dei recettori Wnt LRP5 e LRP6. In assenza di DKK1, potenzia la segnalazione Wnt-beta-catenina mantenendo LRP5 o LRP6 sulla membrana cellulare (https://www.ncbi.nlm.nih.gov/gene?Db=gene&Cmd=DetailsSearch&Term=83999). **Antagonisti noti della segnalazione Wnt includono proteine Dickkopf (Dkk), Wnt Inhibitory Factor-1 (WIF-1) e proteine Frizzled-Related secrete (sFRP)**. L'**espressione ridotta di sFRP è associata all'attivazione aberrante della segnalazione di Wnt e alla tumorigenesi** (https://www.rndsystems.com/research-area/wnt-inhibitors). **KREMEN1** può innescare l'**apoptosi** in **maniera indipendente da Wnt** e **questa attività apoptotica è inibita dal legame del ligando DKK1**. Svolge un ruolo nello sviluppo degli arti; attenua la segnalazione Wnt nell'arto in via di sviluppo per consentire il normale patterning dell'arto e può anche regolare negativamente la formazione ossea. Modula le decisioni sul destino delle cellule nella coclea in via di sviluppo con un ruolo inibitorio nella specificazione del destino delle cellule ciliate (https://www.genecards.org/cgi-bin/carddisp.pl?gene=KREMEN1). Le malattie associate a **KREMEN1** includono *la* ***displasia ectodermica 13***, *il* ***tipo di capelli/denti*** *e la* ***malattia delle mani***, *dei* ***piedi e della bocca***. *Tra le sue vie correlate vi sono la* ***segnalazione tramite GPCR*** *e* ***la regolazione negativa della segnalazione TCF-dipendente da parte degli antagonisti del ligando WNT***. Un importante paralogo di questo gene è **KREMEN2** (https://www.genecards.org/cgi-bin/carddisp.pl?gene=KREMEN1).

PREDICTED: Branchiostoma belcheri ADAM 17-like protease (LOC109472890), mRNA

Sequence ID: XM_019772757.1Length: 694Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 512 to 528GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
CDS: Putative 1      1     S  W  R  H  L  P
Query                4    TCCTGGAGACACCTCCC  20
                          |||||||||||||||||
Sbjct                512  TCCTGGAGACACCTCCC  528
CDS:PREDICTED: ADAM  148   S  W  R  H  L  P
```

/prodotto="ADAM 17-like protease"

ADAM 17-like protease

Una disintegrina e metalloproteasi 17 (**ADAM17**), chiamata anche **TACE** (*enzima di conversione del fattore di necrosi tumorale α*), è un enzima che appartiene alla **famiglia delle proteine ADAM delle disintegrine e delle metalloproteasi** (https://en.wikipedia.org/wiki/ADAM17). **Si ritiene che ADAM17 sia coinvolto nell'elaborazione del fattore di necrosi tumorale alfa (TNF-α) sulla superficie della cellula e dall'interno delle membrane intracellulari della rete trans-Golgi**. Questo processo, noto anche come "spargimento", comporta la scissione e il rilascio di un ectodominio solubile dalle proproteine legate alla membrana (come il **pro-TNF-α**), ed è di *nota importanza fisiologica*. **ADAM17** è stata la prima "**sheddase**" [enzimi che si legano alla membrana e che scindono le porzioni extracellulari delle proteine transmembrana, rilasciando gli ectodomini solubili dalla superficie cellulare (https://en.wikipedia.org/wiki/Sheddase)] ad essere identificata e si ritiene che svolga anche un ruolo nel **rilascio di una varietà diversificata di citochine ancorate alla membrana**, **molecole di adesione cellulare, recettori, ligandi ed enzimi**. La **liberazione proteolitica di TNF-α solubile è catalizzata da ADAM17** (https://en.wikipedia.org/wiki/ADAM17). **ADAM17** è stato scoperto come un **mediatore cruciale della resistenza alla radioterapia** ed è stato anche dimostrato che **la radioterapia attiva ADAM17 nel carcinoma polmonare non a piccole cellule, che si traduce nella perdita di più fattori di sopravvivenza, nell'attivazione della via del fattore di crescita e nella resistenza al trattamento indotta dalla radioterapia** (https://en.wikipedia.org/wiki/ADAM17). **ADAM17** può svolgere un ruolo di primo piano nella **via di segnalazione di Notch**, durante il rilascio proteolitico del dominio intracellulare di Notch (dal recettore Notch1) che avviene in seguito al legame con il ligando. **ADAM17** *regola anche la via di segnalazione della chinasi MAP* regolando lo spargimento dell'anfiregulina del ligando EGFR nella ghiandola mammaria. **ADAM17** ha anche un ruolo nello spargimento di L-selectina, una molecola di adesione cellulare (https://en.wikipedia.org/wiki/ADAM17). È stato documentato che **ADAM17** funzionale è espresso ubiquitariamente nel *colon umano*, con una maggiore attività nella mucosa del colon di pazienti con *colite ulcerosa*. Altri esperimenti hanno anche suggerito che l'**espressione di ADAM17 può essere inibita dall'etanolo** (https://en.wikipedia.org/wiki/ADAM17).

PREDICTED: Poecilia reticulata netrin-1-like (LOC103480490), transcript variant X1, mRNA
Sequence ID: XM_008435452.2Length: 2971Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 417 to 433 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
CDS: Putative 1       1       P  G  D  T  S
Query                 4    TCCTGGAGACACCTCCC   20
                           |||||||||||||||||
Sbjct                 417  TCCTGGAGACACCTCCC   433
CDS:PREDICTED: netri  28      P  G  D  T  S
```

/product="netrin-1-like isoform X1"

NTR_netrin-1_like

Dominio NTR, sottofamiglia simile a Netrin-1; Il dominio NTR C-terminale di netrine è anche chiamato dominio C nel contesto di C. elegans netrin UNC-6. Le netrine sono proteine secrete che funzionano come segnali tropici nella direzione della crescita degli assoni e della migrazione cellulare durante lo sviluppo neurale. Queste proteine possono essere chemioattrattive per alcuni neuroni e chemopellenti per altri. Nel caso della netrina-1, le risposte di attrazione e repulsione sono mediate dalle famiglie di recettori DCC e UNC-5. Le attività biologiche di C. elegans UNC-6, che possono attrarre o respingere cellule o assoni in migrazione, sono mediate dai suoi diversi domini. **È stato dimostrato che il dominio NTR C-terminale di UNC-6 inibisce l'attività di ramificazione degli assoni** (https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=239634).

PREDICTED: Erinaceus europaeus integrin subunit beta 8 (ITGB8), transcript variant X1, mRNA
Sequence ID: XM_007532261.2Length: 3622Number of Matches: 1
Related Information Gene-associated gene details Genome Data Viewer-aligned genomic context
Range 1: 513 to 529 GenBank Graphics

```
Score          Expect  Identities        Gaps        Strand


34.2 bits(17)  47      17/17(100%)  0/17(0%)  Plus/Plus


Query  4    TCCTGGAGACACCTCCC  20
            |||||||||||||||||
Sbjct  513  TCCTGGAGACACCTCCC  529
```

Integrin subunit beta 8 (ITGB8)

Questo gene è un membro della **famiglia della catena beta dell'integrina** e codifica per una **proteina di membrana di tipo I** a passaggio singolo con un **dominio VWFA** e quattro ripetizioni ricche di **cisteina**. Questa proteina si lega in modo non covalente a una subunità alfa per formare un complesso integrinico eterodimerico. In generale, i complessi di integrine mediano le interazioni cellula-cellula e cellula-matrice extracellulare e **questo complesso gioca un ruolo nella proliferazione epiteliale delle vie aeree umane**. Sono state descritte varianti di splicing alternativo che codificano diverse isoforme proteiche; tuttavia, non tutte le varianti sono state completamente caratterizzate (https://www.genecards.org/cgi-bin/carddisp.pl?gene=ITGB8). **ITGB8** è richiesto durante la **vasculogenesi** (per somiglianza) (https://www.genecards.org/cgi-bin/carddisp.pl?gene=ITGB8). Le malattie associate a ITGB8 includono la **malformazione arterovenosa** e la **cardiomiopatia ventricolare destra aritmogena**. Tra i suoi percorsi correlati ci sono **Sertoli-Sertoli Cell Junction Dynamics** e **ERK Signaling**. Le annotazioni di Gene Ontology (GO) relative a questo gene includono il *legame al recettore di segnalazione* e il *legame alle proteine della matrice extracellulare*. Un importante paralogo di questo gene è **ITGB5** [***Testis Secretory Sperm-Binding Protein Li 217p*** *è un gene che codifica per proteine. Le malattie associate a ITGB5 includono l'****adenocarcinoma dei villi*** *e l'****osteopetrosi, autosomica dominante 2****.* ***Integrin alpha-V/beta-5 (ITGAV:ITGB5)*** *è un recettore per la fibronectina, riconosce la sequenza R-G-D nel suo ligando e agisce come* ***recettore per l'adenovirus di tipo C*** (https://www.genecards.org/cgi-bin/carddisp.pl?gene=ITGB5). *Un importante paralogo di questo gene è* ***ITGB3*** (è un gene che codifica per proteine. Le malattie associate a ITGB3 includono la ***tromboastenia di Glanzmann 2*** e il ***disturbo emorragico, di tipo piastrinico, 24***. ***L'integrina alfa-V/beta-3 (ITGAV:ITGB3)*** *è un recettore per citotactina, fibronectina, laminina, metalloproteinasi-2 della matrice, osteopontina, osteomodulina, protrombina, trombospondina, vitronectina e il* ***fattore di von Willebrand*** ***L'integrina alfa-IIb/beta-3 (ITGA2B:ITGB3)*** *è un recettore per fibronectina, fibrinogeno, plasminogeno, protrombina, trombospondina e vitronectina. (https://www.genecards.org/cgi-bin/carddisp.pl?gene=ITGB3)* **L'integrina alfa-V:beta-8 (ITGAV:ITGB8)** è un recettore per la **fibronectina**. Riconosce la sequenza RGD nei suoi ligandi. **L'integrina alfa-V:beta-6** (**ITGAV:ITGB6**) media il rilascio dipendente da RGD del fattore di crescita trasformante beta-1 (**TGF-beta-1**) dal peptide regolatorio associato alla latenza (**LAP**), svolgendo così un ruolo chiave nell'attivazione *TGF-beta-1* sulla superficie delle **cellule T** regolatorie attivate (Tregs) (https://www.genecards.org/cgi-bin/carddisp.pl?gene=ITGB8).

PREDICTED: Peromyscus maniculatus bairdii RIMS-binding protein 3-like (LOC102920774), mRNA Sequence ID: XM_006993043.2Length: 5301Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 3591 to 3607 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
CDS: Putative 1       1        L   E   T   P   P
Query                 4      TCCTGGAGACACCTCCC   20
                             |||||||||||||||||
Sbjct                 3591   TCCTGGAGACACCTCCC   3607
CDS:PREDICTED: RIMS-  1171   F   L   E   T   P   P
```

PREDICTED: Lepisosteus oculatus collagen alpha-6(VI) chain-like (LOC102696460), transcript variant X8, mRNA

Sequence ID: XM_015356881.1Length: 9315Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 8079 to 8095 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
CDS: Putative 1       1        L   E   T   P   P
Query                 4      TCCTGGAGACACCTCCC   20
                             |||||||||||||||||
Sbjct                 8079   TCCTGGAGACACCTCCC   8095
CDS:PREDICTED: colla  2594   I   L   E   T   P   P
```

PREDICTED: Lepisosteus oculatus CTS telomere maintenance complex component 1 (ctc1), mRNA

Sequence ID: XM_015340475.1Length: 3774Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 2518 to 2534 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
CDS: Putative 1       1       P   S   W   R   H   L
Query                 1      CCGTCCTGGAGACACCT   17
                             |||||||||||||||||
Sbjct                 2518   CCGTCCTGGAGACACCT   2534
CDS:PREDICTED: LOW Q  812     P   S   W   R   H   L
```

PREDICTED: Balaenoptera acutorostrata scammoni immunoglobulin superfamily member 9 (IGSF9), transcript variant X2, mRNA

Sequence ID: XM_007171793.1Length: 4045Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 698 to 714 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
CDS: Putative 1        1       L  E  T  P  P
Query                  4    TCCTGGAGACACCTCCC  20
                            |||||||||||||||||
Sbjct                  698  TCCTGGAGACACCTCCC  714
CDS:protein turtle h   136  F  L  E  T  P  P
```

PREDICTED: Pteropus giganteus immunoglobulin superfamily member 9 (IGSF9), transcript variant X7, mRNA

Sequence ID: XM_039839994.1Length: 3888Number of Matches: 1

Range 1: 427 to 443 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
Query  4    TCCTGGAGACACCTCCC  20
            |||||||||||||||||
Sbjct  427  TCCTGGAGACACCTCCC  443
```

PREDICTED: Chelonia mydas fatty acid 2-hydroxylase (FA2H), mRNA

Sequence ID: XM_037877813.1Length: 4650Number of Matches: 1

Range 1: 3432 to 3448 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
Query  1     CCGTCCTGGAGACACCT  17
             |||||||||||||||||
Sbjct  3432  CCGTCCTGGAGACACCT  3448
```

Human DNA sequence from clone CTA-57G9 on chromosome 22q12.1, complete sequence

Sequence ID: Z95116.1Length: 113872Number of Matches: 1

Related Information
Genome Data Viewer-aligned genomic context
Range 1: 39664 to 39680 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Plus

```
Query  4      TCCTGGAGACACCTCCC  20
              |||||||||||||||||
Sbjct  39664  TCCTGGAGACACCTCCC  39680
```

PREDICTED: Marmota flaviventris G protein-coupled receptor 35 (Gpr35), transcript variant X2, mRNA

Sequence ID: XM_027951751.2Length: 5254Number of Matches: 1

Range 1: 4396 to 4412 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Minus

```
Query  4     TCCTGGAGACACCTCCC  20
             |||||||||||||||||
Sbjct  4412  TCCTGGAGACACCTCCC  4396
```

PREDICTED: Microcaecilia unicolor U6 snRNA biogenesis phosphodiesterase 1 (USB1), transcript variant X2, mRNA

Sequence ID: XM_030203583.1Length: 2123Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 847 to 863 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Minus

```
CDS: Putative 1       5        Q  L  C  R  G
Query                 4     TCCTGGAGACACCTCCC  20
                            |||||||||||||||||
Sbjct                 863   TCCTGGAGACACCTCCC  847
CDS:U6 snRNA phospho  245   D  Q  L  C  R  G
```

PREDICTED: Salmo trutta chromodomain-helicase-DNA-binding protein 8-like (LOC115157310), transcript variant X4, mRNA

Sequence ID: XM_029705456.1Length: 8951Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 2733 to 2749 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Minus

```
CDS: Putative 1        5        G   P   S   V   E

Query                  3     GTCCTGGAGACACCTCC  19

                             |||||||||||||||||

Sbjct                  2749  GTCCTGGAGACACCTCC  2733

CDS:chromodomain-hel   758      G   P   S   V   E
```

PREDICTED: Alligator sinensis RNA polymerase III subunit E (POLR3E), transcript variant X2, mRNA

Sequence ID: XM_025207015.1Length: 2865Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 2106 to 2122 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Minus

```
Query  1     CCGTCCTGGAGACACCT  17

             |||||||||||||||||

Sbjct  2122  CCGTCCTGGAGACACCT  2106
```

Pipistrellus pipistrellus genome assembly, chromosome: 10

Sequence ID: LR862366.1Length: 71504835Number of Matches: 4

Range 1: 24388946 to 24388962 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
34.2 bits(17)	47	17/17(100%)	0/17(0%)	Plus/Minus

```
Query  1         CCGTCCTGGAGACACCT  17

                 |||||||||||||||||

Sbjct  24388962  CCGTCCTGGAGACACCT  24388946
```

Range 2: 24843859 to 24843873 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	739	15/15(100%)	0/15(0%)	Plus/Plus

```
Query  3         GTCCTGGAGACACCT  17

                 |||||||||||||||

Sbjct  24843859  GTCCTGGAGACACCT  24843873
```

Range 3: 60766454 to 60766472 GenBank Graphics

Score Expect Identities Gaps Strand

30.2 bits(15) 739 18/19(95%) 0/19(0%) Plus/Plus

```
Query  1          CCGTCCTGGAGACACCTCC  19
                  ||||||||||| |||||||
Sbjct  60766454   CCGTCCTGGAGCCACCTCC  60766472
```

Range 4: 14167176 to 14167190 GenBank Graphics

Score Expect Identities Gaps Strand

30.2 bits(15) 739 15/15(100%) 0/15(0%) Plus/Minus

```
Query  3          GTCCTGGAGACACCT  17
                  |||||||||||||||
Sbjct  14167190   GTCCTGGAGACACCT  14167176
```

Rattus norvegicus 3 BAC CH230-11N5 (Children's Hospital Oakland Research Institute) complete sequence

Sequence ID: AC097745.8Length: 238007Number of Matches: 1

Related Information

Genome Data Viewer-aligned genomic context

Range 1: 70029 to 70045 GenBank Graphics

Score Expect Identities Gaps Strand

34.2 bits(17) 47 17/17(100%) 0/17(0%) Plus/Minus

```
Query  4      TCCTGGAGACACCTCCC  20
              |||||||||||||||||
Sbjct  70045  TCCTGGAGACACCTCCC  70029
```

Wallaby DNA sequence from clone MEKBa-201B9, complete sequence

Sequence ID: CR848708.12Length: 194524Number of Matches: 1

Range 1: 65208 to 65224 GenBank Graphics

Score Expect Identities Gaps Strand

34.2 bits(17) 47 17/17(100%) 0/17(0%) Plus/Minus

```
Query  3      GTCCTGGAGACACCTCC  19
              |||||||||||||||||
Sbjct  65224  GTCCTGGAGACACCTCC  65208
```

PREDICTED: Trachypithecus francoisi G protein-coupled receptor kinase 6 (GRK6), transcript variant X3, mRNA

Sequence ID: XM_033180016.1Length: 2965Number of Matches: 1

Range 1: 2577 to 2592 GenBank Graphics

```
Score           Expect  Identities       Gaps        Strand

32.2 bits(16)  187    16/16(100%)  0/16(0%)  Plus/Plus

Query  3     GTCCTGGAGACACCTC  18
             ||||||||||||||||
Sbjct  2577  GTCCTGGAGACACCTC  2592
```

PREDICTED: Trachypithecus francoisi mediator of DNA damage checkpoint 1 (MDC1), transcript variant X5, mRNA

Sequence ID: XM_033219555.1Length: 7117Number of Matches: 1

Range 1: 14 to 29 GenBank Graphics

```
Score           Expect  Identities       Gaps        Strand

32.2 bits(16)  187    16/16(100%)  0/16(0%)  Plus/Plus

Query  5   CCTGGAGACACCTCCC  20
           ||||||||||||||||
Sbjct  14  CCTGGAGACACCTCCC  29
```

PREDICTED: Rhinolophus ferrumequinum immunoglobulin superfamily member 9 (IGSF9), transcript variant X4, mRNA

Sequence ID: XM_033094038.1Length: 3900Number of Matches: 1

Range 1: 542 to 557 GenBank Graphics

```
Score           Expect  Identities       Gaps        Strand

32.2 bits(16)  187    16/16(100%)  0/16(0%)  Plus/Plus

CDS: Putative 1       1        L  E  T  P  P
Query                 4     TCCTGGAGACACCTCC  19
                            ||||||||||||||||
Sbjct                 542   TCCTGGAGACACCTCC  557
CDS:protein turtle h  75    F  L  E  T  P  P
```

PREDICTED: Catharus ustulatus Snf2 related CREBBP activator protein (SRCAP), mRNA

Sequence ID: XM_033084517.1Length: 6317Number of Matches: 1

Range 1: 5500 to 5519 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	187	19/20(95%)	0/20(0%)	Plus/Plus

```
CDS: Putative 1      1        V  L  E  T  P  P
Query                1     CCGTCCTGGAGACACCTCCC  20
                           ||||||||||||| ||||||
Sbjct                5500  CCGTCCTGGAGACCCCTCCC  5519
CDS:helicase SRCAP [ 1795  T  V  L  E  T  P  P
```

PREDICTED: Tyto alba alba zinc finger protein 639 (ZNF639), transcript variant X5, mRNA

Sequence ID: XM_033006391.1Length: 5893Number of Matches: 1

Range 1: 2178 to 2193 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	187	16/16(100%)	0/16(0%)	Plus/Plus

```
Query  3     GTCCTGGAGACACCTC  18
             ||||||||||||||||
Sbjct  2178  GTCCTGGAGACACCTC  2193
```

PREDICTED: Chiroxiphia lanceolata leucine rich repeats and immunoglobulin like domains 1 (LRIG1), mRNA

Sequence ID: XM_032698791.1Length: 6396Number of Matches: 1

Related Information

Genome Data Viewer-aligned genomic context

Range 1: 2275 to 2290 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	187	16/16(100%)	0/16(0%)	Plus/Plus

```
CDS: Putative 1      1        V  L  E  T  P
Query                1     CCGTCCTGGAGACACC  16
                           ||||||||||||||||
Sbjct                2275  CCGTCCTGGAGACACC  2290
CDS:leucine-rich rep 676   T  V  L  E  T  P
```

PREDICTED: Etheostoma spectabile collagen alpha-1(VII) chain-like (LOC116673180), transcript variant X3, mRNA

Sequence ID: XM_032505355.1Length: 9627Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 1513 to 1528 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	187	16/16(100%)	0/16(0%)	Plus/Plus

```
CDS: Putative 1       1        P  G  D  T  S
Query                 4      TCCTGGAGACACCTCC  19
                             ||||||||||||||||
Sbjct                 1513   TCCTGGAGACACCTCC  1528
CDS:collagen alpha-1  376      P  G  D  T  S
```

PREDICTED: Camelus ferus ataxin 7 (ATXN7), transcript variant X3, mRNA

Sequence ID: XM_032458136.1Length: 6922Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 3283 to 3298 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	187	16/16(100%)	0/16(0%)	Plus/Plus

```
Query  5     CCTGGAGACACCTCCC  20
             ||||||||||||||||
Sbjct  3283  CCTGGAGACACCTCCC  3298
```

PREDICTED: Piliocolobus tephrosceles G protein-coupled receptor kinase 6 (GRK6), transcript variant X2, mRNA

Sequence ID: XM_023185134.3Length: 2937Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 2610 to 2625 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	187	16/16(100%)	0/16(0%)	Plus/Plus

```
Query  3     GTCCTGGAGACACCTC  18
             ||||||||||||||||
Sbjct  2610  GTCCTGGAGACACCTC  2625
```

PREDICTED: Anarrhichthys ocellatus SRY-box transcription factor 2 (sox2), transcript variant X7, misc_RNA

Sequence ID: XR_004213533.1Length: 2961Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 1167 to 1182 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	187	16/16(100%)	0/16(0%)	Plus/Plus

```
Query  2     CGTCCTGGAGACACCT  17
             ||||||||||||||||
Sbjct  1167  CGTCCTGGAGACACCT  1182
```

PREDICTED: Vicugna pacos ataxin 7 (ATXN7), mRNA

Sequence ID: XM_031686336.1Length: 6506Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 2851 to 2866 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	187	16/16(100%)	0/16(0%)	Plus/Plus

```
Query  5     CCTGGAGACACCTCCC  20
             ||||||||||||||||
Sbjct  2851  CCTGGAGACACCTCCC  2866
```

PREDICTED: Phalacrocorax carbo T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA

Sequence ID: XM_009502555.1Length: 4743Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 2337 to 2352 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	199	16/16(100%)	0/16(0%)	Plus/Plus

```
CDS: Putative 1       1       R  P  G  D  T
Query                 1     CCGTCCTGGAGACACC  16
                            ||||||||||||||||
Sbjct                 2337  CCGTCCTGGAGACACC  2352
CDS:PREDICTED: LOW Q  780     R  P  G  D  T
```

/prodotto="LOW QUALITY PROTEIN: T-lymphoma invasion and metastasis-inducing protein 1"

L’invasione del linfoma T e la proteina 1 che induce metastasi (Tiam1) è un fattore di scambio guanina (GEF) per CDC42 e la famiglia Rho GTPasi Rac1, che svolge un ruolo importante nell'adesione cellula-matrice e nella migrazione cellulare. **Tiam1 è coinvolto in più fasi della tumorigenesi** (https://www.ebi.ac.uk/interpro/entry/InterPro/IPR033360/). “**L’invasione del linfoma T e la proteina 1** che induce la **metastasi (Tiam1)** è coinvolta nei **processi di tumorigenesi**, *tra cui migrazione cellulare, adesione e invasione, proteolisi, riorganizzazione del citoscheletro, trasformazione morfologica cellulare e segnalazione intracellulare*. Questi processi sono anche fondamentali per l’**impianto dell’embrione**, sebbene il ruolo di Tiam1 durante l’impianto dell’embrione rimanga poco compreso.” (https://pubmed.ncbi.nlm.nih.gov/18765636/; https://www.uniprot.org/uniprot/Q13009).

PREDICTED: Oncorhynchus kisutch vasopressin V2 receptor (LOC109869858), transcript variant X4, mRNA

Sequence ID: XM_031803871.1Length: 3004Number of Matches: 1

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Range 1: 1071 to 1086 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	199	16/16(100%)	0/16(0%)	Plus/Minus

```
CDS: Putative 1       5      G  P  S  V  E
Query                 4     TCCTGGAGACACCTCC  19
                            ||||||||||||||||
Sbjct                 1086  TCCTGGAGACACCTCC  1071
CDS:vasopressin V2 r  223    G  P  S  V  E
```

/prodotto="vasopressin V2 receptor"

Il **recettore 2 della vasopressina (V2R)**, o **recettore 2 della vasopressina dell'arginina** (chiamato ufficialmente **AVPR2**), è una proteina che agisce come **recettore per la vasopressina**. **AVPR2** appartiene alla sottofamiglia dei recettori G-proteina-accoppiati. La sua attività è mediata dal tipo G_s di proteine G, che stimolano ciclasi (https://en.wikipedia.org/wiki/Vasopressin_receptor_2). L’**AVPR2** è espresso nel *tubulo renale*, prevalentemente nella *membrana delle cellule del tubulo contorto distale e dei dotti collettori, nel tessuto polmonare fetale e nel* ***cancro del polmone****, gli ultimi due associati a splicing alternativo*. **AVPR2 è espresso anche al di fuori del rene nell’endotelio vascolare**. **La stimolazione provoca il rilascio del fattore di von Willebrand e del fattore VIII dalle cellule endoteliali** (https://en.wikipedia.org/wiki/Vasopressin_receptor_2). Poiché il **fattore di von Willebrand** aiuta a stabilizzare i **livelli circolanti di fattore VIII**, l’**analogo della vasopressina desmopressina** può essere utilizzato per **stimolare il recettore AVPR2 e aumentare i livelli di fattore VIII circolante**. **Questo è utile nel trattamento dell’emofilia A e della malattia di Von Willebrand**. Nel rene, la proprietà principale dell’**AVPR2** è quella di rispondere all’**arginina vasopressina** stimolando i meccanismi che concentrano l’urina e mantengono l’omeostasi dell’acqua nell’organismo (https://en.wikipedia.org/wiki/Vasopressin_receptor_2). **Quando la funzione di AVPR2 viene persa, si manifesta la malattia diabete insipido nefrogenico (NDI)**. È stato dimostrato che la **funzione del recettore 2 della vasopressina** è influenzata in modo deleterio da **mutazioni puntiformi nel suo gene**. Alcune di queste mutazioni, quando espresse, fanno sì che il *recettore rimanga nel citosol* (https://en.wikipedia.org/wiki/Vasopressin_receptor_2).

Bacillus paranthracis strain MN1F chromosome, complete genome

GenBank: CP048687.1

FASTA Graphics

Go to:

```
LOCUS       CP048687                  15 bp    DNA     linear   BCT 17-FEB-2020
DEFINITION  Bacillus paranthracis strain MN1F chromosome, complete genome.
ACCESSION   CP048687 REGION: 3474988..3475002
VERSION     CP048687.1
DBLINK      BioProject: PRJNA605734
            BioSample: SAMN14074934
KEYWORDS    .
SOURCE      Bacillus paranthracis
  ORGANISM  Bacillus paranthracis
            Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus;
            Bacillus cereus group.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Sousa,L.
  TITLE     Bacillus paranthracis BCCL
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 15)
  AUTHORS   Sousa,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-FEB-2020) Genetic Department, UNICAMP, Rua Bertrand
            Russel, s/n, Campinas 6109, Brazil
COMMENT     ##Genome-Assembly-Data-START##
            Assembly Method       :: Velvet v. 1.2.10
            Genome Representation :: Full
            Expected Final Version :: Yes
            Genome Coverage       :: 80.0x
            Sequencing Technology :: PacBio
            ##Genome-Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..15
                     /organism="Bacillus paranthracis"
                     /mol_type="genomic DNA"
                     /strain="MN1F"
                     /isolation_source="book surface"
                     /db_xref="taxon:2026186"
                     /country="Brazil: Campinas"
                     /lat_lon="22.54 S 47.3 W"
                     /collection_date="Aug-2019"
                     /collected_by="Leandro Pio de Sousa"
ORIGIN
        1 ccgtcctgga gacac  //
```

Bacillus paranthracis strain MN1F chromosome, complete genome

Sequence ID: CP048687.1Length: 5687871Number of Matches: 1

Range 1: 3474988 to 3475002 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	770	15/15(100%)	0/15(0%)	Plus/Plus

```
Query  1        CCGTCCTGGAGACAC  15
                |||||||||||||||
Sbjct  3474988  CCGTCCTGGAGACAC  3475002
```

Bacillus paranthracis strain CFSAN068816 chromosome, complete genome

GenBank: CP045777.1

FASTA Graphics

Go to:

```
LOCUS       CP045777                  15 bp    DNA     linear   BCT 11-NOV-2019
DEFINITION  Bacillus paranthracis strain CFSAN068816 chromosome, complete
            genome.
ACCESSION   CP045777 REGION: 2000897..2000911
VERSION     CP045777.1
DBLINK      BioProject: PRJNA541977
            BioSample: SAMN10574728
KEYWORDS    .
SOURCE      Bacillus paranthracis
  ORGANISM  Bacillus paranthracis
            Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus;
            Bacillus cereus group.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Mafiz,A., Kastanis,G. and Gonzalez Escalona,N.
  TITLE     Closed genomes of twenty-eight foodborne pathogens from the CFSAN
            verification set by a combination of long and short-reads
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 15)
  AUTHORS   Mafiz,A., Kastanis,G. and Gonzalez Escalona,N.
  TITLE     Direct Submission
JOURNAL   Submitted (01-NOV-2019) ORS/DM/MMSB, Food and Drug
          Administration-College Park, 5001 Campus Drive, College Park, MD
          20740-3835, USA
COMMENT     The annotation was added by the NCBI Prokaryotic Genome Annotation
            Pipeline (PGAP). Information about PGAP can be found here:
            https://www.ncbi.nlm.nih.gov/genome/annotation_prok/

            ##Genome-Assembly-Data-START##
            Assembly Method        :: SPAdes, CANU v. 3.12.0, 1.7
            Genome Representation  :: Full
```

```
          Expected Final Version :: Yes
          Genome Coverage        :: 84, 43, 113, 105, 195, 264x
          Sequencing Technology  :: Oxford Nanopore GridION, Illumina MiSeq
          ##Genome-Assembly-Data-END##

          ##Genome-Annotation-Data-START##
          Annotation Provider               :: NCBI
          Annotation Date                   :: 11/04/2019 10:11:02
          Annotation Pipeline               :: NCBI Prokaryotic Genome
                                               Annotation Pipeline (PGAP)
          Annotation Method                 :: Best-placed reference protein
                                               set; GeneMarkS-2+
          Annotation Software revision      :: 4.10
          Features Annotated                :: Gene; CDS; rRNA; tRNA; ncRNA;
                                               repeat_region
          Genes (total)                     :: 5,736
          CDSs (total)                      :: 5,585
          Genes (coding)                    :: 5,463
          CDSs (with protein)               :: 5,463
          Genes (RNA)                       :: 151
          rRNAs                             :: 14, 14, 14 (5S, 16S, 23S)
          complete rRNAs                    :: 14, 14, 14 (5S, 16S, 23S)
          tRNAs                             :: 104
          ncRNAs                            :: 5
          Pseudo Genes (total)              :: 122
          CDSs (without protein)            :: 122
          Pseudo Genes (ambiguous residues) :: 0 of 122
          Pseudo Genes (frameshifted)       :: 49 of 122
          Pseudo Genes (incomplete)         :: 63 of 122
          Pseudo Genes (internal stop)      :: 27 of 122
          Pseudo Genes (multiple problems)  :: 15 of 122
          ##Genome-Annotation-Data-END##
FEATURES             Location/Qualifiers
     source          1..15
                     /organism="Bacillus paranthracis"
                     /mol_type="genomic DNA"
                     /strain="CFSAN068816"
                     /isolation_source="Mac and Cheese"
                     /db_xref="taxon:2026186"
                     /country="USA:CT"
                     /collection_date="2009-06-11"
                     /collected_by="FDA"
     gene            <1..>15
                     /gene="rplS"
                     /locus_tag="GH772_11805"
```

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     CDS             <1..>15
                     /gene="rplS"
                     /locus_tag="GH772_11805"
                     /inference="COORDINATES: similar to AA
                     sequence:RefSeq:WP_001186515.1"
                     /note="Derived by automated computational analysis using
                     gene prediction method: Protein Homology."
                     /codon_start=2
                     /transl_table=11
                     /product="50S ribosomal protein L19"
                     /protein_id="QGG18348.1"
                     /translation="MQQLIAEITKGQLKTDLPSFRPGDTLRVHVKVVEGTRERIQLFE
                     GVVIKRRGGGISETFTVRKISYGVGVERTFPVHTPRIAKIEVLRRGKVRRAKLYYLRN
                     LRGKKARIKEIR"
ORIGIN
            1 ccgtcctgga gacac
//
```

Bacillus paranthracis strain CFSAN068816 chromosome, complete genome

Sequence ID: CP045777.1Length: 5351395Number of Matches: 1

Range 1: 2000897 to 2000911 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	770	15/15(100%)	0/15(0%)	Plus/Plus

```
CDS: Putative 1        1            R   P   G   D   T
Query                  1          CCGTCCTGGAGACAC   15
                                  |||||||||||||||
Sbjct                  2000897    CCGTCCTGGAGACAC   2000911
CDS:50S ribosomal pr   21           R   P   G   D   T
```

/prodotto="50S ribosomal protein L19"

50S ribosomal protein L19

50S, approssimativamente equivalente alla **subunità ribosomiale 60S nelle cellule eucariotiche** (quelle degli *ESSERI UMANI*), è la **subunità più grande del ribosoma 70S dei procarioti** (cioè **batteri** e **archaea**). È il **sito di inibizione di antibiotici** come i macrolidi, il cloramfenicolo, la clindamicina e le pleuromutiline. Include l'RNA ribosomiale 5S e l'RNA ribosomiale 23S. La **subunità 50S** è composta principalmente da **proteine** ma contiene anche **RNA a filamento singolo** noto come **RNA ribosomiale** (**rRNA**). (https://en.wikipedia.org/wiki/Prokaryotic_large_ribosomal_subunit). L'rRNA forma strutture secondarie e terziarie per mantenere la struttura e svolgere le funzioni catalitiche del ribosoma. **50S** include l'*attività che catalizza la formazione del legame peptidico* (reazione di trasferimento del peptidile), *previene l'idrolisi prematura del polipeptide*, *fornisce un sito di legame per i fattori della proteina G* (aiuta l'inizio, l'allungamento e la terminazione) e *aiuta il ripiegamento delle proteine dopo la sintesi* (https://en.wikipedia.org/wiki/Prokaryotic_large_ribosomal_subunit). Una **proteina ribosomiale**

(*proteina r o rProtein*) è una qualsiasi delle proteine che, insieme all'rRNA, costituiscono le subunità ribosomiali coinvolte nel *processo cellulare di traduzione*. ***E. coli, altri batteri e Archaea*** hanno **una subunità piccola 30S** e **una subunità grande 50S**, mentre gli **esseri umani** e i **lieviti** hanno una **subunità piccola 40S e una subunità grande 60S**. Le *subunità equivalenti sono spesso numerate in modo diverso tra batteri, Archaea, lieviti e umani* (https://en.wikipedia.org/wiki/Ribosomal_protein). Le subunità dei ribosomi, la **piccola subunità 40S** e la **grande subunità 60S**, insieme sono composte da 4 specie di RNA e circa 80 proteine strutturalmente distinte. **RPL19** (***proteina ribosomiale L19***) è un gene che codifica per proteine. Le malattie associate a **RPL19** includono la **Psoriasi 13** e l'**Adenoma del retto** [l'*espressione fecale* di **RPL19** è associata a *stadi avanzati del cancro del colon-retto (**CRC**)* e dipende dai *livelli sierici dell'antigene carcinoembrionario* (**CEA**) nel predire la prognosi dei pazienti con *CRC* (https://onlinelibrary.wiley.com/doi/full/10.1111/j.1582-4934.2008.00253.x]. Tra i percorsi correlati a **RPL19** vi sono il **metabolismo delle proteine** e il **ciclo di vita dell'HIV** (https://hivinfo.nih.gov/understanding-hiv/fact-sheets/hiv-life-cycle; https://www.genecards.org/cgi-bin/carddisp.pl?gene=RPL19). Le annotazioni di Gene Ontology (GO) relative a questo gene includono il *costituente strutturale del ribosoma* (https://www.genecards.org/cgi-bin/carddisp.pl?gene=RPL19). E' stato accertato che i livelli dell'**mRNA** che codifica per la **proteina ribosomiale L19** era più abbondante nei campioni di **cancro al seno** che esprimono alti livelli di **erbB-2** [il gene *erbB-2* (o *HER-2* o *neu*) è *amplificato e sovraespresso* in circa un terzo dei **tumori della mammella**, **dello stomaco e dell'ovaio**. Il **livello di espressione dell'mRNA di L19** variava in un intervallo da 1 a 64 volte tra i campioni di tumore. (https://pubmed.ncbi.nlm.nih.gov/8095182/). Il gene che codifica per la **proteina ribosomiale L19** (**RPL19**) è *sovraespresso* anche nelle **cellule prostatiche umane maligne**, rivelando che RPL19 è un predittore sensibile della **progressione del cancro alla prostata** (https://pubmed.ncbi.nlm.nih.gov/16609016/). Nell'**Homo Sapiens**, il gene **RPL19** (https://www.genenames.org/data/gene-symbol-report/#!/hgnc_id/HGNC:10312) codifica per una proteina ribosomiale che è un componente della ***subunità 60S***. La proteina appartiene alla famiglia delle proteine ribosomiali **L19E**. **L19** contribuisce all'assemblaggio delle **subunità ribosomiali 50S** (https://pubmed.ncbi.nlm.nih.gov/7559342/).
La proteina ribosomiale L19/L19e è assente nei batteri (https://www.sciencedirect.com/science/article/abs/pii/S1055790398906078?via%3Dihub; http://www.ebi.ac.uk/interpro/entry/InterPro/IPR023638/). Si trova nel citoplasma. Come è tipico per i geni che codificano per proteine ribosomiali, ci sono più pseudogeni elaborati di questo gene dispersi attraverso il genoma. Questo gene ha espressione ubiquitaria nell'**ovaio**, nel **linfonodo** e in altri **25 tessuti** (https://www.genecards.org/cgi-bin/carddisp.pl?gene=RPL19; https://pubmed.ncbi.nlm.nih.gov/1577483/; https://en.wikipedia.org/wiki/60S_ribosomal_protein_L19; https://www.omim.org/entry/180466; https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=235418; https://supfam.org/SUPERFAMILY/cgi-bin/scop.cgi?ipid=SSF48140; https://pubmed.ncbi.nlm.nih.gov/1577483/).

Anche se è riportato che **la proteina ribosomiale L19/L19e è assente nei batteri**, **tre mutanti di Escherichia coli** **che apparentemente mancavano della proteina L19 sui loro ribosomi**, sono stati analizzati da una serie di test immunologici per determinare se la proteina era effettivamente mancante. Solo un test su tre ha evidenziato una forma **drasticamente alterata della proteina L19 presente sul ribosoma**. **La posizione della proteina ribosomiale L19 è stata determinata sulla superficie della grande subunità**. Essa era situata alla **base della particella 50 S** di fronte alla piccola subunità, sul lato in cui l'appendice a bastoncello ha origine (https://www.jbc.org/article/S0021-9258(17)43077-8/pdf).

Inoltre, analizzando l'essenzialità o il contributo alla crescita di ciascuno dei **quattro geni nell'operone trmD di Escherichia coli (rpsP, 21K, trmD e rplS)** e dei **geni fiancheggianti ffh e 16K** mediante un metodo genetico inverso, gli autori hanno scoperto che una **delezione-inserimento nel secondo gene, 21K, dell'operone trmD ha provocato l'accumulo di un assemblaggio intermedio della subunità ribosomiale 50S, come risultato di effetti polari sull'espressione di un gene a valle, rplS, che codifica**

per la proteina ribosomiale L19. Questa scoperta suggerisce che L19, precedentemente non considerata una proteina di assemblaggio, contribuisce all'assemblaggio delle subunità ribosomiali 50S (https://pubmed.ncbi.nlm.nih.gov/7559342/).

Per ulteriori approfondimenti:

https://www.uniprot.org/uniprot/P0A7K6; http://www.ebi.ac.uk/interpro/entry/InterPro/IPR000196/;

https://prosite.expasy.org/PDOC00455; http://www.ebi.ac.uk/interpro/entry/InterPro/IPR001857/.

Bacillus anthracis strain FDAARGOS_702 chromosome

GenBank: CP054800.1

FASTA Graphics

Go to:

```
LOCUS       CP054800                  15 bp    DNA     linear   BCT 17-JUN-2020
DEFINITION  Bacillus anthracis strain FDAARGOS_702 chromosome.
ACCESSION   CP054800 REGION: 4251568..4251582
VERSION     CP054800.1
DBLINK      BioProject: PRJNA231221
            BioSample: SAMN11056417
KEYWORDS    .
SOURCE      Bacillus anthracis
  ORGANISM  Bacillus anthracis
            Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus;
            Bacillus cereus group.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Sozhamannan,S., Rosenzweig,N., Tallon,L., Sadzewicz,L.,
            Vavikolanu,K., Mehta,A., Aluvathingal,J., Nadendla,S., Yan,Y. and
            Sichtig,H.
  TITLE     FDA dAtabase for Regulatory Grade micrObial Sequences (FDA-ARGOS):
            Supporting development and validation of Infectious Disease Dx
            tests
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 15)
  AUTHORS   Sozhamannan,S., Rosenzweig,N., Tallon,L., Sadzewicz,L.,
            Vavikolanu,K., Mehta,A., Aluvathingal,J., Nadendla,S., Yan,Y. and
            Sichtig,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-NOV-2019) Center for Devices and Radiological Health,
            US Food and Drug Administration, 10903 New Hampshire Avenue, Silver
            Spring, MD 20993-0002, USA
COMMENT     Assembly not circularized.
            The annotation was added by the NCBI Prokaryotic Genome Annotation
            Pipeline (PGAP). Information about PGAP can be found here:
            https://www.ncbi.nlm.nih.gov/genome/annotation_prok/
```

```
            ##Genome-Assembly-Data-START##
            Assembly Method       :: SMRT v. 2.3.0, HGAP v. 3, SPAdes v. 3.6.0
            Genome Coverage       :: 923.93x
            Sequencing Technology :: Pacbio; Illumina
            ##Genome-Assembly-Data-END##

            ##Genome-Annotation-Data-START##
            Annotation Provider                :: NCBI
            Annotation Date                    :: 06/10/2020 00:01:37
            Annotation Pipeline                :: NCBI Prokaryotic Genome
                                                  Annotation Pipeline (PGAP)
            Annotation Method                  :: Best-placed reference protein
                                                  set; GeneMarkS-2+
            Annotation Software revision       :: 4.11
            Features Annotated                 :: Gene; CDS; rRNA; tRNA; ncRNA;
                                                  repeat_region
            Genes (total)                      :: 5,533
            CDSs (total)                       :: 5,400
            Genes (coding)                     :: 5,101
            CDSs (with protein)                :: 5,101
            Genes (RNA)                        :: 133
            rRNAs                              :: 11, 11, 11 (5S, 16S, 23S)
            complete rRNAs                     :: 11, 11, 11 (5S, 16S, 23S)
            tRNAs                              :: 95
            ncRNAs                             :: 5
            Pseudo Genes (total)               :: 299
            CDSs (without protein)             :: 299
            Pseudo Genes (ambiguous residues)  :: 0 of 299
            Pseudo Genes (frameshifted)        :: 215 of 299
            Pseudo Genes (incomplete)          :: 38 of 299
            Pseudo Genes (internal stop)       :: 67 of 299
            Pseudo Genes (multiple problems)   :: 18 of 299
            ##Genome-Annotation-Data-END##
FEATURES             Location/Qualifiers
     source          1..15
                     /organism="Bacillus anthracis"
                     /mol_type="genomic DNA"
                     /strain="FDAARGOS_702"
                     /culture_collection="FDA:FDAARGOS_702"
                     /db_xref="taxon:1392"
                     /country="USA: MD"
                     /collected_by="U.S. Army Edgewood Chemical Biological
                     Center"
                     /note="genetically modified strain"
     gene            <1..>15
```

```
                     /gene="rplS"
                     /locus_tag="FOC10_22455"
     CDS             <1..>15
                     /gene="rplS"
                     /locus_tag="FOC10_22455"
                     /inference="COORDINATES: similar to AA
                     sequence:RefSeq:NP_389486.2"
                     /note="Derived by automated computational analysis using
                     gene prediction method: Protein Homology."
                     /codon_start=2
                     /transl_table=11
                     /product="50S ribosomal protein L19"
                     /protein_id="QKU16142.1"
                     /translation="MQQLIAEITKGQLKTDLPSFRPGDTLRVHVKVVEGTRERIQLFE
                     GVVIKRRGGGISETFTVRKISYGVGVERTFPVHTPRIAKIEVLRRGKVRRAKLYYLRN
                     LRGKKARIKEIR"
ORIGIN
        1 ccgtcctgga gacac
//
```

Bacillus anthracis strain FDAARGOS_702 chromosome

Sequence ID: CP054800.1Length: 5272559Number of Matches: 1

Range 1: 4251568 to 4251582 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	770	15/15(100%)	0/15(0%)	Plus/Plus

```
CDS: Putative 1       1          R  P  G  D  T
Query                 1        CCGTCCTGGAGACAC  15
                               |||||||||||||||
Sbjct                 4251568  CCGTCCTGGAGACAC  4251582
CDS:50S ribosomal pr  21         R  P  G  D  T
```

/prodotto="50S ribosomal protein L19"

Bacillus anthracis strain Sterne 34F2 genome

GenBank: CP019726.1

FASTA Graphics

Go to:

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LOCUS       CP019726                  15 bp    DNA     linear   BCT 21-FEB-2017
DEFINITION  Bacillus anthracis strain Sterne 34F2 genome.
ACCESSION   CP019726 REGION: 3607405..3607419
VERSION     CP019726.1
DBLINK      BioProject: PRJNA357857
```

```
            BioSample: SAMN06161234
KEYWORDS    .
SOURCE      Bacillus anthracis
  ORGANISM  Bacillus anthracis
            Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus;
            Bacillus cereus group.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Koren,S., Walenz,B.P., Berlin,K., Miller,J.R., Bergman,N.H. and
            Phillippy,A.M.
  TITLE     Canu: scalable and accurate long-read assembly via adaptive k-mer
            weighting and repeat separation
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 15)
  AUTHORS   Koren,S., Walenz,B.P., Berlin,K., Miller,J.R., Bergman,N.H. and
            Phillippy,A.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-2017) CSGB, NHGRI/NIH, NIH 49 Convent Drive Room
            4A03, Bethesda, MD 20892, USA
COMMENT     Bacteria and source DNA available from NBACC.   Gap of
            approximately 10-20 kbp between the last and first base of
            chromosome.

            ##Genome-Assembly-Data-START##
            Assembly Method        :: Canu + Pilon v. 1.3
            Assembly Name          :: Canu Nanopore Assembly followed by 3
                                      rounds Pilon polishing
            Genome Representation  :: Full
            Expected Final Version :: Yes
            Genome Coverage        :: 100.0x
            Sequencing Technology  :: Oxford Nanopore
            ##Genome-Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..15
                     /organism="Bacillus anthracis"
                     /mol_type="genomic DNA"
                     /strain="Sterne 34F2"
                     /isolation_source="lab strain"
                     /db_xref="taxon:1392"
                     /collection_date="17-Nov-2015"
ORIGIN
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//
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Bacillus anthracis strain Sterne 34F2 genome

Sequence ID: CP019726.1Length: 5209112Number of Matches: 1

Range 1: 3607405 to 3607419 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	770	15/15(100%)	0/15(0%)	Plus/Plus

```
Query  1        CCGTCCTGGAGACAC  15
                |||||||||||||||
Sbjct  3607405  CCGTCCTGGAGACAC  3607419
```

PREDICTED: Manis javanica maestro heat like repeat family member 6 (MROH6), transcript variant X6, misc_RNA

Sequence ID: XR_005062615.1Length: 10081Number of Matches: 1

Range 1: 1629 to 1643 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	786	15/15(100%)	0/15(0%)	Plus/Plus

```
Query  5     CCTGGAGACACCTCC  19
             |||||||||||||||
Sbjct  1629  CCTGGAGACACCTCC  1643
```

**/prodotto="maestro heat like repeat family member 6,
transcript variant X6"**

Per approfondimenti:

https://www.ncbi.nlm.nih.gov/gene/642475; https://www.uniprot.org/uniprot/Q8NDA8

PREDICTED: Manis pentadactyla PALM2 and AKAP2 fusion (PALM2AKAP2), transcript variant X11, mRNA

Sequence ID: XM_036903349.1Length: 6723Number of Matches: 1

Range 1: 1705 to 1719 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	786	15/15(100%)	0/15(0%)	Plus/Plus

```
CDS: Putative 1       1        V  L  E  T
Query                 1      CCGTCCTGGAGACAC  15
                             |||||||||||||||
Sbjct                 1705   CCGTCCTGGAGACAC  1719
CDS:A-kinase anchor   480    T  V  L  E  T
```

/prodotto="A-kinase anchor protein 2 isoform X11"

AKAP2 (**A-Kinase Anchoring Protein 2**) è un gene che codifica una proteina. Le malattie associate con **AKAP2** include **Kallmann Syndrome**. Si lega alla subunità regolatrice (RII) della proteina chinasi A. Può essere coinvolto nello stabilire la polarità nei sistemi di segnalazione o nell'integrazione delle isoforme PKA-RII con gli effettori a valle per catturare, amplificare e concentrare i segnali diffusi e transcellulari trasportati dal cAMP (per similarità). (https://www.uniprot.org/uniprot/Q9Y2D5; https://www.genecards.org/cgi-bin/carddisp.pl?gene=PALM2AKAP2).

PREDICTED: Manis javanica uncharacterized LOC108399514 (LOC108399514), transcript variant X6, ncRNA

Sequence ID: XR_005053859.1Length: 2450Number of Matches: 1

Range 1: 101 to 115 GenBank Graphics

```
Score           Expect  Identities      Gaps        Strand

30.2 bits(15)  786    15/15(100%)  0/15(0%)  Plus/Minus

Query  6     CTGGAGACACCTCCC  20
             |||||||||||||||
Sbjct  115   CTGGAGACACCTCCC  101
```

PREDICTED: Falco cherrug cancer susceptibility 1 (CASC1), transcript variant X6, mRNA

Sequence ID: XM_027797425.1Length: 5389Number of Matches: 1

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Range 1: 326 to 340 GenBank Graphics

```
Score           Expect  Identities      Gaps        Strand

30.2 bits(15)  786    15/15(100%)  0/15(0%)  Plus/Minus

Query  3     GTCCTGGAGACACCT  17
             |||||||||||||||
Sbjct  340   GTCCTGGAGACACCT  326
```

Cancer susceptibility 1 (CASC1)

Casc1, alias Las1, è uno dei sei geni che costituiscono l'aplotipo del locus 1 (Pas1) di **suscettibilità dell'adenoma polmonare del topo**. **La suscettibilità al cancro 1 è una proteina che nell'uomo è codificata dal gene CASC1** (https://en.wikipedia.org/wiki/Cancer_susceptibility_1 https://www.wikigenes.org/e/gene/e/55259.html).

4.2 LA SEQUENZA “AES (2)” E I RISULTATI DELLA RICERCA BLAST

Quella mostrata qui di seguito è la sequenza totale del *3’-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*.

C TCGAGCTGGT ACTGCATGCA 3900
CGCAATGCTA GCTGCCCCTT TC**CCGTCCTG GGTACCCCGA GTCTCCCCCG** 3950
ACCTCGGGTC CCAGGTATGC TCCCACCTCC ACCTGCCCCA CTCACCACCT 4000
CTGCTAGTTC CAGACACCTC CCAAGCACGC AGCAATGCAG CTCAAAACGC 4050
TTAGCCTAGC CACACCCCCA CGGGAAACAG CAGTGATTAA CCTTTAGCAA 4100
TAAACGAAAG TTTAACTAAG CTATACTAAC CCCAGGGTTG GTCAATTTCG 4150
TGCCAGCCAC ACCCTGGAGC TAGC

Le **lettere nere in grassetto** sono le lettere poste tra i **DUE spezzoni di sequenza** che costituiscono la **Sequenza “ANTHRAX”** (la sequenza discussa nel paragrafo precedente). La sequenza **Query** (**CCGTCCTGGACCTCGGGTCCCAGGTATGCTCCCACCTC CCCACCTGCCCCACTCACCACCTAGACACCTCCC**) mostrata sotto è formata dai segmenti della **Sequenza “ANTHRAX”** e dalle lettere che li dividono. Questa nuova sequenza è stata definita **Sequenza “AES (2)”** (***Amino-terminal Enhancer of Split*** *o potenziatore ammino-terminale dell’mRNA diviso*. Per il significato di **AES** si rimanda allo studio del Capitolo II di questo documento). Questa sequenza è stata sottoposta ad una ricerca BLAST e nelle pagine seguenti sono mostrati gli *allineamenti significativi* ottenuti e gli “**organismi**” e i “**prodotti**” a cui tali allineamenti si riferiscono. **I risultati dei “prodotti” identificati dalla ricerca BLAST sono coerenti** (ovvero l’atteso ***Amino-terminal Enhancer of Split***, uno dei componenti principali del *3’-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*) **con quanto dichiarato nel documento scaricato dalla WHO** (https://berthub.eu/articles/11889.doc), documento relativo al “codice sorgente” integrale del Vaccino mRNA Sars-Cov-2 BioNTech/Pfizer (BNT162b2). In altri termini, le **sorprese** mostrate nel paragrafo precedente dalla ricerca BLAST su alcune parti costituenti la **Sequenza “AES (2)”** (le parti corrispondenti alla **Sequenza “ANTHRAX”**) emergono **SOLO** se alcuni elementi costitutivi della stessa (le **lettere in grassetto**) vengono omessi, ottenendo così la **Sequenza “ANTHRAX”**.

QUERY : **CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACC TCCACCTGCCCCACTCACCACCTCTGCTAGTTCCAGACACCTCCC**

Search Parameters

Program	blastn
Word size	28
Expect value	0.05
Hitlist size	**5000**
Match/Mismatch scores	1,-2
Gapcosts	0,2.5
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

SEQUENZE SELEZIONATE: 65

Description	Name	Taxid	Score	Score	cover	Value	Ident	Len	Accession
Homo sapiens gp130 associated protein GAM mRNA, complete cds	human	9606	174	174	99%	8,00E-40	97.98	1317	AF072902.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	172	172	99%	3,00E-39	97.98	1805	XM_034945921.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	172	172	99%	3,00E-39	97.98	1808	XM_034945920.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	172	172	99%	3,00E-39	97.98	1731	XM_034945919.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	172	172	99%	3,00E-39	97.98	1891	XM_034945918.1
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	172	172	99%	3,00E-39	97.98	1798	NM_001130.6
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	172	172	99%	3,00E-39	97.98	1795	NM_198970.2
Eukaryotic synthetic construct chromosome 19	NA	111789	172	345	99%	3,00E-39	97.98	64242768	CP034522.1
Eukaryotic synthetic construct chromosome 19	NA	111789	172	345	99%	3,00E-39	97.98	64242768	CP034497.1
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	172	172	99%	3,00E-39	97.98	1512	XM_016937029.2
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	172	172	99%	3,00E-39	97.98	1683	XM_016937028.2
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	172	172	99%	3,00E-39	97.98	1693	XM_016937027.2
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	172	172	99%	3,00E-39	97.98	1888	XM_024351913.1
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	172	172	99%	3,00E-39	97.98	1891	XM_024351912.1
PREDICTED: Homo sapiens TLE family member 5, transcriptional...	human	9606	172	172	99%	3,00E-39	97.98	1881	XM_006722664.1
Homo sapiens DNA, chromosome 19, nearly complete genome	human	9606	172	172	99%	3,00E-39	97.98	59105444	AP023479.1
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	172	172	99%	3,00E-39	97.98	17057	NG_029870.1
Homo sapiens cDNA clone IMAGE:3464459, **** WARNING: chimeric...	human	9606	172	172	99%	3,00E-39	97.98	2395	BC040415.1
Homo sapiens cDNA clone IMAGE:4120426, **** WARNING: chimeric...	human	9606	172	172	99%	3,00E-39	97.98	3387	BC007797.1
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	172	172	99%	3,00E-39	97.98	1754	NM_198969.1
Homo sapiens cDNA FLJ37835 fis, clone BRSSN2010110, weakly...	human	9606	172	172	99%	3,00E-39	97.98	3276	AK095154.1
Homo sapiens cDNA FLJ37272 fis, clone BRAMY2012091, highly...	human	9606	172	172	99%	3,00E-39	97.98	1884	AK094591.1
Homo sapiens PP2150 mRNA, complete cds	human	9606	172	172	99%	3,00E-39	97.98	1035	AF269289.1
Homo sapiens chromosome 19, cosmid F23613, complete sequence	human	9606	172	172	99%	3,00E-39	97.98	42301	AC005944.1
Human homolog of Drosophila enhancer of split m9/m10 mRNA,...	human	9606	172	172	99%	3,00E-39	97.98	1288	U04241.1
PREDICTED: Gorilla gorilla gorilla TLE family member 5,...	western lowl...	9595	167	167	99%	1,00E-37	96.97	1586	XM_031007483.1
PREDICTED: Gorilla gorilla gorilla TLE family member 5,...	western lowl...	9595	167	167	99%	1,00E-37	96.97	1804	XM_031007481.1
PREDICTED: Gorilla gorilla gorilla TLE family member 5,...	western lowl...	9595	167	167	99%	1,00E-37	96.97	1807	XM_031007480.1
Homo sapiens isolate CHM13 chromosome 19	human	9606	167	167	99%	1,00E-37	96.97	61707364	CP068259.2
PREDICTED: Hylobates moloch TLE family member 5, transcription...	silvery gibbon	81572	161	161	99%	6,00E-36	95.96	1672	XM_032176817.1

PREDICTED: Nomascus leucogenys TLE family member 5,...	northern whi...	61853	161	161	99%	6,00E-36	95.96	1839	XM_030795556.1
Homo sapiens chromosome 19 groucho protein homolog (AES) gene,...	human	9606	156	156	99%	3,00E-34	94.95	12683	AH007143.2
PREDICTED: Pongo abelii amino-terminal enhancer of split-like...	Sumatran ora...	9601	148	148	95%	5,00E-32	94.74	1251	XR_654387.2
PREDICTED: Piliocolobus tephrosceles TLE family member 5,...	Ugandan red ...	591936	147	147	99%	2,00E-31	93.14	1796	XM_026455495.2
PREDICTED: Theropithecus gelada amino-terminal enhancer of spl...	gelada	9565	141	141	99%	8,00E-30	92.16	1689	XM_025366152.1
PREDICTED: Theropithecus gelada amino-terminal enhancer of spl...	gelada	9565	141	141	99%	8,00E-30	92.16	1743	XM_025366151.1
PREDICTED: Theropithecus gelada amino-terminal enhancer of spl...	gelada	9565	141	141	99%	8,00E-30	92.16	1699	XM_025366150.1
PREDICTED: Theropithecus gelada amino-terminal enhancer of spl...	gelada	9565	141	141	99%	8,00E-30	92.16	1896	XM_025366148.1
PREDICTED: Cercocebus atys amino-terminal enhancer of split...	sooty mangabey	9531	141	141	99%	8,00E-30	92.16	1606	XM_012073023.1
PREDICTED: Cercocebus atys amino-terminal enhancer of split...	sooty mangabey	9531	141	141	99%	8,00E-30	92.16	1553	XM_012073022.1
PREDICTED: Mandrillus leucophaeus amino-terminal enhancer of...	drill	9568	141	141	99%	8,00E-30	92.16	1619	XM_011967328.1
PREDICTED: Mandrillus leucophaeus amino-terminal enhancer of...	drill	9568	141	141	99%	8,00E-30	92.16	1680	XM_011967327.1
PREDICTED: Chlorocebus sabaeus TLE family member 5,...	green monkey	60711	141	141	99%	8,00E-30	92.16	1699	XM_007994751.2
PREDICTED: Chlorocebus sabaeus TLE family member 5,...	green monkey	60711	141	141	99%	8,00E-30	92.16	1812	XM_007994750.2
PREDICTED: Trachypithecus francoisi TLE family member 5,...	Francois's l...	54180	135	135	99%	4,00E-28	91.18	1752	XM_033199976.1
PREDICTED: Trachypithecus francoisi TLE family member 5,...	Francois's l...	54180	135	135	99%	4,00E-28	91.18	1877	XM_033199975.1
PREDICTED: Trachypithecus francoisi TLE family member 5,...	Francois's l...	54180	135	135	99%	4,00E-28	91.18	1876	XM_033199974.1
PREDICTED: Papio anubis TLE family member 5, transcriptional...	olive baboon	9555	135	135	99%	4,00E-28	91.18	1630	XM_031660129.1
PREDICTED: Papio anubis TLE family member 5, transcriptional...	olive baboon	9555	135	135	99%	4,00E-28	91.18	1866	XM_021930524.2
PREDICTED: Macaca mulatta TLE family member 5, transcriptional...	Rhesus monkey	9544	135	135	99%	4,00E-28	91.18	1767	XM_028839658.1
PREDICTED: Macaca mulatta TLE family member 5, transcriptional...	Rhesus monkey	9544	135	135	99%	4,00E-28	91.18	1876	XM_028839657.1
PREDICTED: Macaca mulatta TLE family member 5, transcriptional...	Rhesus monkey	9544	135	135	99%	4,00E-28	91.18	1879	XM_028839656.1
PREDICTED: Macaca mulatta TLE family member 5, transcriptional...	Rhesus monkey	9544	135	135	99%	4,00E-28	91.18	1614	XM_028839655.1
PREDICTED: Macaca mulatta TLE family member 5, transcriptional...	Rhesus monkey	9544	135	135	99%	4,00E-28	91.18	1617	XM_028839654.1
PREDICTED: Macaca nemestrina amino-terminal enhancer of split...	pig-tailed m...	9545	135	135	99%	4,00E-28	91.18	1660	XM_011748007.2
PREDICTED: Pongo abelii amino-terminal enhancer of split (AES)...	Sumatran ora...	9601	135	135	99%	4,00E-28	91.18	1592	XM_024236904.1
PREDICTED: Pongo abelii amino-terminal enhancer of split (AES)...	Sumatran ora...	9601	135	135	99%	4,00E-28	91.18	1686	XM_024236903.1
PREDICTED: Pongo abelii amino-terminal enhancer of split (AES)...	Sumatran	9601	135	135	99%	4,00E-28	91.18	1689	XM_024236902.1

	ora...								
PREDICTED: Pongo abelii amino-terminal enhancer of split (AES)...	Sumatran ora...	9601	135	135	99%	4,00E-28	91.18	1723	XM_024236901.1
PREDICTED: Macaca fascicularis amino-terminal enhancer of spli...	crab-eating ...	9541	135	135	99%	4,00E-28	91.18	1617	XM_015440156.1
Macaca fascicularis TLE family member 5, transcriptional...	crab-eating ...	9541	135	135	99%	4,00E-28	91.18	1232	NM_001285171.1
PREDICTED: Trachypithecus francoisi TLE family member 5-like...	Francois's l...	54180	130	130	99%	2,00E-26	90.20	1344	XM_033189604.1
PREDICTED: Rhinopithecus bieti amino-terminal enhancer of spli...	black snub-n...	61621	130	130	99%	2,00E-26	90.20	1747	XM_017847996.1
PREDICTED: Rhinopithecus bieti amino-terminal enhancer of spli...	black snub-n...	61621	130	130	99%	2,00E-26	90.20	1653	XM_017847995.1
PREDICTED: Otolemur garnettii amino-terminal enhancer of split...	small-eared ...	30611	56.5	56.5	71%	3,00E-04	81.25	1580	XM_012804464.2

CAPITOLO V

LA SEQUENZA “BAT CORONAVIRUS”, “12S” E I RISULTATI DELLE RICERCHE BLAST

OBIETTIVI DEL CAPITOLO V

In questo capitolo sono mostrati i risultati delle ricerche BLAST effettuate su **due sequenze**:

1) la **Sequenza "BAT CORONAVIRUS"** (**AAAACGCGCTAACACC**), la **terza sequenza** ottenuta dalla fusione di **QUATTRO** segmenti di sequenza non contigui del *3'-UTR*;

2) la **Sequenza "12S"** (**AAAACGCTTAGCCTAGCCACACC**), ***Mitochondrial encoded 12S ribosomal RNA***, uno dei componenti principali del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer* (per il significato di ***12S*** si rimanda allo studio del Capitolo II di questo documento).

La **Sequenza "BAT CORONAVIRUS"** è così chiamata perché tra gli allineamenti significativi di questa sequenza sono stati identificati **due sconcertanti segmenti di sequenza specifici del CORONAVIRUS del Pipistrello** (**BAT**). Il "prodotto" corrispondente a questi **2** allineamenti significativi è un segmento di sequenza del gene **ORF1a** (**O**pen **R**eading **F**rame, *quadro* o *cornice di lettura aperto*, fase di lettura che consente di codificare un'intera proteina, senza incontrare codoni di stop prematuri e quindi formare una proteina tronca). Nel documento intitolato "I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis", una sequenza **UMANA** del **gene RdRp** [o ***R**NA-**d**ependent **R**NA **p**olymerase* (in italiano ***R**NA **p**olimerasi **R**NA-**d**ipendente*) *del SARS-CoV-2*, parte di ***ORF1ab*** e **specifico del SARS-CoV-2** (*Severe acute respiratory syndrome coronavirus 2 /* ***Human***), è stata oggetto di un approfondito studio (si anche veda il Capitolo VII di questo documento).

La **Sequenza "BAT CORONAVIRUS"** (**AAAACGCGCTAACACC**) del gene **ORF1a** identificata corrisponde alla **sequenza di animoacidi "CVSAF"**. La ricerca BLAST sulla sequenza "**AAAACGCGCTAACACC**" **non ha evidenziato** allineamenti significativi con l'**Homo Sapiens**. Al contrario, la **sequenza di aminoacidi "CVSAF"**, le cui basi corrispondono a quelle della **Sequenza "BAT CORONAVIRUS"**, **ha evidenziato** allineamenti significativi con l'**Homo Sapiens**.

In particolare, sono stati identificati i seguenti "prodotti":

- **PKDREJ**, una proteina che può svolgere un ruolo nella **riproduzione umana** ed è implicata nel **rene policistico autosomico dominante (ADPKD)**;

- "**Schlafen umano 5 (SLFN5)**", che **inibisce o promuove la proliferazione di diversi tipi specifici di cellule cancerose**

- **Exo70**, che svolge ruoli importanti nella **progressione del cancro umano** (in particolare, nel **Cancro del Colon**).

Infine, sono stati identificati numerosi
allineamenti significativi con il batterio Salmonella e con diverse specie del batterio **Pseudomonas** (notevolmente implicato in **patologie polmonari**).

ATTEZIONE:

La necessità di pubblicare in fretta questo documento non ci ha consentito di approfondire **altri importanti allineamenti significativi**. Il ricercatore interessato potrà utilizzare le informazioni pubblicate nelle pagine successive e fare autonomamente gli approfondimenti desiderati.

5.1 LA SEQUENZA “BAT CORONAVIRUS” E I RISULTATI DELLA RICERCA BLAST

Quella mostrata qui di seguito è la sequenza totale del *3’-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*. Le lettere colorate sono i **QUATTRO segmenti di sequenza non contigui** che sono stati identificati in questa ricerca. Essi, uniti insieme, formano la **Sequenza “BAT CORONAVIRUS”**. Questa sequenza è stata sottoposta ad una ricerca BLAST e nelle pagine seguenti sono mostrati gli *allineamenti significativi* ottenuti e gli “**organismi**” e i **prodotti** a cui tali allineamenti si riferiscono.

C TCGAGCTGGT ACTGCATGCA 3900
CGCAATGCTA GCTGCCCCTT TCCCGTCCTG GGTACCCCGA GTCTCCCCCG 3950
ACCTCGGGTC CCAGGTATGC TCCCACCTCC ACCTGCCCCA CTCACCACCT 4000
CTGCTAGTTC CAGACACCTC CCAAGCACGC AGCAATGCAG CTC**AAAACGC** 4050
TTA**GC**C**TA**GC C**ACACC**CCCA CGGGAAACAG CAGTGATTAA CCTTTAGCAA 4100
TAAACGAAAG TTTAACTAAG CTATACTAAC CCCAGGGTTG GTCAATTTCG 4150
TGCCAGCCAC ACCCTGGAGC TAGC

QUERY : AAAACGCGCTAACACC

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	**5000**
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F

SEQUENZE SELEZIONATE: 317

Description	Name	Taxid	Score	Score	cover	Value	Ident	Len	Accession
Apiotrichum mycotoxinovorans strain CICC 1454 chromosome 2	NA	252803	32.2	32.2	100%	185	100.00	10254415	CP053621.1
Apiotrichum mycotoxinovorans strain GMU1709 chromosome IV	NA	252803	32.2	32.2	100%	185	100.00	10238178	CP049824.1
Plectropomus leopardus DNA, chromosome 10, nearly complete...	leopard cora...	160734	32.2	32.2	100%	185	100.00	34657930	AP022709.1
Aphantopus hyperantus genome assembly, chromosome: 24	ringlet	2795564	32.2	32.2	100%	185	100.00	9442922	LR761671.1
Myripristis murdjan genome assembly, chromosome: 15	pinecone sol...	586833	32.2	32.2	100%	185	100.00	33424759	LR597564.1
Hymenolepis microstoma genome assembly, chromosome: 4	NA	85433	32.2	32.2	100%	185	100.00	25589455	LR215995.1
PREDICTED: Ceratina calcarata neuronal PAS domain-containing...	NA	156304	32.2	32.2	100%	185	100.00	2949	XM_018025586.2

Catenovulum sp. CCB-QB4 chromosome, complete genome	NA	2172099	32.2	32.2	100%	185	100.00	5663044	CP026604.1
Pseudomonas sp. S-6-2, complete genome	NA	1931241	32.2	32.2	100%	185	100.00	4035153	CP020100.1
PREDICTED: Struthio camelus australis oxidative stress...	NA	441894	32.2	32.2	100%	185	100.00	2969	XM_009682123.1
Marinomonas sp. CT5 chromosome	NA	2066133	32.2	62.4	100%	185	100.00	4761082	CP025572.1
Suillus discolor uncharacterized protein (F5147DRAFT_697198),...	NA	1912936	32.2	32.2	100%	185	100.00	733	XM_041437501.1
Suillus plorans uncharacterized protein (HD556DRAFT_1417304),...	NA	116603	32.2	32.2	100%	185	100.00	746	XM_041304366.1
Hesperia comma genome assembly, chromosome: 13	commonbrand...	291688	32.2	32.2	100%	185	100.00	18062564	FR990026.1
Mimas tiliae genome assembly, chromosome: 13	NA	522848	32.2	32.2	100%	185	100.00	17674729	HG995251.1
Maniola jurtina genome assembly, chromosome: 24	meadowbrown	191418	32.2	32.2	100%	185	100.00	9430113	HG995231.1
Pyrochroa serraticornis genome assembly, chromosome: 5	NA	346838	32.2	32.2	100%	185	100.00	23092697	HG995156.1
PREDICTED: Passer montanus serine/threonine kinase 39 (STK39),...	Eurasian tre...	9160	32.2	32.2	100%	185	100.00	2854	XM_039701616.1
PREDICTED: Passer montanus serine/threonine kinase 39 (STK39),...	Eurasian tre...	9160	32.2	32.2	100%	185	100.00	2916	XM_039701609.1
PREDICTED: Passer montanus serine/threonine kinase 39 (STK39),...	Eurasian tre...	9160	32.2	32.2	100%	185	100.00	3641	XM_039701601.1
PREDICTED: Passer montanus serine/threonine kinase 39 (STK39),...	Eurasian tre...	9160	32.2	32.2	100%	185	100.00	3024	XM_039701594.1
Notocelia uddmanniana genome assembly, chromosome: 15	NA	1594315	32.2	32.2	100%	185	100.00	25884540	LR991067.1
Hypena proboscidalis genome assembly, chromosome: 3	NA	753189	32.2	32.2	100%	185	100.00	24208453	LR990129.1
Alteromonas sp. KC14	NA	2795689	32.2	32.2	100%	185	100.00	4544939	AP024236.1
Alteromonas sp. KC3	NA	2795688	32.2	32.2	100%	185	100.00	4561647	AP024235.1
Pseudoalteromonas rubra strain S4059 chromosome 1, complete...	NA	43658	32.2	32.2	100%	185	100.00	4595233	CP045429.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome: 7	yellowfin se…	8177	32.2	32.2	100%	185	100.00	31194941	LR884466.1
Danio rerio genome assembly, chromosome: 19	zebrafish	7955	30.2	30.2	93%	730	100.00	49536214	LR812081.1
Scandinavium goeteborgense strain CCUG 66741 chromosome,...	NA	1851514	30.2	30.2	93%	730	100.00	4571204	CP054058.1
Erwiniaceae bacterium PD-1 chromosome, complete genome	NA	2740817	30.2	30.2	93%	730	100.00	4617009	CP054212.1
Felis catus Senzu DNA, chromosome: E3, American Shorthair breed	domestic cat	9685	30.2	30.2	93%	730	100.00	41750578	AP023167.1
Providencia rettgeri strain YPR31 chromosome, complete genome	NA	587	30.2	30.2	93%	730	100.00	4605722	CP053896.1
Pseudomonas sp. gcc21 chromosome, complete	NA	2726989	30.2	30.2	93%	730	100.00	3983233	CP051625.1

genome									
Digitaria exilis annotation	NA	1010633	30.2	30.2	93%	730	100.00	41484145	LR792825.1
Digitaria exilis annotation	NA	1010633	30.2	30.2	93%	730	100.00	42379666	LR792824.1
Dolichospermum flos-aquae CCAP 1403/13F chromosome, complete...	NA	315271	30.2	30.2	93%	730	100.00	5151752	CP051206.1
Digitaria exilis genome assembly, chromosome: 3B	NA	1010633	30.2	30.2	93%	730	100.00	41484145	LR761610.1
Digitaria exilis genome assembly, chromosome: 3A	NA	1010633	30.2	30.2	93%	730	100.00	42379666	LR761609.1
Pseudochaenichthys georgianus genome assembly, chromosome: 5	South Georgi...	52239	30.2	30.2	93%	730	100.00	46241663	LR792550.1
Salmonella enterica subsp. enterica serovar Typhimurium isolat...	NA	90371	30.2	30.2	93%	730	100.00	757502	LR792391.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4813284	CP048775.1
Coregonus sp. 'balchen' genome assembly, chromosome: 30	NA	861768	30.2	30.2	93%	730	100.00	48675208	LR778282.1
Providencia sp. 1709051003 chromosome, complete genome	NA	2603246	30.2	30.2	93%	730	100.00	4649235	CP042861.1
Crassostrea gigas strain QD chromosome 4	Pacificoyster	29159	30.2	30.2	93%	730	100.00	62642562	CP048842.1
Aphantopus hyperantus genome assembly, chromosome: 23	ringlet	2795564	30.2	30.2	93%	730	100.00	10071354	LR761670.1
Shewanella sp. Arc9-LZ chromosome, complete genome	NA	2698686	30.2	30.2	93%	730	100.00	4911031	CP048031.1
Providencia rettgeri BML2576 DNA, complete genome	NA	587	30.2	30.2	93%	730	100.00	4351300	AP022375.1
Providencia rettgeri BML2531 DNA, complete genome	NA	587	30.2	30.2	93%	730	100.00	4696377	AP022373.1
Providencia rettgeri BML2526 DNA, complete genome	NA	587	30.2	30.2	93%	730	100.00	4342905	AP022372.1
Providencia rettgeri BML2496 DNA, complete genome	NA	587	30.2	30.2	93%	730	100.00	4651003	AP022371.1
Trichoderma reesei strain CBS999.97 chromosome I, complete...	NA	51453	30.2	30.2	93%	730	100.00	6822680	CP020875.1
Pseudomonas sp. R76, complete genome	NA	1573711	30.2	30.2	93%	730	100.00	6821900	CP019428.1
Pecten maximus genome assembly, chromosome: 7	NA	6579	30.2	60.5	100%	730	100.00	46316487	LR736844.1
Salmonella enterica subsp. enterica serovar Kentucky strain...	NA	192955	30.2	30.2	93%	730	100.00	4889798	CP043664.1
Salmonella enterica subsp. enterica serovar Kentucky strain...	NA	192955	30.2	30.2	93%	730	100.00	4851336	CP043667.1
Salmonella enterica strain CFSAN096147 chromosome, complete...	NA	28901	30.2	30.2	93%	730	100.00	4757321	CP044257.1
Salmonella enterica subsp. enterica serovar Cubana strain...	NA	189201	30.2	30.2	93%	730	100.00	4963375	CP044186.1
Salmonella enterica subsp. enterica serovar Agona str. 392869-...	NA	1072590	30.2	30.2	93%	730	100.00	4798531	CP015024.2
Salmonella enterica subsp. enterica serovar Agona str. 460004...	NA	1124917	30.2	30.2	93%	730	100.00	4797172	CP011259.2
Chanos chanos genome	milkfish	29144	30.2	30.2	93%	730	100.00	43790413	LR697114.1

assembly, chromosome: 9									
Chanos chanos genome assembly, chromosome: 2	milkfish	29144	30.2	30.2	93%	730	100.00	59736555	LR697107.1
Haemonchus contortus strain NZ_Hco_NP chromosome 1	barberpole…	6289	30.2	30.2	93%	730	100.00	83295456	CP035805.1
Spirosoma sp. KCTC 42546 chromosome, complete genome	NA	2520506	30.2	30.2	93%	730	100.00	8664091	CP041360.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 3	NA	223781	30.2	30.2	93%	730	100.00	79382107	LR606183.1
Salmonella enterica subsp. enterica serovar Goldcoast strain...	NA	260678	30.2	30.2	93%	730	100.00	4645545	CP039169.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4762732	CP025454.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4841410	CP025453.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4763930	CP025452.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4763929	CP025451.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4763902	CP025450.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4763925	CP025449.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4762736	CP025448.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4762730	CP025447.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4794633	CP025446.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4763928	CP025445.1
Companilactobacillus futsaii strain Y97 chromosome, complete...	NA	938155	30.2	30.2	93%	730	100.00	2558218	CP040736.1
Salmonella enterica subsp. enterica strain CFSA231 chromosome,...	NA	59201	30.2	30.2	93%	730	100.00	4834516	CP033350.2
Salmonella enterica subsp. enterica serovar California strain...	NA	29474	30.2	30.2	93%	730	100.00	4833791	CP028900.1
Providencia rettgeri strain Pr-15-2-50 chromosome, complete...	NA	587	30.2	30.2	93%	730	100.00	4649193	CP039844.1
Takifugu rubripes genome assembly, chromosome: 19	torafugu	31033	30.2	30.2	93%	730	100.00	19418397	LR584235.1
Escherichia coli strain 190 chromosome, complete genome	NA	562	30.2	30.2	93%	730	100.00	4905831	CP020520.1
Salmonella enterica subsp. enterica serovar Goldcoast strain...	NA	260678	30.2	30.2	93%	730	100.00	4645553	CP037960.1
Salmonella enterica subsp. enterica serovar Kentucky strain...	NA	192955	30.2	30.2	93%	730	100.00	4847949	CP037917.1
Denticeps clupeoides genome assembly, chromosome: 19	denticle her…	299321	30.2	30.2	93%	730	100.00	19707071	LR535831.1
Salmonella enterica subsp. enterica serovar Montevideo str....	NA	1454601	30.2	30.2	93%	730	100.00	4985589	CP025278.1
Escherichia coli strain WCHEC025970 chromosome, complete genome	NA	562	30.2	30.2	93%	730	100.00	4794992	CP036177.1

Salmonella enterica subsp. enterica serovar Derby strain Sa64...	NA	28144	30.2	30.2	93%	730	100.00	4824198	CP034250.1
Salmonella enterica subsp. enterica serovar Senftenberg strain...	NA	28150	30.2	30.2	93%	730	100.00	4818442	CP034233.1
Shewanella livingstonensis strain LMG 19866 chromosome, comple...	NA	150120	30.2	30.2	93%	730	100.00	4839879	CP034015.1
PREDICTED: Ooceraea biroi L-lactate dehydrogenase C chain-like...	clonalraide…	2015173	30.2	30.2	93%	730	100.00	1338	XM_020032801.2
Salmonella enterica subsp. enterica serovar Mbandaka strain...	NA	192954	30.2	30.2	93%	730	100.00	4709669	CP033343.1
PREDICTED: Trichoplusia ni protein unc-45 homolog B...	cabbagelopper	7111	30.2	30.2	93%	730	100.00	3186	XM_026875489.1
PREDICTED: Ceratina calcarata protein quiver (LOC108625614),...	NA	156304	30.2	30.2	93%	730	100.00	5798	XR_003389280.1
Salmonella enterica subsp. enterica strain 10TTU468x chromosom...	NA	59201	30.2	30.2	93%	730	100.00	4985863	CP032814.1
Salmonella enterica subsp. enterica strain 11TTU1590 chromosom...	NA	59201	30.2	30.2	93%	730	100.00	4985874	CP032817.1
Salmonella enterica subsp. enterica strain 11TTU1615b...	NA	59201	30.2	30.2	93%	730	100.00	4985867	CP032815.1
Pseudomonas fluorescens strain SIK_W1 chromosome, complete genome	NA	294	30.2	30.2	93%	730	100.00	6791087	CP031450.1
Haemonchus contortus, ISE/inbred ISE, WGS project CAVP01000000...	barberpole…	6289	30.2	30.2	93%	730	100.00	45774638	LS997562.1
PREDICTED: Carassius auratus chromodomain-helicase-DNA-binding...	goldfish	7957	30.2	30.2	93%	730	100.00	13254	XM_026265961.1
PREDICTED: Carassius auratus chromodomain-helicase-DNA-binding...	goldfish	7957	30.2	30.2	93%	730	100.00	12862	XM_026265960.1
PREDICTED: Carassius auratus chromodomain-helicase-DNA-binding...	goldfish	7957	30.2	30.2	93%	730	100.00	13620	XM_026265958.1
Enterobacteria phage mEp021, complete genome	NA	1150757	30.2	30.2	93%	730	100.00	54655	MH706966.1
Companilactobacillus zhachilii strain HBUAS52074 chromosome,...	NA	2304606	30.2	30.2	93%	730	100.00	2714973	CP031933.2
Escherichia marmotae strain NCTC11133 genome assembly,...	NA	1499973	30.2	30.2	93%	730	100.00	4450344	LR134340.1
Escherichia marmotae strain NCTC8196 genome assembly,...	NA	1499973	30.2	30.2	93%	730	100.00	4857140	LR134270.1
Salmonella enterica strain SA20043041 chromosome, complete genome	NA	28901	30.2	30.2	93%	730	100.00	4603878	CP030231.1
Salmonella enterica strain SA20044414 chromosome, complete genome	NA	28901	30.2	30.2	93%	730	100.00	4805225	CP030209.1
Rhizophagus irregularis DAOM 181602=DAOM 197198 hypothetical...	NA	747089	30.2	30.2	93%	730	100.00	1350	XM_025329637.1

Bat coronavirus isolate CMR891-892 ORF1a gene, partial cds; an...	NA	1508220	30.2	30.2	93%	730	100.00	28810	**MG693171.1**
Bat coronavirus isolate CMR900 ORF1a, ORF1b, Spike protein,...	NA	1508220	30.2	30.2	93%	730	100.00	28989	**MG693169.1**
Salmonella enterica subsp. enterica serovar Senftenberg strain...	NA	28150	30.2	30.2	93%	730	100.00	5029670	LS483465.1
Salmonella enterica subsp. enterica serovar Derby strain...	NA	28144	30.2	30.2	93%	730	100.00	4884649	CP029486.1
Pseudomonas yamanorum strain LBUM636 chromosome, complete genome	NA	515393	30.2	30.2	93%	730	100.00	6856835	CP012400.2
Salmonella enterica strain 201001922 chromosome	NA	28901	30.2	30.2	93%	730	100.00	4858671	CP028357.1
Salmonella enterica subsp. enterica serovar Kentucky strain...	NA	192955	30.2	30.2	93%	730	100.00	4900326	CP026327.1
Escherichia marmotae strain HT073016 chromosome, complete genome	NA	1499973	30.2	30.2	93%	730	100.00	4671322	CP025979.1
Lactobacillus farciminis KCTC 3681 = DSM 20184, complete genome	NA	936140	30.2	30.2	93%	730	100.00	2551839	CP017702.1
Pseudoalteromonas issachenkonii strain KMM 3549 chromosome I,...	NA	152297	30.2	30.2	93%	730	100.00	3403660	CP011030.1
Pseudoalteromonas tetraodonis strain GFC chromosome I, complet...	NA	43659	30.2	30.2	93%	730	100.00	3399143	CP011041.1
Escherichia coli strain 127 chromosome, complete genome	NA	562	30.2	30.2	93%	730	100.00	4697886	CP023377.1
Lelliottia jeotgali strain PFL01 chromosome, complete genome	NA	1907578	30.2	30.2	93%	730	100.00	4603334	CP018628.1
Salmonella enterica subsp. enterica serovar Derby strain...	NA	28144	30.2	30.2	93%	730	100.00	4850334	CP022494.1
Oryzias latipes strain HNI chromosome 4	Japanese medaka	8090	30.2	30.2	93%	730	100.00	31648822	CP020782.1
Salmonella enterica subsp. enterica serovar Mbandaka strain...	NA	192954	30.2	30.2	93%	730	100.00	4796292	CP022489.1
Trichoderma reesei QM6a chromosome I, complete sequence	NA	431241	30.2	30.2	93%	730	100.00	6835803	CP016232.1
Salmonella enterica subsp. enterica serovar Borreze str....	NA	1242089	30.2	30.2	93%	730	100.00	4777558	CP019407.1
Pseudomonas yamanorum strain LMG 27247 genome assembly,...	NA	515393	30.2	30.2	93%	730	100.00	7087525	LT629793.1
PREDICTED: Ceratina calcarata protein quiver (LOC108625614),...	NA	156304	30.2	30.2	93%	730	100.00	5483	XM_018025723.1
Erwinia phage vB_EamM_Caitlin, complete genome	NA	1883379	30.2	30.2	93%	730	100.00	241147	KX397365.1
PREDICTED: Rhagoletis zephyria uncharacterized LOC108369117...	snowberry fr…	28612	30.2	30.2	93%	730	100.00	6474	XM_017624116.1
Staphylococcus equorum strain	NA	246432	30.2	30.2	93%	730	100.00	2753539	CP013714.1

C2014, complete genome									
Salmonella enterica subsp. enterica serovar Java strain NCTC57...	NA	224729	30.2	30.2	93%	730	100.00	4756780	LT571437.1
Collimonas fungivorans strain Ter6 chromosome, complete genome	NA	158899	30.2	30.2	93%	730	100.00	5599729	CP013232.1
PREDICTED: Dufourea novaeangliae kynurenine/alpha-aminoadipate...	NA	178035	30.2	30.2	93%	730	100.00	1343	XM_015584616.1
Pseudoalteromonas issachenkonii strain KCTC 12958 chromosome I...	NA	152297	30.2	30.2	93%	730	100.00	3402324	CP013350.1
Cronobacter condimenti 1330 strain LMG 26250, complete genome	NA	1073999	30.2	30.2	93%	730	100.00	4347991	CP012264.1
Lactobacillus heilongjiangensis strain DSM 28069, complete genome	NA	1074467	30.2	30.2	93%	730	100.00	2790548	CP012559.1
Lactobacillus farciminis strain CNCM-I-3699-R genome	NA	1612	30.2	30.2	93%	730	100.00	2424118	CP012177.1
Lactobacillus farciminis strain CNCM-I-3699-S genome	NA	1612	30.2	30.2	93%	730	100.00	2423489	CP011952.1
Salmonella enterica subsp. enterica serovar Typhimurium strain...	NA	90371	30.2	30.2	93%	730	100.00	4759372	CP011365.1
Enterobacteriaceae bacterium bta3-1, complete genome	NA	1265478	30.2	30.2	93%	730	100.00	4763672	CP004083.1
PREDICTED: Haliaeetus leucocephalus oxidative stress responsiv...	bald eagle	52644	30.2	30.2	93%	730	100.00	4525	XM_010563176.1
PREDICTED: Haliaeetus albicilla oxidative stress responsive 1...	white-tailed…	8969	30.2	30.2	93%	730	100.00	2367	XM_009923218.1
PREDICTED: Apaloderma vittatum oxidative stress responsive 1...	bar-tailed t…	57397	30.2	30.2	93%	730	100.00	2212	XM_009869115.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	93%	730	100.00	648	LN411653.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	93%	730	100.00	3147	LN119028.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	93%	730	100.00	3747	LN097687.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	93%	730	100.00	7585	LN032367.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	93%	730	100.00	8943	LN022833.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	93%	730	100.00	12637	LN009501.1
Dicrocoelium dendriticum genome assembly...	NA	57078	30.2	30.2	93%	730	100.00	959	LK606254.1
Pseudocercospora fijiensis CIRAD86 uncharacterized protein...	NA	383855	30.2	30.2	93%	730	100.00	1458	XM_007929162.1

Baudoinia panamericana UAMH 10762 uncharacterized protein...	NA	717646	30.2	30.2	93%	730	100.00	1635	XM_007680082.1
Enterobacter asburiae L1, complete genome	NA	1421338	30.2	30.2	93%	730	100.00	4561905	CP007546.1
Salmonella enterica subsp. enterica serovar Agona str. 24249,...	NA	1406860	30.2	30.2	93%	730	100.00	4762840	CP006876.1
Vibrio nigripulchritudo str. SFn1 chromosome, complete genome	NA	28173	30.2	30.2	93%	730	100.00	2212415	FO203527.1
Salmonella enterica subsp. enterica Serovar Cubana str....	NA	1271863	30.2	30.2	93%	730	100.00	4977480	CP006055.1
Salmonella enterica subsp. enterica serovar Mbandaka strain...	NA	192954	30.2	30.2	93%	730	100.00	4765651	CP075100.1
Salmonella enterica strain FDA00008277 chromosome, complete...	NA	28901	30.2	30.2	93%	730	100.00	4612973	CP074650.1
Pseudoalteromonas sp. SiA1 chromosome SiA1-1, complete sequence	NA	2839744	30.2	30.2	93%	730	100.00	3355071	CP076084.1
Thaumasiovibrio subtropicus C4V358 DNA, chromosome 1 complete...	NA	1891207	30.2	60.5	93%	730	100.00	3621685	AP023054.1
Salmonella enterica subsp. enterica serovar Paratyphi B str....	NA	1299077	30.2	30.2	93%	730	100.00	4744898	CP074609.1
Salmonella enterica subsp. enterica serovar Paratyphi B str....	NA	1299078	30.2	30.2	93%	730	100.00	4804097	CP074619.1
Blastobasis adustella genome assembly, chromosome: 4	NA	1869501	30.2	30.2	93%	730	100.00	21401191	OU026117.1
Crocallis elinguaria genome assembly, chromosome: 10	NA	934829	30.2	30.2	93%	730	100.00	20584812	OU026074.1
Danio rerio strain T5D chromosome 19	zebrafish	7955	30.2	30.2	93%	730	100.00	48724230	CP068753.1
Enterobacter asburiae strain L1 delta-T1RM chromosome, complet...	NA	61645	30.2	30.2	93%	730	100.00	4557120	CP074584.1
Hemaris fuciformis genome assembly, chromosome: 21	NA	987953	30.2	30.2	93%	730	100.00	13022490	OU015452.1
Salmonella enterica subsp. enterica serovar Derby str. 626...	NA	1124929	30.2	30.2	93%	730	100.00	4779489	CP074319.1
Salmonella enterica subsp. enterica serovar Agona strain...	NA	58095	30.2	30.2	93%	730	100.00	4834847	CP074278.1
Salmonella enterica subsp. enterica serovar Paratyphi B str....	NA	1299082	30.2	30.2	93%	730	100.00	4700031	CP074222.1
Salmonella enterica subsp. enterica serovar Derby str....	NA	1299223	30.2	30.2	93%	730	100.00	4833413	CP074219.1
Salmonella enterica subsp. enterica serovar Cubana str....	NA	1194157	30.2	30.2	93%	730	100.00	5019202	CP074202.1
Salmonella enterica subsp. enterica serovar Typhimurium strain...	NA	90371	30.2	30.2	93%	730	100.00	4858114	CP074096.1
Salmonella enterica subsp. enterica serovar Typhimurium strain...	NA	90371	30.2	30.2	93%	730	100.00	4858033	CP074098.1
Salmonella enterica subsp. enterica serovar Typhimurium strain...	NA	90371	30.2	30.2	93%	730	100.00	4857880	CP074094.1
PREDICTED: Aquila chrysaetos chrysaetos oxidative stress...	NA	223781	30.2	30.2	93%	730	100.00	4375	XM_030008433.2

PREDICTED: Aquila chrysaetos chrysaetos oxidative stress...	NA	223781	30.2	30.2	93%	730	100.00	4440	XM_030008432.2
Salmonella enterica subsp. enterica strain P22 chromosome,...	NA	59201	30.2	30.2	93%	730	100.00	4936609	CP073326.1
Pseudomonas fluorescens strain JNU01 chromosome, complete genome	NA	294	30.2	30.2	93%	730	100.00	6790443	CP072873.1
Thiothrix unzii strain A1 chromosome, complete genome	NA	111769	30.2	30.2	93%	730	100.00	3584962	CP072793.1
Clostera curtula genome assembly, chromosome: 14	NA	987902	30.2	30.2	93%	730	100.00	17868471	FR997808.1
Autographa pulchrina genome assembly, chromosome: 1	NA	987893	30.2	30.2	93%	730	100.00	15711359	FR997763.1
Chrysoperla carnea genome assembly, chromosome: 5	NA	189513	30.2	30.2	93%	730	100.00	76427138	FR997758.1
Ochropleura plecta genome assembly, chromosome: 11	NA	320037	30.2	30.2	93%	730	100.00	22004161	FR997733.1
Pieris napi genome assembly, chromosome: 13	NA	78633	30.2	30.2	93%	730	100.00	12729147	FR997707.1
Leptidea sinapis genome assembly, chromosome: 47	NA	189913	30.2	30.2	93%	730	100.00	8352274	FR990200.1
Leptidea sinapis genome assembly, chromosome: 46	NA	189913	30.2	60.5	93%	730	100.00	8389505	FR990199.1
Leptidea sinapis genome assembly, chromosome: 44	NA	189913	30.2	30.2	93%	730	100.00	9056786	FR990197.1
Leptidea sinapis genome assembly, chromosome: 43	NA	189913	30.2	30.2	93%	730	100.00	9178371	FR990196.1
Leptidea sinapis genome assembly, chromosome: 42	NA	189913	30.2	60.5	93%	730	100.00	9389464	FR990195.1
Leptidea sinapis genome assembly, chromosome: 36	NA	189913	30.2	60.5	93%	730	100.00	10558824	FR990189.1
Leptidea sinapis genome assembly, chromosome: 27	NA	189913	30.2	60.5	93%	730	100.00	13208167	FR990180.1
Leptidea sinapis genome assembly, chromosome: 22	NA	189913	30.2	30.2	93%	730	100.00	13724482	FR990175.1
Leptidea sinapis genome assembly, chromosome: 13	NA	189913	30.2	30.2	93%	730	100.00	15137125	FR990166.1
Leptidea sinapis genome assembly, chromosome: 9	NA	189913	30.2	30.2	93%	730	100.00	15829655	FR990162.1
Leptidea sinapis genome assembly, chromosome: 6	NA	189913	30.2	60.5	93%	730	100.00	16616829	FR990159.1
Leptidea sinapis genome assembly, chromosome: 5	NA	189913	30.2	30.2	93%	730	100.00	16733303	FR990158.1
Leptidea sinapis genome assembly, chromosome: 4	NA	189913	30.2	30.2	93%	730	100.00	17197042	FR990157.1
Leptidea sinapis genome assembly, chromosome: 2	NA	189913	30.2	30.2	93%	730	100.00	28774503	FR990155.1
Leptidea sinapis genome assembly, chromosome: 1	NA	189913	30.2	30.2	93%	730	100.00	34332082	FR990154.1
Hedya salicella genome assembly, chromosome: 11	NA	1869985	30.2	30.2	93%	730	100.00	25487330	FR990107.1
Erannis defoliaria genome assembly, chromosome: 22	NA	104474	30.2	30.2	93%	730	100.00	16658382	FR990088.1
Erannis defoliaria genome assembly, chromosome: 1	NA	104474	30.2	30.2	93%	730	100.00	26948889	FR990066.1
Hesperia comma genome assembly, chromosome: 8	commonbrand...	291688	30.2	30.2	93%	730	100.00	19699062	FR990021.1
Fabriciana adippe genome assembly, chromosome: 26	high brown f…	405009	30.2	30.2	93%	730	100.00	11411053	FR990008.1
Anthocharis cardamines genome assembly,	orangetip	227532	30.2	30.2	93%	730	100.00	12760991	FR989959.1

chromosome: 9									
Pheosia gnoma genome assembly, chromosome: 15	NA	988018	30.2	30.2	93%	730	100.00	9390674	FR989909.1
Biston betularia genome assembly, chromosome: 2	pepper-and-s…	82595	30.2	30.2	93%	730	100.00	17079257	FR989864.1
Escherichia coli O89m:H10 strain MIN12 chromosome, complete...	NA	2810405	30.2	30.2	93%	730	100.00	4896568	CP069657.1
Mucilaginibacter gossypii strain P3 chromosome, complete genome	NA	551996	30.2	30.2	93%	730	100.00	7187733	CP071878.1
Abrostola tripartita genome assembly, chromosome: 8	NA	938171	30.2	30.2	93%	730	100.00	14446605	HG996494.1
Dolichospermum sp. DL01 chromosome, complete genome	NA	2717871	30.2	30.2	93%	730	100.00	4827232	CP050884.1
Lycaena phlaeas genome assembly, chromosome: 15	commoncopper	282391	30.2	60.5	93%	730	100.00	15869936	HG995178.1
Lycaena phlaeas genome assembly, chromosome: 4	commoncopper	282391	30.2	30.2	93%	730	100.00	21478936	HG995166.1
PREDICTED: Ornithorhynchus anatinus calcium voltage-gated...	platypus	9258	30.2	30.2	93%	730	100.00	7752	XM_029077601.2
PREDICTED: Ornithorhynchus anatinus calcium voltage-gated...	platypus	9258	30.2	30.2	93%	730	100.00	7792	XM_029077600.2
PREDICTED: Ornithorhynchus anatinus calcium voltage-gated...	platypus	9258	30.2	30.2	93%	730	100.00	7805	XM_007670954.4
PREDICTED: Ornithorhynchus anatinus calcium voltage-gated...	platypus	9258	30.2	30.2	93%	730	100.00	7812	XM_029077599.2
PREDICTED: Ornithorhynchus anatinus calcium voltage-gated...	platypus	9258	30.2	30.2	93%	730	100.00	7826	XM_007670953.4
Vanessa cardui genome assembly, chromosome: 4	NA	171605	30.2	30.2	93%	730	100.00	16000791	LR999928.1
Noctua pronuba genome assembly, chromosome: 6	large yellow…	214277	30.2	30.2	93%	730	100.00	18652114	LR999898.1
Boloria selene genome assembly, chromosome: 20	silvermeado…	191398	30.2	30.2	93%	730	100.00	11693184	HG993152.1
Boloria selene genome assembly, chromosome: 17	silvermeado…	191398	30.2	30.2	93%	730	100.00	12528241	HG993149.1
Nymphalis polychloros genome assembly, chromosome: 5	blackleg tor	171594	30.2	30.2	93%	730	100.00	15828811	HG992246.1
Lysandra coridon genome assembly, chromosome: 74	NA	268709	30.2	30.2	93%	730	100.00	4691659	HG992129.1
Trichoderma reesei strain QM6a x CBS999.97 isolate...	NA	51453	30.2	30.2	93%	730	100.00	6849918	CP021311.1
Trichoderma reesei strain QM6a x CBS999.97 isolate...	NA	51453	30.2	30.2	93%	730	100.00	6830440	CP021304.1
Trichoderma reesei strain QM6a x CBS999.97 isolate...	NA	51453	30.2	30.2	93%	730	100.00	6834820	CP021297.1
Trichoderma reesei strain QM6a x CBS999.97 isolate...	NA	51453	30.2	30.2	93%	730	100.00	6801106	CP021290.1
Trichoderma reesei strain CBS999.97 chromosome I, complete...	NA	51453	30.2	30.2	93%	730	100.00	6822241	CP020724.1
Sulfitobacter mediterraneus strain SC7-37 chromosome, complete...	NA	83219	30.2	30.2	93%	730	100.00	3648427	CP068998.1
Digitaria exilis genome assembly, chromosome: 3B	NA	1010633	30.2	30.2	93%	730	100.00	41484145	LR994609.1

Digitaria exilis genome assembly, chromosome: 3A	NA	1010633	30.2	30.2	93%	730	100.00	42379666	LR994608.1
Candidatus Xiphinematobacter sp. isolate P15 chromosome,...	NA	1903058	30.2	30.2	93%	730	100.00	917845	CP068477.1
Candidatus Xiphinematobacter sp. isolate P18 chromosome,...	NA	1903058	30.2	30.2	93%	730	100.00	915441	CP068476.1
Candidatus Xiphinematobacter sp. isolate P21 chromosome,...	NA	1903058	30.2	30.2	93%	730	100.00	926970	CP068475.1
Candidatus Xiphinematobacter sp. isolate P22 chromosome,...	NA	1903058	30.2	30.2	93%	730	100.00	909775	CP068474.1
Candidatus Xiphinematobacter sp. isolate P23 chromosome,...	NA	1903058	30.2	30.2	93%	730	100.00	917278	CP068473.1
Trachurus trachurus genome assembly, chromosome: 15	Atlantic hor…	36212	30.2	30.2	93%	730	100.00	31049438	LR991643.1
Trachurus trachurus genome assembly, chromosome: 21	Atlantic hor…	36212	30.2	30.2	93%	730	100.00	35833567	LR991636.1
Lymantria monacha genome assembly, chromosome: 15	black-arched…	78897	30.2	30.2	93%	730	100.00	32374437	LR991096.1
Notocelia uddmanniana genome assembly, chromosome: 16	NA	1594315	30.2	30.2	93%	730	100.00	25713929	LR991068.1
Noctua fimbriata genome assembly, chromosome: 11	NA	753202	30.2	30.2	93%	730	100.00	19516206	LR990931.1
Apotomis turbidana genome assembly, chromosome: 9	NA	1100916	30.2	30.2	93%	730	100.00	27591186	LR990288.1
Notodonta dromedarius genome assembly, chromosome: 7	NA	753204	30.2	30.2	93%	730	100.00	12718468	LR990166.1
Euproctis similis genome assembly, chromosome: 8	NA	987935	30.2	30.2	93%	730	100.00	25819771	LR990111.1
Euproctis similis genome assembly, chromosome: 6	NA	987935	30.2	30.2	93%	730	100.00	26031934	LR990109.1
Crinalium epipsammum PCC 9333, complete genome	NA	1173022	30.2	30.2	93%	730	100.00	5315554	CP003620.1
Alteromonas macleodii str. 'Black Sea 11', complete genome	NA	1004785	30.2	30.2	93%	730	100.00	4480507	CP003845.1
Desulfosporosinus meridiei DSM 13257, complete genome	NA	768704	30.2	30.2	93%	730	100.00	4873567	CP003629.1
Erynnis tages genome assembly, chromosome: 16	NA	520884	30.2	30.2	93%	730	100.00	10932516	LR990087.1
Scaeva pyrastri genome assembly, chromosome: 2	NA	219539	30.2	30.2	93%	730	100.00	86161057	LR989928.1
Pararge aegeria genome assembly, chromosome: 7	speckedwood…	116150	30.2	30.2	93%	730	100.00	20310676	LR990899.1
Endotricha flammealis genome assembly, chromosome: 26	NA	1101095	30.2	30.2	93%	730	100.00	10105287	LR990879.1
Endotricha flammealis genome assembly, chromosome: 19	NA	1101095	30.2	30.2	93%	730	100.00	14456893	LR990871.1
Endotricha flammealis genome assembly, chromosome: 16	NA	1101095	30.2	30.2	93%	730	100.00	15316319	LR990868.1
Xestia xanthographa genome assembly, chromosome: 17	NA	988049	30.2	30.2	93%	730	100.00	30801917	LR990658.1
Phalera bucephala genome assembly, chromosome: 25	NA	753216	30.2	30.2	93%	730	100.00	18324721	LR990634.1
Chlorobi bacterium isolate Ribe_18-Q3-R11-54_MAXAC.096_cln...	NA	2268192	30.2	30.2	93%	730	100.00	3152895	CP065014.1
PREDICTED: Tachyglossus aculeatus calcium voltage-gated channe...	Australian e…	9261	30.2	30.2	93%	730	100.00	7452	XM_038740942.1
PREDICTED: Tachyglossus aculeatus calcium voltage-gated channe...	Australian e…	9261	30.2	30.2	93%	730	100.00	7467	XM_038740941.1

PREDICTED: Tachyglossus aculeatus calcium voltage-gated channe...	Australian e…	9261	30.2	30.2	93%	730	100.00	7473	XM_038740940.1
PREDICTED: Tachyglossus aculeatus calcium voltage-gated channe...	Australian e…	9261	30.2	30.2	93%	730	100.00	7488	XM_038740939.1
Salmonella enterica subsp. enterica serovar Derby strain 14-Sa...	NA	28144	30.2	30.2	93%	730	100.00	4901442	CP066545.1
Salmonella enterica subsp. enterica serovar Agona strain CVM...	NA	58095	30.2	30.2	93%	730	100.00	4891101	CP051402.1
Salmonella enterica subsp. enterica serovar Agona strain CVM...	NA	58095	30.2	30.2	93%	730	100.00	4933457	CP051356.1
Salmonella enterica subsp. enterica serovar Derby strain CVM...	NA	28144	30.2	30.2	93%	730	100.00	4865042	CP053048.1
3_Tms_b3v08	NA	170555	30.2	30.2	93%	730	100.00	641249	OB792843.1
Salmonella enterica strain GX1006 chromosome, complete genome	NA	28901	30.2	30.2	93%	730	100.00	4688541	CP060585.1
Proteus penneri strain FDAARGOS_874 chromosome, complete genome	NA	102862	30.2	30.2	93%	730	100.00	3850796	CP065722.1
Campylobacter concisus strain P1CDO3 chromosome, complete genome	NA	199	30.2	30.2	93%	730	100.00	2051359	CP049266.1
Campylobacter concisus strain P11CDO-S1 chromosome, complete...	NA	199	30.2	30.2	93%	730	100.00	2025227	CP049264.1
1_Tdi_b3v08	NA	61478	30.2	30.2	93%	730	100.00	150540	OA565818.1
Campylobacter concisus strain H9O-S2 chromosome, complete genome	NA	199	30.2	30.2	93%	730	100.00	2025058	CP049232.1
Campylobacter concisus strain P15UCO-S2 chromosome, complete...	NA	199	30.2	30.2	93%	730	100.00	1943962	CP049234.1
Companilactobacillus futsaii strain CQ16Z11 chromosome, comple...	NA	938155	30.2	30.2	93%	730	100.00	2625189	CP064860.1
Companilactobacillus futsaii strain Chongqingii CQ16Z1...	NA	938155	30.2	30.2	93%	730	100.00	2625188	CP064761.1
Escherichia coli isolate MSB1_5C-sc-2280313 genome assembly,...	NA	562	30.2	30.2	93%	730	100.00	4567116	LR890576.1
Macrobrachium nipponense isolate FS-2020 chromosome 15	NA	159736	30.2	30.2	93%	730	100.00	93504222	CP062026.1
Macrobrachium nipponense isolate FS-2020 chromosome 21	NA	159736	30.2	30.2	93%	730	100.00	84091324	CP062019.1
Macrobrachium nipponense isolate FS-2020 chromosome 35	NA	159736	30.2	30.2	93%	730	100.00	67553775	CP062046.1
Pseudomonas poae strain PMA22 chromosome, complete genome	NA	200451	30.2	30.2	93%	730	100.00	6530734	CP063073.1
Vibrio bathopelagicus strain Sal10 chromosome II, complete...	NA	2777577	30.2	30.2	93%	730	100.00	2018969	CP062501.1
Salmonella enterica subsp. enterica serovar Goldcoast strain...	NA	260678	30.2	30.2	93%	730	100.00	4646755	CP062225.1

Salmonella enterica subsp. enterica serovar Goldcoast strain...	NA	260678	30.2	30.2	93%	730	100.00	4645545	CP062223.1
PREDICTED: Rhagoletis pomonella uncharacterized LOC118734500...	apple maggot	28610	30.2	30.2	93%	730	100.00	10485	XM_036464219.1
Poecilia reticulata genome assembly, chromosome: 3	guppy	8081	30.2	30.2	93%	730	100.00	34494140	LR880647.1
Marinomonas arctica strain BSI20414 chromosome, complete genome	NA	383750	30.2	30.2	93%	730	100.00	4540024	CP061081.1
Carposina sasakii isolate BJYQ chromosome 03	NA	252295	30.2	30.2	93%	730	100.00	17046891	CP053150.1
Providencia rettgeri strain FZB001 chromosome	NA	587	30.2	30.2	93%	730	100.00	4581419	CP060821.1
Providencia rettgeri strain YPR25 chromosome, complete genome	NA	587	30.2	30.2	93%	730	100.00	4605722	CP060726.1
Olivibacter sp. SDN3 chromosome, complete genome	NA	2764720	30.2	30.2	93%	730	100.00	6118654	CP060497.1
Proteus vulgaris strain P3M chromosome, complete genome	NA	585	30.2	30.2	93%	730	100.00	3935122	CP060211.1
Companilactobacillus pabuli strain NFFJ11 chromosome, complete...	NA	2714036	30.2	30.2	93%	730	100.00	2435232	CP049366.1
Escherichia marmotae strain RHBSTW-00605 chromosome, complete...	NA	1499973	30.2	30.2	93%	730	100.00	4866904	CP056697.1
Escherichia marmotae strain RHBSTW-00777 chromosome, complete...	NA	1499973	30.2	30.2	93%	730	100.00	4754030	CP056165.1
Escherichia marmotae strain RHBSTW-00814 chromosome, complete...	NA	1499973	30.2	30.2	93%	730	100.00	4946508	CP056159.1
Providencia rettgeri strain P01 chromosome, complete genome	NA	587	30.2	30.2	93%	730	100.00	4601020	CP059298.1
Escherichia marmotae strain RHB24-C12 chromosome, complete genome	NA	1499973	30.2	30.2	93%	730	100.00	4766686	CP058209.1
Escherichia marmotae strain RHB42-C09 chromosome, complete genome	NA	1499973	30.2	30.2	93%	730	100.00	4594602	CP058207.1
Providencia rettgeri strain G0519 chromosome, complete genome	NA	587	30.2	30.2	93%	730	100.00	4493347	CP058958.1
Neptunomonas phycophila strain Scap09 chromosome	NA	1572645	30.2	30.2	93%	730	100.00	3976465	CP041336.1
Salmonella enterica subsp. enterica serovar Kentucky strain...	NA	192955	30.2	30.2	93%	730	100.00	4831443	CP039439.1
Danio rerio genome assembly, chromosome: 19	zebrafish	7955	30.2	30.2	93%	730	100.00	49847318	LR812056.1
Danio rerio strain Nadia (NA) genome assembly, chromosome: 19	zebrafish	7955	30.2	30.2	93%	730	100.00	48376370	LR812587.1
Collimonas fungivorans Ter331 chromosome, complete genome	NA	1005048	30.2	30.2	93%	730	100.00	5186898	CP002745.1
Zebrafish DNA sequence from clone CH1073-416D3 in linkage grou...	zebrafish	7955	30.2	30.2	93%	730	100.00	34589	CU915255.6
Pseudoalteromonas sp. SM9913 chromosome I, complete	NA	234831	30.2	30.2	93%	730	100.00	3332787	CP001796.1

sequence									
Methylotenera versatilis 301 chromosome, complete genome	NA	666681	30.2	30.2	93%	730	100.00	3059871	CP002056.1
Micromonas commoda predicted protein mRNA	NA	296587	30.2	30.2	93%	730	100.00	782	XM_002500928.1
Micromonas sp. RCC299 chromosome 3, complete sequence	NA	296587	30.2	30.2	93%	730	100.00	1759951	CP001324.1
Salmonella enterica subsp. enterica serovar Agona str. SL483,...	NA	454166	30.2	30.2	93%	730	100.00	4798660	CP001138.1
Trichomonas vaginalis G3 hypothetical protein (TVAG_204340)...	NA	412133	30.2	30.2	93%	730	100.00	1086	XM_001308021.1
Maricaulis maris MCS10 chromosome, complete genome	NA	394221	30.2	30.2	93%	730	100.00	3368780	CP000449.1
Shewanella frigidimarina NCIMB 400, complete genome	NA	318167	30.2	30.2	93%	730	100.00	4845257	CP000447.1
Acinetobacter sp. ADP1 complete genome	NA	62977	30.2	30.2	93%	730	100.00	3598621	CR543861.1

Bat coronavirus isolate CMR891-892 ORF1a gene, partial cds; and ORF1b, Spike protein, ORF3, Membrane protein, capsid, hypothetical protein ORFx, and hypothetical protein ORFy genes, complete cds

GenBank: MG693171.1

FASTA Graphics

Go to:

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LOCUS       MG693171                  15 bp ss-RNA     linear   VRL 23-MAR-2020
DEFINITION  Bat coronavirus isolate CMR891-892 ORF1a gene, partial cds; and
            ORF1b, Spike protein, ORF3, Membrane protein, capsid, hypothetical
            protein ORFx, and hypothetical protein ORFy genes, complete cds.
ACCESSION   MG693171 REGION: 10291..10305
VERSION     MG693171.1
KEYWORDS    .
SOURCE      Bat coronavirus
  ORGANISM  Bat coronavirus
            Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes;
            Nidovirales; Cornidovirineae; Coronaviridae; Coronavirinae;
            unclassified Coronavirinae.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Yinda,C.K., Ghogomu,S.M., Conceicao-Neto,N., Beller,L.,
            Deboutte,W., Vanhulle,E., Maes,P., Van Ranst,M. and
            Matthijnssens,J.
  TITLE     Cameroonian fruit bats harbor divergent viruses, including
            rotavirus H, bastroviruses, and picobirnaviruses using an
            alternative genetic code
  JOURNAL   Virus Evol 4 (1), vey008 (2018)
   PUBMED   29644096
  REMARK    Publication Status: Online-Only
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REFERENCE   2  (bases 1 to 15)
  AUTHORS   Yinda,C.K., Ghogomu,S.M., Conceicao-Neto,N., Deboutte,W.,
            Vanhulle,E., Maes,P., Van Ranst,M. and Matthijnssens,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-DEC-2017) Department of Microbiology and Immunology,
            Rega Institute, University of Leuven, Herestraat 49, Leuven,
            Flemish Brabant 3000, Belgium
COMMENT     ##Assembly-Data-START##
            Assembly Method       :: SPAdes v. 3.9.0
            Sequencing Technology :: Sanger dideoxy sequencing; Illumina
            ##Assembly-Data-END##
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Bat coronavirus isolate CMR891-892 ORF1a gene, partial cds; and ORF1b, Spike protein, ORF3, Membrane protein, capsid, hypothetical protein ORFx, and hypothetical protein ORFy genes, complete cds

Sequence ID: MG693171.1Length: 28810Number of Matches: 1

Range 1: 10291 to 10305GenBank Graphics

Score	Expect	Identities	Gaps	Strand
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/prodotto="ORF1a"

ORF1a

ORF1a (**Open Reading Frame**, quadro o cornice di lettura aperto, fase di lettura che consente di codificare un'intera proteina, senza incontrare codoni di stop prematuri e quindi formare una proteina tronca - https://it.wikipedia.org/wiki/Open_reading_frame). **ORF1ab**, *il gene più grande di SARS-CoV-2*, contiene **frame di lettura aperti sovrapposti** che codificano per le **poliproteine PP1ab** e **PP1a**. Le poliproteine vengono scisse per produrre *16 proteine non strutturali*, **NSP1-16**. La produzione della **proteina più lunga** (**PP1ab**) o **più corta** (**PP1a**) dipende da un evento di *frameshifting ribosomiale -1* (https://www.ncbi.nlm.nih.gov/gene/43740578). Un articolo riporta lo sviluppo di un **nuovo test SARS-CoV-2 RT-PCR** basato su **ORF1a** (dell'**ESSERE UMANO**) - **Viroselect** - che mostra un'elevata concordanza con i test convenzionali e la capacità di risolvere i risultati inconcludenti generati durante il picco dell'epidemia in India (https://www.sciencedirect.com/science/article/pii/S1201971221003179). Per il rilevamento di **SARS-CoV-2** sono stati utilizzati *campioni di tamponi orofaringei/rinofaringei* raccolti da **casi sospetti di COVID-19** nel **mezzo di trasporto virale** (**VTM**) (https://www.sciencedirect.com/science/article/pii/S1201971221003179).

Bat coronavirus isolate CMR900 ORF1a, ORF1b, Spike protein, ORF3, Membrane protein, capsid, hypothetical protein ORFx, and hypothetical protein ORFy genes, complete cds

GenBank: MG693169.1

FASTA Graphics

Go to:

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LOCUS       MG693169                  15 bp ss-RNA     linear   VRL 23-MAR-2020
DEFINITION  Bat coronavirus isolate CMR900 ORF1a, ORF1b, Spike protein, ORF3,
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ACCESSION   MG693169 REGION: 10481..10495
VERSION     MG693169.1
KEYWORDS    .
SOURCE      Bat coronavirus
  ORGANISM  Bat coronavirus
            Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes;
            Nidovirales; Cornidovirineae; Coronaviridae; Coronavirinae;
            unclassified Coronavirinae.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Yinda,C.K., Ghogomu,S.M., Conceicao-Neto,N., Beller,L.,
            Deboutte,W., Vanhulle,E., Maes,P., Van Ranst,M. and
            Matthijnssens,J.
  TITLE     Cameroonian fruit bats harbor divergent viruses, including
            rotavirus H, bastroviruses, and picobirnaviruses using an
            alternative genetic code
  JOURNAL   Virus Evol 4 (1), vey008 (2018)
   PUBMED   29644096
  REMARK    Publication Status: Online-Only
REFERENCE   2  (bases 1 to 15)
  AUTHORS   Yinda,C.K., Ghogomu,S.M., Conceicao-Neto,N., Deboutte,W.,
            Vanhulle,E., Maes,P., Van Ranst,M. and Matthijnssens,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-DEC-2017) Department of Microbiology and Immunology,
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            Flemish Brabant 3000, Belgium
COMMENT     ##Assembly-Data-START##
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            Sequencing Technology :: Sanger dideoxy sequencing; Illumina
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Bat coronavirus isolate CMR900 ORF1a, ORF1b, Spike protein, ORF3, Membrane protein, capsid, hypothetical protein ORFx, and hypothetical protein ORFy genes, complete cds

Sequence ID: MG693169.1Length: 28989Number of Matches: 1

Range 1: 10481 to 10495GenBank Graphics

Score	Expect	Identities	Gaps	Strand
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Query                 1       AAAACGCGCTAACAC  15
                              |||||||||||||||
Sbjct                 10495   AAAACGCGCTAACAC  10481
CDS:ORF1a [Bat coron  3424       F   A   S   V   C
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5.2 LA SEQUENZA DI AMINOACIDI “CVSAF” DEL BAT CORONAVIRUS E I RISULTATI DELLA RICERCA BLAST

Nel paragrafo precedente abbiamo visto che tra gli allineamenti significativi della **Sequenza “BAT CORONAVIRUS”** (**AAAACGCGCTAACACC**) sono stati identificati due sconcertanti segmenti di sequenza **specifici del CORONAVIRUS del Pipistrello (BAT)**. Il “prodotto” corrispondente a questi 2 allineamenti significativi è stato un segmento di sequenza del gene **ORF1a**, ovvero la **sequenza di animoacidi “CVSAF”**. La ricerca BLAST sulla sequenza “**AAAACGCGCTAACACC**” **non ha evidenziato** allineamenti significativi con l’**Homo Sapiens**. In questo paragrafo mostriamo i risultati della ricerca BLAST sulla **sequenza di animoacidi “CVSAF”**. Sorprendentemente, questa sequenza di aminoacidi, le cui basi corrispondono a quelle della **Sequenza “BAT CORONAVIRUS”**, **ha evidenziato** allineamenti significativi con l’**Homo Sapiens**. In particolare, è stata identificata una proteina (la proteina **PKDREJ**) che può svolgere un ruolo nella **riproduzione umana** e che è implicata nel **rene policistico autosomico dominante (ADPKD)**. Il gene funzionale **PKDREJ** si trova nella sequenza genomica del **cromosoma umano 22** e ha un pattern di espressione molto ristretto; la trascrizione di circa 8 kb è stata trovata **esclusivamente nel testicolo**, in coincidenza con i ***tempi di maturazione degli spermatozoi***. Un altro allineamento si riferisce al prodotto “**Schlafen umano 5 (SLFN5)”** che **inibisce o promuove la proliferazione di diversi tipi specifici di cellule cancerose**. **SLFN5** umano svolge **ruoli inibitori** nella progressione dell’**Adenocarcinoma Polmonare** umano e legando il **Dna virale** reprime la trascrizione del **Virus dell’Herpes Simplex 1**. Al contrario, un’**elevata espressione** della proteina **SLFN5** nei pazienti con **Metaplasia Intestinale** è correlata alla **progressione** verso il **Cancro Gastrico**. Infine, un altro “prodotto” identificato è stato **Exo70**, un componente chiave del **complesso Exocyst**, che svolge ruoli importanti nella **progressione del cancro umano** oltre che nell’esocitosi e potrebbe essere un **promettente fattore prognostico negativo** e un **potenziale bersaglio terapeutico per il** **Cancro del Colon** (per ulteriori informazioni vedi le pagine successive).

SELEZIONE DI ALLINEAMENTI SIGNIFICATIVI

PKDREJ, partial [Homo sapiens]
Sequence ID: ABR22603.1Length: 2255Number of Matches: 1
Related Information
Gene-associated gene details
Range 1: 2134 to 2138 GenPept Graphics

Score	Expect	Identities	Positives	Gaps
19.3 bits(38)	112466	5/5(100%)	5/5(100%)	0/5(0%)

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Query  1     CVSAF  5
             CVSAF
Sbjct  2134  CVSAF  2138
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/prodotto="PKDREJ"

Polycystic Kidney Disease and Receptor for Egg Jelly-related protein precursor (PKDREJ).

Questo gene **senza introni** codifica per un membro della **famiglia delle proteine della policistina**. La proteina codificata contiene 11 domini transmembrana, un dominio del recettore per la gelatina d'uovo (**REJ**), un dominio del sito proteolitico del recettore accoppiato alla proteina **G (GPS)** e un dominio della policistina-1, lipossigenasi, alfa-tossina **(PLAT)**. **Questa proteina può svolgere un ruolo nella riproduzione umana**. Sono state descritte varianti di splicing alternative, ma la loro natura biologica non è stata determinata (https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=285288; https://www.ncbi.nlm.nih.gov/gene/10343). Le mutazioni nelle **policistine-1 e -2** (**PC1** e **PC2**) causano il **rene policistico autosomico dominante (ADPKD)**, che è caratterizzato dallo sviluppo progressivo di *cisti renali epiteliali*, che alla fine portano all'*insufficienza renale*. Gli autori hanno constatato che la sensibilità del **canale PC2** ai cambiamenti della **concentrazione intracellulare di Ca(2+)** è *carente* in un mutante trovato nei **pazienti con ADPKD**. La disfunzione di tali mutanti può provocare l'accoppiamento difettoso di PC2 all'omeostasi intracellulare di Ca(2+) associata alla patogenesi dell'ADPKD (https://pubmed.ncbi.nlm.nih.gov/11264013/). Studi precedenti avevano mostrato una somiglianza di sequenza tra una regione della proteina del *rene policistico autosomico dominante* **(ADPKD)**, la *policistina-1* e una *glicoproteina spermatica di riccio di mare* coinvolta nella *fecondazione*, il **recettore per la gelatina di uova (suREJ)**. Gli autori hanno trovato una *regione significativa di omologia* con un ampio frame di lettura aperto nella sequenza genomica del **cromosoma umano 22**. Questa regione è il gene funzionale **PKDREJ**, ma a differenza della **policistina-1**, ha un pattern di espressione molto ristretto; la trascrizione di circa 8 kb è stata trovata **esclusivamente nel testicolo**, in coincidenza con i ***tempi di maturazione degli spermatozoi*** (https://pubmed.ncbi.nlm.nih.gov/9949214/).

polycystic kidney disease and receptor for egg jelly-related protein precursor [Homo sapiens]
Sequence ID: NP_006062.1Length: 2253Number of Matches: 1
See 3 more title(s) See all Identical Proteins(IPG) Related Information Gene-associated gene details
Genome Data Viewer-aligned genomic context
Identical Proteins-Identical proteins to NP_006062.1
Range 1: 2132 to 2136 GenPept Graphics

```
Score          Expect    Identities    Positives    Gaps

19.3 bits(38)  112467  5/5(100%)  5/5(100%)  0/5(0%)

Query  1     CVSAF  5
             CVSAF
Sbjct  2132  CVSAF  2136
```

/prodotto=”polycystic kidney disease and receptor for egg jelly-related protein"

likely ortholog of mouse schlafen 5 [Homo sapiens]
Sequence ID: EAW80159.1Length: 994Number of Matches: 1
Related Information
Gene-associated gene details
Range 1: 318 to 322 GenPept Graphics

```
Score          Expect    Identities    Positives    Gaps

19.3 bits(38)  112768  5/5(100%)  5/5(100%)  0/5(0%)

Query  1    CVSAF  5
            CVSAF
Sbjct  318  CVSAF  322
```

/prodotto="likely ortholog of mouse schlafen 5"

SLFN5 membro della famiglia schlafen 5 [Homo sapiens (umano)]

SLFN5 ha un’espressione ubiquitaria nei **linfonodi**, nella **vescica urinaria** e in altri **24 tessuti** (https://www.ncbi.nlm.nih.gov/gene/162394; https://www.genenames.org/data/gene-symbol-report/#!/hgnc_id/HGNC:28286) e può avere un ruolo nella differenziazione delle cellule ematopoietiche (https://www.uniprot.org/uniprot/Q8CBA2). E’ noto che lo **Schlafen umano 5 (SLFN5) inibisce o promuove la proliferazione di diversi tipi specifici di cellule cancerose**. Alcuni studiosi hanno studiato l’espressione di **SLFN5** nell’**adenocarcinoma polmonare (LUAC)**. Essi hanno scoperto che il **knockdown di SLFN5 endogeno** *sovraregola la proliferazione delle cellule tumorali mentre inibisce l’apoptosi*. Al contrario, la ***sovraespressione di SLFN5 esogeno*** *ha inibito la proliferazione cellulare in vitro e in vivo e ha promosso l'apoptosi*. Questi risultati suggeriscono che l’**SLFN5 umano svolge ruoli inibitori nella progressione del LUAC** attraverso la via *PTEN/PI3K/AKT/mTOR*, fornendo un futuro potenziale *bersaglio per lo sviluppo di farmaci per la terapia del cancro del polmone* (https://pubmed.ncbi.nlm.nih.gov/33860045/). Da un altro studio si è scoperto che **SLFN5** lega il **DNA virale** per reprimere la trascrizione del **Virus dell’Herpes Simplex 1** limitando l’accessibilità dell’*RNA polimerasi II ai promotori virali* (https://pubmed.ncbi.nlm.nih.gov/33432153/). Diversamente, altri sudiosi hanno evidenziato **l’elevata espressione della proteina SLFN5 nei pazienti con Metaplasia Intestinale era correlata alla progressione verso Cancro Gastrico** (https://pubmed.ncbi.nlm.nih.gov/27032393/).

schlafen family member 5 isoform 1 [Homo sapiens]
Sequence ID: NP_659412.3Length: 891Number of Matches: 1
See 4 more title(s) See all Identical Proteins(IPG)
Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Identical Proteins-Identical proteins to NP_659412.3
Range 1: 215 to 219 GenPept Graphics

Score	Expect	Identities	Positives	Gaps
19.3 bits(38)	112831	5/5(100%)	5/5(100%)	0/5(0%)

```
Query  1    CVSAF  5
            CVSAF
Sbjct  215  CVSAF  219
```

/prodotto="schlafen family member 5 isoform 1"

SLFN5 protein [Homo sapiens]
Sequence ID: AAI25202.1Length: 891Number of Matches: 1
Related Information
Gene-associated gene details
Range 1: 215 to 219 GenPept Graphics

Score	Expect	Identities	Positives	Gaps
19.3 bits(38)	112831	5/5(100%)	5/5(100%)	0/5(0%)

```
Query  1    CVSAF  5
            CVSAF
Sbjct  215  CVSAF  219
```

/prodotto="SLFN5 protein"

unnamed protein product [Homo sapiens]
Sequence ID: BAG64373.1Length: 891Number of Matches: 1
Related Information
Gene-associated gene details
Range 1: 215 to 219 GenPept Graphics

Score	Expect	Identities	Positives	Gaps
19.3 bits(38)	112831	5/5(100%)	5/5(100%)	0/5(0%)

```
Query  1    CVSAF  5
            CVSAF
Sbjct  215  CVSAF  219
```

unnamed protein product, partial [Homo sapiens]

Sequence ID: BAB70788.1Length: 782Number of Matches: 1

Related Information

Gene-associated gene details

Range 1: 215 to 219 GenPept Graphics

```
Score           Expect   Identities     Positives      Gaps


19.3 bits(38)  112915  5/5(100%)  5/5(100%)  0/5(0%)


Query  1     CVSAF  5
             CVSAF
Sbjct  215   CVSAF  219
```

exocyst complex component 7 isoform X1 [Homo sapiens]

Sequence ID: XP_024306436.1Length: 763Number of Matches: 1

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Range 1: 316 to 320 GenPept Graphics

```
Score           Expect   Identities     Positives      Gaps


19.3 bits(38)  112932  5/5(100%)  5/5(100%)  0/5(0%)


Query  1     CVSAF  5
             CVSAF
Sbjct  316   CVSAF  320
```

/prodotto="exocyst complex component 7 isoform X1"

Componente 7 del Complesso Esocistico (conosciuto anche come EX070)

La proteina codificata da questo gene è un **componente del complesso esocisti**. Il **complesso di esocisti** svolge un ruolo critico nel **traffico vescicolare** e nella **via secretoria** mirando alle **vescicole post-Golgi** verso la **membrana plasmatica**. La proteina codificata è necessaria per l'assemblaggio del complesso esocisti e l'aggancio del complesso alla membrana plasmatica. La proteina codificata può anche svolgere un *ruolo nello splicing del pre-mRNA* attraverso le interazioni con il **fattore di elaborazione del pre-mRNA 19**. Per questo gene sono state osservate varianti di trascrizione con splicing alternativo che codificano più isoforme e uno pseudogene di questo gene si trova sul **braccio lungo del cromosoma 4**. La sua espressione è onnipresente nella **prostata**, nel **cervello** e in altri **25 tessuti** (https://www.ncbi.nlm.nih.gov/gene/23265; https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=397277). **Exo70**, un componente chiave del **complesso Exocyst**, svolge ruoli importanti nella **progressione del cancro umano** oltre che nell'esocitosi. Attraverso il guadagno e la perdita di Exo70 nelle cellule del **cancro del colon**, gli autori hanno scoperto che Exo70 potrebbe **migliorare la capacità di migrazione delle cellule del cancro del colon**. Nel loro insieme, i loro studi hanno rivelato che Exo70 potrebbe essere un **promettente fattore prognostico negativo** e un **potenziale bersaglio terapeutico per il cancro del colon** (https://pubmed.ncbi.nlm.nih.gov/28698570/).

5.3 LA SEQUENZA “12S” E I RISULTATI DELLA RICERCA BLAST

Quella mostrata qui di seguito è la sequenza totale del *3’-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*.

C TCGAGCTGGT ACTGCATGCA 3900
CGCAATGCTA GCTGCCCCTT TCCCGTCCTG GGTACCCCGA GTCTCCCCCG 3950
ACCTCGGGTC CCAGGTATGC TCCCACCTCC ACCTGCCCCA CTCACCACCT 4000
CTGCTAGTTC CAGACACCTC CCAAGCACGC AGCAATGCAG CTC**AAAACGC** 4050
TTAGCCTAGC **CACACC**CCCA CGGGAAACAG CAGTGATTAA CCTTTAGCAA 4100
TAAACGAAAG TTTAACTAAG CTATACTAAC CCCAGGGTTG GTCAATTTCG 4150
TGCCAGCCAC ACCCTGGAGC TAGC

Le **lettere nere in grassetto** sono le lettere poste tra i **QUATTRO spezzoni di sequenza** che costituiscono la **Sequenza “BAT CORONAVIRUS”** (la sequenza discussa nel paragrafo precedente). La sequenza **Query** (**AAAACGCTTAGCCTAGCCACACC**) mostrata sotto è formata dai segmenti della **Sequenza “BAT CORONAVIRUS”** e dalle lettere che li dividono. Questa nuova sequenza è stata definita **Sequenza “12S”** (***Mitochondrial encoded 12S ribosomal RNA***. Per il significato di **12S** si rimanda allo studio del Capitolo II di questo documento). Questa sequenza è stata sottoposta ad una ricerca BLAST e nelle pagine seguenti sono mostrati gli *allineamenti significativi* ottenuti e gli “**organismi**” e i “**prodotti**” a cui tali allineamenti si riferiscono. **I risultati dei “prodotti” identificati dalla ricerca BLAST sono coerenti** (ovvero l’atteso ***Mitochondrial encoded 12S ribosomal RNA***, uno dei componenti principali del *3’-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*) **con quanto dichiarato nel documento scaricato dalla WHO** (https://berthub.eu/articles/11889.doc), documento relativo al “codice sorgente” integrale del Vaccino mRNA Sars-Cov-2 BioNTech/Pfizer (BNT162b2). In altri termini, le **sorprese** mostrate nel paragrafo precedente dalla ricerca BLAST su alcune parti costituenti la **Sequenza “12S”** (le parti corrispondenti alla **Sequenza “BAT CORONAVIRUS”**) emergono **SOLO** se alcuni elementi costitutivi della stessa (le **lettere in grassetto**) vengono omessi, ottenendo così la **Sequenza “BAT CORONAVIRUS”**.

QUERY: **AAAACGCTTAGCCTAGCCACACC**

Search Parameters

Program	blastn
Word size	28
Expect value	0.05
Hitlist size	**5000**
Match/Mismatch scores	1,-2
Gapcosts	0,2.5
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

SEQUENZE SELEZIONATE: 100

Description	Name	Taxid	Score	Score	cover	Value	Ident	Len	Accession
Homo sapiens isolate Yami73 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MN482545.1
Homo sapiens isolate Yami70 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16570	MN482544.1
Homo sapiens isolate Yami68 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MN482543.1
Homo sapiens isolate Yami64 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16567	MN482542.1
Homo sapiens isolate Yami60 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16560	MN482541.1
Homo sapiens isolate Yami59 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16560	MN482540.1
Homo sapiens isolate Yami58 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16560	MN482539.1
Homo sapiens isolate Yami56 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16560	MN482538.1
Homo sapiens isolate Yami53 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16560	MN482537.1
Homo sapiens isolate Yami50 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16560	MN482536.1
Homo sapiens isolate Yami49 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16560	MN482535.1
Homo sapiens isolate Yami32 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16560	MN482534.1
Homo sapiens isolate Yami3 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16567	MN482533.1
Homo sapiens isolate Yami25 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16559	MN482532.1
Homo sapiens isolate Yami21 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16567	MN482531.1
Homo sapiens isolate Yami16 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16560	MN482530.1
Homo sapiens isolate Yami44 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MN482529.1
Homo sapiens isolate Yami34 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MN482528.1
Homo sapiens isolate AmiTW144 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MN482527.1
Homo sapiens isolate AmiTW140 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16567	MN482526.1

Homo sapiens isolate AmiA37 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MN482525.1
Homo sapiens isolate AmiA39 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MN482524.1
Homo sapiens isolate AmiA38 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16567	MN482523.1
Homo sapiens isolate AmiA36 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16567	MN482522.1
Homo sapiens isolate AmiA29b mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16559	MN482521.1
Homo sapiens isolate AmiA7 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MN482520.1
Homo sapiens isolate AmiTW109 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16570	MN482519.1
Homo sapiens isolate AmiTW106 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MN482518.1
Homo sapiens isolate AmiA8 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16572	MN482517.1
Homo sapiens isolate AmiA35 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16562	MN482516.1
Homo sapiens isolate AmiA26 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16569	MN482515.1
Homo sapiens isolate AmiA2 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16569	MN482514.1
Homo sapiens isolate AmiA14 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16569	MN482513.1
Chain AA, 12S mitochondrial rRNA	human	9606	46.1	46.1	100%	0.019	100.00	954	7OG4_AA
Homo sapiens isolate VSO47_D1j1a1b mitochondrion, complete ge	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886215.2
Homo sapiens isolate VSO39_A2bb2 mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886214.2
Homo sapiens isolate VSO38_D1 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16560	MW886213.2
Homo sapiens isolate VSO36_C1b3a mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886212.2
Homo sapiens isolate VDO5_B2ak1 mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16562	MW886210.2
Homo sapiens isolate VA6_B2b2b mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16561	MW886208.2
Homo sapiens isolate VA45_C1d1b1a mitochondrion, complete gen	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886205.2

Homo sapiens isolate VA34_D1j1a2 mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886203.2
Homo sapiens isolate VA24_C1b16a2 mitochondrion, complete gen	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886202.2
Homo sapiens isolate VA23_D1j1a1 mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16572	MW886201.2
Homo sapiens isolate VA22_D1v mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16570	MW886200.2
Homo sapiens isolate VA16_D1 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886198.2
Homo sapiens isolate VA13_C1b16a1a mitochondrion, complete ge	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886197.2
Homo sapiens isolate SUM5_D1j1a2 mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16564	MW886194.2
Homo sapiens isolate SUM32_D1j1a2 mitochondrion, complete gen	human	9606	46.1	46.1	100%	0.019	100.00	16564	MW886193.2
Homo sapiens isolate SUM25_D1j2 mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16571	MW886191.2
Homo sapiens isolate SRC5_D1j1a1b mitochondrion, complete gen	human	9606	46.1	46.1	100%	0.019	100.00	16572	MW886190.2
Homo sapiens isolate SRC31_A2bd mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886189.2
Homo sapiens isolate SRC30_B2z1 mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16563	MW886188.2
Homo sapiens isolate SRC1_A2bb2 mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886187.2
Homo sapiens isolate SRC19_B2z1 mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886186.2
Homo sapiens isolate SRC15_D1j1a1b mitochondrion, complete ge	human	9606	46.1	46.1	100%	0.019	100.00	16573	MW886185.2
Homo sapiens isolate SRC13_B2b mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16562	MW886184.2
Homo sapiens isolate SCM65_A2ax mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886182.2
Homo sapiens isolate RC81_C1d1f mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886181.2
Homo sapiens isolate RC80_B2ak1 mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16562	MW886180.2
Homo sapiens isolate RC49_A2bc mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886179.2
Homo sapiens isolate RC12_D1v mitochondrion,	human	9606	46.1	46.1	100%	0.019	100.00	16570	MW886178.2

complete genome									
Homo sapiens isolate M92_D1g5a1a mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16570	MW886177.2
Homo sapiens isolate M79_B2 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16560	MW886176.2
Homo sapiens isolate M77_D1f4 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16570	MW886175.2
Homo sapiens isolate M74_C1d1 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886174.2
Homo sapiens isolate M72_A2ax mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886173.2
Homo sapiens isolate M63_C1d1f mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886170.2
Homo sapiens isolate M62_D1j1a2 mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16566	MW886169.2
Homo sapiens isolate M59_A2bb1 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16569	MW886168.2
Homo sapiens isolate M58_B2ab1b mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16561	MW886167.2
Homo sapiens isolate M56_C1b18a mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886166.2
Homo sapiens isolate M46_C1b16 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886164.2
Homo sapiens isolate M45_C1b19a mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886163.2
Homo sapiens isolate M3_C1b19a mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886162.2
Homo sapiens isolate M33_D1v mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16570	MW886161.2
Homo sapiens isolate M32_B2am1 mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16562	MW886160.2
Homo sapiens isolate M22_C1b16a mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16564	MW886158.2
Homo sapiens isolate M16_D1j1a1a mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16569	MW886156.2
Homo sapiens isolate LTM48_C1c10 mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16564	MW886155.2
Homo sapiens isolate LTM40_A2ba mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886153.2
Homo sapiens isolate LTM39_C1b3a mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886152.2

Homo sapiens isolate LTM38_C1d1b1a mitochondrion, complete ge	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886151.2
Homo sapiens isolate LTM37_A2ba mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886150.2
Homo sapiens isolate LTM33_C1b16a mitochondrion, complete gen	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886149.2
Homo sapiens isolate LTM31_C1c mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16567	MW886148.2
Homo sapiens isolate LTM20_C1d1f mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886146.2
Homo sapiens isolate LTM18_D1g5a1a mitochondrion, complete ge	human	9606	46.1	46.1	100%	0.019	100.00	16571	MW886145.2
Homo sapiens isolate LTM15_A2bb1 mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886144.2
Homo sapiens isolate LTM12_C1b16a2 mitochondrion, complete ge	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886143.2
Homo sapiens isolate LPA9_C1b15 mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16567	MW886142.2
Homo sapiens isolate LMT23_D1u1 mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16574	MW886140.2
Homo sapiens isolate LC3_A2bc mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16568	MW886139.2
Homo sapiens isolate LC36_C1b19a mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886138.2
Homo sapiens isolate JOV46_A2bb2 mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16569	MW886137.2
Homo sapiens isolate JOV40_A2p mitochondrion, complete genome	human	9606	46.1	46.1	100%	0.019	100.00	16570	MW886136.2
Homo sapiens isolate JOV3_B2ak1 mitochondrion, complete genom	human	9606	46.1	46.1	100%	0.019	100.00	16561	MW886135.2
Homo sapiens isolate JOV28_C1d1f mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886132.2
Homo sapiens isolate CHA35_C1b16 mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886130.2
Homo sapiens isolate CA34_C1b16b mitochondrion, complete geno	human	9606	46.1	46.1	100%	0.019	100.00	16565	MW886128.2

CAPITOLO VI

LA SEQUENZA “ZINC FINGER”, “AES (3)” E I RISULTATI DELLE RICERCHE BLAST

OBIETTIVI DEL CAPITOLO VI

In questo capitolo sono mostrati i risultati delle ricerche BLAST effettuate su **due sequenze**:

1) la **Sequenza "ZINC FINGER"** (**CCGTCCTGGACTCACCACC**), la **quarta sequenza** ottenuta dalla fusione di **DUE** segmenti di sequenza non contigui del *3'-UTR*;

2) la **Sequenza "AES (3)"** (**CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCG GGTCCCAGGTATGCTCCCACCTCCACCTGCCCCACTCACCACC**), l'***Amino-terminal Enhancer of Split*** *o potenziatore ammino-terminale dell'mRNA diviso*, uno dei componenti principali del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer* (per il significato di **AES** si rimanda allo studio del Capitolo II di questo documento).

La **Sequenza "ZINC FINGER"** è così chiamata perché la proteina **ZINC FINGER** è uno degli allineamenti significativi più frequentemente identificato dalla ricerca BLAST. Sono state riscontrate ben **100** sequenze di questa proteina.

Le nucleasi a dita di zinco (ZFN) ***possono essere utilizzate per alterare con precisione i genomi di organismi superiori***. *Insieme a* ***CRISPR/Cas9*** *e* **TALEN**, *ZFN sono uno strumento importante nel campo dell'editing del genoma* (ingegneria genetica). Gli **ZFN** sono utilizzati anche per creare una **nuova generazione di modelli di malattie genetiche** chiamati **modelli isogeni di malattie umane**. **Il ruolo degli ZNF nello sviluppo, nella progressione e nelle metastasi del cancro** sta diventando un argomento di ricerca interessante e gli ***ZFN*** possono essere usati anche nella ***terapia genica***, ma il successo dipende dall'efficace inserimento di geni terapeutici in un appropriato sito bersaglio, **senza causare danno cellulare, mutazioni oncogene o una risposta immunitaria**. Però, se i **domini a dita di zinco** non sono sufficientemente specifici per il loro sito bersaglio o non mirano a un sito univoco all'interno del genoma di interesse, ***può verificarsi una scissione fuori bersaglio***. Tale scissione fuori bersaglio può produrre **riarrangiamenti cromosomici e/o morte cellulare e integrazione casuale del DNA del donatore**. Inoltre, come per molte **proteine estranee inserite nel corpo umano**, esiste il rischio di una **risposta immunologica contro l'agente terapeutico** e le **cellule in cui sono attivi**. Gli **ZFN** possono creare anche **alleli mutanti ereditabili** che possono essere propagati nelle generazioni successive (Per approfondimenti sugli **ZFN** si veda la pagina 459 e le pagine successive). Lo **ione Zinco** e le **proteine Zinc Finger** sono state già citate rispettivamente nel Capitolo III e IV di questo documento. Allo stesso modo, le **proteine Zinc Finger** sono state oggetto approfondito di studio in "I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis" (Si vedano le pagine 189, 230, 232, 238, 248 e 255).

ATTENZIONE: La necessità di pubblicare in fretta questo documento non ci ha consentito di approfondire **altri importanti allineamenti significativi**. Il ricercatore interessato potrà utilizzare le informazioni pubblicate nelle pagine successive e fare autonomamente gli approfondimenti desiderati.

6.1 LA SEQUENZA “ZINC FINGER” E I RISULTATI DELLA RICERCA BLAST

Quella mostrata qui di seguito è la sequenza totale del *3’-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*. Le lettere colorate sono i **DUE segmenti di sequenza non contigui** che sono stati identificati in questa ricerca. Essi, uniti insieme, formano la **Sequenza “ZINC FINGER”**. Questa sequenza è stata sottoposta ad una ricerca BLAST e nelle pagine seguenti sono mostrati gli *allineamenti significativi* ottenuti e gli “**organismi**” e i **prodotti** a cui tali allineamenti si riferiscono**.**

C TCGAGCTGGT ACTGCATGCA 3900
CGCAATGCTA GCTGCCCCTT TC**CCGTCCTG G**GTACCCCGA GTCTCCCCCG 3950
ACCTCGGGTC CCAGGTATGC TCCCACCTCC ACCTGCCCC**A CTCACCACC**T 4000
CTGCTAGTTC CAGACACCTC CCAAGCACGC AGCAATGCAG CTCAAAACGC 4050
TTAGCCTAGC CACACCCCCA CGGGAAACAG CAGTGATTAA CCTTTAGCAA 4100
TAAACGAAAG TTTAACTAAG CTATACTAAC CCCAGGGTTG GTCAATTTCG 4150
TGCCAGCCAC ACCCTGGAGC TAGC

QUERY : CCGTCCTGGACTCACCACC

Search Parameters	
Program	blastn
Word size	7
Expect value	1000
Hitlist size	5000
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

SEQUENZE SELEZIONATE: 2459

Description	Name	Taxid	Score	Score	cover	Value	Ident	Len	Accession
PREDICTED: Acinonyx jubatus uncharacterized LOC113604911...	cheetah	32536	38.2	38.2	100%	3.2	100.00	6350	XR_003426934.1
PREDICTED: Felis catus uncharacterized LOC109498453...	domesti	9685	38.2	38.2	100%	3.2	100.00	6382	XR_002155301.2
PREDICTED: Panthera pardus uncharacterized LOC109269083...	leopard	9691	38.2	38.2	100%	3.2	100.00	6344	XR_002080935.1
PREDICTED: Puma yagouaroundi uncharacterized LOC121044053...	jaguaru	1608482	38.2	38.2	100%	3.2	100.00	6883	XR_005797085.1
Serratia liquefaciens strain HUMV-21, complete genome	NA	614	36.2	36.2	94%	13	100.00	5326657	CP011303.1
PREDICTED: Xenopus laevis protein tyrosine phosphatase,...	African	8355	36.2	36.2	94%	13	100.00	4869	XM_018237411.2
PREDICTED: Xenopus laevis protein tyrosine phosphatase,...	African	8355	36.2	36.2	94%	13	100.00	4673	XM_041577731.1
Xenopus laevis hypothetical	African	8355	36.2	36.2	94%	13	100.00	3111	BC078054.1

protein MGC83117, mRNA (cDNA clone...									
Xenopus laevis protein tyrosine phosphatase, non-receptor type...	African	8355	36.2	36.2	94%	13	100.00	3407	NM_001091402.1
Canis lupus familiaris breed Labrador retriever chromosome 13a	dog	9615	34.2	64.4	94%	50	100.00	63905973	CP050604.1
Canis lupus familiaris breed Labrador retriever chromosome 18a	dog	9615	34.2	34.2	89%	50	100.00	55362250	CP050597.1
Canis lupus familiaris breed Labrador retriever chromosome 13b	dog	9615	34.2	64.4	94%	50	100.00	63899846	CP050644.1
Canis lupus familiaris breed Labrador retriever chromosome 18b	dog	9615	34.2	34.2	89%	50	100.00	55343242	CP050607.1
Citrobacter sp. S40-1-2 chromosome, complete genome	NA	2664854	34.2	34.2	89%	50	100.00	4948530	CP045840.1
Citrobacter sp. H12-3-2 chromosome, complete genome	NA	2664853	34.2	34.2	89%	50	100.00	4948530	CP045837.1
Thalassophryne amazonica genome assembly, chromosome: 14	NA	390379	34.2	64.4	89%	50	100.00	99266177	LR722979.1
Citrobacter portucalensis strain FDAARGOS_617 chromosome,...	NA	1639133	34.2	34.2	89%	50	100.00	4926736	CP044098.1
Citrobacter portucalensis isolate MGYG-HGUT-01705 genome...	NA	1639133	34.2	34.2	89%	50	100.00	4945242	LR698971.1
Myripristis murdjan genome assembly, chromosome: 13	pinecon	586833	34.2	34.2	89%	50	100.00	42404719	LR597562.1
Canis lupus familiaris clone Zoey_032_1115 sequence, complete...	dog	9615	34.2	34.2	89%	50	100.00	30003	MK829538.1
Citrobacter portucalensis strain Effluent_1 chromosome, comple...	NA	1639133	34.2	34.2	89%	50	100.00	5018095	CP039327.1
PREDICTED: Camellia sinensis uncharacterized LOC114291753...	NA	4442	34.2	34.2	89%	50	100.00	1338	XM_028235618.1
PREDICTED: Coffea eugenioides uncharacterized transmembrane...	NA	49369	34.2	34.2	89%	50	100.00	2231	XM_027309888.1
PREDICTED: Coffea eugenioides uncharacterized transmembrane...	NA	49369	34.2	34.2	89%	50	100.00	1919	XM_027299621.1
PREDICTED: Coffea arabica uncharacterized transmembrane protei...	coffee	13443	34.2	34.2	89%	50	100.00	2206	XM_027265251.1
PREDICTED: Coffea arabica uncharacterized transmembrane protei...	coffee	13443	34.2	34.2	89%	50	100.00	2228	XM_027260180.1
Citrobacter youngae strain L6 chromosome, complete genome	NA	133448	34.2	34.2	89%	50	100.00	4945156	CP021963.1
Citrobacter freundii complex sp. CFNIH9 chromosome, complete...	NA	2077149	34.2	34.2	89%	50	100.00	5016446	CP026238.1
Larimichthys crocea genome assembly, chromosome: V	large y	215358	34.2	34.2	89%	50	100.00	34017524	LT972194.1
Citrobacter sp. 30_2 genome	NA	1639133	34.2	34.2	89%	50	100.00	4945242	CP022311.1
Cyberlindnera jadinii NRRL Y-1542 hypothetical protein	NA	983966	34.2	34.2	89%	50	100.00	1895	XM_020217106.1

partial...									
PREDICTED: Branchiostoma belcheri protein-arginine deiminase...	Belcher	7741	34.2	34.2	89%	50	100.00	2408	XM_019786151.1
Citrobacter portucalensis strain P10159, complete genome	NA	1639133	34.2	34.2	89%	50	100.00	5080321	CP012554.1
Actinoplanes friuliensis DSM 7358, complete genome	NA	1246995	34.2	34.2	89%	50	100.00	9376071	CP006272.1
Cervus elaphus genome assembly, chromosome: 14	red dee	9860	34.2	94.6	89%	50	100.00	81685338	OU343091.1
Ocypus olens genome assembly, chromosome: 7	NA	662956	34.2	34.2	89%	50	100.00	59741579	OU343053.1
Acomys percivali genome assembly, chromosome: 16	Perciva	83527	34.2	1122	100%	50	100.00	78221726	OU015757.1
Acomys dimidiatus genome assembly, chromosome: 16	NA	60744	34.2	1305	100%	50	100.00	77604179	OU015389.1
Acomys kempi genome assembly, chromosome: 16	Kemp's	83762	34.2	1547	100%	50	100.00	78196808	OU015370.1
Citrobacter freundii strain Colony300 chromosome	NA	546	34.2	34.2	89%	50	100.00	5016456	CP075521.1
PREDICTED: Gigantopelta aegis Krueppel-like factor luna...	NA	1735272	34.2	34.2	89%	50	100.00	2651	XM_041491676.1
Citrobacter sp. MGH105 chromosome, complete genome	NA	1686380	34.2	34.2	89%	50	100.00	5093209	CP073048.2
Citrobacter portucalensis strain PNUCL1 chromosome, complete...	NA	1639133	34.2	34.2	89%	50	100.00	4825730	CP048388.1
Citrobacter sp. BIDMC108 chromosome, complete genome	NA	1686385	34.2	34.2	89%	50	100.00	5145556	CP073007.1
Sus scrofa scrofa breed NS chromosome 10	NA	415978	34.2	64.4	100%	50	100.00	71502813	CP071561.1
Hedya salicella genome assembly, chromosome: 22	NA	1869985	34.2	34.2	89%	50	100.00	15760218	FR990118.1
Musa acuminata subsp. malaccensis strain Doubled-haploid Pahan...	wild Ma	214687	34.2	96.6	94%	50	100.00	42818424	HG996471.1
Canis lupus genome assembly, chromosome: 18	gray wo	9612	34.2	34.2	89%	50	100.00	57593331	HG994402.1
Canis lupus genome assembly, chromosome: 13	gray wo	9612	34.2	64.4	94%	50	100.00	65443671	HG994397.1
Rhizoctonia solani strain AG-1 IA isolate XN chromosome 13	NA	456999	34.2	34.2	89%	50	100.00	2271624	CP059670.1
Rhizoctonia solani strain AG-1 IA isolate XN chromosome 11	NA	456999	34.2	34.2	89%	50	100.00	2099829	CP059668.1
Citrobacter sp. B72 chromosome, complete genome	NA	2807631	34.2	34.2	89%	50	100.00	5030371	CP069801.1
Citrobacter portucalensis strain Colony224 chromosome	NA	1639133	34.2	34.2	89%	50	100.00	5079742	CP069773.1
Phalera bucephala genome assembly, chromosome: 4	NA	753216	34.2	34.2	89%	50	100.00	39665024	LR990613.1
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4695	XM_038685417.1
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4566	XM_038685416.1
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4591	XM_038685415.1

PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4938	XM_038685414.1
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	5020	XM_038685413.1
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	5007	XM_038685412.1
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	5012	XM_038685410.1
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	5059	XM_038685409.1
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4753	XM_038685408.1
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4760	XM_038685407.1
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4695	XM_038424387.1
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4566	XM_005628113.4
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4591	XM_005628111.4
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4938	XM_005628110.4
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	5020	XM_022426892.2
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	5007	XM_014118758.3
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	5012	XM_014118757.3
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	5059	XM_014118756.3
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4753	XM_022426891.2
PREDICTED: Canis lupus familiaris **ZINC finger** protein 7 (**ZNF7**)...	dog	9615	34.2	34.2	89%	50	100.00	4760	XM_014118754.3
1_Tps_b3v08	NA	170557	34.2	34.2	89%	50	100.00	435	OD266263.1
Poecilia reticulata genome assembly, chromosome: 19	guppy	8081	34.2	34.2	89%	50	100.00	25553809	LR880663.1
Citrobacter freundii strain	NA	546	34.2	34.2	89%	50	100.00	5128689	CP060662.1

MGH281 chromosome, complete genome									
Citrobacter freundii strain MGH281C chromosome, complete genome	NA	546	34.2	34.2	89%	50	100.00	5128186	CP060659.1
Citrobacter freundii strain MGH279 chromosome, complete genome	NA	546	34.2	34.2	89%	50	100.00	5128721	CP060650.1
Citrobacter freundii strain MGH283 chromosome, complete genome	NA	546	34.2	34.2	89%	50	100.00	5125085	CP060654.1
Acomys russatus genome assembly, chromosome: 29	golden	60746	34.2	1636	100%	50	100.00	47664281	LR877240.1
Acomys russatus genome assembly, chromosome: 20	golden	60746	34.2	701	100%	50	100.00	74893780	LR877231.1
Acomys russatus genome assembly, chromosome: 6	golden	60746	34.2	670	89%	50	100.00	89442464	LR877217.1
Acomys russatus genome assembly, chromosome: 5	golden	60746	34.2	1368	100%	50	100.00	79927262	LR877216.1
PREDICTED: Canis lupus dingo **ZINC finger** protein 7 (**ZNF7**),...	dingo	286419	34.2	34.2	89%	50	100.00	4705	XM_035713804.1
PREDICTED: Canis lupus dingo **ZINC finger** protein 7 (**ZNF7**),...	dingo	286419	34.2	34.2	89%	50	100.00	4567	XM_025450675.2
PREDICTED: Canis lupus dingo **ZINC finger** protein 7 (**ZNF7**),...	dingo	286419	34.2	34.2	89%	50	100.00	4593	XM_025450673.2
PREDICTED: Canis lupus dingo **ZINC finger** protein 7 (**ZNF7**),...	dingo	286419	34.2	34.2	89%	50	100.00	4938	XM_025450671.2
PREDICTED: Canis lupus dingo **ZINC finger** protein 7 (**ZNF7**),...	dingo	286419	34.2	34.2	89%	50	100.00	5032	XM_025450670.2
PREDICTED: Canis lupus dingo **ZINC finger** protein 7 (**ZNF7**),...	dingo	286419	34.2	34.2	89%	50	100.00	5018	XM_025450669.2
PREDICTED: Canis lupus dingo **ZINC finger** protein 7 (**ZNF7**),...	dingo	286419	34.2	34.2	89%	50	100.00	5081	XM_025450668.2
PREDICTED: Canis lupus dingo **ZINC finger** protein 7 (**ZNF7**),...	dingo	286419	34.2	34.2	89%	50	100.00	5068	XM_025450667.2
PREDICTED: Canis lupus dingo **ZINC finger** protein 7 (**ZNF7**),...	dingo	286419	34.2	34.2	89%	50	100.00	4753	XM_025450666.2
PREDICTED: Canis lupus dingo **ZINC finger** protein 7 (**ZNF7**),...	dingo	286419	34.2	34.2	89%	50	100.00	4760	XM_025450665.2
Arvicola amphibius genome assembly, chromosome: 15	Eurasia	1047088	34.2	96.6	89%	50	100.00	55452225	LR862395.1
Citrobacter freundii strain RHB30-C03 chromosome, complete genome	NA	546	34.2	34.2	89%	50	100.00	5062205	CP057323.1
Citrobacter freundii strain RHB30-C04 chromosome, complete genome	NA	546	34.2	34.2	89%	50	100.00	4928912	CP057319.1
Canis familiaris chromosome 18,	dog	9615	34.2	34.2	89%	50	100.00	194179	AC188659.9

clone XX-484I11, complete...									
Canis familiaris chromosome 18, clone XX-127C6, complete sequence	dog	9615	34.2	34.2	89%	50	100.00	209069	AC187029.8
Danio aesculapii genome assembly, chromosome: 21	NA	1142201	32.2	32.2	84%	196	100.00	46978008	LR812501.1
Danio rerio genome assembly, chromosome: 21	zebrafi	7955	32.2	32.2	84%	196	100.00	47178121	LR812083.1
Danio rerio genome assembly, chromosome: 5	zebrafi	7955	32.2	32.2	84%	196	100.00	72587816	LR812067.1
Mycolicibacterium smegmatis strain FDAARGOS_679 chromosome	NA	1772	32.2	32.2	84%	196	100.00	6993871	CP054795.1
Felis catus Senzu DNA, chromosome: D4, American Shorthair breed	domesti	9685	32.2	32.2	84%	196	100.00	96896805	AP023164.1
Felis catus Senzu DNA, chromosome: D2, American Shorthair breed	domesti	9685	32.2	92.7	89%	196	100.00	90643714	AP023162.1
PREDICTED: Notolabrus celidotus monoacylglycerol...	New Zea	1203425	32.2	32.2	84%	196	100.00	657	XM_034684129.1
PREDICTED: Pantherophis guttatus msh homeobox 2 (MSX2), mRNA	NA	94885	32.2	32.2	84%	196	100.00	1653	XM_034405303.1
PREDICTED: Esox lucius clusterin-like protein 1 (LOC105019346)...	norther	8010	32.2	32.2	84%	196	100.00	1936	XM_034289293.1
PREDICTED: Esox lucius clusterin-like protein 1 (LOC105019346)...	norther	8010	32.2	32.2	84%	196	100.00	1930	XM_034289292.1
PREDICTED: Esox lucius clusterin-like protein 1 (LOC105019346)...	norther	8010	32.2	32.2	84%	196	100.00	1944	XM_034289291.1
PREDICTED: Esox lucius clusterin-like protein 1 (LOC105019346)...	norther	8010	32.2	32.2	84%	196	100.00	1938	XM_034289290.1
PREDICTED: Esox lucius clusterin-like protein 1 (LOC105019346)...	norther	8010	32.2	32.2	84%	196	100.00	1938	XM_034289289.1
PREDICTED: Esox lucius clusterin-like protein 1 (LOC105019346)...	norther	8010	32.2	32.2	84%	196	100.00	1925	XM_034289288.1
Digitaria exilis annotation	NA	1010633	32.2	32.2	84%	196	100.00	38778756	LR792829.1
Digitaria exilis genome assembly, chromosome: 5B	NA	1010633	32.2	32.2	84%	196	100.00	38778756	LR761614.1
Streptomyces sp. RPA4-5 chromosome	NA	2721245	32.2	32.2	84%	196	100.00	9051652	CP050976.1
Canis lupus familiaris breed Labrador retriever chromosome 05a	dog	9615	32.2	122	94%	196	100.00	86926571	CP050595.1
Canis lupus familiaris breed Labrador retriever chromosome 05b	dog	9615	32.2	122	94%	196	100.00	86915062	CP050642.1
Rhizobium leguminosarum bv. trifolii strain 9B plasmid pRL9b5,...	NA	386	32.2	32.2	84%	196	100.00	464641	CP050099.1
Coregonus sp. 'balchen' genome assembly, chromosome: 33	NA	861768	32.2	32.2	84%	196	100.00	44662967	LR778285.1
Coregonus sp. 'balchen' genome assembly, chromosome: 29	NA	861768	32.2	32.2	84%	196	100.00	48977775	LR778281.1
Plectropomus leopardus DNA,	leopard	160734	32.2	32.2	84%	196	100.00	34657930	AP022709.1

chromosome 10, nearly complete...									
Epinephelus fuscoguttatus DNA, LG7, complete sequence	brown-m	293821	32.2	32.2	84%	196	100.00	47170333	AP022681.1
Epinephelus fuscoguttatus DNA, LG5, complete sequence	brown-m	293821	32.2	32.2	84%	196	100.00	47245075	AP022679.1
PREDICTED: Nematostella vectensis uncharacterized LOC5520139...	starlet	45351	32.2	32.2	84%	196	100.00	4339	XM_032365275.1
Mycolicibacterium confluentis JCM 13671 DNA, nearly complete...	NA	28047	32.2	32.2	84%	196	100.00	5876557	AP022612.1
Kwoniella shandongensis uncharacterized protein (CI109_005626)...	NA	1734106	32.2	32.2	84%	196	100.00	1158	XM_032006755.1
Lutra lutra genome assembly, chromosome: 12	Eurasia	9657	32.2	62.4	94%	196	100.00	96445735	LR738414.1
PREDICTED: Xenopus tropicalis cadherin related family member 3...	tropica	8364	32.2	32.2	84%	196	100.00	4187	XM_002933109.5
PREDICTED: Oncorhynchus kisutch scavenger receptor cysteine-ri...	coho sa	8019	32.2	32.2	84%	196	100.00	1350	XM_031819582.1
Callithrix jacchus chromosome 1 clone CH259-373M7, complete...	white-t	9483	32.2	32.2	84%	196	100.00	167022	AC279283.1
Sciurus vulgaris genome assembly, chromosome: 17	Eurasia	55149	32.2	62.4	84%	196	100.00	75034025	LR738628.1
Sciurus carolinensis genome assembly, chromosome: 17	gray sq	30640	32.2	32.2	84%	196	100.00	66045118	LR738607.1
Sciurus carolinensis genome assembly, chromosome: 15	gray sq	30640	32.2	94.6	100%	196	100.00	83138899	LR738605.1
Neostethus bicornis genome assembly, chromosome: 23	NA	300306	32.2	32.2	84%	196	100.00	16621776	LR738562.1
Caligus rogercresseyi isolate FCH chromosome 6	NA	217165	32.2	32.2	84%	196	100.00	30259579	CP045895.1
Armillaria ostoyae strain C18/9 genome assembly, chromosome: LG6	NA	47428	32.2	32.2	84%	196	100.00	4611551	LR732080.1
Streptomyces platensis strain ATCC 23948 chromosome, complete...	NA	58346	32.2	32.2	84%	196	100.00	8501012	CP023691.1
PREDICTED: Calypte anna protein tyrosine phosphatase...	Anna's	9244	32.2	32.2	84%	196	100.00	1710	XM_030444066.1
PREDICTED: Calypte anna protein tyrosine phosphatase...	Anna's	9244	32.2	32.2	84%	196	100.00	2340	XM_030444065.1
Geotrypetes seraphini genome assembly, chromosome: 13	NA	260995	32.2	32.2	84%	196	100.00	83871185	LR699158.1
Chloropicon primus strain CCMP1205 chromosome 9, complete...	NA	1764295	32.2	32.2	84%	196	100.00	781388	CP031042.1
PREDICTED: Suricata suricatta chloride voltage-gated channel 6...	meerkat	37032	32.2	32.2	84%	196	100.00	6236	XM_029945911.1
PREDICTED: Suricata suricatta acyl-CoA oxidase 3, pristanoyl...	meerkat	37032	32.2	32.2	84%	196	100.00	2557	XM_029952568.1
Gadus morhua genome assembly, chromosome: 14	Atlanti	8049	32.2	32.2	84%	196	100.00	29586942	LR633956.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15425	XM_029827528.1
PREDICTED: Takifugu rubripes	torafug	31033	32.2	32.2	84%	196	100.00	15416	XM_029827523.1

transmembrane protein KIAA1109...									
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15485	XM_029827517.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15521	XM_029827516.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15569	XM_029827510.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15653	XM_029827505.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15662	XM_029827499.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15686	XM_029827490.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15695	XM_029827480.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15734	XM_029827473.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15740	XM_029827467.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15740	XM_029827461.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15743	XM_029827451.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15743	XM_029827446.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15743	XM_029827443.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15837	XM_029827437.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	15746	XM_029827426.1
PREDICTED: Takifugu rubripes transmembrane protein KIAA1109...	torafug	31033	32.2	32.2	84%	196	100.00	16477	XM_029827425.1
Myripristis murdjan genome assembly, chromosome: 15	pinecon	586833	32.2	32.2	84%	196	100.00	33424759	LR597564.1
Sphaeramia orbicularis genome assembly, chromosome: 22	orbicul	375764	32.2	32.2	84%	196	100.00	56303883	LR597479.1
Salarias fasciatus genome assembly, chromosome: 10	jewelle	181472	32.2	32.2	84%	196	100.00	28124721	LR597445.1
Salarias fasciatus genome assembly, chromosome: 7	jewelle	181472	32.2	32.2	84%	196	100.00	33379828	LR597442.1
Takifugu rubripes genome assembly, chromosome: 15	torafug	31033	32.2	126	84%	196	100.00	16705553	LR584240.2
Takifugu rubripes genome assembly, chromosome: 2	torafug	31033	32.2	96.6	84%	196	100.00	15686389	LR584245.2

PREDICTED: Labrus bergylta monoacylglycerol O-acyltransferase ...	ballan	56723	32.2	32.2	84%	196	100.00	1366	XM_020631159.2
Takifugu rubripes genome assembly, chromosome: 13	torafug	31033	32.2	32.2	84%	196	100.00	21507415	LR584232.1
Scleropages formosus genome assembly, chromosome: 21	Asian b	113540	32.2	32.2	84%	196	100.00	25217654	LR584086.1
Scleropages formosus genome assembly, chromosome: 6	Asian b	113540	32.2	32.2	84%	196	100.00	38292110	LR584071.1
Echeneis naucrates genome assembly, chromosome: 12	live sh	173247	32.2	32.2	84%	196	100.00	20416991	LR584053.1
Betta splendens genome assembly, chromosome: 9	Siamese	158456	32.2	32.2	84%	196	100.00	32137567	LR132023.2
Betta splendens genome assembly, chromosome: 4	Siamese	158456	32.2	32.2	84%	196	100.00	34863213	LR132005.2
Gouania willdenowi genome assembly, chromosome: 15	blunt-s	441366	32.2	32.2	84%	196	100.00	37027010	LR131987.1
Brassica rapa genome, scaffold: A01	field m	3711	32.2	32.2	84%	196	100.00	37915545	LR031571.1
Rhizobium jaguaris strain CCGE525 chromosome, complete genome	NA	1312183	32.2	32.2	84%	196	100.00	4575315	CP032694.1
PREDICTED: Eumetopias jubatus **testis** expressed 22 (**TEX22**),...	Steller	34886	32.2	32.2	84%	196	100.00	3034	XM_028095781.1
Cupriavidus taiwanensis isolate Cupriavidus taiwanensis SWF...	NA	164546	32.2	32.2	84%	196	100.00	577503	LT984815.1
Cupriavidus taiwanensis isolate Cupriavidus taiwanensis STM 36...	NA	164546	32.2	32.2	84%	196	100.00	599597	LT984805.1
Cupriavidus taiwanensis isolate Cupriavidus taiwanensis STM 60...	NA	164546	32.2	64.4	84%	196	100.00	586796	LT984799.1
PREDICTED: Callorhinus ursinus **testis** expressed 22 (**TEX22**),...	norther	34884	32.2	32.2	84%	196	100.00	2105	XM_025869237.1
PREDICTED: Callorhinus ursinus **testis** expressed 22 (**TEX22**),...	norther	34884	32.2	32.2	84%	196	100.00	2304	XM_025869235.1
PREDICTED: Melanaphis sacchari elongation of very long chain...	NA	742174	32.2	32.2	84%	196	100.00	2502	XM_025343660.1
Mycolicibacterium smegmatis MKD8 chromosome, complete genome	NA	1214915	32.2	32.2	84%	196	100.00	7119169	CP027541.1
Scophthalmus maximus chromosome 19	turbot	52904	32.2	64.4	84%	196	100.00	20258455	CP026261.1
Scophthalmus maximus chromosome 15	turbot	52904	32.2	32.2	84%	196	100.00	21783159	CP026257.1
Streptomyces nigra strain 452 chromosome, complete genome	NA	1827580	32.2	32.2	84%	196	100.00	7641029	CP029043.1
Bos mutus isolate yakQH1 chromosome 22	wild ya	72004	32.2	32.2	84%	196	100.00	59497618	CP027090.1
PREDICTED: Equus caballus ubiquitin specific peptidase 31...	horse	9796	32.2	32.2	84%	196	100.00	10582	XM_023616128.1
PREDICTED: Equus caballus ubiquitin specific peptidase 31...	horse	9796	32.2	32.2	84%	196	100.00	10687	XM_023616127.1
PREDICTED: Enhydra lutris kenyoni **testis** expressed 22...	NA	391180	32.2	32.2	84%	196	100.00	3071	XM_022505424.1
Drosophila melanogaster strain	fruit f	7227	32.2	62.4	89%	196	100.00	21146568	CP023338.1

rover (forR) chromosome 2R									
Drosophila melanogaster strain sitter (fors) chromosome 2R	fruit f	7227	32.2	62.4	89%	196	100.00	21146707	CP023332.1
PREDICTED: Limulus polyphemus SCY1-like protein 2...	Atlanti	6850	32.2	32.2	84%	196	100.00	2288	XM_022403167.1
PREDICTED: Limulus polyphemus SCY1-like protein 2...	Atlanti	6850	32.2	32.2	84%	196	100.00	2989	XM_022403165.1
PREDICTED: Limulus polyphemus SCY1-like protein 2...	Atlanti	6850	32.2	32.2	84%	196	100.00	3052	XM_022403159.1
PREDICTED: Limulus polyphemus SCY1-like protein 2...	Atlanti	6850	32.2	32.2	84%	196	100.00	3089	XM_022403153.1
Oryzias latipes strain HSOK chromosome 14	Japanes	8090	32.2	62.4	94%	196	100.00	30545418	CP020634.1
Oryzias latipes strain HSOK chromosome 10	Japanes	8090	32.2	32.2	84%	196	100.00	33971696	CP020630.1
Oryzias latipes strain HSOK chromosome 3	Japanes	8090	32.2	32.2	84%	196	100.00	39097270	CP020623.1
Oryzias latipes strain HNI chromosome 10	Japanes	8090	32.2	32.2	84%	196	100.00	28873095	CP020788.1
Oryzias latipes strain Hd-rR chromosome 23 sequence	Japanes	8090	32.2	32.2	84%	196	100.00	24400806	CP020687.1
Oryzias latipes strain Hd-rR chromosome 10 sequence	Japanes	8090	32.2	62.4	100%	196	100.00	31218526	CP020674.1
Streptomyces sp. 1H-SSA4 genome	NA	2014920	32.2	32.2	84%	196	100.00	10989391	CP022161.1
PREDICTED: Carlito syrichta receptor-type tyrosine-protein...	Philipp	1868482	32.2	32.2	84%	196	100.00	895	XM_008068355.2
PREDICTED: Numida meleagris dynamin 3 (DNM3), transcript varia...	helmete	8996	32.2	32.2	84%	196	100.00	7645	XR_002441228.1
PREDICTED: Numida meleagris dynamin 3 (DNM3), transcript varia...	helmete	8996	32.2	32.2	84%	196	100.00	7675	XR_002441227.1
PREDICTED: Drosophila serrata DNA N6-methyl adenine demethylas...	NA	7274	32.2	32.2	84%	196	100.00	9554	XM_020954113.1
Parageobacillus thermoglucosidasius strain TM242 chromosome,...	NA	1426	32.2	32.2	84%	196	100.00	3872522	CP016916.1
TPA: Oryzias latipes strain Hd-rR, complete genome assembly,...	Japanes	8090	32.2	32.2	84%	196	100.00	24050845	HF933229.1
TPA: Oryzias latipes strain Hd-rR, complete genome assembly,...	Japanes	8090	32.2	62.4	100%	196	100.00	27595823	HF933216.1
Parageobacillus thermoglucosidasius strain NCIMB 11955...	NA	1426	32.2	32.2	84%	196	100.00	3873105	CP016622.1
PREDICTED: Ictalurus punctatus peptidyl arginine deiminase 2...	channel	7998	32.2	32.2	84%	196	100.00	3205	XM_017479675.1
PREDICTED: Ictalurus punctatus peptidyl arginine deiminase 2...	channel	7998	32.2	32.2	84%	196	100.00	2911	XM_017479674.1
PREDICTED: Homo sapiens uncharacterized LOC105370052...	human	9606	32.2	32.2	84%	196	100.00	2191	XR_945491.2

PREDICTED: Homo sapiens uncharacterized LOC105370052...	human	9606	32.2	32.2	84%	196	100.00	2188	XR_945490.2
PREDICTED: Nicotiana tabacum uncharacterized LOC107765892...	common	4097	32.2	32.2	84%	196	100.00	1585	XM_016584590.1
Frondihabitans sp. PAMC28766 plasmid 2, complete sequence	NA	1795630	32.2	32.2	84%	196	100.00	135614	CP014515.1
PREDICTED: Polistes dominula glutamyl aminopeptidase-like...	Europea	743375	32.2	32.2	84%	196	100.00	3516	XM_015316071.1
PREDICTED: Equus asinus ubiquitin specific peptidase 31 (USP31...	ass	9793	32.2	32.2	84%	196	100.00	10150	XM_014864726.1
PREDICTED: Polistes canadensis glutamyl aminopeptidase-like...	NA	91411	32.2	32.2	84%	196	100.00	3111	XM_014745286.1
PREDICTED: Dinoponera quadriceps protein FAM69C (LOC106749459)...	NA	609295	32.2	32.2	84%	196	100.00	1688	XM_014628912.1
Parageobacillus thermoglucosidasius strain DSM 2542 chromosome...	NA	1426	32.2	32.2	84%	196	100.00	3873116	CP012712.1
Cronobacter universalis NCTC 9529 plasmid pCUNV1, complete...	NA	1074000	32.2	32.2	84%	196	100.00	129777	CP012258.1
PREDICTED: Chinchilla lanigera uncharacterized LOC102004835...	long-ta	34839	32.2	32.2	84%	196	100.00	517	XR_264266.2
Ovis canadensis canadensis isolate 43U chromosome 19 sequence	NA	112262	32.2	32.2	84%	196	100.00	60532937	CP011904.1
Ovis canadensis canadensis isolate 43U chromosome 13 sequence	NA	112262	32.2	62.4	89%	196	100.00	83176208	CP011898.1
PREDICTED: Condylura cristata **ZINC finger** with KRAB and SCAN...	star-no	143302	32.2	32.2	84%	196	100.00	6917	XM_012734646.1
Xanthophyllomyces dendrorhous genome assembly Xden1, scaffold...	NA	264483	32.2	32.2	84%	196	100.00	2340728	LN483167.1
Pseudozyma hubeiensis SY62 multidrug resistance protein partia...	NA	1305764	32.2	32.2	84%	196	100.00	6120	XM_012333928.1
Mycobacterium smegmatis genome assembly NCTC8159, chromosome : 1	NA	1772	32.2	32.2	84%	196	100.00	6983267	LN831039.1
Mycobacterium smegmatis strain INHR2, complete genome	NA	1772	32.2	32.2	84%	196	100.00	6988302	CP009496.1
Mycobacterium smegmatis strain INHR1, complete genome	NA	1772	32.2	32.2	84%	196	100.00	6988337	CP009495.1
Mycobacterium smegmatis str. MC2 155, complete genome	NA	246196	32.2	32.2	84%	196	100.00	6988269	CP009494.1
PREDICTED: Nicotiana sylvestris uncharacterized LOC104245614...	wood to	4096	32.2	32.2	84%	196	100.00	1558	XM_009801234.1
Drosophila melanogaster chromosome 2R	fruit f	7227	32.2	62.4	89%	196	100.00	25286936	AE013599.5
Drosophila melanogaster longitudinals lacking (lola), transcri...	fruit f	7227	32.2	32.2	84%	196	100.00	2146	NM_170617.5

Drosophila melanogaster longitudinals lacking (lola), transcri...	fruit f	7227	32.2	32.2	84%	196	100.00	3875	NM_176131.5
PREDICTED: Equus przewalskii ubiquitin specific peptidase 31...	Przewal	9798	32.2	32.2	84%	196	100.00	11035	XM_008536259.1
Solanum pennellii chromosome ch06, complete genome	NA	28526	32.2	32.2	84%	196	100.00	60730942	HG975445.1
Exserohilum turcica Et28A uncharacterized protein...	NA	671987	32.2	32.2	84%	196	100.00	2136	XM_008029790.1
Melampsora larici-populina 98AG31 uncharacterized protein...	NA	747676	32.2	32.2	84%	196	100.00	1677	XM_007418352.1
Brassica rapa genome assembly, chromosome: A01	field m	3711	32.2	32.2	84%	196	100.00	39217719	LS974617.2
Thunnus maccoyii genome assembly, chromosome: 21	souther	8240	32.2	32.2	84%	196	100.00	27656739	OU343211.1
Cervus elaphus genome assembly, chromosome: 31	red dee	9860	32.2	32.2	84%	196	100.00	55169878	OU343108.1
Cervus elaphus genome assembly, chromosome: 26	red dee	9860	32.2	32.2	84%	196	100.00	50001067	OU343103.1
Cervus elaphus genome assembly, chromosome: 24	red dee	9860	32.2	32.2	84%	196	100.00	71624245	OU343101.1
Cervus elaphus genome assembly, chromosome: 6	red dee	9860	32.2	32.2	84%	196	100.00	51846305	OU343083.1
Cervus elaphus genome assembly, chromosome: 4	red dee	9860	32.2	64.4	84%	196	100.00	68741660	OU343081.1
Cervus elaphus genome assembly, chromosome: 3	red dee	9860	32.2	32.2	84%	196	100.00	55858895	OU343080.1
Ypsolopha scabrella genome assembly, chromosome: 7	NA	1870435	32.2	32.2	84%	196	100.00	31326399	OU342967.1
Zebrafish DNA sequence from clone CH1073-516L1 in linkage grou...	zebrafi	7955	32.2	32.2	84%	196	100.00	10409	FO681329.2
Acomys percivali genome assembly, chromosome: 13	Perciva	83527	32.2	2422	94%	196	100.00	86120762	OU015754.1
Acomys dimidiatus genome assembly, chromosome: 15	NA	60744	32.2	1483	94%	196	100.00	80520786	OU015388.1
Acomys kempi genome assembly, chromosome: 14	Kemp's	83762	32.2	2545	89%	196	100.00	99561253	OU015368.1
Acomys kempi genome assembly, chromosome: 18	Kemp's	83762	32.2	908	100%	196	100.00	9247165	OU015372.1
PREDICTED: Alosa sapidissima Era-like **12S** mitochondrial rRNA...	America	34773	32.2	32.2	84%	196	100.00	2471	XM_042091173.1
PREDICTED: Alosa sapidissima Era-like **12S** mitochondrial rRNA...	America	34773	32.2	32.2	84%	196	100.00	2502	XM_042091172.1
Danio rerio strain T5D chromosome 21	zebrafi	7955	32.2	32.2	84%	196	100.00	45833048	CP068755.1
Zeuzera pyrina genome assembly, chromosome: 27	NA	1101072	32.2	32.2	84%	196	100.00	14506622	OU015644.1
Caprimulgus europaeus genome assembly, chromosome: 24	Eurasia	111811	32.2	32.2	84%	196	100.00	7570459	OU015548.1
Streptopelia turtur genome assembly, chromosome: 29	NA	177155	32.2	32.2	84%	196	100.00	22405544	OU015479.1
PREDICTED: Xenopus laevis cadherin related family member 3 L...	African	8355	32.2	32.2	84%	196	100.00	3870	XM_041586522.1
PREDICTED: Betta splendens dynein, axonemal, heavy chain	Siamese	158456	32.2	32.2	84%	196	100.00	14555	XM_041070346.1

5 lik...									
Ochropleura plecta genome assembly, chromosome: 18	NA	320037	32.2	32.2	84%	196	100.00	20456218	FR997740.1
PREDICTED: Aegilops tauschii subsp. strangulata uncharacterize...	NA	200361	32.2	32.2	84%	196	100.00	1880	XR_005756841.1
PREDICTED: Aegilops tauschii subsp. strangulata uncharacterize...	NA	200361	32.2	32.2	84%	196	100.00	2178	XR_002227980.2
Meleagris gallopavo genome assembly, chromosome: Z	turkey	9103	32.2	32.2	84%	196	100.00	76077877	HG999683.1
PREDICTED: Hirundo rustica protein tyrosine phosphatase...	Barn sw	43150	32.2	32.2	84%	196	100.00	2012	XM_040064193.1
PREDICTED: Hirundo rustica protein tyrosine phosphatase...	Barn sw	43150	32.2	32.2	84%	196	100.00	5018	XM_040064183.1
Hecatera dysodea genome assembly, chromosome: 25	NA	988125	32.2	32.2	84%	196	100.00	15320587	HG995312.1
Mimas tiliae genome assembly, chromosome: 23	NA	522848	32.2	32.2	84%	196	100.00	11870120	HG995261.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon	72036	32.2	32.2	84%	196	100.00	39563600	HG994581.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon	72036	32.2	32.2	84%	196	100.00	53400701	HG994580.1
Canis lupus genome assembly, chromosome: 5	gray wo	9612	32.2	122	94%	196	100.00	89778077	HG994385.1
Micromonosporaceae bacterium DSM 106523 chromosome, complete...	NA	2811111	32.2	32.2	84%	196	100.00	5699854	CP070499.1
Spilosoma lubricipeda genome assembly, chromosome: 7	NA	875880	32.2	32.2	84%	196	100.00	22815533	HG992281.1
Colias croceus genome assembly, chromosome: 30	clouded	72248	32.2	32.2	84%	196	100.00	5078220	HG991988.1
Colias croceus genome assembly, chromosome: 12	clouded	72248	32.2	32.2	84%	196	100.00	11204669	HG991970.1
Colias croceus genome assembly, chromosome: 2	clouded	72248	32.2	32.2	84%	196	100.00	13248411	HG991960.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon	72036	32.2	32.2	84%	196	100.00	39563600	LR794185.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon	72036	32.2	32.2	84%	196	100.00	53400701	LR794184.1
Digitaria exilis genome assembly, chromosome: 5B	NA	1010633	32.2	32.2	84%	196	100.00	38778756	LR994613.1
Syritta pipiens genome assembly, chromosome: 2	NA	34682	32.2	32.2	84%	196	100.00	86509480	LR994572.1
Notodonta dromedarius genome assembly, chromosome: 24	NA	753204	32.2	32.2	84%	196	100.00	8740623	LR990183.1
Uncultured Alteromonas sp. AD1000-15-F07 genomic sequence	NA	1245944	32.2	32.2	84%	196	100.00	34821	JX888731.1
Mycobacterium smegmatis str. MC2 155, complete genome	NA	246196	32.2	32.2	84%	196	100.00	6988208	CP001663.1
Nibea albiflora genome assembly, chromosome: 22	white f	240163	32.2	32.2	84%	196	100.00	15878150	LR699045.1
Nibea albiflora genome assembly, chromosome: 7	white f	240163	32.2	32.2	84%	196	100.00	25201542	LR699030.1
Clitopilus hobsonii strain QYL-10 chromosome 6	NA	648681	32.2	32.2	84%	196	100.00	4299753	CP068002.1
PREDICTED: Tachyglossus aculeatus vexin (VXN), mRNA	Austral	9261	32.2	32.2	84%	196	100.00	986	XM_038766708.1
1_Tps_b3v08	NA	170557	32.2	32.2	84%	196	100.00	3434	OD032048.1

Synechococcus sp. CBW1006 chromosome, complete genome	NA	1353138	32.2	32.2	84%	196	100.00	3860130	CP060396.1
1_Tdi_b3v08	NA	61478	32.2	32.2	84%	196	100.00	174867	OA565456.1
Darwinula stevensoni	NA	69355	32.2	32.2	84%	196	100.00	29012	LR903164.1
PREDICTED: **MANIS JAVANICA** **RAB43, member RAS oncogene family...**	Malayan	9974	32.2	32.2	84%	196	100.00	4484	XM_017659866.2
PREDICTED: Phyllostomus discolor retinoid isomerohydrolase RPE...	pale sp	89673	32.2	32.2	84%	196	100.00	2410	XM_036026271.1
PREDICTED: Phyllostomus discolor retinoid isomerohydrolase RPE...	pale sp	89673	32.2	32.2	84%	196	100.00	2599	XM_028513446.2
Streptomyces libani subsp. rufus NBRC 15424 DNA, complete genome	NA	249582	32.2	32.2	84%	196	100.00	8522827	AP023408.1
PREDICTED: Anopheles albimanus voltage-dependent calcium chann...	NA	7167	32.2	32.2	84%	196	100.00	5689	XM_035918474.1
Acomys russatus genome assembly, chromosome: 26	golden	60746	32.2	822	100%	196	100.00	53312271	LR877237.1
Acomys russatus genome assembly, chromosome: 24	golden	60746	32.2	640	94%	196	100.00	60479378	LR877235.1
Acomys russatus genome assembly, chromosome: 21	golden	60746	32.2	243	94%	196	100.00	61132863	LR877232.1
Acomys russatus genome assembly, chromosome: 19	golden	60746	32.2	3629	94%	196	100.00	66025038	LR877230.1
Acomys russatus genome assembly, chromosome: 16	golden	60746	32.2	1999	100%	196	100.00	47487087	LR877227.1
Acomys russatus genome assembly, chromosome: 14	golden	60746	32.2	1241	94%	196	100.00	62749011	LR877225.1
Acomys russatus genome assembly, chromosome: 13	golden	60746	32.2	787	94%	196	100.00	72247343	LR877224.1
Acomys russatus genome assembly, chromosome: 9	golden	60746	32.2	485	94%	196	100.00	66475698	LR877220.1
Acomys russatus genome assembly, chromosome: 8	golden	60746	32.2	878	89%	196	100.00	77196262	LR877219.1
Acomys russatus genome assembly, chromosome: 4	golden	60746	32.2	1301	89%	196	100.00	85305823	LR877215.1
Onychomys torridus genome assembly, chromosome: 14	souther	38674	32.2	32.2	84%	196	100.00	84754330	LR877201.1
Onychomys torridus genome assembly, chromosome: 13	souther	38674	32.2	62.4	89%	196	100.00	78371027	LR877200.1
Rhizobium leguminosarum bv. trifolii strain RCAM1365 plasmid...	NA	386	32.2	32.2	84%	196	100.00	497560	CP050516.1
Arvicola amphibius genome assembly, chromosome: 14	Eurasia	1047088	32.2	64.4	84%	196	100.00	63161238	LR862394.1
Pipistrellus Pipistrellus genome assembly, chromosome: 14	common	59474	32.2	62.4	100%	196	100.00	51672279	LR862370.1
Arvicola amphibius genome assembly, chromosome: 16	Eurasia	1047088	32.2	32.2	84%	196	100.00	51382976	LR862396.1
PREDICTED: Electrophorus electricus tubby-related protein 4-li...	electri	8005	32.2	32.2	84%	196	100.00	7677	XM_027032921.2
Exserohilum turcica Et28A chromosome 4	NA	671987	32.2	32.2	84%	196	100.00	3003811	CP054630.1
Danio rerio genome assembly, chromosome: 23	zebrafi	7955	32.2	32.2	84%	196	100.00	47467499	LR812060.1
Danio rerio genome assembly,	zebrafi	7955	32.2	32.2	84%	196	100.00	48052324	LR812058.1

chromosome: 21									
Danio rerio genome assembly, chromosome: 5	zebrafi	7955	32.2	32.2	84%	196	100.00	74433922	LR812042.1
Danio rerio genome assembly, chromosome: 1	zebrafi	7955	32.2	62.4	84%	196	100.00	59963668	LR812038.1
Danio rerio genome assembly, chromosome: 21	zebrafi	7955	32.2	32.2	84%	196	100.00	43492497	LR812614.1
Danio rerio genome assembly, chromosome: 5	zebrafi	7955	32.2	32.2	84%	196	100.00	67558190	LR812598.1
Danio rerio genome assembly, chromosome: 1	zebrafi	7955	32.2	62.4	84%	196	100.00	56285942	LR812594.1
Danio rerio strain Nadia (NA) genome assembly, chromosome: 21	zebrafi	7955	32.2	32.2	84%	196	100.00	44761126	LR812589.1
Danio rerio strain Nadia (NA) genome assembly, chromosome: 15	zebrafi	7955	32.2	32.2	84%	196	100.00	46203510	LR812583.1
Danio rerio strain Cooch Behar (CB) genome assembly, chromosom...	zebrafi	7955	32.2	32.2	84%	196	100.00	42543634	LR812564.1
Danio kyathit genome assembly, chromosome: 21	NA	242068	32.2	32.2	84%	196	100.00	57145428	LR812539.1
Parageobacillus thermoglucosidasius C56-YS93 chromosome,...	NA	634956	32.2	32.2	84%	196	100.00	3893306	CP002835.1
Geobacillus sp. Y4.1MC1, complete genome	NA	581103	32.2	32.2	84%	196	100.00	3840330	CP002293.1
Verticillium alfalfae VaMs.102 MPE1 partial mRNA	NA	526221	32.2	32.2	84%	196	100.00	2188	XM_003008688.1
MACACA MULATTA BAC clone CH250-38N17 from chromosome 10,...	Rhesus	9544	32.2	32.2	84%	196	100.00	190233	AC197615.4
Mycobacterium smegmatis str. MC2 155, complete genome	NA	246196	32.2	32.2	84%	196	100.00	6988209	CP000480.1
Drosophila melanogaster clone BACR16P22, complete sequence	fruit f	7227	32.2	32.2	84%	196	100.00	179325	AC007418.9
Sus scrofa clone RP44-524D11, complete sequence	pig	9823	32.2	32.2	84%	196	100.00	69000	AC096852.3
Drosophila melanogaster GM09276 full length cDNA	fruit f	7227	32.2	32.2	84%	196	100.00	1260	AY060963.1
Fugu rubripes cosmid 151J19 covering the WT1, reticulocalbin a...	torafug	31033	32.2	32.2	84%	196	100.00	45565	AL021531.1
Homo sapiens 12 BAC RP11-158L12 (Roswell Park Cancer Institute...	human	9606	32.2	32.2	84%	196	100.00	178315	AC122688.5
Drosophila melanogaster, chromosome 2R, region 47A-47B, BAC...	fruit f	7227	32.2	32.2	84%	196	100.00	168567	AC007398.6
Drosophila melanogaster lola mRNA for Lola protein isoform N,...	fruit f	7227	32.2	32.2	84%	196	100.00	3729	AB107345.1
Drosophila melanogaster lola mRNA for Lola protein isoform M,...	fruit f	7227	32.2	32.2	84%	196	100.00	2000	AB107344.1
Drosophila melanogaster lola mRNA for Lola protein isoform N,...	fruit f	7227	32.2	32.2	84%	196	100.00	3729	AB107325.1
Drosophila melanogaster lola mRNA for Lola protein isoform M,...	fruit f	7227	32.2	32.2	84%	196	100.00	2000	AB107324.1

Drosophila melanogaster lola mRNA for Lola protein isoform N,...	fruit f	7227	32.2	32.2	84%	196	100.00	3873	AB107305.1
Drosophila melanogaster lola mRNA for Lola protein isoform M,...	fruit f	7227	32.2	32.2	84%	196	100.00	2144	AB107304.1
Drosophila melanogaster lola mRNA for Lola protein isoform N,...	fruit f	7227	32.2	32.2	84%	196	100.00	3932	AB107285.1
Drosophila melanogaster lola mRNA for Lola protein isoform M,...	fruit f	7227	32.2	32.2	84%	196	100.00	2203	AB107284.1
Danio aesculapii genome assembly, chromosome: 16	NA	1142201	30.2	30.2	78%	774	100.00	57624524	LR812499.1
Erithacus rubecula genome assembly, chromosome: 4	Europea	37610	30.2	30.2	78%	774	100.00	68599267	LR812106.1
Erithacus rubecula genome assembly, chromosome: 22	Europea	37610	30.2	30.2	78%	774	100.00	10967517	LR812125.1
Erithacus rubecula genome assembly, chromosome: 15	Europea	37610	30.2	30.2	78%	774	100.00	19110993	LR812118.1
Erithacus rubecula genome assembly, chromosome: 10	Europea	37610	30.2	30.2	78%	774	100.00	29524214	LR812113.1
Erithacus rubecula genome assembly, chromosome: 9	Europea	37610	30.2	30.2	78%	774	100.00	34931163	LR812111.1
Danio rerio genome assembly, chromosome: 15	zebrafi	7955	30.2	30.2	78%	774	100.00	49376335	LR812077.1
Danio rerio genome assembly, chromosome: 18	zebrafi	7955	30.2	30.2	78%	774	100.00	52041376	LR812080.1
Danio rerio genome assembly, chromosome: 7	zebrafi	7955	30.2	60.5	84%	774	100.00	73594634	LR812069.1
Streptomyces fulvissimus strain NA06532 chromosome, complete...	NA	68202	30.2	30.2	78%	774	100.00	7790974	CP054926.1
Streptomyces coelicolor strain M1154/pAMX4/pGP1416 chromosome,...	NA	1902	30.2	30.2	78%	774	100.00	8585093	CP050522.1
Bacillus altitudinis strain SCU11 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3755707	CP038517.1
PREDICTED: Maniola hyperantus sodium/potassium-transporting...	ringlet	2795564	30.2	30.2	78%	774	100.00	974	XM_034968923.1
Bacillus altitudinis strain 11-1-1 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3879167	CP054136.1
Mycobacterium tuberculosis strain FDAARGOS_756 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4414577	CP054014.1
Mycobacterium tuberculosis strain FDAARGOS_757 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4417931	CP054013.1
Gossypium arboreum cultivar Shixiya1 chromosome 12	NA	29729	30.2	30.2	78%	774	100.00	94637005	CP053561.1
Felis catus Senzu DNA, chromosome: F1, American Shorthair breed	domesti	9685	30.2	30.2	78%	774	100.00	74990155	AP023168.1
Felis catus Senzu DNA, chromosome: E1, American Shorthair breed	domesti	9685	30.2	30.2	78%	774	100.00	65441144	AP023165.1
PREDICTED: Trachemys scripta elegans DS cell adhesion molecule...	NA	31138	30.2	30.2	78%	774	100.00	2132	XM_034753142.1
PREDICTED: Trachemys scripta elegans DS cell adhesion	NA	31138	30.2	30.2	78%	774	100.00	4556	XM_034753134.1

molecule...									
PREDICTED: Trachemys scripta elegans DS cell adhesion molecule...	NA	31138	30.2	30.2	78%	774	100.00	6991	XM_034753123.1
Nocardioides sp. zg-579 chromosome, complete genome	NA	2663857	30.2	30.2	78%	774	100.00	4391338	CP053660.1
Apiotrichum mycotoxinovorans strain CICC 1454 chromosome 1	NA	252803	30.2	30.2	78%	774	100.00	7496769	CP053620.1
PREDICTED: Ailuropoda melanoleuca **ZINC finger** protein 7 (**ZNF7**)...	giant p	9646	30.2	30.2	78%	774	100.00	5133	XM_019802657.2
PREDICTED: Ailuropoda melanoleuca **ZINC finger** protein 7 (**ZNF7**)...	giant p	9646	30.2	30.2	78%	774	100.00	5219	XM_034668832.1
PREDICTED: Ailuropoda melanoleuca **ZINC finger** protein 7 (**ZNF7**)...	giant p	9646	30.2	30.2	78%	774	100.00	5129	XM_011228508.3
PREDICTED: Notolabrus celidotus dynein, axonemal, heavy chain ...	New Zea	1203425	30.2	30.2	78%	774	100.00	13734	XM_034678523.1
PREDICTED: Drosophila innubila threonine aspartase 1...	NA	198719	30.2	30.2	78%	774	100.00	1698	XM_034628135.1
PREDICTED: Hippoglossus hippoglossus transcription initiation...	Atlanti	8267	30.2	30.2	78%	774	100.00	4306	XM_034578183.1
PREDICTED: Crassostrea gigas filamin-A (LOC105348068), mRNA	Pacific	29159	30.2	30.2	78%	774	100.00	10470	XM_020075242.2
Fusarium oxysporum Fo5176 chromosome 7	NA	660025	30.2	30.2	78%	774	100.00	4366300	CP053266.1
PREDICTED: Pantherophis guttatus estrogen related receptor bet...	NA	94885	30.2	30.2	78%	774	100.00	1519	XM_034418179.1
PREDICTED: Pantherophis guttatus estrogen related receptor bet...	NA	94885	30.2	30.2	78%	774	100.00	1796	XM_034418178.1
PREDICTED: Pantherophis guttatus estrogen related receptor bet...	NA	94885	30.2	30.2	78%	774	100.00	1733	XM_034418177.1
PREDICTED: Pantherophis guttatus estrogen related receptor bet...	NA	94885	30.2	30.2	78%	774	100.00	1638	XM_034418176.1
PREDICTED: Pantherophis guttatus estrogen related receptor bet...	NA	94885	30.2	30.2	78%	774	100.00	1701	XM_034418175.1
PREDICTED: Thrips palmi uncharacterized LOC117647478...	NA	161013	30.2	30.2	78%	774	100.00	4591	XM_034389234.1
PREDICTED: Prunus dulcis uncharacterized LOC117637086...	almond	3755	30.2	30.2	78%	774	100.00	3338	XM_034371880.1
PREDICTED: Prunus dulcis uncharacterized LOC117637086...	almond	3755	30.2	30.2	78%	774	100.00	3422	XM_034371870.1
PREDICTED: Prunus dulcis uncharacterized LOC117637086...	almond	3755	30.2	30.2	78%	774	100.00	3428	XM_034371863.1
Fusarium oxysporum Fo47 chromosome V	NA	660027	30.2	30.2	78%	774	100.00	4523040	CP052042.1

Mycobacterium tuberculosis strain 4860 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4394156	CP053092.1
PREDICTED: Gymnodraco acuticeps KIAA0753 ortholog (kiaa0753),...	NA	8218	30.2	30.2	78%	774	100.00	3574	XM_034207037.1
PREDICTED: Gymnodraco acuticeps KIAA0753 ortholog (kiaa0753),...	NA	8218	30.2	30.2	78%	774	100.00	3583	XM_034207036.1
PREDICTED: Gymnodraco acuticeps pyridoxal kinase-like...	NA	8218	30.2	30.2	78%	774	100.00	2404	XM_034236919.1
PREDICTED: Thalassophryne amazonica steroid hormone receptor...	NA	390379	30.2	30.2	78%	774	100.00	2485	XM_034162198.1
PREDICTED: Thalassophryne amazonica steroid hormone receptor...	NA	390379	30.2	30.2	78%	774	100.00	1831	XR_004558463.1
PREDICTED: Thalassophryne amazonica steroid hormone receptor...	NA	390379	30.2	30.2	78%	774	100.00	1861	XM_034162197.1
PREDICTED: Melopsittacus undulatus DS cell adhesion molecule...	budgeri	13146	30.2	30.2	78%	774	100.00	6811	XM_034074654.1
PREDICTED: Trematomus bernacchii KIAA0753 ortholog (kiaa0753),...	emerald	40690	30.2	30.2	78%	774	100.00	3182	XM_034112914.1
PREDICTED: Trematomus bernacchii KIAA0753 ortholog (kiaa0753),...	emerald	40690	30.2	30.2	78%	774	100.00	3191	XM_034112913.1
PREDICTED: Pseudochaenichthys georgianus pyridoxal kinase-like...	South G	52239	30.2	30.2	78%	774	100.00	2573	XM_034110369.1
Mycobacterium tuberculosis strain RW-TB008 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4379910	CP048071.1
PREDICTED: Tursiops truncatus uncharacterized LOC117312364...	common	9739	30.2	30.2	78%	774	100.00	6226	XR_004526587.1
PREDICTED: Tursiops truncatus glutaminyl-peptide...	common	9739	30.2	30.2	78%	774	100.00	1066	XM_019942895.2
PREDICTED: Tursiops truncatus glutaminyl-peptide...	common	9739	30.2	30.2	78%	774	100.00	1066	XM_019942894.2
PREDICTED: Fukomys damarensis gamma-aminobutyric acid type A...	Damara	885580	30.2	30.2	78%	774	100.00	9560	XM_010640191.2
PREDICTED: Cryptotermes secundus UPF0577 protein KIAA1324-like...	NA	105785	30.2	30.2	78%	774	100.00	3671	XM_033753000.1
Bacillus velezensis strain UCMB5140 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3980571	CP051463.1
Digitaria exilis annotation	NA	1010633	30.2	30.2	78%	774	100.00	60747861	LR792838.1
Digitaria exilis genome assembly, chromosome: UA	NA	1010633	30.2	30.2	78%	774	100.00	60747861	LR761623.1
PREDICTED: Orcinus orca glutaminyl-peptide cyclotransferase...	killer	9733	30.2	30.2	78%	774	100.00	1068	XM_033419269.1
PREDICTED: Orcinus orca glutaminyl-peptide cyclotransferase...	killer	9733	30.2	30.2	78%	774	100.00	1071	XM_033419268.1

PREDICTED: Belonocnema treatae uncharacterized LOC117175816...	NA	1159321	30.2	30.2	78%	774	100.00	9796	XM_033365573.1
PREDICTED: Belonocnema treatae uncharacterized LOC117175816...	NA	1159321	30.2	30.2	78%	774	100.00	8747	XM_033365571.1
Vibrio parahaemolyticus strain 2012V-1116 chromosome 1	NA	670	30.2	30.2	78%	774	100.00	3383078	CP051113.1
Streptomyces sp. RLB1-33 chromosome, complete genome	NA	2721243	30.2	30.2	100%	774	94.74	12127650	CP050974.1
Pseudochaenichthys georgianus genome assembly, chromosome: 21	South G	52239	30.2	30.2	78%	774	100.00	39591329	LR792566.1
Pseudochaenichthys georgianus genome assembly, chromosome: 19	South G	52239	30.2	30.2	78%	774	100.00	28991432	LR792564.1
Pseudochaenichthys georgianus genome assembly, chromosome: 7	South G	52239	30.2	30.2	78%	774	100.00	45376657	LR792552.1
Canis lupus familiaris breed Labrador retriever chromosome 07a	dog	9615	30.2	60.5	94%	774	100.00	80755643	CP050606.1
Canis lupus familiaris breed Labrador retriever chromosome 17a	dog	9615	30.2	60.5	84%	774	100.00	64150251	CP050603.1
Canis lupus familiaris breed Labrador retriever chromosome 21a	dog	9615	30.2	30.2	78%	774	100.00	51019060	CP050601.1
Canis lupus familiaris breed Labrador retriever chromosome 11a	dog	9615	30.2	30.2	78%	774	100.00	73584800	CP050600.1
Canis lupus familiaris breed Labrador retriever chromosome 32a	dog	9615	30.2	30.2	78%	774	100.00	65817495	CP050598.1
Canis lupus familiaris breed Labrador retriever chromosome 09a	dog	9615	30.2	30.2	78%	774	100.00	60580822	CP050593.1
Canis lupus familiaris breed Labrador retriever chromosome 23a	dog	9615	30.2	60.5	84%	774	100.00	52268927	CP050590.1
Canis lupus familiaris breed Labrador retriever chromosome 14a	dog	9615	30.2	30.2	78%	774	100.00	62855878	CP050589.1
Canis lupus familiaris breed Labrador retriever chromosome 28a	dog	9615	30.2	30.2	100%	774	94.74	41217541	CP050584.1
Canis lupus familiaris breed Labrador retriever chromosome 29a	dog	9615	30.2	30.2	78%	774	100.00	41746788	CP050580.1
Canis lupus familiaris breed Labrador retriever chromosome 12a	dog	9615	30.2	30.2	78%	774	100.00	72572423	CP050578.1
Canis lupus familiaris breed Labrador retriever chromosome 16a	dog	9615	30.2	30.2	78%	774	100.00	54734298	CP050577.1
Canis lupus familiaris breed Labrador retriever chromosome 02a	dog	9615	30.2	30.2	78%	774	100.00	83829384	CP050574.1
Canis lupus familiaris breed Labrador retriever chromosome 04a	dog	9615	30.2	30.2	100%	774	94.74	86937822	CP050572.1
Canis lupus familiaris breed	dog	9615	30.2	30.2	78%	774	100.00	38035513	CP050570.1

Labrador retriever chromosome 26a									
Canis lupus familiaris breed Labrador retriever chromosome 07b	dog	9615	30.2	60.5	94%	774	100.00	80755819	CP050637.1
Canis lupus familiaris breed Labrador retriever chromosome 09b	dog	9615	30.2	30.2	78%	774	100.00	60598474	CP050635.1
Canis lupus familiaris breed Labrador retriever chromosome 32b	dog	9615	30.2	30.2	78%	774	100.00	65810985	CP050634.1
Canis lupus familiaris breed Labrador retriever chromosome 23b	dog	9615	30.2	60.5	84%	774	100.00	52281894	CP050632.1
Canis lupus familiaris breed Labrador retriever chromosome 11b	dog	9615	30.2	30.2	78%	774	100.00	73564375	CP050630.1
Canis lupus familiaris breed Labrador retriever chromosome 29b	dog	9615	30.2	30.2	78%	774	100.00	41750700	CP050629.1
Canis lupus familiaris breed Labrador retriever chromosome 28b	dog	9615	30.2	30.2	100%	774	94.74	41256193	CP050626.1
Canis lupus familiaris breed Labrador retriever chromosome 04b	dog	9615	30.2	30.2	100%	774	94.74	86945037	CP050625.1
Canis lupus familiaris breed Labrador retriever chromosome 21b	dog	9615	30.2	30.2	78%	774	100.00	51014097	CP050624.1
Canis lupus familiaris breed Labrador retriever chromosome 14b	dog	9615	30.2	30.2	78%	774	100.00	62857718	CP050623.1
Canis lupus familiaris breed Labrador retriever chromosome 16b	dog	9615	30.2	30.2	78%	774	100.00	54760087	CP050618.1
Canis lupus familiaris breed Labrador retriever chromosome 12b	dog	9615	30.2	30.2	78%	774	100.00	72555136	CP050616.1
Canis lupus familiaris breed Labrador retriever chromosome 17b	dog	9615	30.2	60.5	84%	774	100.00	64169108	CP050614.1
Canis lupus familiaris breed Labrador retriever chromosome 02b	dog	9615	30.2	30.2	78%	774	100.00	83851004	CP050613.1
Canis lupus familiaris breed Labrador retriever chromosome 26b	dog	9615	30.2	30.2	78%	774	100.00	38033444	CP050610.1
Bacillus velezensis strain S4 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4065174	CP050424.1
Mycobacterium sp. DL440 chromosome	NA	2675523	30.2	30.2	78%	774	100.00	6381854	CP050191.1
Phytohabitans flavus NBRC 107702 DNA, complete genome	NA	1076124	30.2	30.2	78%	774	100.00	9607004	AP022870.1
PREDICTED: Catharus ustulatus acetyl-CoA carboxylase beta...	Swainso	91951	30.2	30.2	78%	774	100.00	8158	XM_033075801.1
PREDICTED: Tyto alba alba DS cell adhesion molecule (**DSCAM**),...	NA	507980	30.2	30.2	78%	774	100.00	1337	XM_033011403.1
PREDICTED: Tyto alba alba DS cell adhesion molecule	NA	507980	30.2	30.2	78%	774	100.00	5795	XR_004409769.1

(**DSCAM**),...									
PREDICTED: Tyto alba alba DS cell adhesion molecule (**DSCAM**),...	NA	507980	30.2	30.2	78%	774	100.00	3747	XM_033011401.1
PREDICTED: Tyto alba alba DS cell adhesion molecule (**DSCAM**),...	NA	507980	30.2	30.2	78%	774	100.00	4743	XM_033011399.1
PREDICTED: Tyto alba alba DS cell adhesion molecule (**DSCAM**),...	NA	507980	30.2	30.2	78%	774	100.00	6221	XM_033011398.1
PREDICTED: Tyto alba alba DS cell adhesion molecule (**DSCAM**),...	NA	507980	30.2	30.2	78%	774	100.00	6608	XM_033011397.1
PREDICTED: Tyto alba alba protein tyrosine phosphatase...	NA	507980	30.2	30.2	78%	774	100.00	1600	XM_033010620.1
PREDICTED: Tyto alba alba protein tyrosine phosphatase...	NA	507980	30.2	30.2	78%	774	100.00	2263	XM_033010619.1
PREDICTED: Amblyraja radiata cadherin EGF LAG seven-pass G-typ...	thorny	386614	30.2	30.2	78%	774	100.00	10540	XM_033039749.1
PREDICTED: Amblyraja radiata cadherin EGF LAG seven-pass G-typ...	thorny	386614	30.2	30.2	78%	774	100.00	10549	XM_033039748.1
PREDICTED: Amblyraja radiata cadherin EGF LAG seven-pass G-typ...	thorny	386614	30.2	30.2	78%	774	100.00	10582	XM_033039747.1
PREDICTED: Amblyraja radiata tonsoku like, DNA repair protein...	thorny	386614	30.2	30.2	78%	774	100.00	4607	XM_033039307.1
PREDICTED: Strigops habroptila protein tyrosine phosphatase...	Kakapo	2489341	30.2	30.2	78%	774	100.00	1435	XM_030469976.2
Apiotrichum mycotoxinovorans strain GMU1709 chromosome II	NA	252803	30.2	30.2	78%	774	100.00	7427248	CP049822.1
PREDICTED: Lontra canadensis aryl-hydrocarbon receptor repress...	Norther	76717	30.2	30.2	78%	774	100.00	2248	XM_032861814.1
PREDICTED: Chelonoidis abingdonii DS cell adhesion molecule...	Abingdo	106734	30.2	30.2	78%	774	100.00	1637	XM_032791679.1
PREDICTED: Chelonoidis abingdonii DS cell adhesion molecule...	Abingdo	106734	30.2	30.2	78%	774	100.00	4364	XM_032791678.1
PREDICTED: Chelonoidis abingdonii DS cell adhesion molecule...	Abingdo	106734	30.2	30.2	78%	774	100.00	2783	XM_032791677.1
PREDICTED: Chelonoidis abingdonii DS cell adhesion molecule...	Abingdo	106734	30.2	30.2	78%	774	100.00	4066	XM_032791676.1
PREDICTED: Chelonoidis abingdonii protein tyrosine phosphatase...	Abingdo	106734	30.2	30.2	78%	774	100.00	1706	XM_032789678.1
PREDICTED: Chelonoidis abingdonii protein tyrosine phosphatase...	Abingdo	106734	30.2	30.2	78%	774	100.00	2404	XM_032789668.1
Coregonus sp. 'balchen' genome assembly, chromosome: 11	NA	861768	30.2	30.2	78%	774	100.00	63177489	LR778263.1
Coregonus sp. 'balchen' genome assembly, chromosome: 1	NA	861768	30.2	30.2	78%	774	100.00	93459789	LR778253.1
Bacillus altitudinis strain ZAP62 chromosome	NA	293387	30.2	30.2	78%	774	100.00	4041532	CP049589.1

Mycobacterium tuberculosis strain 5005 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4418311	CP049108.1
PREDICTED: Chiroxiphia lanceolata uncharacterized LOC116797582...	lance-t	296741	30.2	30.2	78%	774	100.00	12307	XR_004360689.1
PREDICTED: Chiroxiphia lanceolata acetyl-CoA carboxylase beta...	lance-t	296741	30.2	30.2	78%	774	100.00	9690	XM_032706092.1
PREDICTED: Nasonia vitripennis enoyl-CoA hydratase...	jewel w	7425	30.2	30.2	78%	774	100.00	1376	XM_001604387.6
PREDICTED: Chiroxiphia lanceolata protein tyrosine phosphatase...	lance-t	296741	30.2	30.2	78%	774	100.00	1678	XM_032688001.1
PREDICTED: Chiroxiphia lanceolata protein tyrosine phosphatase...	lance-t	296741	30.2	30.2	78%	774	100.00	6176	XM_032687992.1
Crassostrea gigas strain QD chromosome 4	Pacific	29159	30.2	30.2	78%	774	100.00	62642562	CP048842.1
Mycobacterium tuberculosis strain TCDC11 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4418417	CP046728.2
Plectropomus leopardus DNA, chromosome 19, nearly complete...	leopard	160734	30.2	30.2	78%	774	100.00	28624681	AP022718.1
Plectropomus leopardus DNA, chromosome 17, nearly complete...	leopard	160734	30.2	30.2	78%	774	100.00	31444801	AP022716.1
Epinephelus fuscoguttatus DNA, LG22, complete sequence	brown-m	293821	30.2	30.2	78%	774	100.00	37548733	AP022696.1
Epinephelus fuscoguttatus DNA, LG18, complete sequence	brown-m	293821	30.2	30.2	78%	774	100.00	41318902	AP022692.1
Epinephelus fuscoguttatus DNA, LG2, complete sequence	brown-m	293821	30.2	30.2	78%	774	100.00	52288159	AP022676.1
Epinephelus fuscoguttatus DNA, LG1, complete sequence	brown-m	293821	30.2	30.2	78%	774	100.00	52788389	AP022675.1
PREDICTED: Camelus ferus **ZINC finger** protein 7 (**ZNF7**),...	Wild Ba	419612	30.2	30.2	78%	774	100.00	6494	XM_032468256.1
PREDICTED: Camelus ferus **ZINC finger** protein 7 (**ZNF7**),...	Wild Ba	419612	30.2	30.2	78%	774	100.00	6137	XM_032468255.1
PREDICTED: Camelus ferus **ZINC finger** protein 7 (**ZNF7**),...	Wild Ba	419612	30.2	30.2	78%	774	100.00	5521	XM_032468254.1
PREDICTED: Camelus ferus **ZINC finger** protein 7 (**ZNF7**),...	Wild Ba	419612	30.2	30.2	78%	774	100.00	5603	XM_032468253.1
PREDICTED: Camelus ferus **ZINC finger** protein 7 (**ZNF7**),...	Wild Ba	419612	30.2	30.2	78%	774	100.00	5606	XM_032468252.1
PREDICTED: Camelus ferus **ZINC finger** protein 7 (**ZNF7**),...	Wild Ba	419612	30.2	30.2	78%	774	100.00	5810	XM_032468251.1
PREDICTED: Camelus ferus **ZINC finger** protein 7 (**ZNF7**),...	Wild Ba	419612	30.2	30.2	78%	774	100.00	5813	XM_032468250.1
PREDICTED: Camelus ferus	Wild Ba	419612	30.2	30.2	78%	774	100.00	4411	XM_032461208.1

junctophilin 2 (JPH2), mRNA									
PREDICTED: Coturnix japonica uncharacterized LOC107306501...	Japanes	93934	30.2	30.2	78%	774	100.00	6512	XR_001552164.2
PREDICTED: Drosophila ananassae PX domain-containing protein...	NA	7217	30.2	30.2	78%	774	100.00	3480	XM_001960967.3
PREDICTED: Coturnix japonica RAB11 family interacting protein ...	Japanes	93934	30.2	30.2	100%	774	94.74	3427	XM_015877196.2
Aphantopus hyperantus genome assembly, chromosome: 1	ringlet	2795564	30.2	30.2	78%	774	100.00	18856181	LR761647.1
Crassostrea gigas genome assembly, linkage group: LG8	Pacific	29159	30.2	30.2	78%	774	100.00	58462999	LR761641.1
Nitrospira sp. KM1 DNA, complete genome	NA	1936990	30.2	30.2	78%	774	100.00	4509223	AP022671.1
PREDICTED: Phoca vitulina **ZINC finger** protein 7 (**ZNF7**),...	harbor	9720	30.2	30.2	78%	774	100.00	5514	XM_032415540.1
PREDICTED: Phoca vitulina **ZINC finger** protein 7 (**ZNF7**),...	harbor	9720	30.2	30.2	78%	774	100.00	5405	XM_032415539.1
PREDICTED: Phoca vitulina **ZINC finger** protein 7 (**ZNF7**),...	harbor	9720	30.2	30.2	78%	774	100.00	5548	XM_032415538.1
PREDICTED: Phoca vitulina **ZINC finger** protein 7 (**ZNF7**),...	harbor	9720	30.2	30.2	78%	774	100.00	5438	XM_032415537.1
PREDICTED: Phoca vitulina **ZINC finger** protein 7 (**ZNF7**),...	harbor	9720	30.2	30.2	78%	774	100.00	5370	XM_032415536.1
PREDICTED: Phoca vitulina **ZINC finger** protein 7 (**ZNF7**),...	harbor	9720	30.2	30.2	78%	774	100.00	5756	XM_032415535.1
PREDICTED: Phoca vitulina **ZINC finger** protein 7 (**ZNF7**),...	harbor	9720	30.2	30.2	78%	774	100.00	5878	XM_032415534.1
PREDICTED: Phoca vitulina **ZINC finger** protein 7 (**ZNF7**),...	harbor	9720	30.2	30.2	78%	774	100.00	5769	XM_032415533.1
Streptomyces sp. S4.7 chromosome, complete genome	NA	2705439	30.2	30.2	100%	774	94.74	7920066	CP048397.1
Mycolicibacterium helvum JCM 30396 DNA, complete genome	NA	1534349	30.2	30.2	78%	774	100.00	6400811	AP022596.1
PREDICTED: Mustela erminea aryl-hydrocarbon receptor repressor...	ermine	36723	30.2	30.2	78%	774	100.00	5428	XM_032337869.1
PREDICTED: Thamnophis elegans estrogen related receptor beta...	Western	35005	30.2	30.2	78%	774	100.00	1185	XM_032224567.1
PREDICTED: Thamnophis elegans estrogen related receptor beta...	Western	35005	30.2	30.2	78%	774	100.00	1469	XM_032224558.1
PREDICTED: Aythya fuligula estrogen related receptor beta...	tufted	219594	30.2	30.2	78%	774	100.00	1356	XM_032188954.1
PREDICTED: Aythya fuligula estrogen related receptor beta...	tufted	219594	30.2	30.2	78%	774	100.00	1185	XM_032188952.1
PREDICTED: Aythya fuligula	tufted	219594	30.2	30.2	78%	774	100.00	1315	XM_032188951.1

estrogen related receptor beta...									
PREDICTED: Aythya fuligula DS cell adhesion molecule (DSCAM),...	tufted	219594	30.2	30.2	78%	774	100.00	1615	XM_032188250.1
PREDICTED: Aythya fuligula DS cell adhesion molecule (DSCAM),...	tufted	219594	30.2	30.2	78%	774	100.00	4048	XM_032188242.1
PREDICTED: Aythya fuligula DS cell adhesion molecule (DSCAM),...	tufted	219594	30.2	30.2	78%	774	100.00	6126	XM_032188234.1
Aspergillus alliaceus Calcipressin (BDW43DRAFT_34037), mRNA	NA	209559	30.2	30.2	78%	774	100.00	1534	XM_032049936.1
PREDICTED: Corvus moneduloides protein tyrosine phosphatase...	New Cal	1196302	30.2	30.2	78%	774	100.00	2117	XM_032121496.1
PREDICTED: Corvus moneduloides protein tyrosine phosphatase...	New Cal	1196302	30.2	30.2	78%	774	100.00	1779	XM_032121488.1
PREDICTED: Corvus moneduloides supervillin (SVIL), transcript...	New Cal	1196302	30.2	30.2	78%	774	100.00	8420	XM_032100684.1
PREDICTED: Corvus moneduloides grainyhead like transcription...	New Cal	1196302	30.2	30.2	78%	774	100.00	5017	XM_032104296.1
PREDICTED: Corvus moneduloides grainyhead like transcription...	New Cal	1196302	30.2	30.2	78%	774	100.00	5044	XM_032104295.1
PREDICTED: Corvus moneduloides grainyhead like transcription...	New Cal	1196302	30.2	30.2	78%	774	100.00	5052	XM_032104294.1
PREDICTED: Corvus moneduloides grainyhead like transcription...	New Cal	1196302	30.2	30.2	78%	774	100.00	5079	XM_032104293.1
Bacillus velezensis strain SRCM102747 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4100473	CP028211.1
Bacillus velezensis strain SRCM102746 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3963855	CP028210.1
Bacillus velezensis strain SRCM102744 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4100472	CP028208.1
Bacillus velezensis strain SRCM102743 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3963851	CP028207.1
Bacillus velezensis strain SRCM102742 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4018060	CP028206.1
Bacillus velezensis strain SRCM102741 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4018059	CP028205.1
Solanum pinnatisectum cultivar CGN17745 chromosome 3	tansyle	50273	30.2	30.2	78%	774	100.00	62237402	CP047566.1
Trichoderma reesei strain CBS999.97 chromosome V, complete...	NA	51453	30.2	30.2	78%	774	100.00	4096940	CP020877.1
Streptomyces sp. HM190 chromosome, complete genome	NA	2695266	30.2	30.2	78%	774	100.00	7762826	CP047318.1
Mycobacterium tuberculosis strain TCDC3 chromosome	NA	1773	30.2	30.2	78%	774	100.00	4413983	CP047258.1

Bacillus velezensis strain DH8043 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3966723	CP047268.1
Lutra lutra genome assembly, chromosome: X	Eurasia	9657	30.2	30.2	78%	774	100.00	99689450	LR738421.1
Lutra lutra genome assembly, chromosome: 17	Eurasia	9657	30.2	120	100%	774	100.00	60348511	LR738419.1
Lutra lutra genome assembly, chromosome: 15	Eurasia	9657	30.2	30.2	78%	774	100.00	69992071	LR738417.1
Mycobacterium tuberculosis strain TCDC7 chromosome	NA	1773	30.2	30.2	78%	774	100.00	4641184	CP047163.1
Mycobacterium tuberculosis strain TCDC10 chromosome	NA	1773	30.2	30.2	78%	774	100.00	4419577	CP047164.1
Streptomyces sp. Tu 2975 chromosome, complete genome	NA	2676871	30.2	30.2	78%	774	100.00	7623788	CP047140.1
PREDICTED: Sarcophilus harrisii DS cell adhesion molecule...	Tasmani	9305	30.2	30.2	78%	774	100.00	6552	XM_031959192.1
PREDICTED: Sarcophilus harrisii DS cell adhesion molecule...	Tasmani	9305	30.2	30.2	78%	774	100.00	6775	XM_031959191.1
PREDICTED: Nasonia vitripennis enoyl-CoA hydratase...	jewel w	7425	30.2	30.2	78%	774	100.00	1176	XM_016984045.2
Bacillus velezensis strain BA-26 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4035062	CP046918.1
Vibrio parahaemolyticus strain 2013V-1174 chromosome 1, comple...	NA	670	30.2	30.2	78%	774	100.00	3369685	CP046787.1
PREDICTED: Xenopus tropicalis fidgetin like2 (fignl2), mRNA	tropica	8364	30.2	30.2	78%	774	100.00	9845	XM_004911907.3
Bacillus sp. ms-22 chromosome, complete genome	NA	2683680	30.2	30.2	78%	774	100.00	3629561	CP046653.1
PREDICTED: Anarrhichthys ocellatus KIAA0753 ortholog (kiaa0753...	wolf-ee	433405	30.2	30.2	78%	774	100.00	5729	XR_004213721.1
PREDICTED: Anarrhichthys ocellatus KIAA0753 ortholog (kiaa0753...	wolf-ee	433405	30.2	30.2	78%	774	100.00	4580	XM_031873640.1
PREDICTED: Anarrhichthys ocellatus KIAA0753 ortholog (kiaa0753...	wolf-ee	433405	30.2	30.2	78%	774	100.00	4622	XM_031873639.1
PREDICTED: Anarrhichthys ocellatus KIAA0753 ortholog (kiaa0753...	wolf-ee	433405	30.2	30.2	78%	774	100.00	4625	XM_031873638.1
Mycobacterium tuberculosis strain SIT745/EAI1-MYS chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4414742	CP046529.1
Bacillus velezensis strain HN-Q-8 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4004056	CP045711.1
PREDICTED: Oncorhynchus kisutch microtubule-associated protein...	coho sa	8019	30.2	30.2	78%	774	100.00	6888	XM_031806591.1
PREDICTED: Oncorhynchus kisutch microtubule-associated protein...	coho sa	8019	30.2	30.2	78%	774	100.00	6903	XM_020462947.2
PREDICTED: Oncorhynchus kisutch microtubule-associated protein...	coho sa	8019	30.2	30.2	78%	774	100.00	6960	XM_031806590.1
PREDICTED: Oncorhynchus kisutch microtubule-associated	coho sa	8019	30.2	30.2	78%	774	100.00	6975	XM_020462946.2

protein...									
PREDICTED: Oncorhynchus kisutch microtubule-associated protein...	coho sa	8019	30.2	30.2	78%	774	100.00	7005	XM_031806589.1
PREDICTED: Oncorhynchus kisutch microtubule-associated protein...	coho sa	8019	30.2	30.2	78%	774	100.00	7020	XM_020462945.2
PREDICTED: Oncorhynchus kisutch microtubule-associated protein...	coho sa	8019	30.2	30.2	78%	774	100.00	7079	XM_020462943.2
PREDICTED: Oncorhynchus kisutch microtubule-associated protein...	coho sa	8019	30.2	30.2	78%	774	100.00	7098	XM_020462944.2
PREDICTED: Oncorhynchus kisutch microtubule-associated protein...	coho sa	8019	30.2	30.2	78%	774	100.00	7110	XM_020462942.2
PREDICTED: Oncorhynchus kisutch microtubule-associated protein...	coho sa	8019	30.2	30.2	78%	774	100.00	7113	XM_020462941.2
PREDICTED: Oncorhynchus kisutch mucin-2-like (LOC116374719), mRNA	coho sa	8019	30.2	30.2	78%	774	100.00	4624	XM_031829274.1
PREDICTED: Oncorhynchus kisutch scavenger receptor cysteine-ri...	coho sa	8019	30.2	30.2	78%	774	100.00	1628	XM_031820781.1
PREDICTED: Oncorhynchus kisutch uncharacterized LOC116365180...	coho sa	8019	30.2	30.2	78%	774	100.00	345	XR_004208077.1
PREDICTED: Oncorhynchus kisutch uncharacterized LOC116365072...	coho sa	8019	30.2	30.2	78%	774	100.00	349	XR_004208065.1
PREDICTED: Oncorhynchus kisutch uncharacterized LOC116364640...	coho sa	8019	30.2	30.2	78%	774	100.00	353	XR_004208030.1
PREDICTED: Oncorhynchus kisutch uncharacterized LOC116364462...	coho sa	8019	30.2	30.2	78%	774	100.00	345	XR_004208002.1
PREDICTED: Oncorhynchus kisutch uncharacterized LOC116364450...	coho sa	8019	30.2	30.2	78%	774	100.00	352	XR_004207999.1
PREDICTED: Oncorhynchus kisutch uncharacterized LOC116360140...	coho sa	8019	30.2	30.2	78%	774	100.00	346	XR_004206927.1
PREDICTED: Oncorhynchus kisutch uncharacterized LOC109877147...	coho sa	8019	30.2	30.2	78%	774	100.00	848	XM_031814793.1
Mycobacterium tuberculosis strain FDAARGOS_751 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4441988	CP046308.1
Mycobacterium tuberculosis strain FDAARGOS_750 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4434666	CP046309.1
Haloactinobacterium sp. HY164 chromosome, complete genome	NA	2675754	30.2	30.2	78%	774	100.00	5648255	CP046175.1
PREDICTED: Vicugna pacos **ZINC finger** protein 7 (**ZNF7**),...	alpaca	30538	30.2	30.2	78%	774	100.00	4815	XM_015245211.2
PREDICTED: Vicugna pacos **ZINC finger** protein 7 (**ZNF7**),...	alpaca	30538	30.2	30.2	78%	774	100.00	4331	XM_031690499.1
PREDICTED: Vicugna pacos	alpaca	30538	30.2	30.2	78%	774	100.00	4818	XM_031690498.1

ZINC finger protein 7 (**ZNF7**),...									
PREDICTED: Vicugna pacos junctophilin 2 (JPH2), mRNA	alpaca	30538	30.2	30.2	78%	774	100.00	4025	XM_031687976.1
PREDICTED: Vicugna pacos proline-rich protein 23A...	alpaca	30538	30.2	30.2	78%	774	100.00	1747	XM_031676897.1
Sciurus vulgaris genome assembly, chromosome: 15	Eurasia	55149	30.2	30.2	78%	774	100.00	90997183	LR738626.1
Sciurus vulgaris genome assembly, chromosome: 14	Eurasia	55149	30.2	151	89%	774	100.00	99237486	LR738625.1
Sciurus carolinensis genome assembly, chromosome: 18	gray sq	30640	30.2	60.5	78%	774	100.00	41557064	LR738608.1
Neostethus bicornis genome assembly, chromosome: 8	NA	300306	30.2	30.2	78%	774	100.00	26260016	LR738556.1
Neostethus bicornis genome assembly, chromosome: 21	NA	300306	30.2	30.2	78%	774	100.00	30721030	LR738549.1
PREDICTED: Clupea harengus protein-glutamine...	Atlanti	7950	30.2	30.2	78%	774	100.00	2372	XM_031566961.1
PREDICTED: Clupea harengus protein-glutamine...	Atlanti	7950	30.2	30.2	78%	774	100.00	2520	XM_031566960.1
PREDICTED: Clupea harengus 39S ribosomal protein L23,...	Atlanti	7950	30.2	30.2	78%	774	100.00	1036	XM_012832377.2
PREDICTED: Clupea harengus PH domain leucine-rich...	Atlanti	7950	30.2	30.2	100%	774	94.74	7499	XM_031563328.1
Mycobacterium tuberculosis strain AUSMDU00018547 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4414769	CP045962.1
PREDICTED: Nymphaea colorata uncharacterized LOC116262305...	NA	210225	30.2	30.2	78%	774	100.00	3846	XM_031641544.1
Fusarium fujikuroi strain Augusto2 chromosome V	NA	5127	30.2	30.2	78%	774	100.00	4490296	CP023093.1
Fusarium fujikuroi strain I1.3 chromosome V	NA	5127	30.2	30.2	78%	774	100.00	4532787	CP023105.1
Fusarium fujikuroi strain CSV1 chromosome V	NA	5127	30.2	30.2	78%	774	100.00	4485856	CP023081.1
Mycobacterium tuberculosis variant bovis strain Mb3601 genome...	NA	1765	30.2	30.2	78%	774	100.00	4365068	LR699570.1
Streptomyces tsukubensis strain AT3 chromosome, complete genome	NA	83656	30.2	30.2	100%	774	94.74	8615214	CP045178.1
PREDICTED: Camelus dromedarius **ZINC finger** protein 7 (**ZNF7**),...	Arabian	9838	30.2	30.2	78%	774	100.00	6608	XM_010998732.2
PREDICTED: Camelus dromedarius **ZINC finger** protein 7 (**ZNF7**),...	Arabian	9838	30.2	30.2	78%	774	100.00	6124	XM_031439946.1
PREDICTED: Camelus dromedarius **ZINC finger** protein 7 (**ZNF7**),...	Arabian	9838	30.2	30.2	78%	774	100.00	5855	XM_031439945.1
PREDICTED: Camelus dromedarius **ZINC finger** protein 7 (**ZNF7**),...	Arabian	9838	30.2	30.2	78%	774	100.00	5959	XM_031439944.1
PREDICTED: Camelus dromedarius junctophilin 2 (JPH2), mRNA	Arabian	9838	30.2	30.2	78%	774	100.00	4411	XM_031433768.1
PREDICTED: Mastomys coucha uncharacterized LOC116072356...	souther	35658	30.2	30.2	78%	774	100.00	1338	XR_004111411.1

PREDICTED: Mastomys coucha uncharacterized LOC116072356...	souther	35658	30.2	30.2	78%	774	100.00	1405	XR_004111410.1
PREDICTED: Mastomys coucha uncharacterized LOC116072356...	souther	35658	30.2	30.2	78%	774	100.00	1297	XR_004111409.1
PREDICTED: Mastomys coucha uncharacterized LOC116072356...	souther	35658	30.2	30.2	78%	774	100.00	1180	XR_004111408.1
PREDICTED: Mastomys coucha haptoglobin (LOC116070147), mRNA	souther	35658	30.2	30.2	100%	774	94.74	1303	XM_031341373.1
Fusarium proliferatum ET1 non-ribosomal peptide synthetase...	NA	1227346	30.2	30.2	78%	774	100.00	7422	XM_031234467.1
Nannochloropsis oceanica strain BR2 chromosome 17	NA	145522	30.2	30.2	78%	774	100.00	830381	CP044592.1
Nannochloropsis oceanica strain KB1 chromosome 17	NA	145522	30.2	30.2	78%	774	100.00	783173	CP044560.1
Fusarium odoratissimum NRRL 54006 uncharacterized protein...	NA	1089451	30.2	30.2	78%	774	100.00	7570	XM_031209697.1
Fusarium odoratissimum NRRL 54006 uncharacterized protein...	NA	1089451	30.2	30.2	78%	774	100.00	9895	XM_031209696.1
Fusarium odoratissimum NRRL 54006 uncharacterized protein...	NA	1089451	30.2	30.2	78%	774	100.00	9029	XM_031209694.1
Fusarium oxysporum NRRL 32931 uncharacterized protein...	NA	660029	30.2	30.2	78%	774	100.00	7489	XM_031183306.1
Fusarium oxysporum NRRL 32931 uncharacterized protein...	NA	660029	30.2	30.2	78%	774	100.00	6815	XM_031183308.1
Fusarium oxysporum NRRL 32931 uncharacterized protein...	NA	660029	30.2	30.2	78%	774	100.00	7576	XM_031183305.1
Streptomyces coelicolor A3(2) strain CFB_NBC_0001 chromosome,...	NA	100226	30.2	30.2	78%	774	100.00	8667664	CP042324.1
Phialemoniopsis curvata uncharacterized protein (E0L32_007294)...	NA	1093900	30.2	30.2	78%	774	100.00	2190	XM_031142023.1
PREDICTED: Geospiza fortis grainyhead like transcription facto...	medium	48883	30.2	30.2	78%	774	100.00	4877	XM_014306759.2
PSEUDOMONAS umsongensis strain GO16 chromosome	NA	198618	30.2	30.2	78%	774	100.00	7269974	CP044409.1
Vibrio parahaemolyticus G2910 K55_G2910 genomic sequence	NA	670	30.2	30.2	78%	774	100.00	73400	MK482085.1
Mycobacterium tuberculosis strain L chromosome, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4416671	CP044345.1
Bacillus velezensis strain FJAT-46737 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3995978	CP044133.1
Thalassophryne amazonica genome assembly, chromosome: 21	NA	390379	30.2	60.5	84%	774	100.00	40587171	LR722986.1
Thalassophryne amazonica genome assembly, chromosome: 20	NA	390379	30.2	120	78%	774	100.00	70111961	LR722985.1
Thalassophryne amazonica genome assembly, chromosome: 19	NA	390379	30.2	181	94%	774	100.00	72818716	LR722984.1
Thalassophryne amazonica	NA	390379	30.2	151	78%	774	100.00	77050466	LR722982.1

genome assembly, chromosome: 17									
Thalassophryne amazonica genome assembly, chromosome: 16	NA	390379	30.2	90.7	78%	774	100.00	92122960	LR722981.1
Thalassophryne amazonica genome assembly, chromosome: 13	NA	390379	30.2	120	78%	774	100.00	99659484	LR722978.1
PREDICTED: Camarhynchus parvulus grainyhead like transcription...	NA	87175	30.2	30.2	78%	774	100.00	4927	XM_030946441.1
Streptomyces kanamyceticus strain ATCC 12853 chromosome,...	NA	1967	30.2	30.2	78%	774	100.00	10133897	CP023699.1
PREDICTED: Globicephala melas uncharacterized LOC115863712...	long-fi	9731	30.2	30.2	78%	774	100.00	6257	XR_004043637.1
PREDICTED: Globicephala melas glutaminyl-peptide...	long-fi	9731	30.2	30.2	78%	774	100.00	1070	XM_030857918.1
PREDICTED: Globicephala melas glutaminyl-peptide...	long-fi	9731	30.2	30.2	78%	774	100.00	1068	XM_030857917.1
PREDICTED: Delphinapterus leucas uncharacterized LOC111181698...	beluga	9749	30.2	30.2	78%	774	100.00	6134	XR_004023989.1
PREDICTED: Delphinapterus leucas uncharacterized LOC111181698...	beluga	9749	30.2	30.2	78%	774	100.00	5886	XR_002646566.2
PREDICTED: Chanos chanos SPHK1 interactor, AKAP domain...	milkfis	29144	30.2	30.2	78%	774	100.00	5100	XM_030765183.1
PREDICTED: Chanos chanos sperm flagellar 2 (spef2), mRNA	milkfis	29144	30.2	30.2	78%	774	100.00	5082	XM_030791702.1
Bacillus altitudinis strain CHB19 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3867833	CP043559.1
Bacillus amyloliquefaciens strain ARP23 chromosome, complete...	NA	1390	30.2	30.2	78%	774	100.00	4018867	CP035899.1
Bacillus velezensis strain ONU 553 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3934563	CP043416.1
PREDICTED: Cannabis sativa uncharacterized aarF...	NA	3483	30.2	30.2	78%	774	100.00	2531	XM_030637679.1
PREDICTED: Cannabis sativa uncharacterized aarF...	NA	3483	30.2	30.2	78%	774	100.00	2534	XM_030637672.1
PREDICTED: Gopherus evgoodei protein tyrosine phosphatase...	Goodes	1825980	30.2	30.2	78%	774	100.00	2350	XM_030552712.1
PREDICTED: Gopherus evgoodei protein tyrosine phosphatase...	Goodes	1825980	30.2	30.2	78%	774	100.00	1701	XM_030552710.1
PREDICTED: Gopherus evgoodei protein tyrosine phosphatase...	Goodes	1825980	30.2	30.2	78%	774	100.00	2315	XM_030552709.1
PREDICTED: Gopherus evgoodei protein tyrosine phosphatase...	Goodes	1825980	30.2	30.2	78%	774	100.00	2459	XM_030552708.1
PREDICTED: Gopherus evgoodei DS cell adhesion molecule (**DSCAM**)...	Goodes	1825980	30.2	30.2	78%	774	100.00	1867	XM_030577517.1
PREDICTED: Gopherus evgoodei DS cell adhesion	Goodes	1825980	30.2	30.2	78%	774	100.00	2990	XM_030577508.1

molecule (**DSCAM**)...									
PREDICTED: Gopherus evgoodei DS cell adhesion molecule (**DSCAM**)...	Goodes	1825980	30.2	30.2	78%	774	100.00	4981	XM_030577499.1
PREDICTED: Gopherus evgoodei DS cell adhesion molecule (**DSCAM**)...	Goodes	1825980	30.2	30.2	78%	774	100.00	3014	XM_030577488.1
PREDICTED: Gopherus evgoodei DS cell adhesion molecule (**DSCAM**)...	Goodes	1825980	30.2	30.2	78%	774	100.00	4296	XM_030577483.1
PREDICTED: Gopherus evgoodei DS cell adhesion molecule (**DSCAM**)...	Goodes	1825980	30.2	30.2	78%	774	100.00	6859	XM_030577471.1
PREDICTED: Strigops habroptila protein tyrosine phosphatase...	Kakapo	2489341	30.2	30.2	78%	774	100.00	2078	XM_030469967.1
PREDICTED: Strigops habroptila protein tyrosine phosphatase...	Kakapo	2489341	30.2	30.2	78%	774	100.00	4676	XM_030469959.1
PREDICTED: Strigops habroptila protein tyrosine phosphatase...	Kakapo	2489341	30.2	30.2	78%	774	100.00	1711	XM_030469949.1
PREDICTED: Strigops habroptila protein tyrosine phosphatase...	Kakapo	2489341	30.2	30.2	78%	774	100.00	2296	XM_030469940.1
PREDICTED: Strigops habroptila DS cell adhesion molecule...	Kakapo	2489341	30.2	30.2	78%	774	100.00	3356	XR_003990146.1
PREDICTED: Strigops habroptila DS cell adhesion molecule...	Kakapo	2489341	30.2	30.2	78%	774	100.00	4106	XM_030477065.1
PREDICTED: Strigops habroptila DS cell adhesion molecule...	Kakapo	2489341	30.2	30.2	78%	774	100.00	6623	XM_030477064.1
PREDICTED: Strigops habroptila DS cell adhesion molecule...	Kakapo	2489341	30.2	30.2	78%	774	100.00	6697	XM_030477062.1
Mycobacterium tuberculosis variant bovis strain 1 chromosome	NA	1765	30.2	30.2	78%	774	100.00	4349904	CP040832.1
PREDICTED: Sparus aurata dynein heavy chain 5, axonemal-like...	gilthea	8175	30.2	30.2	78%	774	100.00	14547	XM_030398060.1
PREDICTED: Drosophila navojoa Krueppel homolog 1 (LOC108656122...	NA	7232	30.2	30.2	78%	774	100.00	2166	XM_018108065.2
Chanos chanos genome assembly, chromosome: 14	milkfis	29144	30.2	30.2	78%	774	100.00	21941848	LR697119.1
Chanos chanos genome assembly, chromosome: 6	milkfis	29144	30.2	30.2	78%	774	100.00	50300218	LR697111.1
Chanos chanos genome assembly, chromosome: 2	milkfis	29144	30.2	30.2	78%	774	100.00	59736555	LR697107.1
Chanos chanos genome assembly, chromosome: 1	milkfis	29144	30.2	30.2	78%	774	100.00	63121898	LR697106.1
Chanos chanos genome assembly, chromosome: 15	milkfis	29144	30.2	30.2	78%	774	100.00	20460689	LR697120.1
Bacillus altitudinis strain Cr2-1 chromosome	NA	293387	30.2	30.2	78%	774	100.00	3748650	CP031774.1
Mycobacterium tuberculosis strain MT-0080 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4426525	CP041207.1
PREDICTED: Sphaeramia orbicularis dynein heavy chain 5,...	orbicul	375764	30.2	30.2	78%	774	100.00	13658	XM_030123886.1
PREDICTED: Sphaeramia orbicularis putative sodium-coupled...	orbicul	375764	30.2	30.2	78%	774	100.00	1663	XM_030128745.1
PREDICTED: Sphaeramia orbicularis transcription	orbicul	375764	30.2	30.2	78%	774	100.00	5150	XM_030125035.1

initiation...									
PREDICTED: Sphaeramia orbicularis transcription initiation...	orbicul	375764	30.2	30.2	78%	774	100.00	5297	XM_030125025.1
PREDICTED: Sphaeramia orbicularis GTPase Era, mitochondrial-li...	orbicul	375764	30.2	30.2	78%	774	100.00	1657	XM_030130560.1
Sparus aurata genome assembly, chromosome: 21	gilthea	8175	30.2	30.2	78%	774	100.00	35160130	LR537141.1
Sparus aurata genome assembly, chromosome: 19	gilthea	8175	30.2	30.2	78%	774	100.00	31047742	LR537139.1
Sparus aurata genome assembly, chromosome: 2	gilthea	8175	30.2	30.2	78%	774	100.00	36133474	LR537122.1
Haemonchus contortus strain NZ_Hco_NP chromosome 4	barber	6289	30.2	30.2	78%	774	100.00	92053285	CP035804.1
Haemonchus contortus strain NZ_Hco_NP chromosome 2	barber	6289	30.2	30.2	78%	774	100.00	77295023	CP035801.1
PREDICTED: Aquila chrysaetos chrysaetos DS cell adhesion...	NA	223781	30.2	30.2	78%	774	100.00	2310	XM_030020088.1
PREDICTED: Aquila chrysaetos chrysaetos DS cell adhesion...	NA	223781	30.2	30.2	78%	774	100.00	4726	XM_030020087.1
PREDICTED: Salarias fasciatus snake venom serine protease...	jewelle	181472	30.2	30.2	78%	774	100.00	940	XM_030094550.1
PREDICTED: Salarias fasciatus kallikrein-6-like (LOC115390356)...	jewelle	181472	30.2	30.2	78%	774	100.00	1093	XM_030094198.1
PREDICTED: Myripristis murdjan pyridoxal kinase-like...	pinecon	586833	30.2	30.2	78%	774	100.00	2473	XM_030081288.1
PREDICTED: Manacus vitellinus acetyl-CoA carboxylase beta...	golden-	328815	30.2	30.2	78%	774	100.00	9463	XM_029961183.1
PREDICTED: Manacus vitellinus protein tyrosine phosphatase...	golden-	328815	30.2	30.2	78%	774	100.00	1556	XM_029959393.1
PREDICTED: Terrapene carolina triunguis protein tyrosine...	Three-t	2587831	30.2	30.2	78%	774	100.00	1575	XM_026660897.2
PREDICTED: Terrapene carolina triunguis Down syndrome cell...	Three-t	2587831	30.2	30.2	78%	774	100.00	5583	XM_029911625.1
PREDICTED: Terrapene carolina triunguis Down syndrome cell...	Three-t	2587831	30.2	30.2	78%	774	100.00	5637	XM_029911623.1
PREDICTED: Terrapene carolina triunguis Down syndrome cell...	Three-t	2587831	30.2	30.2	78%	774	100.00	5586	XM_029911464.1
PREDICTED: Terrapene carolina triunguis Down syndrome cell...	Three-t	2587831	30.2	30.2	78%	774	100.00	5640	XM_029911462.1
Gadus morhua genome assembly, chromosome: 20	Atlanti	8049	30.2	30.2	78%	774	100.00	24843429	LR633962.1
Gadus morhua genome assembly, chromosome: 11	Atlanti	8049	30.2	30.2	78%	774	100.00	30713045	LR633953.1
Gadus morhua genome assembly, chromosome: 9	Atlanti	8049	30.2	30.2	78%	774	100.00	26487948	LR633951.1
Gadus morhua genome assembly, chromosome: 7	Atlanti	8049	30.2	30.2	78%	774	100.00	34137969	LR633949.1
Gadus morhua genome assembly, chromosome: 6	Atlanti	8049	30.2	30.2	78%	774	100.00	27762770	LR633948.1
Gadus morhua genome assembly, chromosome: 1	Atlanti	8049	30.2	30.2	78%	774	100.00	30875876	LR633943.1
PREDICTED: Takifugu rubripes transcription cofactor...	torafug	31033	30.2	30.2	78%	774	100.00	2221	XM_003963404.3

PREDICTED: Takifugu rubripes transcription cofactor...	torafug	31033	30.2	30.2	78%	774	100.00	2219	XM_011602560.2
PREDICTED: Takifugu rubripes transcription cofactor...	torafug	31033	30.2	30.2	78%	774	100.00	2308	XM_011602558.2
PREDICTED: Takifugu rubripes SCO-spondin-like (LOC105419748),...	torafug	31033	30.2	30.2	78%	774	100.00	17441	XM_029843166.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 16	NA	223781	30.2	60.5	84%	774	100.00	30610376	LR606196.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 7	NA	223781	30.2	60.5	78%	774	100.00	47779391	LR606187.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 4	NA	223781	30.2	30.2	78%	774	100.00	77266225	LR606184.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: Z	NA	223781	30.2	60.5	78%	774	100.00	88216475	LR606180.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 21	NA	223781	30.2	30.2	78%	774	100.00	24756580	LR606201.1
Aquila chrysaetos chrysaetos genome assembly, chromosome: 17	NA	223781	30.2	30.2	78%	774	100.00	29699254	LR606197.1
PREDICTED: Salmo trutta microtubule-associated protein tau-lik...	river t	8032	30.2	30.2	78%	774	100.00	8031	XM_029705014.1
PREDICTED: Salmo trutta microtubule-associated protein tau-lik...	river t	8032	30.2	30.2	78%	774	100.00	8151	XM_029705013.1
PREDICTED: Salmo trutta microtubule-associated protein tau-lik...	river t	8032	30.2	30.2	78%	774	100.00	8226	XM_029705012.1
PREDICTED: Salmo trutta microtubule-associated protein tau-lik...	river t	8032	30.2	30.2	78%	774	100.00	8239	XM_029705011.1
PREDICTED: Salmo trutta microtubule-associated protein tau-lik...	river t	8032	30.2	30.2	78%	774	100.00	8242	XM_029705010.1
PREDICTED: Oncorhynchus nerka mitochondrial import receptor...	sockeye	8023	30.2	30.2	78%	774	100.00	1376	XM_029657969.1
PREDICTED: Oncorhynchus nerka mitochondrial import receptor...	sockeye	8023	30.2	30.2	78%	774	100.00	1371	XM_029657968.1
PREDICTED: Oncorhynchus nerka microtubule-associated protein...	sockeye	8023	30.2	30.2	78%	774	100.00	6897	XM_029623603.1
PREDICTED: Oncorhynchus nerka microtubule-associated protein...	sockeye	8023	30.2	30.2	78%	774	100.00	6975	XM_029623602.1
PREDICTED:	sockeye	8023	30.2	30.2	78%	774	100.00	7020	XM_029623601.1

Oncorhynchus nerka microtubule-associated protein...									
PREDICTED: Oncorhynchus nerka microtubule-associated protein...	sockeye	8023	30.2	30.2	78%	774	100.00	7425	XM_029623600.1
PREDICTED: Oncorhynchus nerka microtubule-associated protein...	sockeye	8023	30.2	30.2	78%	774	100.00	7075	XM_029623598.1
PREDICTED: Oncorhynchus nerka microtubule-associated protein...	sockeye	8023	30.2	30.2	78%	774	100.00	6986	XM_029623597.1
PREDICTED: Oncorhynchus nerka microtubule-associated protein...	sockeye	8023	30.2	30.2	78%	774	100.00	7090	XM_029623596.1
PREDICTED: Oncorhynchus nerka microtubule-associated protein...	sockeye	8023	30.2	30.2	78%	774	100.00	7107	XM_029623595.1
PREDICTED: Oncorhynchus nerka microtubule-associated protein...	sockeye	8023	30.2	30.2	78%	774	100.00	7110	XM_029623594.1
PREDICTED: Oncorhynchus nerka uncharacterized LOC115121394...	sockeye	8023	30.2	30.2	78%	774	100.00	683	XR_003862316.1
Myripristis murdjan genome assembly, chromosome: 21	pinecon	586833	30.2	30.2	78%	774	100.00	33919319	LR597570.1
Myripristis murdjan genome assembly, chromosome: 17	pinecon	586833	30.2	60.5	94%	774	100.00	35810529	LR597566.1
Sphaeramia orbicularis genome assembly, chromosome: 21	orbicul	375764	30.2	30.2	78%	774	100.00	59908307	LR597478.1
Sphaeramia orbicularis genome assembly, chromosome: 20	orbicul	375764	30.2	60.5	78%	774	100.00	47041096	LR597477.1
Sphaeramia orbicularis genome assembly, chromosome: 3	orbicul	375764	30.2	60.5	94%	774	100.00	63265450	LR597460.1
Sphaeramia orbicularis genome assembly, chromosome: 2	orbicul	375764	30.2	30.2	78%	774	100.00	30694919	LR597459.1
Sphaeramia orbicularis genome assembly, chromosome: 1	orbicul	375764	30.2	30.2	78%	774	100.00	59520452	LR597458.1
Salarias fasciatus genome assembly, chromosome: 23	jewelle	181472	30.2	60.5	89%	774	100.00	41705463	LR597457.1
Salarias fasciatus genome assembly, chromosome: 19	jewelle	181472	30.2	60.5	89%	774	100.00	26030347	LR597454.1
Salarias fasciatus genome assembly, chromosome: 17	jewelle	181472	30.2	30.2	78%	774	100.00	22427289	LR597452.1
Salarias fasciatus genome assembly, chromosome: 16	jewelle	181472	30.2	30.2	78%	774	100.00	34246461	LR597451.1
Salarias fasciatus genome assembly, chromosome: 12	jewelle	181472	30.2	30.2	78%	774	100.00	32729575	LR597447.1

Salarias fasciatus genome assembly, chromosome: 11	jewelle	181472	30.2	60.5	78%	774	100.00	36057378	LR597446.1
Salarias fasciatus genome assembly, chromosome: 6	jewelle	181472	30.2	60.5	78%	774	100.00	41296897	LR597441.1
Salarias fasciatus genome assembly, chromosome: 4	jewelle	181472	30.2	30.2	78%	774	100.00	27169852	LR597439.1
Salarias fasciatus genome assembly, chromosome: 2	jewelle	181472	30.2	30.2	78%	774	100.00	35747288	LR597437.1
Bacillus velezensis strain At1 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3888990	CP041145.1
PREDICTED: Nannospalax galili myelin protein zero like 1...	Upper G	1026970	30.2	30.2	78%	774	100.00	3797	XM_008829366.3
PREDICTED: Nannospalax galili myelin protein zero like 1...	Upper G	1026970	30.2	30.2	78%	774	100.00	3898	XM_008829365.3
Myxococcus xanthus strain GH3.5.6c2, complete genome	NA	34	30.2	30.2	78%	774	100.00	9321034	CP017169.1
Myxococcus xanthus strain GH5.1.9c20, complete genome	NA	34	30.2	30.2	78%	774	100.00	9262965	CP017170.1
Myxococcus xanthus strain KF3.2.8c11, complete genome	NA	34	30.2	30.2	78%	774	100.00	8952969	CP017171.1
Myxococcus xanthus strain KF4.3.9c1, complete genome	NA	34	30.2	30.2	78%	774	100.00	9429999	CP017172.1
Myxococcus xanthus strain MC3.3.5c16, complete genome	NA	34	30.2	30.2	78%	774	100.00	9316378	CP017173.1
Myxococcus xanthus strain MC3.5.9c15, complete genome	NA	34	30.2	30.2	78%	774	100.00	9316447	CP017174.1
Agaricus bisporus strain KMCC00540 chromosome 5	NA	5341	30.2	30.2	78%	774	100.00	2758943	CP039877.1
Cryptococcus wingfieldii strain CBS7118 chromosome 6, complete...	NA	5619	30.2	30.2	78%	774	100.00	1575190	CP034266.1
Bacillus altitudinis strain HQ-51-Ba chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3701797	CP040747.1
Streptopelia turtur genome assembly, chromosome: 14	NA	177155	30.2	30.2	78%	774	100.00	18481186	LR594565.1
Streptopelia turtur genome assembly, chromosome: 7	NA	177155	30.2	30.2	78%	774	100.00	42930475	LR594557.1
Takifugu rubripes genome assembly, chromosome: 12	torafug	31033	30.2	30.2	78%	774	100.00	13571579	LR584248.2
Takifugu rubripes genome assembly, chromosome: 10	torafug	31033	30.2	30.2	78%	774	100.00	12556898	LR584251.2
Syngnathus acus genome assembly, chromosome: 19	greater	161584	30.2	30.2	78%	774	100.00	8952397	LR594603.1
Syngnathus acus genome assembly, chromosome: 17	greater	161584	30.2	30.2	78%	774	100.00	11896884	LR594602.1
Syngnathus acus genome assembly, chromosome: 12	greater	161584	30.2	30.2	78%	774	100.00	12111329	LR594597.1
Syngnathus acus genome assembly, chromosome: 10	greater	161584	30.2	60.5	78%	774	100.00	28444102	LR594595.1
Syngnathus acus genome assembly, chromosome: 9	greater	161584	30.2	30.2	78%	774	100.00	20014430	LR594594.1
Syngnathus acus genome assembly, chromosome: 6	greater	161584	30.2	30.2	78%	774	100.00	17680260	LR594592.1
Syngnathus acus genome assembly, chromosome: 1	greater	161584	30.2	30.2	78%	774	100.00	18448286	LR594587.1
Bacillus altitudinis strain GQYP101 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3880448	CP040514.1
PREDICTED: Protobothrops mucrosquamatus estrogen	NA	103944	30.2	30.2	78%	774	100.00	1315	XM_015814247.2

related...									
Gossypioides kirkii chromosome KI_06	NA	47615	30.2	30.2	78%	774	100.00	60359545	CP032248.1
PREDICTED: Monodon monoceros NADH-cytochrome b5 reductase 3...	narwhal	40151	30.2	30.2	78%	774	100.00	3068	XM_029207214.1
Streptomyces hawaiiensis strain ATCC 12236 chromosome, complet...	NA	67305	30.2	30.2	78%	774	100.00	8876928	CP021978.1
Brevundimonas vancanneytii strain NCTC9239 genome assembly,...	NA	1325724	30.2	30.2	78%	774	100.00	3383349	LR588407.1
Mycobacterium tuberculosis variant bovis strain Danish 1331...	NA	1765	30.2	30.2	78%	774	100.00	4411814	CP039850.1
Mycobacterium tuberculosis variant bovis strain Danish...	NA	1765	30.2	30.2	78%	774	100.00	4332698	CP039851.1
PREDICTED: Antrostomus carolinensis protein tyrosine phosphata...	chuck-w	279965	30.2	30.2	78%	774	100.00	1652	XM_010174806.2
PREDICTED: Prosopis alba AAA-ATPase At4g25835-like...	NA	207710	30.2	30.2	78%	774	100.00	1859	XM_028943902.1
PREDICTED: Prosopis alba G-type lectin S-receptor-like...	NA	207710	30.2	30.2	78%	774	100.00	3467	XM_028936956.1
PREDICTED: Macaca mulatta uncharacterized LOC114680155...	Rhesus	9544	30.2	30.2	100%	774	94.74	8466	XR_003732213.1
Bacillus velezensis strain LPL-K103 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3933292	CP039380.1
Streptomyces antimycoticus NBRC 100767 DNA, complete genome	NA	68175	30.2	30.2	78%	774	100.00	11000615	AP019620.1
Plasmodium gonderi hypothetical protein, conserved (PGO_083060...	NA	77519	30.2	30.2	78%	774	100.00	11058	XM_028687528.1
Salmo trutta genome assembly, chromosome: 21	river t	8032	30.2	30.2	78%	774	100.00	52728040	LR584437.1
Salmo trutta genome assembly, chromosome: 18	river t	8032	30.2	30.2	78%	774	100.00	59142494	LR584435.1
Salmo trutta genome assembly, chromosome: 17	river t	8032	30.2	30.2	78%	774	100.00	59764774	LR584426.1
Salmo trutta genome assembly, chromosome: 33	river t	8032	30.2	30.2	78%	774	100.00	44893998	LR584414.1
Salmo trutta genome assembly, chromosome: 9	river t	8032	30.2	30.2	78%	774	100.00	49359203	LR584409.1
Rhinatrema bivittatum genome assembly, chromosome: 18	two-lin	194408	30.2	30.2	78%	774	100.00	61353747	LR584404.1
Rhinatrema bivittatum genome assembly, chromosome: 16	two-lin	194408	30.2	30.2	78%	774	100.00	74781573	LR584402.1
Rhinatrema bivittatum genome assembly, chromosome: 12	two-lin	194408	30.2	30.2	78%	774	100.00	87785054	LR584398.1
Takifugu rubripes genome assembly, chromosome: 11	torafug	31033	30.2	30.2	78%	774	100.00	16367601	LR584241.1
Takifugu rubripes genome assembly, chromosome: 3	torafug	31033	30.2	30.2	78%	774	100.00	17484280	LR584237.1
Scleropages formosus genome assembly, chromosome: 18	Asian b	113540	30.2	30.2	78%	774	100.00	26243056	LR584083.1
Scleropages formosus genome assembly, chromosome: 5	Asian b	113540	30.2	30.2	78%	774	100.00	38535925	LR584070.1
Scleropages formosus genome assembly, chromosome: 2	Asian b	113540	30.2	30.2	78%	774	100.00	43577283	LR584067.1

Scleropages formosus genome assembly, chromosome: 1	Asian b	113540	30.2	30.2	78%	774	100.00	54115380	LR584066.1
Echeneis naucrates genome assembly, chromosome: 23	live sh	173247	30.2	30.2	78%	774	100.00	16494136	LR584064.1
Echeneis naucrates genome assembly, chromosome: 8	live sh	173247	30.2	30.2	78%	774	100.00	20381986	LR584049.1
Nannochloropsis oceanica strain LAMB2011 chromosome 17	NA	145522	30.2	30.2	78%	774	100.00	877916	CP038114.1
Bacillus amyloliquefaciens strain FS1092 chromosome, complete...	NA	1390	30.2	30.2	78%	774	100.00	4240930	CP038028.1
PREDICTED: Physeter catodon glutaminyl-peptide cyclotransferas...	sperm w	9755	30.2	30.2	78%	774	100.00	1078	XM_028497105.1
PREDICTED: Gouania willdenowi chromosome 8 C17orf53 homolog...	blunt-s	441366	30.2	30.2	78%	774	100.00	3454	XM_028456323.1
Betta splendens genome assembly, chromosome: 11	Siamese	158456	30.2	30.2	78%	774	100.00	16885281	LR132019.2
Betta splendens genome assembly, chromosome: 5	Siamese	158456	30.2	30.2	78%	774	100.00	21146536	LR132018.2
Betta splendens genome assembly, chromosome: 14	Siamese	158456	30.2	30.2	78%	774	100.00	17358772	LR132016.2
Mastacembelus armatus genome assembly, chromosome: 23	zig-zag	205130	30.2	30.2	78%	774	100.00	16453789	LR535855.1
Denticeps clupeoides genome assembly, chromosome: 13	denticl	299321	30.2	30.2	78%	774	100.00	21794296	LR535825.1
Denticeps clupeoides genome assembly, chromosome: 10	denticl	299321	30.2	30.2	78%	774	100.00	22713814	LR535822.1
Denticeps clupeoides genome assembly, chromosome: 8	denticl	299321	30.2	30.2	78%	774	100.00	23378448	LR535820.1
Denticeps clupeoides genome assembly, chromosome: 4	denticl	299321	30.2	30.2	78%	774	100.00	35364899	LR535816.1
PREDICTED: Parambassis ranga epithelial membrane protein 2...	Indian	210632	30.2	30.2	78%	774	100.00	1983	XM_028411335.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	4361	XM_028395703.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	4026	XM_028395702.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	4022	XM_028395700.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	5464	XM_028395699.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	3990	XM_028395698.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	4079	XM_028395697.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	5533	XM_028395696.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	5468	XM_028395695.1
PREDICTED: Parambassis	Indian	210632	30.2	30.2	78%	774	100.00	4430	XM_028395694.1

ranga steroid hormone receptor ERR2...									
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	4439	XM_028395693.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	4442	XM_028395692.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	5537	XM_028395691.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	4502	XM_028395690.1
PREDICTED: Parambassis ranga steroid hormone receptor ERR2...	Indian	210632	30.2	30.2	78%	774	100.00	4511	XM_028395689.1
PREDICTED: Parambassis ranga P2Y purinoceptor 6-like...	Indian	210632	30.2	30.2	78%	774	100.00	1109	XM_028430435.1
PREDICTED: Glycine soja **ZINC finger** CCCH domain-containing...	NA	3848	30.2	30.2	78%	774	100.00	5420	XM_028380610.1
PREDICTED: Glycine soja **ZINC finger** CCCH domain-containing...	NA	3848	30.2	30.2	78%	774	100.00	5835	XM_028380609.1
Nocardia cyriacigeorgica strain 30**12S**TDY6756504 genome assembl...	NA	135487	30.2	30.2	78%	774	100.00	6476621	LR215973.1
Anabas testudineus genome assembly, chromosome: 1	climbin	64144	30.2	30.2	78%	774	100.00	27357120	LR132051.1
Anabas testudineus genome assembly, chromosome: 12	climbin	64144	30.2	30.2	100%	774	94.74	19394341	LR132041.1
Anabas testudineus genome assembly, chromosome: 10	climbin	64144	30.2	30.2	78%	774	100.00	23456640	LR132037.1
Gouania willdenowi genome assembly, chromosome: 3	blunt-s	441366	30.2	30.2	78%	774	100.00	46057556	LR132003.1
Gouania willdenowi genome assembly, chromosome: 1	blunt-s	441366	30.2	30.2	78%	774	100.00	45933286	LR131998.1
Gouania willdenowi genome assembly, chromosome: 9	blunt-s	441366	30.2	30.2	78%	774	100.00	43149712	LR131997.1
Gouania willdenowi genome assembly, chromosome: 8	blunt-s	441366	30.2	30.2	78%	774	100.00	34658348	LR131991.1
Gouania willdenowi genome assembly, chromosome: 22	blunt-s	441366	30.2	30.2	78%	774	100.00	34676616	LR131988.1
Parambassis ranga genome assembly, chromosome: 8	Indian	210632	30.2	30.2	78%	774	100.00	18866916	LR131980.1
Parambassis ranga genome assembly, chromosome: 3	Indian	210632	30.2	30.2	78%	774	100.00	26339914	LR131975.1
Parambassis ranga genome assembly, chromosome: 22	Indian	210632	30.2	30.2	78%	774	100.00	20675483	LR131973.1
Parambassis ranga genome assembly, chromosome: 2	Indian	210632	30.2	60.5	84%	774	100.00	46703924	LR131970.1
Parambassis ranga genome assembly, chromosome: 19	Indian	210632	30.2	30.2	78%	774	100.00	24703432	LR131969.1
Streptomyces sp. WAC 06738 chromosome, complete genome	NA	2203210	30.2	30.2	78%	774	100.00	8324535	CP029618.1
Bacillus altitudinis strain SGAir0031 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3812575	CP022319.2
PREDICTED: Larimichthys crocea dynein heavy chain 5,	large y	215358	30.2	30.2	78%	774	100.00	14060	XM_027274426.1

axonemal...									
Bacillus velezensis strain MH25 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4118468	CP034176.1
Bacillus velezensis strain 1B-23 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4141063	CP033967.1
PREDICTED: Tachysurus fulvidraco voltage-dependent R-type...	yellow	1234273	30.2	30.2	78%	774	100.00	7709	XM_027170822.1
PREDICTED: Tachysurus fulvidraco calpain-2 catalytic...	yellow	1234273	30.2	30.2	78%	774	100.00	2084	XM_027157818.1
PREDICTED: Tachysurus fulvidraco calpain-2 catalytic...	yellow	1234273	30.2	30.2	78%	774	100.00	2057	XM_027157817.1
Brassica rapa genome, scaffold: Brapa_scaffold_139	field m	3711	30.2	30.2	78%	774	100.00	101524	LR031676.1
Brassica rapa genome, scaffold: A06	field m	3711	30.2	30.2	78%	774	100.00	55319261	LR031569.1
PREDICTED: Lagenorhynchus obliquidens glutaminyl-peptide...	Pacific	90247	30.2	30.2	78%	774	100.00	1075	XM_027113367.1
PREDICTED: Lagenorhynchus obliquidens glutaminyl-peptide...	Pacific	90247	30.2	30.2	78%	774	100.00	1073	XM_027113366.1
PREDICTED: Acinonyx jubatus uncharacterized LOC113595677...	cheetah	32536	30.2	60.5	78%	774	100.00	2737	XR_003416247.1
PREDICTED: Acinonyx jubatus uncharacterized LOC113595677...	cheetah	32536	30.2	60.5	78%	774	100.00	2721	XR_003416246.1
PREDICTED: Acinonyx jubatus uncharacterized LOC113595677...	cheetah	32536	30.2	60.5	78%	774	100.00	2738	XR_003416245.1
PREDICTED: Acinonyx jubatus uncharacterized LOC113595677...	cheetah	32536	30.2	60.5	78%	774	100.00	2769	XR_003416244.1
PREDICTED: Acinonyx jubatus uncharacterized LOC113595677...	cheetah	32536	30.2	60.5	78%	774	100.00	2769	XR_003416243.1
PREDICTED: Acinonyx jubatus uncharacterized LOC113595677...	cheetah	32536	30.2	60.5	78%	774	100.00	2768	XR_003416242.1
PREDICTED: Acinonyx jubatus uncharacterized LOC113595677...	cheetah	32536	30.2	60.5	78%	774	100.00	2752	XR_003416241.1
PREDICTED: Acinonyx jubatus uncharacterized LOC113595677...	cheetah	32536	30.2	60.5	78%	774	100.00	1067	XR_003416240.1
PREDICTED: Acinonyx jubatus uncharacterized LOC113595677...	cheetah	32536	30.2	60.5	78%	774	100.00	2720	XR_003416239.1
Arthrobacter phage Hestia, complete genome	NA	2419609	30.2	30.2	78%	774	100.00	51476	MH910036.1
Mycobacterium tuberculosis strain DKC2 genome assembly,...	NA	1773	30.2	30.2	78%	774	100.00	4409544	LR027516.1
Herbaspirillum rubrisubalbicans strain DSM 11543 chromosome,...	NA	80842	30.2	30.2	78%	774	100.00	5617593	CP024996.1
Mycobacterium tuberculosis variant bovis BCG strain BCG_S49...	NA	33892	30.2	30.2	78%	774	100.00	4294423	CP033311.1
Mycobacterium tuberculosis variant bovis BCG strain BCG-S48...	NA	33892	30.2	30.2	78%	774	100.00	4294448	CP033310.1

Malassezia restricta CBS 7877 chromosome IV	NA	425264	30.2	30.2	78%	774	100.00	839175	CP033151.1
Arthrobacter phage Richie, complete genome	NA	2419967	30.2	30.2	78%	774	100.00	53867	MH834625.1
Arthrobacter phage Auxilium, complete genome	NA	2419948	30.2	30.2	78%	774	100.00	49447	MH834598.1
PREDICTED: Athene cunicularia estrogen related receptor beta...	burrowi	194338	30.2	30.2	78%	774	100.00	5393	XM_026849616.1
PREDICTED: Athene cunicularia protein tyrosine phosphatase,...	burrowi	194338	30.2	30.2	78%	774	100.00	3720	XM_026841425.1
PREDICTED: Athene cunicularia DS cell adhesion molecule (**DSCAM**...	burrowi	194338	30.2	30.2	78%	774	100.00	6705	XM_026868377.1
PREDICTED: Microtus ochrogaster NSE1 homolog, SMC5-SMC6 comple...	prairie	79684	30.2	30.2	78%	774	100.00	2612	XM_005351187.3
PREDICTED: Microtus ochrogaster NSE1 homolog, SMC5-SMC6 comple...	prairie	79684	30.2	30.2	78%	774	100.00	2730	XM_013347809.2
PREDICTED: Zonotrichia albicollis grainyhead like transcriptio...	white-t	44394	30.2	30.2	78%	774	100.00	5022	XM_026793584.1
PREDICTED: Zonotrichia albicollis protein tyrosine phosphatase...	white-t	44394	30.2	30.2	78%	774	100.00	2134	XM_005486723.3
PREDICTED: Zonotrichia albicollis protein tyrosine phosphatase...	white-t	44394	30.2	30.2	78%	774	100.00	5166	XM_005486722.3
Serratia sp. 1D1416 chromosome, complete genome	NA	2447890	30.2	30.2	78%	774	100.00	5552047	CP032738.1
Aspergillus thermomutatus hypothetical protein (CDV56_106180),...	NA	41047	30.2	30.2	78%	774	100.00	2301	XM_026759799.1
PREDICTED: Pseudonaja textilis estrogen related receptor beta...	NA	8673	30.2	30.2	78%	774	100.00	1185	XM_026705292.1
PREDICTED: Pseudonaja textilis estrogen related receptor beta...	NA	8673	30.2	30.2	78%	774	100.00	1308	XM_026705285.1
PREDICTED: Pseudonaja textilis estrogen related receptor beta...	NA	8673	30.2	30.2	78%	774	100.00	1353	XM_026705280.1
PREDICTED: Pseudonaja textilis estrogen related receptor beta...	NA	8673	30.2	30.2	78%	774	100.00	1468	XM_026705271.1
PREDICTED: Notechis scutatus estrogen related receptor beta...	mainlan	8663	30.2	30.2	78%	774	100.00	1185	XM_026664265.1
PREDICTED: Notechis scutatus estrogen related receptor beta...	mainlan	8663	30.2	30.2	78%	774	100.00	1468	XM_026664264.1
PREDICTED: Ursus arctos horribilis uncharacterized LOC11326659...	NA	116960	30.2	30.2	78%	774	100.00	5204	XR_003320435.1
PREDICTED: Ursus arctos horribilis uncharacterized LOC11326659...	NA	116960	30.2	30.2	78%	774	100.00	5234	XR_003320434.1
PREDICTED: Hyposmocoma kahamanoa plexin A3 (LOC113239717), mRNA	NA	1477025	30.2	30.2	78%	774	100.00	6531	XM_026476809.1
PREDICTED: Frankliniella occidentalis E3 ubiquitin-protein...	western	133901	30.2	30.2	100%	774	94.74	2383	XM_026427295.1
PREDICTED: Frankliniella occidentalis E3 ubiquitin-protein...	western	133901	30.2	30.2	100%	774	94.74	2538	XM_026427294.1
PREDICTED: Frankliniella	western	133901	30.2	30.2	100%	774	94.74	2782	XM_026427293.1

occidentalis E3 ubiquitin-protein...									
PREDICTED: Frankliniella occidentalis E3 ubiquitin-protein...	western	133901	30.2	30.2	100%	774	94.74	2663	XM_026427291.1
PREDICTED: Frankliniella occidentalis uncharacterized...	western	133901	30.2	30.2	78%	774	100.00	1988	XM_026422904.1
PREDICTED: Frankliniella occidentalis uncharacterized...	western	133901	30.2	30.2	78%	774	100.00	1991	XM_026422896.1
Haemonchus contortus, ISE/inbred ISE, WGS project CAVP01000000...	barber	6289	30.2	30.2	78%	774	100.00	51826579	LS997565.1
PREDICTED: Vombatus ursinus DS cell adhesion molecule (**DSCAM**),...	common	29139	30.2	30.2	78%	774	100.00	5991	XM_027843631.1
Streptomyces sp. M2 chromosome, complete genome	NA	646637	30.2	30.2	78%	774	100.00	8718751	CP028834.1
PREDICTED: Empidonax traillii acetyl-CoA carboxylase beta...	willow	164674	30.2	30.2	78%	774	100.00	8711	XM_027894364.1
PREDICTED: Empidonax traillii protein tyrosine phosphatase,...	willow	164674	30.2	30.2	78%	774	100.00	6130	XM_027885345.1
PREDICTED: Empidonax traillii protein tyrosine phosphatase,...	willow	164674	30.2	30.2	78%	774	100.00	1649	XM_027885344.1
PREDICTED: Falco peregrinus protein tyrosine phosphatase,...	peregri	8954	30.2	30.2	78%	774	100.00	2602	XM_027792228.1
PREDICTED: Falco cherrug protein tyrosine phosphatase,...	Saker f	345164	30.2	30.2	78%	774	100.00	2597	XM_027798972.1
Anopheles stephensi strain Indian chromosome X	Asian m	30069	30.2	30.2	78%	774	100.00	16301208	CP032298.1
Anopheles stephensi strain SDA-500 chromosome X	Asian m	30069	30.2	30.2	78%	774	100.00	16423912	CP032231.1
Bacillus aerophilus strain 232 chromosome, complete genome	NA	293389	30.2	30.2	78%	774	100.00	3829464	CP026008.1
Lateolabrax maculatus linkage group 7 sequence	spotted	315492	30.2	30.2	78%	774	100.00	27713553	CP032604.1
Lateolabrax maculatus linkage group 6 sequence	spotted	315492	30.2	30.2	78%	774	100.00	27759045	CP032603.1
Lateolabrax maculatus linkage group 5 sequence	spotted	315492	30.2	60.5	89%	774	100.00	27893061	CP032602.1
Lateolabrax maculatus linkage group 3 sequence	spotted	315492	30.2	30.2	78%	774	100.00	29073605	CP032600.1
Lateolabrax maculatus linkage group 2 sequence	spotted	315492	30.2	30.2	78%	774	100.00	29991467	CP032595.1
Lateolabrax maculatus linkage group 20 sequence	spotted	315492	30.2	30.2	78%	774	100.00	21427312	CP032594.1
Lateolabrax maculatus linkage group 19 sequence	spotted	315492	30.2	30.2	78%	774	100.00	22300342	CP032593.1
Lateolabrax maculatus linkage group 17 sequence	spotted	315492	30.2	30.2	78%	774	100.00	22597543	CP032591.1
Lateolabrax maculatus linkage group 16 sequence	spotted	315492	30.2	30.2	78%	774	100.00	23356654	CP032590.1
Lateolabrax maculatus linkage group 14 sequence	spotted	315492	30.2	60.5	84%	774	100.00	23620959	CP032588.1
Lateolabrax maculatus linkage group 12 sequence	spotted	315492	30.2	90.7	78%	774	100.00	24885600	CP032586.1
Lateolabrax maculatus linkage group 11 sequence	spotted	315492	30.2	30.2	78%	774	100.00	25037391	CP032585.1
Takifugu bimaculatus chromosome 19	NA	433685	30.2	30.2	78%	774	100.00	13896840	CP034985.1
Lateolabrax maculatus chromosome Lm22	spotted	315492	30.2	30.2	78%	774	100.00	21943731	CP027283.1

Lateolabrax maculatus chromosome Lm20	spotted	315492	30.2	30.2	78%	774	100.00	21152183	CP027281.1
Lateolabrax maculatus chromosome Lm10	spotted	315492	30.2	30.2	78%	774	100.00	17765475	CP027271.1
Lateolabrax maculatus chromosome Lm9	spotted	315492	30.2	30.2	78%	774	100.00	20127546	CP027270.1
Lateolabrax maculatus chromosome Lm8	spotted	315492	30.2	30.2	78%	774	100.00	21392500	CP027269.1
Lateolabrax maculatus chromosome Lm6	spotted	315492	30.2	60.5	78%	774	100.00	27060119	CP027267.1
Lateolabrax maculatus chromosome Lm5	spotted	315492	30.2	120	78%	774	100.00	21471159	CP027266.1
Lateolabrax maculatus chromosome Lm4	spotted	315492	30.2	30.2	78%	774	100.00	19156603	CP027265.1
Lateolabrax maculatus chromosome Lm2	spotted	315492	30.2	30.2	78%	774	100.00	22535790	CP027263.1
Lateolabrax maculatus chromosome Lm1	spotted	315492	30.2	30.2	78%	774	100.00	22914103	CP027262.1
PREDICTED: Corapipo altera acetyl-CoA carboxylase beta (ACACB)...	White-r	415028	30.2	30.2	78%	774	100.00	8709	XM_027652004.1
PREDICTED: Neopelma chrysocephalum acetyl-CoA carboxylase beta...	saffron	114329	30.2	30.2	78%	774	100.00	8709	XM_027689325.1
PREDICTED: Neopelma chrysocephalum protein tyrosine phosphatas...	saffron	114329	30.2	30.2	78%	774	100.00	1470	XM_027677056.1
PREDICTED: Neopelma chrysocephalum protein tyrosine phosphatas...	saffron	114329	30.2	30.2	78%	774	100.00	6039	XM_027677048.1
Eukaryotic synthetic construct chromosome 13	NA	111789	30.2	60.5	89%	774	100.00	96089878	CP034516.1
Eukaryotic synthetic construct chromosome 16	NA	111789	30.2	30.2	78%	774	100.00	98200793	CP034494.1
Eukaryotic synthetic construct chromosome 14	NA	111789	30.2	30.2	78%	774	100.00	88289540	CP034492.1
Eukaryotic synthetic construct chromosome 13	NA	111789	30.2	60.5	89%	774	100.00	96089878	CP034491.1
Malassezia restricta epsin (MRET_3018), partial mRNA	NA	76775	30.2	30.2	78%	774	100.00	1209	XM_027629645.1
Homo sapiens PR/SET domain 16 (PRDM16), RefSeqGene on chromoso...	human	9606	30.2	30.2	78%	774	100.00	376444	NG_029576.2
PREDICTED: Bos indicus x Bos taurus neurocalcin delta (NCALD),...	hybrid	30522	30.2	30.2	78%	774	100.00	3174	XM_027561420.1
PREDICTED: Bos indicus x Bos taurus neurocalcin delta (NCALD),...	hybrid	30522	30.2	30.2	78%	774	100.00	3277	XM_027561419.1
PREDICTED: Bos indicus x Bos taurus neurocalcin delta (NCALD),...	hybrid	30522	30.2	30.2	78%	774	100.00	3296	XM_027561418.1
PSEUDOMONAS poae strain CAP-2018 chromosome, complete genome	NA	200451	30.2	30.2	78%	774	100.00	7371963	CP034537.1
Corynebacterium matruchotii strain NCTC10206 genome assembly,...	NA	43768	30.2	30.2	78%	774	100.00	2878842	LR134504.1
Streptomyces sp. CB09001 chromosome, complete genome	NA	2083284	30.2	30.2	78%	774	100.00	7787608	CP026730.1
PREDICTED: Dromaius	emu	8790	30.2	30.2	78%	774	100.00	5896	XM_026121588.1

novaehollandiae DS cell adhesion molecule...									
PREDICTED: Dromaius novaehollandiae MOB kinase activator 3A...	emu	8790	30.2	30.2	78%	774	100.00	2272	XM_026114160.1
PREDICTED: Dromaius novaehollandiae protein tyrosine...	emu	8790	30.2	30.2	78%	774	100.00	2131	XM_026094320.1
PREDICTED: Dromaius novaehollandiae protein tyrosine...	emu	8790	30.2	30.2	78%	774	100.00	2307	XM_026094319.1
PREDICTED: Dromaius novaehollandiae protein tyrosine...	emu	8790	30.2	30.2	78%	774	100.00	2319	XM_026094318.1
PREDICTED: Apteryx rowi ST3 beta-galactoside...	Okarito	308060	30.2	30.2	78%	774	100.00	3233	XM_026064650.1
PREDICTED: Apteryx rowi ST3 beta-galactoside...	Okarito	308060	30.2	30.2	78%	774	100.00	3320	XM_026064649.1
PREDICTED: Apteryx rowi ST3 beta-galactoside...	Okarito	308060	30.2	30.2	78%	774	100.00	3325	XM_026064648.1
PREDICTED: Apteryx rowi ST3 beta-galactoside...	Okarito	308060	30.2	30.2	78%	774	100.00	3639	XM_026064647.1
PREDICTED: Apteryx rowi ST3 beta-galactoside...	Okarito	308060	30.2	30.2	78%	774	100.00	3700	XM_026064646.1
PREDICTED: Apteryx rowi ST3 beta-galactoside...	Okarito	308060	30.2	30.2	78%	774	100.00	3709	XM_026064645.1
PREDICTED: Apteryx rowi ST3 beta-galactoside...	Okarito	308060	30.2	30.2	78%	774	100.00	3700	XM_026064644.1
PREDICTED: Apteryx rowi ST3 beta-galactoside...	Okarito	308060	30.2	30.2	78%	774	100.00	3715	XM_026064643.1
PREDICTED: Apteryx rowi ST3 beta-galactoside...	Okarito	308060	30.2	30.2	78%	774	100.00	3812	XM_026064642.1
PREDICTED: Apteryx rowi ST3 beta-galactoside...	Okarito	308060	30.2	30.2	78%	774	100.00	3714	XM_026064641.1
PREDICTED: Apteryx rowi protein tyrosine phosphatase,...	Okarito	308060	30.2	30.2	78%	774	100.00	2135	XM_026063051.1
PREDICTED: Apteryx rowi protein tyrosine phosphatase,...	Okarito	308060	30.2	30.2	78%	774	100.00	5227	XM_026063050.1
PREDICTED: Oryza sativa Japonica Group DDT domain-containing...	Japanes	39947	30.2	30.2	78%	774	100.00	7379	XM_015791315.2
Erythrobacter aureus strain YH-07 plasmid unnamed, complete...	NA	2182384	30.2	30.2	78%	774	100.00	407975	CP031358.1
Micromonospora aurantiaca strain 110B(2018) chromosome, comple...	NA	47850	30.2	30.2	100%	774	94.74	7255264	CP031263.1
PREDICTED: Vulpes vulpes uncharacterized LOC112909427...	red fox	9627	30.2	30.2	78%	774	100.00	788	XR_003233114.1
PREDICTED: Oreochromis niloticus lebercilin-like protein...	Nile ti	8128	30.2	30.2	78%	774	100.00	1761	XM_005474566.4
PREDICTED: Oreochromis niloticus lebercilin-like protein...	Nile ti	8128	30.2	30.2	78%	774	100.00	1821	XM_005474565.4
PREDICTED: Callorhinus ursinus uncharacterized LOC112823520...	norther	34884	30.2	30.2	78%	774	100.00	2829	XR_003208072.1
Paraburkholderia caledonica strain PHRS4 chromosome PHRS4_A,...	NA	134536	30.2	30.2	78%	774	100.00	3862683	CP024905.1
Bacillus amyloliquefaciens strain SH-B74 chromosome,	NA	1390	30.2	30.2	78%	774	100.00	4042190	CP030097.1

complete...									
Mycobacterium tuberculosis strain TBMENG-03 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4359659	CP029065.1
Malassezia restricta strain KCTC 27527 chromosome V, complete...	NA	76775	30.2	30.2	78%	774	100.00	836807	CP030255.1
Aspergillus aculeatinus CBS 121060 hypothetical protein...	NA	1448322	30.2	30.2	78%	774	100.00	1613	XM_025642173.1
Mycobacterium tuberculosis strain H112 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4406346	CP019613.1
Mycobacterium tuberculosis strain H107 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4418796	CP019612.1
Mycobacterium tuberculosis strain H83 chromosome, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4413214	CP019611.1
Mycobacterium tuberculosis strain H54 chromosome, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4416938	CP019610.1
Bacillus velezensis strain DSYZ chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4258978	CP030150.1
Mycobacterium tuberculosis strain RUS_B0 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4418559	CP030093.1
PREDICTED: Bubalus bubalis cytochrome P450 4B1 (LOC102415534),...	water b	89462	30.2	30.2	78%	774	100.00	2060	XM_006052512.2
PREDICTED: Bubalus bubalis neurocalcin delta (NCALD), transcri...	water b	89462	30.2	30.2	78%	774	100.00	4961	XM_006046435.2
Streptomyces cadmiisoli strain ZFG47 chromosome, complete genome	NA	2184053	30.2	30.2	78%	774	100.00	9269371	CP030073.1
Scophthalmus maximus chromosome 6	turbot	52904	30.2	30.2	78%	774	100.00	27411298	CP026248.1
PREDICTED: Alligator sinensis protein tyrosine phosphatase,...	Chinese	38654	30.2	30.2	78%	774	100.00	1507	XM_025204726.1
PREDICTED: Alligator sinensis protein tyrosine phosphatase,...	Chinese	38654	30.2	30.2	78%	774	100.00	4932	XM_025204725.1
PREDICTED: Alligator sinensis protein tyrosine phosphatase,...	Chinese	38654	30.2	30.2	78%	774	100.00	4790	XM_025204724.1
PREDICTED: Alligator sinensis protein tyrosine phosphatase,...	Chinese	38654	30.2	30.2	78%	774	100.00	1641	XM_025204723.1
PREDICTED: Alligator sinensis protein tyrosine phosphatase,...	Chinese	38654	30.2	30.2	78%	774	100.00	4945	XM_025204722.1
PREDICTED: Pelodiscus sinensis uncharacterized LOC102447734...	Chinese	13735	30.2	30.2	78%	774	100.00	1037	XR_003087161.1
PREDICTED: Python bivittatus estrogen related receptor beta...	Burmese	176946	30.2	30.2	78%	774	100.00	1308	XM_025164519.1
PREDICTED: Python bivittatus estrogen related receptor beta...	Burmese	176946	30.2	30.2	78%	774	100.00	1468	XM_007424819.2
Bacillus amyloliquefaciens strain ALB79 chromosome, complete...	NA	1390	30.2	30.2	78%	774	100.00	3982905	CP029071.1
PREDICTED: Cynara cardunculus var. scolymus isoflavone...	NA	59895	30.2	30.2	78%	774	100.00	1674	XM_025117079.1
PREDICTED: Cynara cardunculus var. scolymus isoflavone...	NA	59895	30.2	30.2	78%	774	100.00	1641	XM_025117030.1

Mycobacterium tuberculosis strain LJ338 chromosome	NA	1773	30.2	30.2	78%	774	100.00	4408432	CP029326.1
Bacillus velezensis strain AP183 chromosome	NA	492670	30.2	30.2	78%	774	100.00	4006441	CP029296.1
PREDICTED: Bos taurus uncharacterized LOC112444498...	cattle	9913	30.2	30.2	78%	774	100.00	8501	XR_003032816.1
PREDICTED: Bos taurus grainyhead like transcription factor 2...	cattle	9913	30.2	30.2	78%	774	100.00	10026	XM_002692794.5
PREDICTED: Bos taurus neurocalcin delta (NCALD), transcript...	cattle	9913	30.2	30.2	78%	774	100.00	3391	XM_025001409.1
PREDICTED: Bos taurus neurocalcin delta (NCALD), transcript...	cattle	9913	30.2	30.2	78%	774	100.00	3427	XM_025001408.1
PREDICTED: Bos taurus neurocalcin delta (NCALD), transcript...	cattle	9913	30.2	30.2	78%	774	100.00	3359	XM_025001407.1
PREDICTED: Bos taurus neurocalcin delta (NCALD), transcript...	cattle	9913	30.2	30.2	78%	774	100.00	3305	XM_025001406.1
Bacillus velezensis strain BS-37 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4013888	CP023414.1
Bacillus velezensis strain QST713 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4233757	CP025079.1
Hyaloscypha bicolor E uncharacterized protein...	NA	1095630	30.2	30.2	78%	774	100.00	573	XM_024884572.1
Dongshaea marina strain DM2 chromosome, complete genome	NA	2047966	30.2	30.2	78%	774	100.00	5032832	CP028897.1
Bacillus velezensis strain GYL4 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3975084	CP020874.1
Mycobacterium tuberculosis strain CAS chromosome	NA	1773	30.2	30.2	78%	774	100.00	4394577	CP028428.1
PREDICTED: Physcomitrella patens uncharacterized LOC112283664...	NA	3218	30.2	30.2	78%	774	100.00	1857	XM_024522704.1
PREDICTED: Pan troglodytes rab GTPase-activating protein 1-lik...	chimpan	9598	30.2	30.2	78%	774	100.00	3717	XM_024355115.1
PREDICTED: Pan troglodytes rab GTPase-activating protein 1-lik...	chimpan	9598	30.2	30.2	78%	774	100.00	3683	XM_024355109.1
Mycobacterium tuberculosis strain Beijing2014PNGD chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4404064	CP022704.2
Yamagishiella unicocca DNA, mating locus, mating-type plus...	NA	51707	30.2	30.2	78%	774	100.00	333561	LC314412.1
Mycobacterium tuberculosis strain WC078 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4413712	CP022577.1
Mycobacterium tuberculosis strain WC059 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4413669	CP022578.1
Mycobacterium tuberculosis variant bovis strain 2002/0476...	NA	1765	30.2	30.2	78%	774	100.00	4355637	CP027035.1
Bos mutus isolate yakQH1 chromosome 29	wild ya	72004	30.2	30.2	78%	774	100.00	49314950	CP027097.1
Bos mutus isolate yakQH1 chromosome 28	wild ya	72004	30.2	30.2	78%	774	100.00	41841768	CP027096.1
Bos mutus isolate yakQH1	wild ya	72004	30.2	30.2	78%	774	100.00	45444811	CP027091.1

chromosome 23									
Bos mutus isolate yakQH1 chromosome 21	wild ya	72004	30.2	30.2	78%	774	100.00	67277862	CP027089.1
Bos mutus isolate yakQH1 chromosome 16	wild ya	72004	30.2	60.5	78%	774	100.00	78623970	CP027084.1
Bos mutus isolate yakQH1 chromosome 15	wild ya	72004	30.2	30.2	78%	774	100.00	79990276	CP027083.1
Bos mutus isolate yakQH1 chromosome 14	wild ya	72004	30.2	60.5	89%	774	100.00	81354091	CP027082.1
Bos mutus isolate yakQH1 chromosome 13	wild ya	72004	30.2	60.5	84%	774	100.00	75983851	CP027081.1
Bacillus velezensis strain CGMCC 11640 chromosome, complete...	NA	492670	30.2	30.2	78%	774	100.00	4322979	CP026610.1
Cryptococcus gattii VGII R265 chromosome 1, complete sequence	NA	294750	30.2	30.2	78%	774	100.00	2207848	CP025759.1
PREDICTED: Salvelinus alpinus microtubule-associated protein 4...	Arctic	8036	30.2	30.2	78%	774	100.00	6843	XM_024009684.2
PREDICTED: Salvelinus alpinus microtubule-associated protein 4...	Arctic	8036	30.2	30.2	78%	774	100.00	6919	XM_024009683.2
PREDICTED: Salvelinus alpinus microtubule-associated protein 4...	Arctic	8036	30.2	30.2	78%	774	100.00	6963	XM_024009682.2
PREDICTED: Salvelinus alpinus microtubule-associated protein 4...	Arctic	8036	30.2	30.2	78%	774	100.00	7039	XM_024009681.2
PREDICTED: Salvelinus alpinus microtubule-associated protein 4...	Arctic	8036	30.2	30.2	78%	774	100.00	7113	XM_024009680.2
PREDICTED: Salvelinus alpinus microtubule-associated protein 4...	Arctic	8036	30.2	30.2	78%	774	100.00	7054	XM_024009679.2
Nocardia cyriacigeorgica strain MDA3349 chromosome, complete...	NA	135487	30.2	30.2	78%	774	100.00	6320090	CP026746.1
Mycobacterium tuberculosis strain LJ319 chromosome	NA	1773	30.2	30.2	78%	774	100.00	4399460	CP026742.1
PREDICTED: Chrysemys picta bellii DS cell adhesion molecule...	western	8478	30.2	30.2	78%	774	100.00	5464	XM_024100527.1
PREDICTED: Chrysemys picta bellii DS cell adhesion molecule...	western	8478	30.2	30.2	78%	774	100.00	7151	XM_005304452.3
PREDICTED: Oryzias latipes serine/arginine repetitive matrix...	Japanes	8090	30.2	30.2	78%	774	100.00	8862	XM_023959301.1
PREDICTED: Cyanistes caeruleus protein tyrosine phosphatase,...	blue ti	156563	30.2	30.2	78%	774	100.00	1980	XM_023921135.1
PREDICTED: Paramormyrops kingsleyae pyridoxal kinase (pdxk), mRNA	NA	1676925	30.2	30.2	78%	774	100.00	2243	XM_023792946.1
PREDICTED: Paramormyrops kingsleyae Era like **12S** mitochondrial...	NA	1676925	30.2	30.2	78%	774	100.00	1504	XM_023833006.1
PREDICTED: Paramormyrops kingsleyae Era like **12S** mitochondrial...	NA	1676925	30.2	30.2	78%	774	100.00	1551	XM_023833005.1
PREDICTED: Paramormyrops	NA	1676925	30.2	30.2	78%	774	100.00	1779	XM_023833004.1

kingsleyae Era like **12S** mitochondrial...									
Bacillus altitudinis strain FD48 chromosome	NA	293387	30.2	30.2	78%	774	100.00	3751533	CP025643.1
Aspergillus carbonarius culture ITEM:5010 ochratoxin A...	NA	40993	30.2	30.2	78%	774	100.00	21508	MG701890.1
PREDICTED: Myotis lucifugus tsukushi, small leucine rich...	little	59463	30.2	30.2	78%	774	100.00	2757	XM_006091053.3
PREDICTED: Octodon degus pappalysin-1 (LOC101583960), transcri...	degu	10160	30.2	30.2	78%	774	100.00	6159	XM_023701594.1
PREDICTED: Octodon degus pappalysin-1 (LOC101583960), transcri...	degu	10160	30.2	30.2	78%	774	100.00	6196	XM_004641459.2
Mycobacterium tuberculosis strain MYC004 chromosome	NA	1773	30.2	30.2	78%	774	100.00	4411530	CP024614.1
PREDICTED: Pteropus vampyrus **ZINC finger** protein 74 (ZNF74),...	large f	132908	30.2	30.2	78%	774	100.00	2995	XM_023528269.1
PREDICTED: Pteropus vampyrus **ZINC finger** protein 74 (ZNF74),...	large f	132908	30.2	30.2	78%	774	100.00	3046	XM_023528268.1
PREDICTED: Pteropus vampyrus **ZINC finger** protein 74 (ZNF74),...	large f	132908	30.2	30.2	78%	774	100.00	3473	XM_023528267.1
PREDICTED: Pteropus vampyrus **ZINC finger** protein 74 (ZNF74),...	large f	132908	30.2	30.2	78%	774	100.00	3476	XM_011355914.2
PREDICTED: Pteropus vampyrus **ZINC finger** protein 74 (ZNF74),...	large f	132908	30.2	30.2	78%	774	100.00	3524	XM_011355913.2
PREDICTED: Pteropus vampyrus **ZINC finger** protein 74 (ZNF74),...	large f	132908	30.2	30.2	78%	774	100.00	3527	XM_011355911.2
Bos taurus neurocalcin delta (NCALD), transcript variant 3, mRNA	cattle	9913	30.2	30.2	78%	774	100.00	3338	NM_174398.3
Bos taurus neurocalcin delta (NCALD), transcript variant 2, mRNA	cattle	9913	30.2	30.2	78%	774	100.00	3384	NM_001359912.1
Bos taurus neurocalcin delta (NCALD), transcript variant 1, mRNA	cattle	9913	30.2	30.2	78%	774	100.00	3426	NM_001359911.1
Larimichthys crocea genome assembly, chromosome: VIII	large y	215358	30.2	30.2	78%	774	100.00	29925751	LT972197.1
Mycobacterium tuberculosis strain GG-229-10 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411519	CP025608.1
Mycobacterium tuberculosis strain GG-186-10 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411478	CP025607.1
Mycobacterium tuberculosis strain GG-137-10 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411446	CP025606.1
Mycobacterium tuberculosis strain GG-134-11 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411399	CP025605.1
Mycobacterium tuberculosis strain GG-129-11 chromosome,	NA	1773	30.2	30.2	78%	774	100.00	4411413	CP025604.1

comple...									
Mycobacterium tuberculosis strain GG-121-10 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411510	CP025603.1
Mycobacterium tuberculosis strain GG-109-10 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411463	CP025602.1
Mycobacterium tuberculosis strain GG-90-10 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411602	CP025601.1
Mycobacterium tuberculosis strain GG-77-11 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411508	CP025600.1
Mycobacterium tuberculosis strain GG-45-11 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411469	CP025599.1
Mycobacterium tuberculosis strain GG-37-11 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411526	CP025598.1
Mycobacterium tuberculosis strain GG-36-11 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411469	CP025597.1
Mycobacterium tuberculosis strain GG-27-11 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411443	CP025596.1
Mycobacterium tuberculosis strain GG-20-11 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411504	CP025595.1
Mycobacterium tuberculosis strain GG-5-10 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411442	CP025594.1
Mycobacterium tuberculosis strain GG-111-10 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411563	CP025593.1
Fusarium fujikuroi IMI 58289 non-ribosomal peptide synthetase...	NA	1279085	30.2	30.2	78%	774	100.00	7422	XM_023577125.1
PREDICTED: Otolemur garnettii inhibitor of nuclear factor kapp...	small-e	30611	30.2	30.2	78%	774	100.00	3257	XM_023514601.1
PSEUDOMONAS fluorescens strain 2P24 chromosome, complete genome	NA	294	30.2	30.2	78%	774	100.00	6610571	CP025542.1
PREDICTED: Felis catus uncharacterized LOC105259913...	domesti	9685	30.2	30.2	78%	774	100.00	4127	XR_002739329.1
Bacillus velezensis strain TJ02 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4061552	CP024797.1
Dermabacter jinjuensis strain 32T chromosome, complete genome	NA	1667168	30.2	30.2	78%	774	100.00	2398786	CP023482.1
Bacillus altitudinis strain P-10 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3765752	CP024204.1
Bacillus velezensis strain NKG-1 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4197217	CP024203.1
Bacillus velezensis strain L-1 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4090582	CP023859.1
Bacillus velezensis strain LABIM40 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3972310	CP023748.1
Mycobacterium tuberculosis strain TBV4952 chromosome,	NA	1773	30.2	30.2	78%	774	100.00	4411414	CP023640.1

complete...									
Mycobacterium tuberculosis strain TBV4768 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411173	CP023639.1
Mycobacterium tuberculosis strain TBV4766 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411310	CP023638.1
Mycobacterium tuberculosis strain TBDM2717 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411442	CP023637.1
Mycobacterium tuberculosis strain TBDM2699 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411457	CP023636.1
Mycobacterium tuberculosis strain TBDM2489 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411369	CP023635.1
Mycobacterium tuberculosis strain TBDM2487 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411314	CP023634.1
Mycobacterium tuberculosis strain TBDM2444 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411284	CP023633.1
Mycobacterium tuberculosis strain TBDM2189 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411316	CP023632.1
Mycobacterium tuberculosis strain TBDM1506 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411157	CP023631.1
Mycobacterium tuberculosis strain MDRMA2441 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411454	CP023630.1
Mycobacterium tuberculosis strain MDRMA2260 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411352	CP023629.1
Mycobacterium tuberculosis strain MDRMA2082 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411479	CP023628.1
Mycobacterium tuberculosis strain MDRMA2019 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411229	CP023627.1
Mycobacterium tuberculosis strain MDRMA1565 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411159	CP023626.1
Mycobacterium tuberculosis strain MDRMA863 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411432	CP023625.1
Mycobacterium tuberculosis strain MDRMA701 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411338	CP023624.1
Mycobacterium tuberculosis strain MDRMA203 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411290	CP023623.1
Mycobacterium tuberculosis strain MDRDM827 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411315	CP023622.1
Mycobacterium tuberculosis strain LN2900 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411327	CP023621.1
Mycobacterium tuberculosis strain LN1856 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411299	CP023620.1

Mycobacterium tuberculosis strain LN1100 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411392	CP023619.1
Mycobacterium tuberculosis strain LN3695 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411449	CP023618.1
Mycobacterium tuberculosis strain LN3672 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411335	CP023617.1
Mycobacterium tuberculosis strain LN3668 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411494	CP023616.1
Mycobacterium tuberculosis strain LN3589 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411392	CP023615.1
Mycobacterium tuberculosis strain LN3588 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411379	CP023614.1
Mycobacterium tuberculosis strain LN3584 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411326	CP023613.1
Mycobacterium tuberculosis strain LN2978 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411331	CP023612.1
Mycobacterium tuberculosis strain LN763 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411321	CP023611.1
Mycobacterium tuberculosis strain LN317 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411340	CP023610.1
Mycobacterium tuberculosis strain LN55 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411186	CP023609.1
Mycobacterium tuberculosis strain LE410 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411365	CP023608.1
Mycobacterium tuberculosis strain LE371 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411137	CP023607.1
Mycobacterium tuberculosis strain LE103 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411243	CP023606.1
Mycobacterium tuberculosis strain LE79 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411475	CP023605.1
Mycobacterium tuberculosis strain LE76 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411211	CP023604.1
Mycobacterium tuberculosis strain LE63 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411415	CP023603.1
Mycobacterium tuberculosis strain LE13 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411412	CP023602.1
Mycobacterium tuberculosis strain CSV9577 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411230	CP023601.1
Mycobacterium tuberculosis strain CSV3611 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411439	CP023600.1
Mycobacterium tuberculosis strain CSV383 chromosome,	NA	1773	30.2	30.2	78%	774	100.00	4411115	CP023599.1

complete...									
Mycobacterium tuberculosis strain SLM100 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411394	CP023598.1
Mycobacterium tuberculosis strain SLM088 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411385	CP023597.1
Mycobacterium tuberculosis strain SLM063 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411337	CP023596.1
Mycobacterium tuberculosis strain SLM060 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411134	CP023595.1
Mycobacterium tuberculosis strain SLM056 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411306	CP023594.1
Mycobacterium tuberculosis strain SLM040 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411408	CP023593.1
Mycobacterium tuberculosis strain SLM036 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411342	CP023592.1
Mycobacterium tuberculosis strain TBV5365 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411398	CP023591.1
Mycobacterium tuberculosis strain TBV5362 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411331	CP023590.1
Mycobacterium tuberculosis strain TBV5000 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411318	CP023589.1
Mycobacterium tuberculosis strain TBDM425 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411143	CP023588.1
Mycobacterium tuberculosis strain ME1473 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411217	CP023587.1
Mycobacterium tuberculosis strain MDRMA2491 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411121	CP023586.1
Mycobacterium tuberculosis strain MDRDM1098 chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411148	CP023585.1
Mycobacterium tuberculosis strain MDRDM627 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411215	CP023584.1
Mycobacterium tuberculosis strain MDRDM260 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411280	CP023583.1
Mycobacterium tuberculosis strain LN3756 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411315	CP023582.1
Mycobacterium tuberculosis strain LN2358 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411353	CP023581.1
Mycobacterium tuberculosis strain LN180 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411436	CP023580.1
Mycobacterium tuberculosis strain LE492 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411208	CP023579.1

Mycobacterium tuberculosis strain LE486 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411180	CP023578.1
Mycobacterium tuberculosis strain CSV11678 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411382	CP023577.1
Mycobacterium tuberculosis strain CSV10399 chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4411180	CP023576.1
Mycobacterium tuberculosis strain CSV5769 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411312	CP023575.1
Mycobacterium tuberculosis strain CSV4644 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411271	CP023574.1
Mycobacterium tuberculosis strain CSV4519 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4411288	CP023573.1
PREDICTED: Seriola dumerili KIAA0753 ortholog (kiaa0753),...	greater	41447	30.2	30.2	78%	774	100.00	3654	XM_022759768.1
PREDICTED: Seriola dumerili KIAA0753 ortholog (kiaa0753),...	greater	41447	30.2	30.2	78%	774	100.00	3654	XM_022759767.1
PREDICTED: Seriola dumerili KIAA0753 ortholog (kiaa0753),...	greater	41447	30.2	30.2	78%	774	100.00	3657	XM_022759766.1
PREDICTED: Astyanax mexicanus hydroxypyruvate isomerase...	Mexican	7994	30.2	30.2	78%	774	100.00	1542	XM_022675387.1
PREDICTED: Astyanax mexicanus kyphoscoliosis peptidase...	Mexican	7994	30.2	30.2	78%	774	100.00	4574	XM_007258585.3
PREDICTED: Enhydra lutris kenyoni aryl-hydrocarbon receptor...	NA	391180	30.2	30.2	78%	774	100.00	2193	XM_022512476.1
Mycobacterium tuberculosis strain C3 chromosome	NA	1773	30.2	30.2	78%	774	100.00	4414325	CP023170.1
Mycobacterium tuberculosis strain S3 chromosome	NA	1773	30.2	30.2	78%	774	100.00	4411709	CP023169.1
Lupinus angustifolius cultivar Tanjil chromosome LG-02	narrow-	3871	30.2	30.2	78%	774	100.00	30912075	CP023114.1
Serratia ficaria strain NCTC12148 genome assembly, chromosome: 1	NA	61651	30.2	30.2	78%	774	100.00	5209973	LT906479.1
Bacillus pumilus strain NCTC10337 genome assembly, chromosome: 1	NA	1408	30.2	30.2	78%	774	100.00	3855667	LT906438.1
PREDICTED: Acanthochromis polyacanthus proline-rich protein...	spiny c	80966	30.2	30.2	78%	774	100.00	5015	XM_022202499.1
PREDICTED: Acanthochromis polyacanthus E3 ubiquitin-protein...	spiny c	80966	30.2	30.2	78%	774	100.00	15269	XM_022201953.1
PREDICTED: Acanthochromis polyacanthus KIAA0753 ortholog...	spiny c	80966	30.2	30.2	78%	774	100.00	5858	XM_022196821.1
PREDICTED: Acanthochromis polyacanthus KIAA0753 ortholog...	spiny c	80966	30.2	30.2	78%	774	100.00	5858	XM_022196820.1
PREDICTED: Acanthochromis polyacanthus KIAA0753 ortholog...	spiny c	80966	30.2	30.2	78%	774	100.00	5861	XM_022196819.1
PREDICTED: Acanthochromis polyacanthus transcription	spiny c	80966	30.2	30.2	78%	774	100.00	5449	XM_022198273.1

initiatio...									
PREDICTED: Acanthochromis polyacanthus transcription initiatio...	spiny c	80966	30.2	30.2	78%	774	100.00	5592	XM_022198197.1
PREDICTED: Acanthochromis polyacanthus transcription initiatio...	spiny c	80966	30.2	30.2	78%	774	100.00	5595	XM_022198112.1
PREDICTED: Carica papaya transcription factor E2FA...	papaya	3649	30.2	30.2	78%	774	100.00	2236	XM_022036751.1
PREDICTED: Spinacia oleracea chalcone synthase 3-like...	spinach	3562	30.2	30.2	78%	774	100.00	1466	XM_022004738.1
Bacillus velezensis strain TB1501, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3979382	CP022531.1
Oryzias latipes strain HSOK chromosome 11	Japanes	8090	30.2	30.2	78%	774	100.00	27778217	CP020631.1
Oryzias latipes strain HSOK chromosome 8	Japanes	8090	30.2	30.2	78%	774	100.00	27128663	CP020628.1
Oryzias latipes strain HNI chromosome 14	Japanes	8090	30.2	30.2	78%	774	100.00	28133707	CP020792.1
Oryzias latipes strain HNI chromosome 8	Japanes	8090	30.2	30.2	78%	774	100.00	24535370	CP020786.1
Oryzias latipes strain Hd-rR chromosome 17 sequence	Japanes	8090	30.2	30.2	78%	774	100.00	31792230	CP020681.1
Oryzias latipes strain Hd-rR chromosome 14 sequence	Japanes	8090	30.2	30.2	78%	774	100.00	30598983	CP020678.1
Oryzias latipes strain Hd-rR chromosome 8 sequence	Japanes	8090	30.2	60.5	84%	774	100.00	26239357	CP020672.1
Oryzias latipes strain Hd-rR chromosome 3 sequence	Japanes	8090	30.2	30.2	78%	774	100.00	38248663	CP020667.1
PREDICTED: Chenopodium quinoa **ZINC finger** MYM-type protein...	quinoa	63459	30.2	30.2	78%	774	100.00	1350	XM_021892034.1
Oncorhynchus mykiss TAF7 RNA polymerase II, TATA box binding...	rainbow	8022	30.2	30.2	78%	774	100.00	1471	NM_001165123.2
PREDICTED: Aotus nancymaae uncharacterized LOC110567253...	Ma's ni	37293	30.2	30.2	78%	774	100.00	748	XR_002477691.1
PREDICTED: Aotus nancymaae endoplasmic reticulum-golgi...	Ma's ni	37293	30.2	30.2	78%	774	100.00	3047	XM_012461148.2
PREDICTED: Aotus nancymaae endoplasmic reticulum-golgi...	Ma's ni	37293	30.2	30.2	78%	774	100.00	2898	XM_012461147.2
PREDICTED: Neomonachus schauinslandi potassium two pore domain...	Hawaiia	29088	30.2	30.2	78%	774	100.00	3339	XM_021684622.1
PREDICTED: Meriones unguiculatus sperm acrosome...	Mongoli	10047	30.2	30.2	78%	774	100.00	828	XM_021655912.1
PREDICTED: Meriones unguiculatus spleen associated tyrosine...	Mongoli	10047	30.2	30.2	78%	774	100.00	4308	XM_021643593.1
Mycobacterium tuberculosis strain MTB2 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4417716	CP022014.1
PREDICTED: Lonchura striata domestica protein tyrosine...	Bengale	299123	30.2	30.2	78%	774	100.00	2137	XM_021527797.1
PREDICTED: Lonchura striata domestica protein tyrosine...	Bengale	299123	30.2	30.2	78%	774	100.00	5147	XM_021527796.1
Achromobacter denitrificans strain PR1, complete genome	NA	32002	30.2	30.2	78%	774	100.00	6929205	CP020917.1
PREDICTED: Danio rerio mucin-5AC-like (LOC110438578),	zebrafi	7955	30.2	30.2	78%	774	100.00	6540	XM_021471242.1

mRNA									
PREDICTED: Danio rerio uncharacterized LOC103909155...	zebrafi	7955	30.2	30.2	78%	774	100.00	3867	XM_021478006.1
PREDICTED: Columba livia protein tyrosine phosphatase,...	rock pi	8932	30.2	30.2	78%	774	100.00	1503	XM_021281496.1
PREDICTED: Columba livia DS cell adhesion molecule (**DSCAM**), mRNA	rock pi	8932	30.2	30.2	78%	774	100.00	6262	XM_013370005.2
PREDICTED: Heterocephalus glaber electron transfer flavoprotei...	naked m	10181	30.2	30.2	100%	774	94.74	1357	XM_004872076.2
PREDICTED: Heterocephalus glaber AF4/FMR2 family member 1...	naked m	10181	30.2	30.2	78%	774	100.00	8662	XM_021248856.1
PREDICTED: Heterocephalus glaber AF4/FMR2 family member 1...	naked m	10181	30.2	30.2	78%	774	100.00	8732	XM_004870537.2
PREDICTED: Heterocephalus glaber AF4/FMR2 family member 1...	naked m	10181	30.2	30.2	78%	774	100.00	8757	XM_004870535.2
PREDICTED: Heterocephalus glaber AF4/FMR2 family member 1...	naked m	10181	30.2	30.2	78%	774	100.00	8681	XM_021248855.1
PREDICTED: Heterocephalus glaber AF4/FMR2 family member 1...	naked m	10181	30.2	30.2	78%	774	100.00	8684	XM_021248854.1
Mycobacterium tuberculosis DNA, complete genome, strain: HN-506	NA	1773	30.2	30.2	78%	774	100.00	4413362	AP018036.1
Mycobacterium tuberculosis DNA, complete genome, strain: HN-321	NA	1773	30.2	30.2	78%	774	100.00	4421540	AP018035.1
Mycobacterium tuberculosis DNA, complete genome, strain: HN-205	NA	1773	30.2	30.2	78%	774	100.00	4411033	AP018034.1
PREDICTED: Phascolarctos cinereus Down syndrome cell adhesion...	koala	38626	30.2	30.2	78%	774	100.00	5741	XM_020973916.1
Bordetella genomosp. 9 strain AU14267, complete genome	NA	1416803	30.2	30.2	78%	774	100.00	4497105	CP021110.1
Bordetella genomosp. 9 strain AU17164, complete genome	NA	1416803	30.2	30.2	78%	774	100.00	4587366	CP021109.1
Oryza sativa Indica Group cultivar Shuhui498 chromosome 7...	long-gr	39946	30.2	30.2	78%	774	100.00	30277827	CP018163.1
Oryza sativa Indica Group cultivar Shuhui498 chromosome 3...	long-gr	39946	30.2	30.2	78%	774	100.00	39691490	CP018159.1
Mycobacterium tuberculosis strain Beijing-like/1104 chromosome...	NA	1773	30.2	30.2	78%	774	100.00	4380156	CP017598.1
Mycobacterium tuberculosis strain Beijing-like/50148 chromosom...	NA	1773	30.2	30.2	78%	774	100.00	4444417	CP017597.1
Mycobacterium tuberculosis strain Beijing/391 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4406925	CP017596.1
Mycobacterium tuberculosis strain Beijing-like/38774 chromosom...	NA	1773	30.2	30.2	78%	774	100.00	4431885	CP017595.1

Mycobacterium tuberculosis strain Beijing-like/36918 chromosom...	NA	1773	30.2	30.2	78%	774	100.00	4441591	CP017594.1
Mycobacterium tuberculosis strain Beijing-like/35049 chromosom...	NA	1773	30.2	30.2	78%	774	100.00	4427062	CP017593.1
PREDICTED: Odocoileus virginianus texanus cytochrome P450 4B1...	NA	9880	30.2	30.2	78%	774	100.00	1818	XM_020877137.1
Mycobacterium tuberculosis DNA, complete genome, strain: HN-024	NA	1773	30.2	30.2	78%	774	100.00	4399916	AP018033.1
Mycobacterium tuberculosis strain MTB1, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4433542	CP020381.2
PREDICTED: Monopterus albus pyridoxal kinase-like...	swamp e	43700	30.2	30.2	78%	774	100.00	2201	XM_020621197.1
PREDICTED: Monopterus albus pyridoxal kinase-like...	swamp e	43700	30.2	30.2	78%	774	100.00	2310	XM_020621196.1
PREDICTED: Monopterus albus titin-like (LOC109971935), mRNA	swamp e	43700	30.2	30.2	78%	774	100.00	92088	XM_020620505.1
PREDICTED: Monopterus albus uncharacterized LOC109959152...	swamp e	43700	30.2	30.2	78%	774	100.00	978	XR_002274782.1
PREDICTED: Monopterus albus uncharacterized LOC109959152...	swamp e	43700	30.2	30.2	78%	774	100.00	953	XR_002274778.1
PREDICTED: Monopterus albus uncharacterized LOC109959152...	swamp e	43700	30.2	30.2	78%	774	100.00	965	XR_002274777.1
Homo sapiens ATPase family AAA domain containing 3A (ATAD3A),...	human	9606	30.2	30.2	78%	774	100.00	29545	NG_053035.1
PREDICTED: Prunus persica uncharacterized LOC18788604...	peach	3760	30.2	30.2	78%	774	100.00	3262	XM_007226406.2
PREDICTED: Prunus persica uncharacterized LOC18788604...	peach	3760	30.2	30.2	78%	774	100.00	3346	XM_020555266.1
PREDICTED: Prunus persica uncharacterized LOC18788604...	peach	3760	30.2	30.2	78%	774	100.00	3352	XM_020555265.1
Cyberlindnera jadinii NRRL Y-1542 WD40 repeat-like protein...	NA	983966	30.2	30.2	78%	774	100.00	2559	XM_020216535.1
Bacillus sp. 275, complete genome	NA	1941347	30.2	30.2	78%	774	100.00	4045581	CP019626.1
Mycobacterium tuberculosis TRS10 genome	NA	1334056	30.2	30.2	78%	774	100.00	4411532	CP009195.1
Mycobacterium tuberculosis TRS29 genome	NA	1334075	30.2	30.2	78%	774	100.00	4411532	CP009187.1
Mycobacterium tuberculosis TRS2 genome	NA	1334048	30.2	30.2	78%	774	100.00	4411532	CP009186.1
Mycobacterium tuberculosis TRS22 genome	NA	1334068	30.2	30.2	78%	774	100.00	4411532	CP009183.1
Mycobacterium tuberculosis 1821ADB45 genome	NA	1334084	30.2	30.2	78%	774	100.00	4411532	CP009206.1
Mycobacterium tuberculosis 1821ADB36 genome	NA	1334077	30.2	30.2	78%	774	100.00	4411532	CP009199.1
Mycobacterium tuberculosis 1821ADB40 genome	NA	1334080	30.2	30.2	78%	774	100.00	4411532	CP009202.1
Mycobacterium tuberculosis TRS26 genome	NA	1334072	30.2	30.2	78%	774	100.00	4411532	CP009193.1

Mycobacterium tuberculosis TRS25 genome	NA	1334071	30.2	30.2	78%	774	100.00	4411532	CP009192.1
Mycobacterium tuberculosis TRS24 genome	NA	1334070	30.2	30.2	78%	774	100.00	4411532	CP009191.1
Mycobacterium tuberculosis TRS27 genome	NA	1334073	30.2	30.2	78%	774	100.00	4411532	CP009190.1
Mycobacterium tuberculosis TRS11 genome	NA	1334057	30.2	30.2	78%	774	100.00	4411532	CP009197.1
Mycobacterium tuberculosis TRS8 genome	NA	1334054	30.2	30.2	78%	774	100.00	4411532	CP009196.1
Mycobacterium tuberculosis TRS28 genome	NA	1334074	30.2	30.2	78%	774	100.00	4411532	CP009194.1
Mycobacterium tuberculosis TRS4 genome	NA	1334050	30.2	30.2	78%	774	100.00	4411532	CP009189.1
Mycobacterium tuberculosis TRS6 genome	NA	1334052	30.2	30.2	78%	774	100.00	4411532	CP009188.1
Mycobacterium tuberculosis TRS18 genome	NA	1334064	30.2	30.2	78%	774	100.00	4411532	CP009185.1
Mycobacterium tuberculosis TRS15 genome	NA	1334061	30.2	30.2	78%	774	100.00	4411532	CP009184.1
Mycobacterium tuberculosis TRS12 genome	NA	1334058	30.2	30.2	78%	774	100.00	4411532	CP009182.1
Mycobacterium tuberculosis TRS14 genome	NA	1334060	30.2	30.2	78%	774	100.00	4411532	CP009181.1
Mycobacterium tuberculosis TRS23 genome	NA	1334069	30.2	30.2	78%	774	100.00	4411532	CP009180.1
Mycobacterium tuberculosis TRS5 genome	NA	1334051	30.2	30.2	78%	774	100.00	4411532	CP009179.1
Mycobacterium tuberculosis TRS7 genome	NA	1334053	30.2	30.2	78%	774	100.00	4411532	CP009178.1
Mycobacterium tuberculosis TRS19 genome	NA	1334065	30.2	30.2	78%	774	100.00	4411532	CP009177.1
Mycobacterium tuberculosis TRS21 genome	NA	1334067	30.2	30.2	78%	774	100.00	4411532	CP009176.1
Mycobacterium tuberculosis TRS13 genome	NA	1334059	30.2	30.2	78%	774	100.00	4411532	CP009175.1
Mycobacterium tuberculosis TRS20 genome	NA	1334066	30.2	30.2	78%	774	100.00	4411532	CP009174.1
Mycobacterium tuberculosis TRS17 genome	NA	1334063	30.2	30.2	78%	774	100.00	4411532	CP009173.1
Mycobacterium tuberculosis TRS16 genome	NA	1334062	30.2	30.2	78%	774	100.00	4411532	CP009172.1
Mycobacterium tuberculosis TRS1 genome	NA	1334047	30.2	30.2	78%	774	100.00	4411532	CP009207.1
Mycobacterium tuberculosis 1821ADB44 genome	NA	1334083	30.2	30.2	78%	774	100.00	4411532	CP009205.1
Mycobacterium tuberculosis 1821ADB42 genome	NA	1334082	30.2	30.2	78%	774	100.00	4411532	CP009204.1
Mycobacterium tuberculosis 1821ADB41 genome	NA	1334081	30.2	30.2	78%	774	100.00	4411532	CP009203.1
Mycobacterium tuberculosis 1821ADB38 genome	NA	1334079	30.2	30.2	78%	774	100.00	4411532	CP009201.1
Mycobacterium tuberculosis 1821ADB37 genome	NA	1334078	30.2	30.2	78%	774	100.00	4411532	CP009200.1
Mycobacterium tuberculosis 1821ADB35 genome	NA	1334076	30.2	30.2	78%	774	100.00	4411532	CP009198.1
Mycobacterium tuberculosis TRS9 genome	NA	1334055	30.2	30.2	78%	774	100.00	4411532	CP008702.1
PREDICTED: Paralichthys olivaceus rho guanine nucleotide...	Japanes	8255	30.2	30.2	78%	774	100.00	1934	XM_020108664.1
PREDICTED: Paralichthys	Japanes	8255	30.2	30.2	78%	774	100.00	5436	XM_020079689.1

olivaceus transcription initiation...									
Brachybacterium sp. P6-10-X1, complete genome	NA	1903186	30.2	30.2	78%	774	100.00	4385603	CP017297.1
Mycobacterium bovis AF2122/97 genome assembly, chromosome:...	NA	233413	30.2	30.2	78%	774	100.00	4349904	LT708304.1
PREDICTED: Dendroctonus ponderosae 50S ribosomal protein L27...	mountai	77166	30.2	30.2	100%	774	94.74	589	XM_019907032.1
Mycobacterium caprae strain Allgaeu genome	NA	115862	30.2	30.2	78%	774	100.00	4324961	CP016401.1
PREDICTED: Hippocampus comes LIM domain kinase 2 (limk2),...	tiger t	109280	30.2	30.2	78%	774	100.00	1456	XM_019862661.1
PREDICTED: Hippocampus comes LIM domain kinase 2 (limk2),...	tiger t	109280	30.2	30.2	78%	774	100.00	1732	XM_019862654.1
Mycobacterium tuberculosis H37Ra, complete genome	NA	419947	30.2	30.2	78%	774	100.00	4426109	CP016972.1
Bacillus safensis strain U17-1, complete genome	NA	561879	30.2	30.2	78%	774	100.00	3741804	CP015611.1
Bacillus safensis strain U41, complete genome	NA	561879	30.2	30.2	78%	774	100.00	3735181	CP015610.1
Saccharomycopsis fibuligera x Saccharomycopsis cf. fibuligera...	NA	1725355	30.2	30.2	78%	774	100.00	4911352	CP012809.1
Saccharomycopsis fibuligera strain ATCC 36309 chromosome 1...	NA	4944	30.2	30.2	78%	774	100.00	4909981	CP015978.1
Saccharomycopsis fibuligera strain KPH12 chromosome 1, complet...	NA	4944	30.2	30.2	78%	774	100.00	4889271	CP012823.1
Streptomyces sp. Tue6075, complete genome	NA	1661694	30.2	30.2	78%	774	100.00	7931832	CP010833.1
Pajaroellobacter abortibovis strain BTF92-0548A/99-0131, genome	NA	1882918	30.2	30.2	78%	774	100.00	1821632	CP016908.1
Mycobacterium tuberculosis strain DK9897, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4411511	CP018778.1
Bacillus cellulasensis strain GLB197, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3733835	CP018574.1
PREDICTED: Gavialis gangeticus protein tyrosine phosphatase,...	Gharial	94835	30.2	30.2	78%	774	100.00	2423	XM_019524994.1
PREDICTED: Gavialis gangeticus protein tyrosine phosphatase,...	Gharial	94835	30.2	30.2	78%	774	100.00	2486	XM_019524987.1
PREDICTED: Gavialis gangeticus protein tyrosine phosphatase,...	Gharial	94835	30.2	30.2	78%	774	100.00	2316	XM_019524979.1
Hubei tombus-like virus 8 strain WHCC116238 hypothetical prote...	NA	1923295	30.2	30.2	78%	774	100.00	4326	KX883226.1
Mycobacterium tuberculosis strain M0018684-2, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4359825	CP018305.1
Mycobacterium tuberculosis strain M0002959-6, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4386447	CP018304.1
Mycobacterium tuberculosis strain I0004241-1, complete	NA	1773	30.2	30.2	78%	774	100.00	4386132	CP018303.1

genome									
Mycobacterium tuberculosis strain I0004000-1, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4365724	CP018302.1
Mycobacterium tuberculosis strain I0002801-4, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4376067	CP018301.1
Mycobacterium tuberculosis strain I0002353-6, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4385578	CP018300.1
Bacillus subtilis strain J-5, complete genome	NA	1423	30.2	30.2	78%	774	100.00	4117900	CP018295.1
PREDICTED: Aptenodytes forsteri protein tyrosine phosphatase,...	emperor	9233	30.2	30.2	78%	774	100.00	2187	XM_009284089.2
PREDICTED: Aptenodytes forsteri protein tyrosine phosphatase,...	emperor	9233	30.2	30.2	78%	774	100.00	1674	XM_009284088.2
PREDICTED: Aptenodytes forsteri protein tyrosine phosphatase,...	emperor	9233	30.2	30.2	78%	774	100.00	2314	XM_019473353.1
Mycobacterium tuberculosis DNA, complete genome, strain:...	NA	1773	30.2	30.2	78%	774	100.00	4380602	AP017901.1
Nocardia mangyaensis strain Y48 chromosome, complete genome	NA	2213200	30.2	30.2	78%	774	100.00	7310115	CP018082.1
Kwoniella pini CBS 10737 hypothetical protein partial mRNA	NA	1296096	30.2	30.2	78%	774	100.00	1137	XM_019156321.1
PREDICTED: Cyprinus carpio mediator of RNA polymerase II...	common	7962	30.2	30.2	100%	774	94.74	2149	XM_019095653.1
PREDICTED: Cyprinus carpio dystrophin-like (LOC109078538), mRNA	common	7962	30.2	30.2	78%	774	100.00	549	XM_019093793.1
PREDICTED: Bemisia tabaci protein CASC1-like (LOC109033871), mRNA	NA	7038	30.2	30.2	78%	774	100.00	4432	XM_019046701.1
Mycobacterium tuberculosis strain TB282 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4425860	CP017920.1
Bacillus xiamenensis strain VV3, complete genome	NA	1178537	30.2	30.2	78%	774	100.00	3637729	CP017786.1
Fusarium verticillioides 7600 hypothetical protein (FVEG_03243...	NA	334819	30.2	30.2	78%	774	100.00	7573	XM_018890855.1
Mycobacterium tuberculosis strain 1458, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4402033	CP013475.1
PREDICTED: Musa acuminata subsp. malaccensis cytochrome P450...	wild Ma	214687	30.2	30.2	78%	774	100.00	1818	XM_018822843.1
Streptomyces sp. 2114.2 genome assembly, chromosome: I	NA	1881022	30.2	30.2	78%	774	100.00	8620263	LT629768.1
PSEUDOMONAS umsongensis strain BS3657 genome assembly,...	NA	198618	30.2	30.2	78%	774	100.00	6749275	LT629767.1
PREDICTED: Lates calcarifer titin-like (LOC108874713), mRNA	barramu	8187	30.2	30.2	78%	774	100.00	89380	XM_018663223.1
PREDICTED: Lates calcarifer uncharacterized	barramu	8187	30.2	30.2	78%	774	100.00	2801	XR_001960965.1

LOC108883932...									
PREDICTED: Pyrus x bretschneideri uncharacterized LOC103967766...	Chinese	225117	30.2	30.2	78%	774	100.00	1453	XR_670394.2
PREDICTED: Pyrus x bretschneideri uncharacterized LOC103967766...	Chinese	225117	30.2	30.2	78%	774	100.00	1459	XR_670392.2
PREDICTED: Pyrus x bretschneideri uncharacterized LOC103967766...	Chinese	225117	30.2	30.2	78%	774	100.00	1491	XR_670393.2
Ganoderma lucidum isopentenyl pyrophosphate isomerase (ipi)...	NA	5315	30.2	30.2	78%	774	100.00	2031	HQ377516.1
Ganoderma lucidum isopentenyl pyrophosphate isomerase (ipi)...	NA	5315	30.2	30.2	78%	774	100.00	846	HQ377515.1
Mycobacterium tuberculosis strain Beijing, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4378588	CP011510.1
Streptomyces rubrolavendulae strain MJM4426, complete genome	NA	285473	30.2	30.2	100%	774	94.74	6543262	CP017316.1
Actinoalloteichus hymeniacidonis strain HPA177(T) (=DSM...	NA	340345	30.2	30.2	78%	774	100.00	6306386	CP014859.1
Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protei...	NA	426428	30.2	30.2	78%	774	100.00	9125	XM_018382944.1
Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protei...	NA	426428	30.2	30.2	78%	774	100.00	9804	XM_018382942.1
Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protei...	NA	426428	30.2	30.2	78%	774	100.00	7571	XM_018382941.1
PREDICTED: Manacus vitellinus FA core complex associated prote...	golden-	328815	30.2	30.2	78%	774	100.00	1689	XM_018079314.1
Mycobacterium tuberculosis strain SCAID 252.0, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4439387	CP016888.1
TPA: Oryzias latipes strain Hd-rR, complete genome assembly,...	Japanes	8090	30.2	30.2	78%	774	100.00	25865442	HF933214.1
TPA: Oryzias latipes strain Hd-rR, complete genome assembly,...	Japanes	8090	30.2	30.2	78%	774	100.00	36623554	HF933209.1
Mycobacterium tuberculosis strain SCAID 187.0 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4411829	CP012506.2
Streptomyces noursei ATCC 11455, complete genome	NA	316284	30.2	30.2	78%	774	100.00	9815884	CP011533.1
PREDICTED: Lepidothrix coronata protein tyrosine phosphatase,...	blue-cr	321398	30.2	30.2	78%	774	100.00	1655	XM_017819463.1
PREDICTED: Lepidothrix coronata protein tyrosine phosphatase,...	blue-cr	321398	30.2	30.2	78%	774	100.00	6162	XM_017819462.1
PREDICTED: Lepidothrix coronata acetyl-CoA carboxylase beta...	blue-cr	321398	30.2	30.2	78%	774	100.00	7482	XM_017814297.1
Mycobacterium tuberculosis strain SCAID 320.0, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4406628	CP016794.1
Bacillus cellulasensis strain NJ-V, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3792999	CP012330.1

Mycobacterium bovis strain SP38, complete genome	NA	1765	30.2	30.2	78%	774	100.00	4347648	CP015773.2
PREDICTED: Corvus brachyrhynchos grainyhead like transcription...	America	85066	30.2	30.2	78%	774	100.00	4969	XM_017744981.1
PREDICTED: Corvus brachyrhynchos protein tyrosine phosphatase,...	America	85066	30.2	30.2	78%	774	100.00	1949	XM_017729471.1
Bacillus pumilus strain C4 genome	NA	1408	30.2	30.2	78%	774	100.00	3659360	CP011109.1
Agaricus bisporus var. bisporus H97 chromosome 5, complete...	NA	936046	30.2	30.2	78%	774	100.00	2550681	CP015461.1
Agaricus bisporus var. bisporus strain H39 chromosome 5,...	NA	192523	30.2	30.2	78%	774	100.00	2477729	CP015474.1
PREDICTED: Ictalurus punctatus dynein heavy chain 5,...	channel	7998	30.2	30.2	78%	774	100.00	14578	XM_017473580.1
PREDICTED: Daucus carota subsp. sativus mitochondrial arginine...	NA	79200	30.2	30.2	100%	774	94.74	1979	XM_017395035.1
PREDICTED: Poecilia reticulata programmed cell death 10...	guppy	8081	30.2	30.2	78%	774	100.00	1664	XM_008399283.2
PREDICTED: Drosophila takahashii uncharacterized LOC108060847...	NA	29030	30.2	30.2	78%	774	100.00	436	XM_017146744.1
PREDICTED: Anolis carolinensis estrogen related receptor beta...	green a	28377	30.2	30.2	78%	774	100.00	6445	XM_008121354.2
PREDICTED: Anolis carolinensis estrogen related receptor beta...	green a	28377	30.2	30.2	78%	774	100.00	6377	XM_008121249.2
PREDICTED: Anolis carolinensis estrogen related receptor beta...	green a	28377	30.2	30.2	78%	774	100.00	7439	XM_008121187.2
PREDICTED: Anolis carolinensis estrogen related receptor beta...	green a	28377	30.2	30.2	78%	774	100.00	7389	XM_008121092.2
PREDICTED: Prunus mume uncharacterized LOC103323114...	Japanes	102107	30.2	30.2	78%	774	100.00	3209	XM_008225076.2
Fonsecaea multimorphosa CBS 102226 hypothetical protein partia...	NA	1442371	30.2	30.2	78%	774	100.00	3135	XM_016776852.1
Spizellomyces punctatus DAOM BR117 hypothetical protein...	NA	645134	30.2	30.2	78%	774	100.00	1759	XM_016753935.1
Bacillus velezensis strain SB1216, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3814720	CP015417.1
Bacillus velezensis strain CC09, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4167153	CP015443.1
Cladophialophora immunda hypothetical protein mRNA	NA	569365	30.2	30.2	78%	774	100.00	6821	XM_016393322.1
Exophiala oligosperma hypothetical protein, variant mRNA	NA	215243	30.2	30.2	78%	774	100.00	1627	XM_016405526.1
Exophiala oligosperma hypothetical protein mRNA	NA	215243	30.2	30.2	78%	774	100.00	1711	XM_016405525.1
Bacillus amyloliquefaciens strain B15, complete genome	NA	1390	30.2	30.2	78%	774	100.00	4006754	CP014783.1
Bacillus amyloliquefaciens UMAF6639, complete genome	NA	1333538	30.2	30.2	78%	774	100.00	4034636	CP006058.1
Mycobacterium africanum strain UT307 genome	NA	33894	30.2	30.2	78%	774	100.00	4493502	CP014617.1
Mycobacterium tuberculosis strain PR10 genome	NA	1773	30.2	30.2	78%	774	100.00	4433130	CP010968.1
Mycobacterium tuberculosis variant bovis BCG str. Tokyo 172...	NA	561275	30.2	30.2	78%	774	100.00	4371707	CP014566.1

PREDICTED: Protobothrops mucrosquamatus estrogen related...	NA	103944	30.2	30.2	78%	774	100.00	1185	XM_015814246.1
PREDICTED: Protobothrops mucrosquamatus estrogen related...	NA	103944	30.2	30.2	78%	774	100.00	1317	XM_015814245.1
Bacillus pumilus strain SH-B9, complete genome	NA	1408	30.2	30.2	78%	774	100.00	3787586	CP011007.1
Bacillus pumilus strain SH-B11, complete genome	NA	1408	30.2	30.2	78%	774	100.00	3860091	CP010997.1
Mycobacterium tuberculosis strain 26105, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4426489	CP010340.1
Mycobacterium tuberculosis strain 22103, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4399422	CP010339.1
Mycobacterium tuberculosis strain 37004, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4417090	CP010338.1
Mycobacterium tuberculosis strain 22115, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4401829	CP010337.1
Mycobacterium tuberculosis strain 2279, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4405033	CP010336.1
Mycobacterium tuberculosis strain 2242, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4419839	CP010335.1
Mycobacterium africanum strain 25, complete genome	NA	33894	30.2	30.2	78%	774	100.00	4386422	CP010334.1
Mycobacterium microti strain 12, complete genome	NA	1806	30.2	30.2	78%	774	100.00	4370115	CP010333.1
Mycobacterium bovis strain 30, complete genome	NA	1765	30.2	30.2	78%	774	100.00	4336227	CP010332.1
Mycobacterium bovis BCG strain 26, complete genome	NA	33892	30.2	30.2	78%	774	100.00	4351313	CP010331.1
Mycobacterium tuberculosis strain F28, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4421903	CP010330.1
Mycobacterium tuberculosis strain F1, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4428621	CP010329.1
Bacillus cellulasensis strain ku-bf1 genome	NA	293387	30.2	30.2	78%	774	100.00	3745118	CP014165.1
PREDICTED: Lepisosteus oculatus potassium channel subfamily M...	spotted	7918	30.2	30.2	78%	774	100.00	5954	XM_015360838.1
PREDICTED: Lepisosteus oculatus potassium channel subfamily M...	spotted	7918	30.2	30.2	78%	774	100.00	4560	XM_015360837.1
PREDICTED: Lepisosteus oculatus potassium channel subfamily M...	spotted	7918	30.2	30.2	78%	774	100.00	3733	XM_015360836.1
PREDICTED: Lepisosteus oculatus potassium channel subfamily M...	spotted	7918	30.2	30.2	78%	774	100.00	5343	XM_015360835.1
PREDICTED: Lepisosteus oculatus potassium channel subfamily M...	spotted	7918	30.2	30.2	78%	774	100.00	3619	XM_006637406.2
Mycobacterium bovis strain BCG-1 (Russia), complete genome	NA	1765	30.2	30.2	78%	774	100.00	4370705	CP013741.1
Herbaspirillum rubrisubalbicans M1, complete genome	NA	1078773	30.2	30.2	78%	774	100.00	5611261	CP013737.1
PREDICTED: Calidris pugnax protein tyrosine phosphatase,...	ruff	198806	30.2	30.2	78%	774	100.00	1784	XM_014938599.1
PREDICTED: Calidris pugnax protein tyrosine phosphatase,...	ruff	198806	30.2	30.2	78%	774	100.00	2815	XM_014938598.1
PREDICTED: Sturnus vulgaris coatomer protein complex	Common	9172	30.2	30.2	78%	774	100.00	2396	XM_014882528.1

subunit...									
PREDICTED: Sturnus vulgaris grainyhead-like transcription fact...	Common	9172	30.2	30.2	78%	774	100.00	4496	XM_014894990.1
PREDICTED: Equus asinus **ZINC finger** protein 7 (**ZNF7**), transcri...	ass	9793	30.2	30.2	78%	774	100.00	5429	XM_014858243.1
PREDICTED: Equus asinus **ZINC finger** protein 7 (**ZNF7**), transcri...	ass	9793	30.2	30.2	78%	774	100.00	6935	XM_014858242.1
PREDICTED: Equus asinus **ZINC finger** protein 7 (**ZNF7**), transcri...	ass	9793	30.2	30.2	78%	774	100.00	5852	XM_014858241.1
PREDICTED: Equus asinus **ZINC finger** protein 7 (**ZNF7**), transcri...	ass	9793	30.2	30.2	78%	774	100.00	5647	XM_014858240.1
PREDICTED: Equus asinus **ZINC finger** protein 7 (**ZNF7**), transcri...	ass	9793	30.2	30.2	78%	774	100.00	5951	XM_014858239.1
PREDICTED: Equus asinus **ZINC finger** protein 7 (**ZNF7**), transcri...	ass	9793	30.2	30.2	78%	774	100.00	5693	XM_014858238.1
PREDICTED: Equus asinus **ZINC finger** protein 7 (**ZNF7**), transcri...	ass	9793	30.2	30.2	78%	774	100.00	5853	XM_014858237.1
PREDICTED: Equus asinus **ZINC finger** protein 555 (LOC106834151)...	ass	9793	30.2	30.2	78%	774	100.00	9793	XM_014845624.1
Bacillus pumilus DNA, complete genome, strain: TUAT1	NA	1408	30.2	30.2	78%	774	100.00	3723433	AP014928.1
Bacillus cellulasensis strain NJ-V2, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3787818	CP012482.1
PREDICTED: Myotis brandtii DEAH (Asp-Glu-Ala-His) box...	Brandt'	109478	30.2	30.2	78%	774	100.00	3202	XM_014533344.1
Bacillus cellulasensis strain NJ-M2, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3793419	CP012329.1
Pseudonocardia sp. EC080619-01, complete genome	NA	1096856	30.2	30.2	100%	774	94.74	6149338	CP012184.1
Pseudonocardia sp. EC080610-09, complete genome	NA	1688404	30.2	30.2	100%	774	94.74	6138223	CP012181.1
PREDICTED: Bos mutus neurocalcin delta (NCALD), transcript...	wild ya	72004	30.2	30.2	78%	774	100.00	2910	XM_005887014.2
PREDICTED: Bos mutus neurocalcin delta (NCALD), transcript...	wild ya	72004	30.2	30.2	78%	774	100.00	3157	XM_005887013.2
Drosophila melanogaster long non-coding RNA:CR44344...	fruit f	7227	30.2	30.2	78%	774	100.00	1568	NR_124597.2
Oryza sativa Japonica Group DNA, chromosome 7, cultivar:...	Japanes	39947	30.2	30.2	78%	774	100.00	29697621	AP014963.1
Oryza sativa Japonica Group DNA, chromosome 3, cultivar:...	Japanes	39947	30.2	30.2	78%	774	100.00	36413819	AP014959.1
Oryza sativa Indica Group cultivar RP Bio-226 chromosome 7...	long-gr	39946	30.2	30.2	78%	774	100.00	26660614	CP012615.1
Oryza sativa Indica Group cultivar RP Bio-226 chromosome 3...	long-gr	39946	30.2	30.2	78%	774	100.00	39504267	CP012611.1

Glutamicibacter halophytocola strain KLBMP 5180 chromosome,...	NA	1933880	30.2	30.2	78%	774	100.00	3911798	CP012750.1
PREDICTED: Pseudopodoces humilis protein tyrosine phosphatase,...	Tibetan	181119	30.2	30.2	78%	774	100.00	1715	XM_005517278.2
PREDICTED: Salmo salar microtubule-associated protein 4-like...	Atlanti	8030	30.2	30.2	78%	774	100.00	8140	XM_014140325.1
PREDICTED: Salmo salar microtubule-associated protein 4-like...	Atlanti	8030	30.2	30.2	78%	774	100.00	8204	XM_014140324.1
PREDICTED: Salmo salar microtubule-associated protein 4-like...	Atlanti	8030	30.2	30.2	78%	774	100.00	8212	XM_014140323.1
PREDICTED: Salmo salar microtubule-associated protein 4-like...	Atlanti	8030	30.2	30.2	78%	774	100.00	8222	XM_014140322.1
PREDICTED: Salmo salar mucin-17-like (LOC106605304), mRNA	Atlanti	8030	30.2	30.2	78%	774	100.00	8299	XM_014200820.1
Pseudonocardia sp. EC080625-04, complete genome	NA	1096868	30.2	30.2	100%	774	94.74	6135769	CP010989.1
PREDICTED: Austrofundulus limnaeus myosin phosphatase Rho...	NA	52670	30.2	30.2	78%	774	100.00	8400	XM_014008210.1
PREDICTED: Austrofundulus limnaeus myosin phosphatase Rho...	NA	52670	30.2	30.2	78%	774	100.00	8985	XM_014008209.1
PREDICTED: Austrofundulus limnaeus myosin phosphatase Rho...	NA	52670	30.2	30.2	78%	774	100.00	9207	XM_014008208.1
PREDICTED: Austrofundulus limnaeus myosin phosphatase Rho...	NA	52670	30.2	30.2	78%	774	100.00	9332	XM_014008206.1
PREDICTED: Austrofundulus limnaeus myosin phosphatase Rho...	NA	52670	30.2	30.2	78%	774	100.00	9222	XM_014008205.1
PREDICTED: Austrofundulus limnaeus myosin phosphatase Rho...	NA	52670	30.2	30.2	78%	774	100.00	9347	XM_014008204.1
PREDICTED: Austrofundulus limnaeus myosin phosphatase Rho...	NA	52670	30.2	30.2	78%	774	100.00	9261	XM_014008203.1
Mycobacterium bovis strain BCG-1 genome	NA	1765	30.2	30.2	78%	774	100.00	4363945	CP011455.1
PREDICTED: Thamnophis sirtalis steroid hormone receptor ERR2...	NA	35019	30.2	30.2	78%	774	100.00	2907	XM_014055050.1
PREDICTED: Thamnophis sirtalis steroid hormone receptor ERR2...	NA	35019	30.2	30.2	78%	774	100.00	2781	XM_014055049.1
PREDICTED: Thamnophis sirtalis steroid hormone receptor ERR2...	NA	35019	30.2	30.2	78%	774	100.00	2919	XM_014055048.1
PREDICTED: Apteryx australis mantelli protein tyrosine...	NA	202946	30.2	30.2	78%	774	100.00	1562	XM_013942485.1
PREDICTED: Apteryx australis mantelli protein tyrosine...	NA	202946	30.2	30.2	78%	774	100.00	1440	XM_013942478.1
Mycobacterium bovis BCG strain Russia 368, complete genome	NA	33892	30.2	30.2	78%	774	100.00	4370138	CP009243.1
Eimeria necatrix	NA	51315	30.2	30.2	78%	774	100.00	6516	XM_013577640.1

Nucleotidyltransferase family protein, relate...									
PREDICTED: Chinchilla lanigera **ZINC finger** protein 3 (Znf3),...	long-ta	34839	30.2	30.2	78%	774	100.00	2573	XM_005413761.2
PREDICTED: Chinchilla lanigera **ZINC finger** protein 3 (Znf3),...	long-ta	34839	30.2	30.2	78%	774	100.00	2616	XM_005413760.2
PREDICTED: Chinchilla lanigera **ZINC finger** protein 3 (Znf3),...	long-ta	34839	30.2	30.2	78%	774	100.00	2750	XM_005413758.2
PREDICTED: Chinchilla lanigera **ZINC finger** protein 3 (Znf3),...	long-ta	34839	30.2	30.2	78%	774	100.00	2779	XM_005413759.2
PREDICTED: Chinchilla lanigera **ZINC finger** protein 3 (Znf3),...	long-ta	34839	30.2	30.2	78%	774	100.00	2708	XM_005413757.2
Mycobacterium tuberculosis W-148, complete genome	NA	659019	30.2	30.2	78%	774	100.00	4418548	CP012090.1
Bacillus altitudinis strain GR-8, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3674849	CP009108.1
Luteipulveratus mongoliensis strain MN07-A0370 genome	NA	571913	30.2	30.2	78%	774	100.00	5420910	CP011112.1
PREDICTED: Anser cygnoides domesticus Down syndrome cell...	NA	381198	30.2	30.2	78%	774	100.00	7137	XM_013181234.1
PREDICTED: Anser cygnoides domesticus protein tyrosine...	NA	381198	30.2	30.2	78%	774	100.00	1338	XM_013179359.1
PREDICTED: Anser cygnoides domesticus protein tyrosine...	NA	381198	30.2	30.2	78%	774	100.00	1213	XM_013179358.1
PREDICTED: Anser cygnoides domesticus protein tyrosine...	NA	381198	30.2	30.2	78%	774	100.00	5381	XM_013179357.1
Mycobacterium bovis strain 1595, complete genome	NA	1765	30.2	30.2	78%	774	100.00	4351712	CP012095.1
Myxococcus hansupus strain mixupus, complete genome	NA	1297742	30.2	30.2	78%	774	100.00	9490432	CP012109.1
PREDICTED: Mustela putorius furo aryl hydrocarbon receptor...	domesti	9669	30.2	30.2	78%	774	100.00	3856	XM_013064500.1
Mycobacterium bovis BCG strain 3281, complete genome	NA	33892	30.2	30.2	78%	774	100.00	4410431	CP008744.1
Ovis canadensis canadensis isolate 43U chromosome 25 sequence	NA	112262	30.2	60.5	84%	774	100.00	45421385	CP011910.1
Ovis canadensis canadensis isolate 43U chromosome 23 sequence	NA	112262	30.2	30.2	78%	774	100.00	62403671	CP011908.1
Ovis canadensis canadensis isolate 43U chromosome 22 sequence	NA	112262	30.2	30.2	78%	774	100.00	50890418	CP011907.1
Ovis canadensis canadensis isolate 43U chromosome 21 sequence	NA	112262	30.2	60.5	78%	774	100.00	50119401	CP011906.1
Ovis canadensis canadensis isolate 43U chromosome 17 sequence	NA	112262	30.2	30.2	78%	774	100.00	72372754	CP011902.1
Ovis canadensis canadensis isolate 43U chromosome 16 sequence	NA	112262	30.2	30.2	78%	774	100.00	71803284	CP011901.1
Ovis canadensis canadensis isolate 43U chromosome 15 sequence	NA	112262	30.2	30.2	78%	774	100.00	81015546	CP011900.1
Ovis canadensis canadensis isolate 43U chromosome 14 sequence	NA	112262	30.2	30.2	78%	774	100.00	62800317	CP011899.1
Ovis canadensis canadensis isolate 43U chromosome 8	NA	112262	30.2	30.2	78%	774	100.00	90795278	CP011893.1

sequence									
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	78%	774	100.00	196293	LK066217.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	78%	774	100.00	18604806	LK064876.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	78%	774	100.00	35850568	LK064800.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	78%	774	100.00	1527064	LK065467.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	90.7	78%	774	100.00	37256661	LK391417.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	78%	774	100.00	242259	LK067367.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	78%	774	100.00	17637924	LK064763.1
Apteryx australis mantelli genome assembly AptMant0, scaffold...	NA	202946	30.2	30.2	78%	774	100.00	2740165	LK064678.1
Bacillus velezensis strain G341 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4009746	CP011686.1
Methanosarcina barkeri CM1, complete genome	NA	796385	30.2	30.2	78%	774	100.00	4501171	CP008746.1
Streptomyces sp. CNQ-509 chromosome, complete genome	NA	444103	30.2	30.2	78%	774	100.00	8039333	CP011492.1
TPA: Neospora caninum Liverpool, chromosome chrVIII, complete...	NA	572307	30.2	30.2	78%	774	100.00	6731139	LN714483.1
PREDICTED: Aotus nancymaae endoplasmic reticulum-golgi...	Ma's ni	37293	30.2	30.2	78%	774	100.00	2935	XM_012461146.1
PREDICTED: Aotus nancymaae uncharacterized LOC105721590...	Ma's ni	37293	30.2	30.2	78%	774	100.00	3904	XR_001108373.1
Bacillus altitudinis strain W3, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3745123	CP011150.1
Methanosarcina barkeri 227, complete genome	NA	1434106	30.2	30.2	78%	774	100.00	4447980	CP009530.1
Methanosarcina barkeri MS, complete genome	NA	1434108	30.2	30.2	78%	774	100.00	4533209	CP009528.1
PREDICTED: Cercocebus atys uncharacterized LOC105594419...	sooty m	9531	30.2	30.2	78%	774	100.00	2868	XR_001017998.1
Mycobacterium tuberculosis strain Beijing-like, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4411216	CP010873.1
Mycobacterium tuberculosis strain PR08 genome	NA	1773	30.2	30.2	78%	774	100.00	4392860	CP010895.1
Bacillus amyloliquefaciens subsp. amyloliquefaciens KHG19,...	NA	1292358	30.2	30.2	78%	774	100.00	3953361	CP007242.1
Mycobacterium tuberculosis 18b genome	NA	1452723	30.2	30.2	78%	774	100.00	4411953	CP007299.1
Mycobacterium tuberculosis H37RvSiena, complete genome	NA	1437856	30.2	30.2	78%	774	100.00	4410911	CP007027.1
Streptomyces sp. 769, complete genome	NA	1262452	30.2	30.2	78%	774	100.00	10100774	CP003987.1

PREDICTED: Camelus bactrianus **ZINC finger** protein 7 (**ZNF7**),...	Bactria	9837	30.2	30.2	78%	774	100.00	4863	XM_010961202.1
PREDICTED: Camelus bactrianus **ZINC finger** protein 7 (**ZNF7**),...	Bactria	9837	30.2	30.2	78%	774	100.00	3894	XM_010961201.1
PREDICTED: Camelus bactrianus **ZINC finger** protein 7 (**ZNF7**),...	Bactria	9837	30.2	30.2	78%	774	100.00	4866	XM_010961200.1
PREDICTED: Camelus bactrianus junctophilin 2 (JPH2), mRNA	Bactria	9837	30.2	30.2	78%	774	100.00	2860	XM_010958721.1
Bacillus sp. Pc3, complete genome	NA	1446792	30.2	30.2	78%	774	100.00	3982168	CP010406.1
Mycobacterium tuberculosis str. Kurono DNA, complete genome	NA	1445606	30.2	30.2	78%	774	100.00	4415078	AP014573.1
PREDICTED: Notothenia coriiceps KIAA0753 ortholog (kiaa0753),...	black r	8208	30.2	30.2	78%	774	100.00	3644	XM_010792480.1
PREDICTED: Notothenia coriiceps KIAA0753 ortholog (kiaa0753),...	black r	8208	30.2	30.2	78%	774	100.00	3653	XM_010792479.1
PREDICTED: Notothenia coriiceps pyridoxal (pyridoxine, vitamin...	black r	8208	30.2	30.2	78%	774	100.00	2445	XM_010783104.1
Cucumis melo genomic chromosome, chr_1	muskmel	3656	30.2	30.2	78%	774	100.00	35383099	LN713255.1
Cucumis melo genomic scaffold, anchoredscaffold00019	muskmel	3656	30.2	30.2	78%	774	100.00	5954733	LN681798.1
Bacillus sp. WP8, complete genome	NA	756828	30.2	30.2	78%	774	100.00	3708888	CP010075.1
PREDICTED: Haliaeetus leucocephalus protein tyrosine...	bald ea	52644	30.2	30.2	78%	774	100.00	1646	XM_010583313.1
PREDICTED: Haliaeetus leucocephalus protein tyrosine...	bald ea	52644	30.2	30.2	78%	774	100.00	2648	XM_010583312.1
PREDICTED: Haliaeetus leucocephalus protein tyrosine...	bald ea	52644	30.2	30.2	78%	774	100.00	1854	XM_010583311.1
PREDICTED: Haliaeetus leucocephalus Down syndrome cell adhesio...	bald ea	52644	30.2	30.2	78%	774	100.00	6570	XM_010580406.1
Collimonas arenae strain Cal35, complete genome	NA	279058	30.2	30.2	78%	774	100.00	5603532	CP009962.1
PREDICTED: Balearica regulorum gibbericeps protein tyrosine...	East Af	100784	30.2	30.2	78%	774	100.00	1801	XM_010306337.1
PREDICTED: Phaethon lepturus Down syndrome cell adhesion...	White-t	97097	30.2	30.2	78%	774	100.00	1848	XM_010291637.1
PREDICTED: Phaethon lepturus protein tyrosine phosphatase,...	White-t	97097	30.2	30.2	78%	774	100.00	2122	XM_010297591.1
PREDICTED: Tinamus guttatus protein tyrosine phosphatase,...	white-t	94827	30.2	30.2	78%	774	100.00	1598	XM_010221639.1
PREDICTED: Colius striatus low-density lipoprotein receptor...	speckle	57412	30.2	30.2	78%	774	100.00	752	XM_010202892.1
PREDICTED: Chlamydotis macqueenii protein tyrosine phosphatase...	Macquee	187382	30.2	30.2	78%	774	100.00	729	XM_010119241.1
PREDICTED: Pterocles gutturalis Down syndrome cell adhesion...	yellow-	240206	30.2	30.2	78%	774	100.00	1916	XM_010078165.1
PREDICTED: Pterocles	yellow-	240206	30.2	30.2	78%	774	100.00	1645	XM_010087126.1

gutturalis protein tyrosine phosphatase,...									
PREDICTED: Eurypyga helias Down syndrome cell adhesion molecul...	sunbitt	54383	30.2	30.2	78%	774	100.00	1845	XM_010146526.1
PREDICTED: Buceros rhinoceros silvestris Down syndrome cell...	NA	175836	30.2	30.2	78%	774	100.00	1947	XM_010135805.1
PREDICTED: Buceros rhinoceros silvestris protein tyrosine...	NA	175836	30.2	30.2	78%	774	100.00	1582	XM_010133368.1
Mycobacterium tuberculosis 49-02 complete genome	NA	1427516	30.2	30.2	78%	774	100.00	4412379	HG813240.1
PREDICTED: Chaetura pelagica protein tyrosine phosphatase,...	chimney	8897	30.2	30.2	78%	774	100.00	1567	XM_010006878.1
PREDICTED: Tauraco erythrolophus protein tyrosine phosphatase,...	red-cre	121530	30.2	30.2	78%	774	100.00	1579	XM_009988748.1
PREDICTED: Leptosomus discolor protein tyrosine phosphatase,...	cuckoo	188344	30.2	30.2	78%	774	100.00	1450	XM_009951640.1
PREDICTED: Opisthocomus hoazin protein tyrosine phosphatase,...	NA	30419	30.2	30.2	78%	774	100.00	1783	XM_009938948.1
PREDICTED: Opisthocomus hoazin Down syndrome cell adhesion...	NA	30419	30.2	30.2	78%	774	100.00	6590	XM_009932702.1
PREDICTED: Haliaeetus albicilla protein tyrosine phosphatase,...	white-t	8969	30.2	30.2	78%	774	100.00	1167	XM_009927391.1
PREDICTED: Haliaeetus albicilla Down syndrome cell adhesion...	white-t	8969	30.2	30.2	78%	774	100.00	2410	XM_009924238.1
PREDICTED: Picoides pubescens Down syndrome cell adhesion...	Downy w	118200	30.2	30.2	78%	774	100.00	6626	XM_009905864.1
PREDICTED: Charadrius vociferus protein tyrosine phosphatase,...	killdee	50402	30.2	30.2	78%	774	100.00	1566	XM_009889062.1
PREDICTED: Picoides pubescens protein tyrosine phosphatase,...	Downy w	118200	30.2	30.2	78%	774	100.00	1529	XM_009909908.1
PREDICTED: Picoides pubescens protein tyrosine phosphatase,...	Downy w	118200	30.2	30.2	78%	774	100.00	1476	XM_009909907.1
PREDICTED: Apaloderma vittatum protein tyrosine phosphatase,...	bar-tai	57397	30.2	30.2	78%	774	100.00	1567	XM_009867543.1
PREDICTED: Apaloderma vittatum Down syndrome cell adhesion...	bar-tai	57397	30.2	30.2	78%	774	100.00	2041	XM_009878322.1
PREDICTED: Gavia stellata protein tyrosine phosphatase,...	red-thr	37040	30.2	30.2	78%	774	100.00	899	XM_009815938.1
PREDICTED: Gavia stellata Down syndrome cell adhesion...	red-thr	37040	30.2	30.2	78%	774	100.00	1939	XM_009820497.1
PREDICTED: Struthio camelus australis protein tyrosine...	NA	441894	30.2	30.2	78%	774	100.00	1513	XM_009686059.1
PREDICTED: Struthio camelus australis Down syndrome cell...	NA	441894	30.2	30.2	78%	774	100.00	6139	XM_009679579.1
PREDICTED: Fulmarus glacialis protein tyrosine phosphatase,...	Norther	30455	30.2	30.2	78%	774	100.00	1587	XM_009585853.1
PREDICTED: Fulmarus glacialis Down syndrome cell adhesion...	Norther	30455	30.2	30.2	78%	774	100.00	2062	XM_009579278.1
Phytophthora sojae hypothetical	NA	67593	30.2	30.2	78%	774	100.00	2721	XM_009527689.1

protein partial mRNA									
PREDICTED: Phalacrocorax carbo protein tyrosine phosphatase,...	great c	9209	30.2	30.2	78%	774	100.00	1565	XM_009511704.1
PREDICTED: Nipponia nippon Down syndrome cell adhesion molecul...	crested	128390	30.2	30.2	78%	774	100.00	6540	XM_009473531.1
PREDICTED: Nipponia nippon protein tyrosine phosphatase,...	crested	128390	30.2	30.2	78%	774	100.00	1564	XM_009470701.1
PREDICTED: Pelecanus crispus protein tyrosine phosphatase,...	Dalmati	36300	30.2	30.2	78%	774	100.00	1566	XM_009491657.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	78%	774	100.00	1589	LN218295.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	78%	774	100.00	2568	LN145888.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	78%	774	100.00	4742	LN071533.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	78%	774	100.00	7349	LN034477.1
PREDICTED: Pygoscelis adeliae protein tyrosine phosphatase,...	Adelie	9238	30.2	30.2	78%	774	100.00	1538	XM_009318526.1
PREDICTED: Pygoscelis adeliae protein tyrosine phosphatase,...	Adelie	9238	30.2	30.2	78%	774	100.00	2325	XM_009318525.1
Dicrocoelium dendriticum genome assembly...	NA	57078	30.2	30.2	78%	774	100.00	834	LK668686.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei...	NA	99802	30.2	30.2	78%	774	100.00	10871	LN014259.1
Mycobacterium tuberculosis strain 96121, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4410945	CP009427.1
Mycobacterium tuberculosis strain 96075, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4379376	CP009426.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common	7962	30.2	30.2	78%	774	100.00	728060	LN596728.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common	7962	30.2	30.2	100%	774	94.74	391788	LN595276.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common	7962	30.2	60.5	78%	774	100.00	852171	LN594734.1
Cyprinus carpio genome assembly common carp genome, scaffold...	common	7962	30.2	30.2	78%	774	100.00	453945	LN594316.1
Cyprinus carpio genome assembly common carp genome, scaffold:...	common	7962	30.2	30.2	78%	774	100.00	20606094	LN590685.1
PREDICTED: Acanthisitta chloris acetyl-CoA carboxylase beta...	riflema	57068	30.2	30.2	78%	774	100.00	6687	XM_009081175.1
PREDICTED: Acanthisitta chloris protein tyrosine phosphatase,...	riflema	57068	30.2	30.2	78%	774	100.00	1458	XM_009079776.1
Streptomyces lividans TK24, complete genome	NA	457428	30.2	30.2	78%	774	100.00	8345283	CP009124.1
Mycobacterium tuberculosis strain ZMC13-88, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4411515	CP009101.1
Mycobacterium tuberculosis strain ZMC13-264, complete	NA	1773	30.2	30.2	78%	774	100.00	4411507	CP009100.1

genome									
Mycobacterium tuberculosis strain 0A005DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539433	CP008983.1
Mycobacterium tuberculosis strain 0A029DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008981.1
Mycobacterium tuberculosis strain 0A033DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008980.1
Mycobacterium tuberculosis strain 0A036DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008979.1
Mycobacterium tuberculosis strain 0A087DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008978.1
Mycobacterium tuberculosis strain 0A092DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008977.1
Mycobacterium tuberculosis strain 0A093DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008976.1
Mycobacterium tuberculosis strain 0A094DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008975.1
Mycobacterium tuberculosis strain 0A115DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008974.1
Mycobacterium tuberculosis strain 0A117DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008973.1
Mycobacterium tuberculosis strain 0B026XDR genome	NA	1773	30.2	30.2	78%	774	100.00	4539433	CP008972.1
Mycobacterium tuberculosis strain 0B049XDR genome	NA	1773	30.2	30.2	78%	774	100.00	4539433	CP008971.1
Mycobacterium tuberculosis strain 0B070XDR genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008970.1
Mycobacterium tuberculosis strain 0B076XDR genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008969.1
Mycobacterium tuberculosis strain 0B123ND genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008968.1
Mycobacterium tuberculosis strain 0B169XDR genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008967.1
Mycobacterium tuberculosis strain 0B218DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008966.1
Mycobacterium tuberculosis strain 0B222DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008965.1
Mycobacterium tuberculosis strain 0B228DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008964.1
Mycobacterium tuberculosis strain 0B229DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008963.1
Mycobacterium tuberculosis strain 0B235DS genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008962.1
Mycobacterium tuberculosis strain 0B259XDR genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008961.1
Mycobacterium tuberculosis strain 0B329XDR genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008960.1
Mycobacterium tuberculosis strain 6A024XDR genome	NA	1773	30.2	30.2	78%	774	100.00	4539435	CP008959.1
PREDICTED: Stegastes partitus transcription initiation factor...	bicolor	144197	30.2	30.2	78%	774	100.00	5263	XM_008297440.1
Mycobacterium tuberculosis strain KIT87190, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4410788	CP007809.1
Mycobacterium tuberculosis K, complete genome	NA	1249615	30.2	30.2	78%	774	100.00	4385518	CP007803.1
PREDICTED: Anolis carolinensis estrogen related receptor beta...	green a	28377	30.2	30.2	78%	774	100.00	6325	XM_008121419.1
PREDICTED: Anolis carolinensis estrogen related receptor beta...	green a	28377	30.2	30.2	78%	774	100.00	6273	XM_008121305.1
PREDICTED: Anolis carolinensis estrogen related receptor beta...	green a	28377	30.2	30.2	78%	774	100.00	6589	XM_008121134.1

Pseudocercospora fijiensis CIRAD86 uncharacterized protein...	NA	383855	30.2	30.2	78%	774	100.00	759	XM_007921519.1
PREDICTED: Monodelphis domestica Down syndrome cell adhesion...	gray sh	13616	30.2	30.2	78%	774	100.00	7331	XM_007493072.1
PREDICTED: Python bivittatus estrogen related receptor beta...	Burmese	176946	30.2	30.2	78%	774	100.00	1185	XM_007424818.1
Homo sapiens adenosine monophosphate deaminase 2 (AMPD2),...	human	9606	30.2	30.2	78%	774	100.00	19243	NG_034075.1
Agaricus bisporus var. burnettii JB137-S8 hypothetical protein...	NA	597362	30.2	30.2	78%	774	100.00	2652	XM_007331292.1
Marssonina brunnea f. sp. 'multigermtubi' MB_m1 hypothetical...	NA	1072389	30.2	30.2	78%	774	100.00	2376	XM_007289390.1
PREDICTED: Balaenoptera acutorostrata scammoni chromosome...	NA	310752	30.2	30.2	78%	774	100.00	1014	XM_007186053.1
Mycobacterium bovis BCG str. ATCC 35743, complete genome	NA	998092	30.2	30.2	78%	774	100.00	4334064	CP003494.1
Bacillus pumilus strain MTCC B6033, complete genome	NA	1408	30.2	30.2	78%	774	100.00	3763493	CP007436.1
Mycobacterium tuberculosis CCDC5180, complete genome	NA	443150	30.2	30.2	78%	774	100.00	4414346	CP002885.1
Mycobacterium tuberculosis BT1, complete genome	NA	1010836	30.2	30.2	78%	774	100.00	4399405	CP002883.1
Mycobacterium tuberculosis BT2, complete genome	NA	1010835	30.2	30.2	78%	774	100.00	4401899	CP002882.1
Mycobacterium tuberculosis HKBS1, complete genome	NA	1010834	30.2	30.2	78%	774	100.00	4407929	CP002871.1
Mycobacterium tuberculosis H37Rv, complete genome	NA	83332	30.2	30.2	78%	774	100.00	4411709	CP003248.2
Zebrafish DNA sequence from clone CH211-166G5 in linkage group...	zebrafi	7955	30.2	30.2	78%	774	100.00	121539	CR762399.18
Brassica rapa genome assembly, chromosome: A06	field m	3711	30.2	30.2	78%	774	100.00	58997078	LS974622.2
PREDICTED: Oncorhynchus tshawytscha microtubule-associated...	Chinook	74940	30.2	30.2	78%	774	100.00	6918	XM_024391518.2
PREDICTED: Oncorhynchus tshawytscha microtubule-associated...	Chinook	74940	30.2	30.2	78%	774	100.00	6977	XM_042307916.1
PREDICTED: Oncorhynchus tshawytscha microtubule-associated...	Chinook	74940	30.2	30.2	78%	774	100.00	6998	XM_024391517.2
PREDICTED: Oncorhynchus tshawytscha microtubule-associated...	Chinook	74940	30.2	30.2	78%	774	100.00	7022	XM_042307915.1
PREDICTED: Oncorhynchus tshawytscha microtubule-associated...	Chinook	74940	30.2	30.2	78%	774	100.00	7040	XM_024391516.2
PREDICTED: Oncorhynchus tshawytscha microtubule-associated...	Chinook	74940	30.2	30.2	78%	774	100.00	7123	XM_024391515.2
PREDICTED: Oncorhynchus tshawytscha microtubule-associated...	Chinook	74940	30.2	30.2	78%	774	100.00	7111	XM_024391514.2
PREDICTED: Oncorhynchus tshawytscha microtubule-associated...	Chinook	74940	30.2	30.2	78%	774	100.00	7127	XM_024391513.2

PREDICTED: Oncorhynchus tshawytscha microtubule-associated...	Chinook	74940	30.2	30.2	78%	774	100.00	7129	XM_024391512.2
PREDICTED: Oncorhynchus tshawytscha deleted in malignant brain...	Chinook	74940	30.2	30.2	78%	774	100.00	1522	XM_042312621.1
Bacillus altitudinis strain LZP 02 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3763082	CP075052.1
Thunnus maccoyii genome assembly, chromosome: 16	souther	8240	30.2	60.5	84%	774	100.00	30468816	OU343206.1
Thunnus maccoyii genome assembly, chromosome: 1	souther	8240	30.2	30.2	78%	774	100.00	41002747	OU343191.1
Amphipyra berbera genome assembly, chromosome: 7	NA	987877	30.2	30.2	78%	774	100.00	21870261	OU343128.1
Amphipyra berbera genome assembly, chromosome: Z	NA	987877	30.2	30.2	78%	774	100.00	26789203	OU343121.1
Cervus elaphus genome assembly, chromosome: 33	red dee	9860	30.2	30.2	78%	774	100.00	79323360	OU343110.1
Cervus elaphus genome assembly, chromosome: 23	red dee	9860	30.2	60.5	78%	774	100.00	82663824	OU343100.1
Cervus elaphus genome assembly, chromosome: 17	red dee	9860	30.2	30.2	78%	774	100.00	65067212	OU343094.1
Cervus elaphus genome assembly, chromosome: 16	red dee	9860	30.2	30.2	78%	774	100.00	47758366	OU343093.1
Cervus elaphus genome assembly, chromosome: 15	red dee	9860	30.2	30.2	78%	774	100.00	94138249	OU343092.1
Cervus elaphus genome assembly, chromosome: 13	red dee	9860	30.2	60.5	89%	774	100.00	72175023	OU343090.1
Cervus elaphus genome assembly, chromosome: 10	red dee	9860	30.2	30.2	78%	774	100.00	55766398	OU343087.1
Cervus elaphus genome assembly, chromosome: 8	red dee	9860	30.2	30.2	78%	774	100.00	55694185	OU343085.1
Cervus elaphus genome assembly, chromosome: 7	red dee	9860	30.2	60.5	89%	774	100.00	52316097	OU343084.1
Cervus elaphus genome assembly, chromosome: 2	red dee	9860	30.2	90.7	100%	774	100.00	50834548	OU343079.1
Cervus elaphus genome assembly, chromosome: 1	red dee	9860	30.2	30.2	78%	774	100.00	99365844	OU343078.1
Lineus longissimus genome assembly, chromosome: 3	NA	88925	30.2	30.2	78%	774	100.00	29083594	OU342994.1
Andrena haemorrhoa genome assembly, chromosome: 1	NA	444401	30.2	30.2	78%	774	100.00	59446405	OU342940.1
Pholis gunnellus genome assembly, chromosome: 24	rock gu	56726	30.2	30.2	78%	774	100.00	11275572	OU342827.1
Pholis gunnellus genome assembly, chromosome: 18	rock gu	56726	30.2	30.2	78%	774	100.00	21874052	OU342821.1
Pholis gunnellus genome assembly, chromosome: 9	rock gu	56726	30.2	30.2	78%	774	100.00	27596544	OU342811.1
Cerceris rybyensis genome assembly, chromosome: 13	NA	1167272	30.2	30.2	78%	774	100.00	16240273	OU342801.1
Homo sapiens dopamine receptor D3 (DRD3), RefSeqGene on...	human	9606	30.2	30.2	78%	774	100.00	77698	NG_008842.2
PREDICTED: Pseudopodoces humilis protein tyrosine phosphatase,...	Tibetan	181119	30.2	30.2	78%	774	100.00	1666	XM_005517279.1
Mycobacterium tuberculosis str. Haarlem, complete genome	NA	395095	30.2	30.2	78%	774	100.00	4408224	CP001664.1
Bacillus amyloliquefaciens subsp. plantarum UCMB5113, complete...	NA	1150476	30.2	30.2	78%	774	100.00	3889532	HG328254.1
Streptomyces collinus Tu 365	NA	1214242	30.2	30.2	78%	774	100.00	8272925	CP006259.1

chromosome, complete genome									
Mycobacterium tuberculosis EAI5, complete genome	NA	1306414	30.2	30.2	78%	774	100.00	4391174	CP006578.1
Taurulus bubalis genome assembly, chromosome: 9	NA	61643	30.2	30.2	78%	774	100.00	29138660	OU342719.1
Chrysoteuchia culmella genome assembly, chromosome: 8	NA	1594250	30.2	30.2	78%	774	100.00	24698495	OU342649.1
Acomys percivali genome assembly, chromosome: 18	Perciva	83527	30.2	634	89%	774	100.00	13292943	OU015759.1
Acomys percivali genome assembly, chromosome: 17	Perciva	83527	30.2	483	89%	774	100.00	38986706	OU015758.1
Acomys percivali genome assembly, chromosome: 15	Perciva	83527	30.2	1239	89%	774	100.00	84648590	OU015756.1
Acomys dimidiatus genome assembly, chromosome: 18	NA	60744	30.2	816	78%	774	100.00	14035028	OU015391.1
Acomys dimidiatus genome assembly, chromosome: 13	NA	60744	30.2	3536	89%	774	100.00	85730870	OU015386.1
Acomys dimidiatus genome assembly, chromosome: 17	NA	60744	30.2	453	89%	774	100.00	36818564	OU015390.1
Acomys kempi genome assembly, chromosome: 17	Kemp's	83762	30.2	604	89%	774	100.00	38169830	OU015371.1
Acomys kempi genome assembly, chromosome: 15	Kemp's	83762	30.2	1541	89%	774	100.00	79860018	OU015369.1
Acomys kempi genome assembly, chromosome: 13	Kemp's	83762	30.2	3899	89%	774	100.00	86063037	OU015367.1
PREDICTED: Peromyscus maniculatus bairdii uncharacterized...	prairie	230844	30.2	30.2	78%	774	100.00	1488	XR_006074342.1
PREDICTED: Peromyscus maniculatus bairdii uncharacterized...	prairie	230844	30.2	30.2	78%	774	100.00	1449	XR_006074341.1
PREDICTED: Peromyscus maniculatus bairdii uncharacterized...	prairie	230844	30.2	30.2	78%	774	100.00	1658	XR_006074340.1
PREDICTED: Peromyscus maniculatus bairdii centlein (Cntln),...	prairie	230844	30.2	30.2	78%	774	100.00	4943	XM_015994925.2
PREDICTED: Peromyscus maniculatus bairdii centlein (Cntln),...	prairie	230844	30.2	30.2	78%	774	100.00	5076	XM_042271376.1
PREDICTED: Ovis aries MAP6 domain containing 1 (MAP6D1),...	sheep	9940	30.2	30.2	78%	774	100.00	2830	XM_042233845.1
PREDICTED: Ovis aries cytochrome P450 4B1 (LOC101105114), mRNA	sheep	9940	30.2	30.2	78%	774	100.00	2044	XM_004001941.5
PREDICTED: Aricia agestis collagen alpha-1(XVIII) chain-like...	brown a	91739	30.2	30.2	78%	774	100.00	3979	XM_042131194.1
PREDICTED: Aricia agestis collagen alpha-1(XVIII) chain-like...	brown a	91739	30.2	30.2	78%	774	100.00	4009	XM_042131193.1
PREDICTED: Aricia agestis collagen alpha-1(XVIII) chain-like...	brown a	91739	30.2	30.2	78%	774	100.00	4012	XM_042131192.1
PREDICTED: Aricia agestis collagen alpha-1(XVIII) chain-like...	brown a	91739	30.2	30.2	78%	774	100.00	4018	XM_042131191.1
PREDICTED: Aricia agestis collagen alpha-1(XVIII) chain-like...	brown a	91739	30.2	30.2	78%	774	100.00	4033	XM_042131190.1

PREDICTED: Aricia agestis collagen alpha-1(XVIII) chain-like...	brown a	91739	30.2	30.2	78%	774	100.00	4048	XM_042131189.1
PREDICTED: Aricia agestis collagen alpha-1(XVIII) chain-like...	brown a	91739	30.2	30.2	78%	774	100.00	4054	XM_042131188.1
PREDICTED: Aricia agestis collagen alpha-1(XVIII) chain-like...	brown a	91739	30.2	30.2	78%	774	100.00	4063	XM_042131187.1
TPA: Siphoviridae sp. isolate ctlFw17, partial genome	NA	2170413	30.2	30.2	100%	774	94.74	31471	BK043984.1
Rousettus aegyptiacus IGHV1-69.1, IGHV4-59.1, IGHV1-8.1,...	Egyptia	9407	30.2	30.2	78%	774	100.00	634142	MW800879.1
TPA: Siphoviridae sp. isolate ctHgM15, partial genome	NA	2170413	30.2	30.2	100%	774	94.74	30639	BK021840.1
Dickeya dadantii strain S3-1 chromosome, complete genome	NA	204038	30.2	30.2	78%	774	100.00	5065613	CP076386.1
TPA: Siphoviridae sp. isolate ctDGB3, partial genome	NA	2170413	30.2	30.2	78%	774	100.00	45855	BK023677.1
Bacillus sp. JNUCC-22 chromosome, complete genome	NA	2842457	30.2	30.2	78%	774	100.00	3949366	CP076408.1
PREDICTED: Corvus kubaryi supervillin (SVIL), transcript varia...	Mariana	68294	30.2	30.2	78%	774	100.00	8273	XM_042042977.1
PREDICTED: Corvus kubaryi grainyhead like transcription factor...	Mariana	68294	30.2	30.2	78%	774	100.00	5016	XM_042033029.1
PREDICTED: Corvus kubaryi grainyhead like transcription factor...	Mariana	68294	30.2	30.2	78%	774	100.00	5042	XM_042033028.1
PREDICTED: Corvus kubaryi grainyhead like transcription factor...	Mariana	68294	30.2	30.2	78%	774	100.00	5051	XM_042033027.1
PREDICTED: Corvus kubaryi grainyhead like transcription factor...	Mariana	68294	30.2	30.2	78%	774	100.00	5078	XM_042033026.1
PREDICTED: Melanotaenia boesemani rho GTPase-activating protei...	Boesema	1250792	30.2	30.2	78%	774	100.00	7468	XM_041967908.1
PREDICTED: Melanotaenia boesemani rho GTPase-activating protei...	Boesema	1250792	30.2	30.2	78%	774	100.00	7476	XM_041967907.1
PREDICTED: Melanotaenia boesemani rho GTPase-activating protei...	Boesema	1250792	30.2	30.2	78%	774	100.00	7500	XM_041967906.1
PREDICTED: Corvus kubaryi protein tyrosine phosphatase...	Mariana	68294	30.2	30.2	78%	774	100.00	4906	XM_042032041.1
PREDICTED: Corvus kubaryi protein tyrosine phosphatase...	Mariana	68294	30.2	30.2	78%	774	100.00	2088	XM_042032031.1
PREDICTED: Corvus kubaryi protein tyrosine phosphatase...	Mariana	68294	30.2	30.2	78%	774	100.00	2034	XM_042032020.1
PREDICTED: Corvus kubaryi protein tyrosine phosphatase...	Mariana	68294	30.2	30.2	78%	774	100.00	5117	XM_042032012.1
PREDICTED: Corvus kubaryi protein tyrosine phosphatase...	Mariana	68294	30.2	30.2	78%	774	100.00	5063	XM_042032004.1
PREDICTED: Melanotaenia boesemani sushi, nidogen and EGF-like...	Boesema	1250792	30.2	30.2	78%	774	100.00	4532	XM_042006548.1
PREDICTED: Melanotaenia boesemani sushi, nidogen and EGF-like...	Boesema	1250792	30.2	30.2	78%	774	100.00	4637	XM_042006547.1
PREDICTED: Melanotaenia	Boesema	1250792	30.2	30.2	78%	774	100.00	4646	XM_042006546.1

boesemani sushi, nidogen and EGF-like...									
PREDICTED: Chelmon rostratus NACHT, LRR and PYD...	copperb	109905	30.2	30.2	78%	774	100.00	4488	XM_041963090.1
PREDICTED: Chelmon rostratus NACHT, LRR and PYD...	copperb	109905	30.2	30.2	78%	774	100.00	4492	XM_041963089.1
PREDICTED: Chelmon rostratus NACHT, LRR and PYD...	copperb	109905	30.2	30.2	78%	774	100.00	4520	XM_041963088.1
PREDICTED: Chelmon rostratus NACHT, LRR and PYD...	copperb	109905	30.2	30.2	78%	774	100.00	4503	XM_041963087.1
PREDICTED: Chelmon rostratus NACHT, LRR and PYD...	copperb	109905	30.2	30.2	78%	774	100.00	4507	XM_041963086.1
PREDICTED: Chelmon rostratus NACHT, LRR and PYD...	copperb	109905	30.2	30.2	78%	774	100.00	4511	XM_041963085.1
PREDICTED: Chelmon rostratus NACHT, LRR and PYD...	copperb	109905	30.2	30.2	78%	774	100.00	4540	XM_041963084.1
PREDICTED: Chelmon rostratus NACHT, LRR and PYD...	copperb	109905	30.2	30.2	78%	774	100.00	4522	XM_041963083.1
PREDICTED: Coregonus clupeaformis NHS-like protein 1...	lake wh	59861	30.2	30.2	78%	774	100.00	8181	XM_041848438.1
Streptomyces sp. JCM17656 chromosome, complete genome	NA	2768067	30.2	30.2	100%	774	94.74	10097084	CP075611.1
Mycobacterium tuberculosis R2092 DNA, complete genome	NA	1773	30.2	30.2	78%	774	100.00	4383210	AP024671.1
Fusarium mangiferae non-ribosomal peptide synthetase...	NA	192010	30.2	30.2	78%	774	100.00	7422	XM_041830646.1
Myxococcus xanthus DZ2 chromosome, complete genome	NA	1198133	30.2	60.5	78%	774	100.00	9359382	CP070500.1
PREDICTED: Cheilinus undulatus monoacylglycerol...	humphea	241271	30.2	30.2	78%	774	100.00	1202	XM_041801879.1
PREDICTED: Cheilinus undulatus transcription initiation factor...	humphea	241271	30.2	30.2	78%	774	100.00	3144	XM_041793694.1
PREDICTED: Cheilinus undulatus transcription initiation factor...	humphea	241271	30.2	30.2	78%	774	100.00	7144	XM_041793686.1
PREDICTED: Cheilinus undulatus transcription initiation factor...	humphea	241271	30.2	30.2	78%	774	100.00	3370	XM_041793677.1
PREDICTED: Cheilinus undulatus transcription initiation factor...	humphea	241271	30.2	30.2	78%	774	100.00	7297	XM_041793668.1
PREDICTED: Cheilinus undulatus transcription initiation factor...	humphea	241271	30.2	30.2	78%	774	100.00	3523	XM_041793659.1
PREDICTED: Vulpes lagopus FYVE, RhoGEF and PH domain containin...	Arctic	494514	30.2	30.2	78%	774	100.00	3626	XM_041746118.1
PREDICTED: Taeniopygia guttata grainyhead like transcription...	zebra f	59729	30.2	30.2	78%	774	100.00	4951	XM_030270060.3
PREDICTED: Taeniopygia guttata protein tyrosine phosphatase...	zebra f	59729	30.2	30.2	78%	774	100.00	2130	XM_030265949.3
PREDICTED: Taeniopygia guttata protein tyrosine phosphatase...	zebra f	59729	30.2	30.2	78%	774	100.00	5125	XM_030265950.3
Idaea aversata genome assembly, chromosome: 10	NA	104447	30.2	30.2	78%	774	100.00	15391505	OU026093.1
Crocallis elinguaria genome assembly, chromosome: 3	NA	934829	30.2	30.2	78%	774	100.00	37508892	OU026067.1

Danio rerio strain T5D chromosome 18	zebrafi	7955	30.2	30.2	78%	774	100.00	50937954	CP068752.1
Danio rerio strain T5D chromosome 12	zebrafi	7955	30.2	30.2	78%	774	100.00	49168109	CP068746.1
Danio rerio strain T5D chromosome 7	zebrafi	7955	30.2	30.2	78%	774	100.00	73995704	CP068741.1
Danio rerio strain T5D chromosome 1	zebrafi	7955	30.2	30.2	78%	774	100.00	58785646	CP068735.1
Coccinella septempunctata genome assembly, chromosome: 9	seven-s	41139	30.2	30.2	78%	774	100.00	20753350	OU015582.1
Caprimulgus europaeus genome assembly, chromosome: 18	Eurasia	111811	30.2	30.2	78%	774	100.00	15699869	OU015542.1
Caprimulgus europaeus genome assembly, chromosome: 14	Eurasia	111811	30.2	60.5	84%	774	100.00	22349459	OU015538.1
Caprimulgus europaeus genome assembly, chromosome: 27	Eurasia	111811	30.2	30.2	78%	774	100.00	6260693	OU015551.1
Caprimulgus europaeus genome assembly, chromosome: 26	Eurasia	111811	30.2	120	78%	774	100.00	7503399	OU015550.1
Caprimulgus europaeus genome assembly, chromosome: 9	Eurasia	111811	30.2	60.5	78%	774	100.00	48660147	OU015532.1
Caprimulgus europaeus genome assembly, chromosome: 8	Eurasia	111811	30.2	30.2	78%	774	100.00	50913645	OU015531.1
Fusarium fujikuroi IMI 58289 draft genome, chromosome FFUJ_chr05	NA	1279085	30.2	30.2	78%	774	100.00	4489497	HF679027.1
Salpingoeca rosetta uncharacterized protein (PTSG_08986), mRNA	NA	946362	30.2	30.2	78%	774	100.00	2061	XM_004989727.1
Mycobacterium tuberculosis CCDC5079, complete genome	NA	443149	30.2	30.2	78%	774	100.00	4414325	CP002884.1
Mycobacterium tuberculosis EAI5/NITR206, complete genome	NA	1310115	30.2	30.2	78%	774	100.00	4390306	CP005387.1
Mycobacterium tuberculosis CAS/NITR204, complete genome	NA	1310114	30.2	30.2	78%	774	100.00	4392876	CP005386.1
Mycobacterium tuberculosis str. Haarlem/NITR202, complete genome	NA	1304279	30.2	30.2	78%	774	100.00	4404786	CP004886.1
Streptomyces fulvissimus DSM 40593 chromosome, complete genome	NA	1303692	30.2	30.2	78%	774	100.00	7905758	CP005080.1
PREDICTED: Xenopus laevis transmembrane protein 104 S homeolog...	African	8355	30.2	30.2	78%	774	100.00	2482	XM_041579144.1
PREDICTED: Xenopus laevis transmembrane protein 104 S homeolog...	African	8355	30.2	30.2	78%	774	100.00	2887	XM_041579143.1
PREDICTED: Xenopus laevis transmembrane protein 104 S homeolog...	African	8355	30.2	30.2	78%	774	100.00	2513	XM_018238492.2
PREDICTED: Xenopus laevis transmembrane protein 104 S homeolog...	African	8355	30.2	30.2	78%	774	100.00	2367	XM_018238491.2
PREDICTED: Xenopus laevis transmembrane protein 104 S homeolog...	African	8355	30.2	30.2	78%	774	100.00	2662	XM_018238490.2
PREDICTED: Xenopus laevis transmembrane protein 104 S homeolog...	African	8355	30.2	30.2	78%	774	100.00	2592	XM_018238489.2
PREDICTED: Xenopus laevis	African	8355	30.2	30.2	78%	774	100.00	2477	XM_018238488.2

transmembrane protein 104 S homeolog...									
PREDICTED: Xenopus laevis transmembrane protein 104 L homeolog...	African	8355	30.2	30.2	78%	774	100.00	3158	XM_018235311.2
PREDICTED: Xenopus laevis fidgetin like2 S homeolog (fignl2.S)...	African	8355	30.2	30.2	78%	774	100.00	6291	XM_041584447.1
PREDICTED: Xenopus laevis fidgetin like2 S homeolog (fignl2.S)...	African	8355	30.2	30.2	78%	774	100.00	6389	XM_018250111.2
PREDICTED: Xenopus laevis fidgetin (LOC108708614), transcript...	African	8355	30.2	30.2	78%	774	100.00	9569	XM_018247503.2
PREDICTED: Xenopus laevis fidgetin (LOC108708614), transcript...	African	8355	30.2	30.2	78%	774	100.00	9474	XM_018247502.2
Streptomyces mirabilis strain P16B-1 chromosome, complete genome	NA	68239	30.2	30.2	100%	774	94.74	9103359	CP074102.1
Streptopelia turtur genome assembly, chromosome: 26	NA	177155	30.2	30.2	78%	774	100.00	6472241	LR594575.2
Streptopelia turtur genome assembly, chromosome: 28	NA	177155	30.2	60.5	78%	774	100.00	5368108	LR594574.2
Streptopelia turtur genome assembly, chromosome: 4	NA	177155	30.2	30.2	78%	774	100.00	81365208	LR594554.2
Homo sapiens isolate CHM13 chromosome 16	human	9606	30.2	30.2	78%	774	100.00	96330374	CP068262.2
PREDICTED: Pyrgilauda ruficollis protein tyrosine phosphatase...	rufous-	221976	30.2	30.2	78%	774	100.00	2154	XM_041477624.1
PREDICTED: Pyrgilauda ruficollis protein tyrosine phosphatase...	rufous-	221976	30.2	30.2	78%	774	100.00	5175	XM_041477623.1
PREDICTED: Onychostruthus taczanowskii protein tyrosine...	white-r	356909	30.2	30.2	78%	774	100.00	1693	XM_041399270.1
PREDICTED: Onychostruthus taczanowskii protein tyrosine...	white-r	356909	30.2	30.2	78%	774	100.00	1838	XM_041399269.1
PREDICTED: Onychostruthus taczanowskii protein tyrosine...	white-r	356909	30.2	30.2	78%	774	100.00	5186	XM_041399268.1
Chitinophaga sp. KRA15-503 chromosome, complete genome	NA	2829818	30.2	30.2	78%	774	100.00	8341603	CP073766.1
PREDICTED: Aquila chrysaetos chrysaetos DS cell adhesion...	NA	223781	30.2	30.2	78%	774	100.00	7250	XM_030020086.2
PREDICTED: Aquila chrysaetos chrysaetos protein tyrosine...	NA	223781	30.2	30.2	78%	774	100.00	2104	XM_030012784.2
PREDICTED: Aquila chrysaetos chrysaetos protein tyrosine...	NA	223781	30.2	30.2	78%	774	100.00	2043	XM_041123201.1
PREDICTED: Aquila chrysaetos chrysaetos protein tyrosine...	NA	223781	30.2	30.2	78%	774	100.00	2321	XM_041123200.1
PREDICTED: Aquila chrysaetos chrysaetos protein tyrosine...	NA	223781	30.2	30.2	78%	774	100.00	2206	XM_030012783.2
Gordonia polyisoprenivorans strain C chromosome, complete genome	NA	84595	30.2	30.2	78%	774	100.00	5925347	CP073075.1
Homo sapiens lncRNA for PREDICTED lncRNA (TCONS_00022316)	human	9606	30.2	30.2	78%	774	100.00	2478	OA985574.1
Pseudomassariella vexata translation initiation factor eIF...	NA	1141098	30.2	30.2	78%	774	100.00	744	XM_040854919.1
Cryphonectria parasitica EP155 MFS general substrate	NA	660469	30.2	30.2	78%	774	100.00	1323	XM_040921316.1

transport...									
PREDICTED: Glycine max **ZINC finger** CCCH domain-containing...	soybean	3847	30.2	30.2	78%	774	100.00	5804	XM_014776460.2
PREDICTED: Mesocricetus auratus uncharacterized LOC121132783...	golden	10036	30.2	30.2	78%	774	100.00	3290	XR_005880342.1
PREDICTED: Mesocricetus auratus uncharacterized LOC121132783...	golden	10036	30.2	30.2	78%	774	100.00	3271	XR_005880341.1
Bacillus altitudinis strain 6ww6 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3804206	CP072851.1
Mycobacterium tuberculosis strain H37Rv_CG chromosome, complet...	NA	1773	30.2	30.2	78%	774	100.00	4415999	CP072765.1
Mycobacterium tuberculosis strain CG24 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4459449	CP072761.1
Mycobacterium tuberculosis strain CG21 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4415999	CP072763.1
Mycobacterium tuberculosis strain CG20 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4415998	CP072764.1
Mycobacterium tuberculosis strain CG23 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4432513	CP072762.1
PREDICTED: Gallus gallus uncharacterized LOC100859691...	chicken	9031	30.2	30.2	78%	774	100.00	55314	XR_005842774.1
PREDICTED: Gallus gallus uncharacterized LOC100859691...	chicken	9031	30.2	30.2	78%	774	100.00	55464	XR_005842771.1
PREDICTED: Gallus gallus uncharacterized LOC100859691...	chicken	9031	30.2	30.2	78%	774	100.00	54294	XR_005842769.1
PREDICTED: Lepeophtheirus salmonis uncharacterized LOC12112486...	salmon	72036	30.2	30.2	78%	774	100.00	1651	XM_040720065.1
PREDICTED: Lepeophtheirus salmonis **ZINC finger** protein ubi-d4...	salmon	72036	30.2	30.2	78%	774	100.00	1831	XM_040716884.1
PREDICTED: Ursus maritimus tumor necrosis factor receptor...	polar b	29073	30.2	30.2	78%	774	100.00	3447	XM_040639621.1
PREDICTED: Ursus maritimus tumor necrosis factor receptor...	polar b	29073	30.2	30.2	78%	774	100.00	3480	XM_040639620.1
PREDICTED: Ursus maritimus tumor necrosis factor receptor...	polar b	29073	30.2	30.2	78%	774	100.00	3483	XM_040639619.1
Sus scrofa scrofa breed NS chromosome 18	NA	415978	30.2	30.2	78%	774	100.00	57355364	CP071569.1
Sus scrofa scrofa breed NS chromosome 16	NA	415978	30.2	60.5	84%	774	100.00	81227385	CP071567.1
PREDICTED: Falco naumanni protein tyrosine phosphatase...	lesser	148594	30.2	30.2	78%	774	100.00	1587	XM_040587512.1
PREDICTED: Falco naumanni protein tyrosine phosphatase...	lesser	148594	30.2	30.2	78%	774	100.00	2296	XM_040587511.1
PREDICTED: Cygnus olor estrogen related receptor beta	mute sw	8869	30.2	30.2	78%	774	100.00	6087	XM_040559093.1

(ESRRB),...									
PREDICTED: Cygnus olor estrogen related receptor beta (ESRRB),...	mute sw	8869	30.2	30.2	78%	774	100.00	5604	XM_040559092.1
PREDICTED: Cygnus olor protein tyrosine phosphatase non-recept...	mute sw	8869	30.2	30.2	78%	774	100.00	1669	XM_040549957.1
PREDICTED: Cygnus olor protein tyrosine phosphatase non-recept...	mute sw	8869	30.2	30.2	78%	774	100.00	2307	XM_040549955.1
PREDICTED: Cygnus olor DS cell adhesion molecule (**DSCAM**), mRNA	mute sw	8869	30.2	30.2	78%	774	100.00	6896	XM_040530051.1
Pieris napi genome assembly, chromosome: 22	NA	78633	30.2	30.2	78%	774	100.00	10703985	FR997716.1
Muricauda sp. isolate ih8 chromosome	NA	192149	30.2	30.2	78%	774	100.00	4052258	CP051245.1
Polymorphospora rubra NBRC 101157 DNA, complete genome	NA	338584	30.2	30.2	78%	774	100.00	8365212	AP023359.1
Ochlodes sylvanus genome assembly, chromosome: 19	NA	876063	30.2	30.2	78%	774	100.00	11776845	FR990142.1
Hedya salicella genome assembly, chromosome: 16	NA	1869985	30.2	60.5	78%	774	100.00	23063133	FR990112.1
Erannis defoliaria genome assembly, chromosome: 9	NA	104474	30.2	30.2	78%	774	100.00	19376520	FR990075.1
Hesperia comma genome assembly, chromosome: 8	common	291688	30.2	30.2	78%	774	100.00	19699062	FR990021.1
Pheosia gnoma genome assembly, chromosome: 1	NA	988018	30.2	30.2	78%	774	100.00	11949387	FR989894.1
PREDICTED: Bufo bufo KIAA1109 ortholog (KIAA1109), transcript...	common	8384	30.2	30.2	78%	774	100.00	14911	XM_040418415.1
PREDICTED: Bufo bufo KIAA1109 ortholog (KIAA1109), transcript...	common	8384	30.2	30.2	78%	774	100.00	15052	XM_040418414.1
PREDICTED: Bufo bufo KIAA1109 ortholog (KIAA1109), transcript...	common	8384	30.2	30.2	78%	774	100.00	15109	XM_040418412.1
PREDICTED: Bufo bufo KIAA1109 ortholog (KIAA1109), transcript...	common	8384	30.2	30.2	78%	774	100.00	15118	XM_040418411.1
PREDICTED: Bufo bufo KIAA1109 ortholog (KIAA1109), transcript...	common	8384	30.2	30.2	78%	774	100.00	15157	XM_040418410.1
PREDICTED: Bufo bufo KIAA1109 ortholog (KIAA1109), transcript...	common	8384	30.2	30.2	78%	774	100.00	15683	XM_040418409.1
PREDICTED: Bufo bufo KIAA1109 ortholog (KIAA1109), transcript...	common	8384	30.2	30.2	78%	774	100.00	15250	XM_040418408.1
PREDICTED: Bufo bufo KIAA1109 ortholog (KIAA1109), transcript...	common	8384	30.2	30.2	78%	774	100.00	15336	XM_040418407.1
PREDICTED: Bufo bufo KIAA1109 ortholog (KIAA1109), transcript...	common	8384	30.2	30.2	78%	774	100.00	15776	XM_040418406.1
Bacillus amyloliquefaciens strain XJ5 chromosome, complete genome	NA	1390	30.2	30.2	78%	774	100.00	4160003	CP071970.1
Arthrobacter crystallopoietes strain NT16 chromosome,	NA	37928	30.2	30.2	78%	774	100.00	4381539	CP072014.1

complete...									
Meleagris gallopavo genome assembly, chromosome: 10	turkey	9103	30.2	30.2	78%	774	100.00	29439779	HG999689.1
PREDICTED: Ictidomys tridecemlineatus BUD23 rRNA...	thirtee	43179	30.2	30.2	78%	774	100.00	3206	XM_040278440.1
Mutant Streptomyces lividans strain TK24-YQS040, complete genome	NA	1916	30.2	30.2	78%	774	100.00	8360641	CP071800.1
PSEUDOMONAS fluorescens strain YK-310 chromosome, complete genome	NA	294	30.2	30.2	78%	774	100.00	6498941	CP071797.1
PREDICTED: Oryx dammah cytochrome P450 4B1 (LOC120856190), mRNA	scimita	59534	30.2	30.2	78%	774	100.00	2064	XM_040231240.1
Musa acuminata subsp. malaccensis strain Doubled-haploid Pahan...	wild Ma	214687	30.2	30.2	78%	774	100.00	40528553	HG996468.1
Streptomyces sp. CA-256286 chromosome, complete genome	NA	2801033	30.2	30.2	78%	774	100.00	7726360	CP071044.1
PREDICTED: Simochromis diagramma uncharacterized LOC120745384...	NA	43689	30.2	30.2	78%	774	100.00	2602	XR_005698618.1
Pheosia tremula genome assembly, chromosome: 1	NA	988019	30.2	30.2	78%	774	100.00	12641679	HG995397.1
Atethmia centrago genome assembly, chromosome: 10	NA	988071	30.2	30.2	78%	774	100.00	32762140	HG995376.1
Mimas tiliae genome assembly, chromosome: 1	NA	522848	30.2	30.2	78%	774	100.00	25978239	HG995238.1
Mycobacterium tuberculosis str. Beijing/NITR203, complete genome	NA	1306400	30.2	30.2	78%	774	100.00	4411128	CP005082.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon	72036	30.2	60.5	94%	774	100.00	59812117	HG994593.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon	72036	30.2	30.2	78%	774	100.00	30072609	HG994588.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon	72036	30.2	30.2	78%	774	100.00	43017027	HG994586.1
Canis lupus genome assembly, chromosome: 28	gray wo	9612	30.2	30.2	100%	774	94.74	42479636	HG994413.1
Canis lupus genome assembly, chromosome: 29	gray wo	9612	30.2	30.2	78%	774	100.00	44093449	HG994412.1
Canis lupus genome assembly, chromosome: 26	gray wo	9612	30.2	30.2	78%	774	100.00	46109286	HG994409.1
Canis lupus genome assembly, chromosome: 23	gray wo	9612	30.2	60.5	84%	774	100.00	52955009	HG994406.1
Canis lupus genome assembly, chromosome: 21	gray wo	9612	30.2	30.2	78%	774	100.00	53106277	HG994405.1
Canis lupus genome assembly, chromosome: 14	gray wo	9612	30.2	30.2	78%	774	100.00	62790595	HG994400.1
Canis lupus genome assembly, chromosome: 16	gray wo	9612	30.2	30.2	78%	774	100.00	63665305	HG994398.1
Canis lupus genome assembly, chromosome: 17	gray wo	9612	30.2	60.5	84%	774	100.00	65956162	HG994396.1
Canis lupus genome assembly, chromosome: 9	gray wo	9612	30.2	60.5	94%	774	100.00	66787146	HG994394.1
Canis lupus genome assembly, chromosome: 11	gray wo	9612	30.2	60.5	78%	774	100.00	75747776	HG994391.1
Canis lupus genome assembly, chromosome: 7	gray wo	9612	30.2	60.5	94%	774	100.00	82288100	HG994388.1
Canis lupus genome assembly, chromosome: 2	gray wo	9612	30.2	30.2	78%	774	100.00	86397490	HG994387.1

Canis lupus genome assembly, chromosome: 4	gray wo	9612	30.2	30.2	100%	774	94.74	88630877	HG994386.1
Brassica napus genome assembly, chromosome: A05	rape	3708	30.2	30.2	78%	774	100.00	42112164	HG994359.1
Mutant Streptomyces lividans strain TK24 DG2-P41, complete genome	NA	1916	30.2	30.2	78%	774	100.00	8380771	CP071123.1
Mycobacterium tuberculosis strain 267/47W148 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4411528	CP071128.1
Mycobacterium tuberculosis strain 120/26CAO chromosome, comple...	NA	1773	30.2	30.2	78%	774	100.00	4411524	CP071127.1
Bacillus altitudinis strain 1817 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3729040	CP065591.1
PREDICTED: Pteropus giganteus retrotransposon Gag like 1 (RTL1...	Indian	143291	30.2	30.2	78%	774	100.00	4747	XM_039884230.1
PREDICTED: Pteropus giganteus retrotransposon Gag like 1 (RTL1...	Indian	143291	30.2	30.2	78%	774	100.00	5088	XM_039884229.1
PREDICTED: Passer montanus protein tyrosine phosphatase...	Eurasia	9160	30.2	30.2	78%	774	100.00	3024	XM_039705957.1
PREDICTED: Passer montanus protein tyrosine phosphatase...	Eurasia	9160	30.2	30.2	78%	774	100.00	2043	XM_039705956.1
PREDICTED: Passer montanus protein tyrosine phosphatase...	Eurasia	9160	30.2	30.2	78%	774	100.00	5161	XM_039705955.1
Mycolicibacterium austroafricanum strain MYC221 chromosome	NA	39687	30.2	30.2	100%	774	94.74	6287627	CP070380.1
Streptomyces noursei strain A-2-1 chromosome, complete genome	NA	1971	30.2	30.2	78%	774	100.00	9857535	CP070326.1
Mycobacterium tuberculosis strain 11502 chromosome, complete...	NA	1773	30.2	30.2	78%	774	100.00	4420561	CP070338.1
PREDICTED: Drosophila santomea uncharacterized LOC120447485...	NA	129105	30.2	30.2	100%	774	94.74	5977	XM_039628881.1
PREDICTED: Oreochromis aureus lebercilin-like protein...	NA	47969	30.2	30.2	78%	774	100.00	1645	XM_039622715.1
PREDICTED: Oreochromis aureus lebercilin-like protein...	NA	47969	30.2	30.2	78%	774	100.00	1847	XM_031752624.2
Tachina fera genome assembly, chromosome: X	NA	631328	30.2	30.2	78%	774	100.00	14176217	LR999968.1
Xylota sylvarum genome assembly, chromosome: X	NA	374264	30.2	30.2	78%	774	100.00	17728835	LR999961.1
Boloria selene genome assembly, chromosome: 1	silver	191398	30.2	30.2	78%	774	100.00	16075597	HG993132.1
Eristalis tenax genome assembly, chromosome: 3	drone f	198635	30.2	30.2	78%	774	100.00	77068984	HG993126.1
Spilosoma lubricipeda genome assembly, chromosome: 24	NA	875880	30.2	30.2	78%	774	100.00	14472961	HG992298.1
Mellicta athalia genome assembly, chromosome: 2	NA	113330	30.2	30.2	78%	774	100.00	24877037	HG992178.1
Ennomos fuscantarius genome assembly, chromosome: 19	dusky t	722662	30.2	30.2	100%	774	94.74	14288185	HG992042.1
Amphipyra tragopoginis genome assembly, chromosome: 16	NA	689058	30.2	30.2	78%	774	100.00	26860071	HG992007.1
PREDICTED: Corvus cornix cornix grainyhead like transcription...	NA	932674	30.2	30.2	78%	774	100.00	5012	XM_039568087.1

PREDICTED: Corvus cornix cornix grainyhead like transcription...	NA	932674	30.2	30.2	78%	774	100.00	5043	XM_039568086.1
PREDICTED: Corvus cornix cornix grainyhead like transcription...	NA	932674	30.2	30.2	78%	774	100.00	5048	XM_039568085.1
PREDICTED: Corvus cornix cornix grainyhead like transcription...	NA	932674	30.2	30.2	78%	774	100.00	5079	XM_039568084.1
PREDICTED: Corvus cornix cornix protein tyrosine phosphatase...	NA	932674	30.2	30.2	78%	774	100.00	2117	XM_039548669.1
PREDICTED: Corvus cornix cornix protein tyrosine phosphatase...	NA	932674	30.2	30.2	78%	774	100.00	1779	XM_039548668.1
Bacillus velezensis strain TB918 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3979294	CP069430.1
PREDICTED: Mauremys reevesii estrogen related receptor beta...	Reeves'	260615	30.2	30.2	78%	774	100.00	1997	XM_039535270.1
PREDICTED: Mauremys reevesii estrogen related receptor beta...	Reeves'	260615	30.2	30.2	78%	774	100.00	1326	XM_039535269.1
PREDICTED: Mauremys reevesii estrogen related receptor beta...	Reeves'	260615	30.2	30.2	78%	774	100.00	1374	XM_039535268.1
PREDICTED: Mauremys reevesii estrogen related receptor beta...	Reeves'	260615	30.2	30.2	78%	774	100.00	1898	XM_039535267.1
PREDICTED: Mauremys reevesii estrogen related receptor beta...	Reeves'	260615	30.2	30.2	78%	774	100.00	1961	XM_039535266.1
PREDICTED: Mauremys reevesii estrogen related receptor beta...	Reeves'	260615	30.2	30.2	78%	774	100.00	1404	XM_039535265.1
PREDICTED: Mauremys reevesii estrogen related receptor beta...	Reeves'	260615	30.2	30.2	78%	774	100.00	2338	XM_039535263.1
PREDICTED: Mauremys reevesii estrogen related receptor beta...	Reeves'	260615	30.2	30.2	78%	774	100.00	1783	XM_039535262.1
PREDICTED: Mauremys reevesii protein tyrosine phosphatase...	Reeves'	260615	30.2	30.2	78%	774	100.00	1816	XM_039523232.1
PREDICTED: Mauremys reevesii protein tyrosine phosphatase...	Reeves'	260615	30.2	30.2	78%	774	100.00	5041	XM_039523231.1
PREDICTED: Mauremys reevesii DS cell adhesion molecule (**DSCAM**)...	Reeves'	260615	30.2	30.2	78%	774	100.00	6969	XM_039513797.1
PREDICTED: Mauremys reevesii DS cell adhesion molecule (**DSCAM**)...	Reeves'	260615	30.2	30.2	78%	774	100.00	2006	XM_039513791.1
PREDICTED: Pipra filicauda protein tyrosine phosphatase...	Wire-ta	649802	30.2	30.2	78%	774	100.00	5178	XM_027742951.2
PREDICTED: Pipra filicauda protein tyrosine phosphatase...	Wire-ta	649802	30.2	30.2	78%	774	100.00	2120	XM_027742952.2
PREDICTED: Pipra filicauda acetyl-CoA carboxylase beta (ACACB)...	Wire-ta	649802	30.2	30.2	78%	774	100.00	9190	XM_039384194.1
PREDICTED: Pipra filicauda acetyl-CoA carboxylase beta (ACACB)...	Wire-ta	649802	30.2	30.2	78%	774	100.00	9712	XM_027711260.2
Bacillus velezensis strain GUAL210 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4011788	CP069214.1
PREDICTED: Crotalus tigris estrogen related receptor beta...	Tiger r	88082	30.2	30.2	78%	774	100.00	2883	XM_039351657.1
PREDICTED: Crotalus tigris estrogen related receptor beta...	Tiger r	88082	30.2	30.2	78%	774	100.00	1612	XM_039351656.1
PREDICTED: Crotalus tigris	Tiger r	88082	30.2	30.2	78%	774	100.00	2814	XM_039351655.1

estrogen related receptor beta...									
PREDICTED: Crotalus tigris estrogen related receptor beta...	Tiger r	88082	30.2	30.2	78%	774	100.00	7360	XM_039351654.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon	72036	30.2	60.5	94%	774	100.00	59812117	LR794197.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon	72036	30.2	30.2	78%	774	100.00	30072609	LR794192.1
Lepeophtheirus salmonis strain IoA-00 genome assembly,...	salmon	72036	30.2	30.2	78%	774	100.00	43017027	LR794190.1
PREDICTED: Eucalyptus grandis protein NRT1/ PTR FAMILY 2.8...	NA	71139	30.2	30.2	78%	774	100.00	2423	XM_010040338.3
Bacillus altitudinis strain 63-2-2 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3772571	CP069098.1
Trichoderma reesei strain QM6a x CBS999.97 isolate...	NA	51453	30.2	30.2	78%	774	100.00	4082705	CP021315.1
Trichoderma reesei strain QM6a x CBS999.97 isolate...	NA	51453	30.2	30.2	78%	774	100.00	4151839	CP021294.1
Trichoderma reesei strain CBS999.97 chromosome V, complete...	NA	51453	30.2	30.2	78%	774	100.00	4096578	CP020728.1
Digitaria exilis genome assembly, chromosome: UA	NA	1010633	30.2	30.2	78%	774	100.00	60747861	LR994622.1
Streptomyces fulvissimus strain DF chromosome	NA	68202	30.2	30.2	78%	774	100.00	7800405	CP068598.1
Aspergillus luchuensis RIB2601 DNA, chromosome 6, nearly...	NA	1069201	30.2	30.2	78%	774	100.00	3972571	AP024439.1
Aspergillus luchuensis IFO 4308 DNA, chromosome 6, nearly...	NA	1069201	30.2	30.2	78%	774	100.00	3967242	AP024430.1
Aspergillus chevalieri M1 DNA, chromosome 4, nearly complete...	NA	182096	30.2	30.2	78%	774	100.00	3787471	AP024419.1
Bacillus altitudinis strain ws31 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3741767	CP068389.1
2_Tcm_b3v08	Califor	61474	30.2	30.2	78%	774	100.00	318992	OE179393.1
Medioppia subpectinata	NA	1979941	30.2	30.2	78%	774	100.00	14824	OC856567.1
Trachurus trachurus genome assembly, chromosome: 19	Atlanti	36212	30.2	60.5	89%	774	100.00	25328826	LR991650.1
Trachurus trachurus genome assembly, chromosome: 11	Atlanti	36212	30.2	30.2	78%	774	100.00	33386963	LR991641.1
Trachurus trachurus genome assembly, chromosome: 16	Atlanti	36212	30.2	90.7	94%	774	100.00	35009248	LR991639.1
Trachurus trachurus genome assembly, chromosome: 7	Atlanti	36212	30.2	30.2	78%	774	100.00	35447499	LR991638.1
Trachurus trachurus genome assembly, chromosome: 21	Atlanti	36212	30.2	30.2	78%	774	100.00	35833567	LR991636.1
Trachurus trachurus genome assembly, chromosome: 4	Atlanti	36212	30.2	30.2	78%	774	100.00	36093002	LR991635.1
Trachurus trachurus genome assembly, chromosome: 5	Atlanti	36212	30.2	30.2	78%	774	100.00	36888734	LR991633.1
Trachurus trachurus genome assembly, chromosome: 9	Atlanti	36212	30.2	30.2	78%	774	100.00	37400736	LR991632.1
Trachurus trachurus genome assembly, chromosome: 10	Atlanti	36212	30.2	30.2	78%	774	100.00	38572790	LR991631.1
Trachurus trachurus genome assembly, chromosome: 13	Atlanti	36212	30.2	30.2	78%	774	100.00	40695139	LR991629.1
Lymantria monacha genome assembly, chromosome: 13	black-a	78897	30.2	30.2	78%	774	100.00	33489103	LR991094.1
Notocelia uddmanniana genome assembly, chromosome: Z	NA	1594315	30.2	30.2	78%	774	100.00	75621453	LR991052.1
Noctua fimbriata genome	NA	753202	30.2	30.2	78%	774	100.00	17246417	LR990943.1

assembly, chromosome: 22									
Noctua fimbriata genome assembly, chromosome: 17	NA	753202	30.2	30.2	78%	774	100.00	18339581	LR990938.1
Apotomis turbidana genome assembly, chromosome: 1	NA	1100916	30.2	30.2	78%	774	100.00	42158560	LR990281.1
Aricia agestis genome assembly, chromosome: 20	brown a	91739	30.2	30.2	78%	774	100.00	14495840	LR990276.1
Aricia agestis genome assembly, chromosome: Z	brown a	91739	30.2	30.2	78%	774	100.00	42150342	LR990256.1
Limenitis camilla genome assembly, chromosome: 5	NA	270466	30.2	30.2	78%	774	100.00	16034060	LR990229.1
Hylaea fasciaria genome assembly, chromosome: Z	NA	722673	30.2	30.2	78%	774	100.00	17069495	LR990192.1
Notodonta dromedarius genome assembly, chromosome: 27	NA	753204	30.2	30.2	78%	774	100.00	6596137	LR990186.1
Hypena proboscidalis genome assembly, chromosome: 27	NA	753189	30.2	30.2	78%	774	100.00	11713018	LR990153.1
Hypena proboscidalis genome assembly, chromosome: 17	NA	753189	30.2	30.2	78%	774	100.00	20496581	LR990143.1
Hypena proboscidalis genome assembly, chromosome: 9	NA	753189	30.2	30.2	78%	774	100.00	22648911	LR990135.1
Hypena proboscidalis genome assembly, chromosome: Z	NA	753189	30.2	30.2	78%	774	100.00	34615938	LR990126.1
Euproctis similis genome assembly, chromosome: 5	NA	987935	30.2	30.2	78%	774	100.00	26047333	LR990108.1
Mycobacterium bovis BCG str. Korea 1168P, complete genome	NA	1206780	30.2	30.2	78%	774	100.00	4376711	CP003900.2
Bacillus amyloliquefaciens subsp. plantarum UCMB5036 complete...	NA	1150475	30.2	30.2	78%	774	100.00	3910324	HF563562.1
Mycobacterium tuberculosis H37Rv complete genome	NA	83332	30.2	30.2	78%	774	100.00	4411532	AL123456.3
Myxococcus stipitatus DSM 14675, complete genome	NA	1278073	30.2	30.2	78%	774	100.00	10350586	CP004025.1
Mycobacterium tuberculosis 7199-99 complete genome	NA	1138877	30.2	30.2	78%	774	100.00	4421197	HE663067.1
Mycobacterium canettii CIPT 140070017 complete genome	NA	1205677	30.2	30.2	78%	774	100.00	4524466	FO203510.1
Mycobacterium canettii CIPT 140070010 complete genome	NA	1205674	30.2	30.2	78%	774	100.00	4525948	FO203509.1
Mycobacterium canettii CIPT 140070008 complete genome	NA	1205675	30.2	30.2	78%	774	100.00	4420197	FO203508.1
Mycobacterium canettii CIPT 140060008 complete genome	NA	1205676	30.2	30.2	78%	774	100.00	4432426	FO203507.1
Bacillus velezensis AS43.3, complete genome	NA	1225788	30.2	30.2	78%	774	100.00	3961368	CP003838.1
Agaricus bisporus clone FWBA09-M05, complete sequence	NA	5341	30.2	30.2	78%	774	100.00	36557	AC253743.1
Drosophila melanogaster MIP34701 full insert cDNA	fruit f	7227	30.2	30.2	78%	774	100.00	1603	BT149858.1
Laspeyria flexula genome assembly, chromosome: 7	NA	938238	30.2	30.2	78%	774	100.00	17356636	LR989956.1
Mycobacterium tuberculosis variant microti strain Mycobacteriu...	NA	1806	30.2	30.2	78%	774	100.00	4384561	LR882500.1
Mycobacterium tuberculosis variant microti OV254 strain...	NA	1427372	30.2	30.2	78%	774	100.00	4369915	LR882499.1
Mycobacterium tuberculosis variant microti strain Mycobacteriu...	NA	1806	30.2	30.2	78%	774	100.00	4382575	LR882498.1

Mycobacterium tuberculosis variant microti strain Mycobacteriu...	NA	1806	30.2	30.2	78%	774	100.00	4385022	LR882497.1
Mycobacterium tuberculosis variant microti strain Mycobacteriu...	NA	1806	30.2	30.2	78%	774	100.00	4366549	LR882496.1
5_Tge_b3v08	NA	629358	30.2	30.2	78%	774	100.00	55010	OE844087.1
5_Tge_b3v08	NA	629358	30.2	30.2	78%	774	100.00	272721	OE839738.1
2_Tcm_b3v08	Califor	61474	30.2	30.2	78%	774	100.00	197941	OE179930.1
2_Tcm_b3v08	Califor	61474	30.2	30.2	78%	774	100.00	252207	OE179596.1
2_Tcm_b3v08	Califor	61474	30.2	30.2	78%	774	100.00	264031	OE179548.1
Oppiella nova	NA	334625	30.2	30.2	78%	774	100.00	15769	OC916432.1
Xestia xanthographa genome assembly, chromosome: 24	NA	988049	30.2	30.2	78%	774	100.00	27142919	LR990665.1
Xestia xanthographa genome assembly, chromosome: 20	NA	988049	30.2	90.7	78%	774	100.00	29746777	LR990661.1
Nibea albiflora genome assembly, chromosome: 20	white f	240163	30.2	30.2	78%	774	100.00	22112515	LR699043.1
Nibea albiflora genome assembly, chromosome: 16	white f	240163	30.2	30.2	78%	774	100.00	22261758	LR699039.1
Nibea albiflora genome assembly, chromosome: 4	white f	240163	30.2	30.2	78%	774	100.00	26591590	LR699027.1
Xestia xanthographa genome assembly, chromosome: 8	NA	988049	30.2	30.2	78%	774	100.00	32026937	LR990649.1
Clitopilus hobsonii strain QYL-10 chromosome 7	NA	648681	30.2	30.2	78%	774	100.00	3102588	CP068003.1
Phycisphaerales bacterium isolate...	NA	2052180	30.2	30.2	78%	774	100.00	3355795	CP064987.1
Myxococcus xanthus strain e-3-1 chromosome, complete genome	NA	34	30.2	60.5	78%	774	100.00	9251369	CP068048.1
PREDICTED: Canis lupus familiaris plexin A4 (PLXNA4), transcri...	dog	9615	30.2	30.2	78%	774	100.00	13026	XM_038686098.1
PREDICTED: Canis lupus familiaris plexin A4 (PLXNA4), transcri...	dog	9615	30.2	30.2	78%	774	100.00	12932	XM_038686097.1
PREDICTED: Canis lupus familiaris plexin A4 (PLXNA4), transcri...	dog	9615	30.2	30.2	78%	774	100.00	13023	XM_038686096.1
PREDICTED: Canis lupus familiaris plexin A4 (PLXNA4), transcri...	dog	9615	30.2	30.2	78%	774	100.00	13047	XM_038686095.1
PREDICTED: Canis lupus familiaris uncharacterized LOC119881648...	dog	9615	30.2	30.2	78%	774	100.00	1672	XR_005434791.1
PREDICTED: Canis lupus familiaris plexin A4 (PLXNA4), transcri...	dog	9615	30.2	30.2	78%	774	100.00	13025	XM_539370.7
Micropterus salmoides dynein heavy chain 5, axonemal (dnah5l),...	largemo	27706	30.2	30.2	78%	774	100.00	15862	XM_038696913.1
Dermochelys coriacea tyrosine-protein phosphatase non-receptor...	leather	27794	30.2	30.2	78%	774	100.00	1736	XM_038388444.1
Dermochelys coriacea tyrosine-protein phosphatase non-receptor...	leather	27794	30.2	30.2	78%	774	100.00	3609	XM_038388442.1
Dermochelys coriacea tyrosine-protein phosphatase non-receptor...	leather	27794	30.2	30.2	78%	774	100.00	3553	XM_038388441.1
Dermochelys coriacea LOW	leather	27794	30.2	30.2	78%	774	100.00	6748	XM_038408200.1

QUALITY PROTEIN: Down syndrome cell...									
Dermochelys coriacea protein PHTF2 transcript variant X1...	leather	27794	30.2	30.2	78%	774	100.00	4932	XM_038396678.1
Dermochelys coriacea protein PHTF2 transcript variant X1...	leather	27794	30.2	30.2	78%	774	100.00	5027	XM_038396671.1
Oryza sativa Indica Group cultivar Zhenshan 97 chromosome 7	long-gr	39946	30.2	30.2	78%	774	100.00	30840550	CP056058.1
Oryza sativa Indica Group cultivar Zhenshan 97 chromosome 3	long-gr	39946	30.2	30.2	78%	774	100.00	39636162	CP056054.1
Oryza sativa Indica Group cultivar Minghui 63 chromosome 7	long-gr	39946	30.2	30.2	78%	774	100.00	30877072	CP054682.1
Oryza sativa Indica Group cultivar Minghui 63 chromosome 3	long-gr	39946	30.2	30.2	78%	774	100.00	39893253	CP054678.1
Actinomyces naeslundii strain FDAARGOS_1037 chromosome, comple...	NA	1655	30.2	30.2	78%	774	100.00	3152123	CP066049.1
4_Tte_b3v08	NA	61484	30.2	30.2	78%	774	100.00	430082	OE000160.1
1_Tps_b3v08	NA	170557	30.2	30.2	78%	774	100.00	189296	OD000506.1
1_Tps_b3v08	NA	170557	30.2	30.2	78%	774	100.00	200121	OD000447.1
4_Tbi_b3v08	NA	61472	30.2	30.2	78%	774	100.00	117000	OD566504.1
3_Tce_b3v08	NA	61476	30.2	30.2	78%	774	100.00	184064	OC317742.1
Mycolicibacterium sp. Z-34 chromosome, complete genome	NA	2736649	30.2	30.2	78%	774	100.00	5962395	CP065373.2
1_Tps_b3v08	NA	170557	30.2	30.2	78%	774	100.00	19825	OD009335.1
3_Tms_b3v08	NA	170555	30.2	30.2	78%	774	100.00	421831	OB793115.1
Scyliorhinus canicula chromosome 29	smaller	7830	30.2	30.2	78%	774	100.00	16133577	LR744058.1
Scyliorhinus canicula chromosome 26	smaller	7830	30.2	30.2	78%	774	100.00	24906204	LR744055.1
Scyliorhinus canicula chromosome 21	smaller	7830	30.2	60.5	84%	774	100.00	71046048	LR744050.1
Scyliorhinus canicula chromosome 20	smaller	7830	30.2	30.2	78%	774	100.00	98274498	LR744049.1
4_Tte_b3v08	NA	61484	30.2	30.2	78%	774	100.00	354825	OE000297.1
4_Tbi_b3v08	NA	61472	30.2	30.2	78%	774	100.00	182790	OD565415.1
PREDICTED: Anas platyrhynchos DS cell adhesion molecule (**DSCAM**...	mallard	8839	30.2	30.2	78%	774	100.00	2136	XM_038167528.1
PREDICTED: Anas platyrhynchos DS cell adhesion molecule (**DSCAM**...	mallard	8839	30.2	30.2	78%	774	100.00	3277	XM_038167519.1
PREDICTED: Anas platyrhynchos DS cell adhesion molecule (**DSCAM**...	mallard	8839	30.2	30.2	78%	774	100.00	4559	XM_038167515.1
PREDICTED: Anas platyrhynchos DS cell adhesion molecule (**DSCAM**...	mallard	8839	30.2	30.2	78%	774	100.00	7091	XM_038167513.1
Bacillus velezensis strain LBUM279 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4170117	CP065791.1
PREDICTED: Motacilla alba alba grainyhead like transcription...	NA	1094192	30.2	30.2	78%	774	100.00	3597	XM_038132046.1
PREDICTED: Motacilla alba alba protein tyrosine phosphatase...	NA	1094192	30.2	30.2	78%	774	100.00	2009	XM_038126978.1
PREDICTED: Motacilla alba alba	NA	1094192	30.2	30.2	78%	774	100.00	1996	XM_038126977.1

protein tyrosine phosphatase...									
Myxococcus xanthus strain DK1622::pDPO-Mxn116-Pvan-Tpase...	NA	34	30.2	60.5	78%	774	100.00	9201039	CP065375.1
PREDICTED: Chlorocebus sabaeus uncharacterized LOC119627394...	green m	60711	30.2	30.2	78%	774	100.00	9934	XR_005243594.1
PREDICTED: Kryptolebias marmoratus MICAL-like 1a (micall1a),...	mangrov	37003	30.2	30.2	78%	774	100.00	4050	XM_017417023.3
PREDICTED: Kryptolebias marmoratus MICAL-like 1a (micall1a),...	mangrov	37003	30.2	30.2	78%	774	100.00	4092	XM_017417021.3
PREDICTED: Kryptolebias marmoratus pyridoxal kinase...	mangrov	37003	30.2	30.2	78%	774	100.00	3135	XM_017420604.3
PREDICTED: Kryptolebias marmoratus pyridoxal kinase...	mangrov	37003	30.2	30.2	78%	774	100.00	3137	XM_017420603.3
Notodromas monacha	NA	399045	30.2	30.2	78%	774	100.00	31001	OA885238.1
2_Tsi_b3v08	NA	629360	30.2	30.2	78%	774	100.00	78708	OC003744.1
2_Tsi_b3v08	NA	629360	30.2	30.2	78%	774	100.00	101871	OC002853.1
2_Tsi_b3v08	NA	629360	30.2	30.2	78%	774	100.00	103521	OC002799.1
2_Tsi_b3v08	NA	629360	30.2	30.2	78%	774	100.00	115506	OC002418.1
2_Tsi_b3v08	NA	629360	30.2	30.2	78%	774	100.00	310846	OC000377.1
Bacillus altitudinis strain Ba1449 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3718493	CP065040.1
1_Tdi_b3v08	NA	61478	30.2	30.2	78%	774	100.00	207243	OA565128.1
1_Tdi_b3v08	NA	61478	30.2	30.2	78%	774	100.00	344654	OA564518.1
1_Tdi_b3v08	NA	61478	30.2	30.2	78%	774	100.00	602106	OA564297.1
Darwinula stevensoni	NA	69355	30.2	30.2	78%	774	100.00	12167	LR905488.1
Darwinula stevensoni	NA	69355	30.2	30.2	78%	774	100.00	177198	LR899675.1
Darwinula stevensoni	NA	69355	30.2	30.2	78%	774	100.00	184303	LR899661.1
Cyprideis torosa	NA	163714	30.2	30.2	78%	774	100.00	53550	OB660964.1
PREDICTED: Chelonia mydas DS cell adhesion molecule (**DSCAM**), mRNA	Green s	8469	30.2	30.2	78%	774	100.00	6591	XM_037890275.1
PREDICTED: Nematolebias whitei nucleoporin nup211...	Rio pea	451745	30.2	30.2	78%	774	100.00	8421	XM_037690865.1
Mycobacterium tuberculosis variant bovis BCG strain BCG SL 222...	NA	33892	30.2	30.2	78%	774	100.00	4370706	CP064405.1
PREDICTED: Pygocentrus nattereri pyridoxal (pyridoxine, vitami...	red-bel	42514	30.2	30.2	78%	774	100.00	2768	XM_017691488.2
PREDICTED: Pygocentrus nattereri hydroxypyruvate isomerase...	red-bel	42514	30.2	30.2	78%	774	100.00	1450	XM_017687698.2
PREDICTED: Pygocentrus nattereri hydroxypyruvate isomerase...	red-bel	42514	30.2	30.2	78%	774	100.00	1562	XM_017687697.2
PREDICTED: Triticum dicoccoides putative cysteine-rich...	NA	85692	30.2	30.2	78%	774	100.00	2084	XM_037567046.1
PREDICTED: Triticum dicoccoides putative cysteine-rich...	NA	85692	30.2	30.2	78%	774	100.00	2087	XM_037567044.1
PREDICTED: Triticum dicoccoides putative cysteine-rich...	NA	85692	30.2	30.2	78%	774	100.00	3170	XM_037567043.1
PREDICTED: Triticum dicoccoides putative cysteine-	NA	85692	30.2	30.2	78%	774	100.00	3208	XM_037567042.1

rich...									
PREDICTED: Triticum dicoccoides putative cysteine-rich...	NA	85692	30.2	30.2	78%	774	100.00	3315	XM_037567041.1
PREDICTED: Manduca sexta uncharacterized LOC115452773...	tobacco	7130	30.2	30.2	78%	774	100.00	994	XM_030181372.2
PREDICTED: Falco rusticolus retina and anterior neural fold...	gyrfalc	120794	30.2	30.2	78%	774	100.00	1941	XR_005103786.1
PREDICTED: Falco rusticolus protein tyrosine phosphatase...	gyrfalc	120794	30.2	30.2	78%	774	100.00	2748	XM_037379337.1
Mycobacterium orygis strain MUHC/MB/EPTB/Orygis/51145...	NA	1305738	30.2	30.2	78%	774	100.00	4352172	CP063804.1
Vibrio parahaemolyticus strain VP366 capsule biosythesis gene...	NA	670	30.2	30.2	78%	774	100.00	42433	MT898320.1
Vibrio parahaemolyticus strain VP2 capsule biosynthesis gene...	NA	670	30.2	30.2	78%	774	100.00	37003	MT898293.1
Vibrio parahaemolyticus strain VP19 capsule biosythesis gene...	NA	670	30.2	30.2	78%	774	100.00	37003	MT898273.1
Vibrio parahaemolyticus strain VP180 capsule biosythesis gene...	NA	670	30.2	30.2	78%	774	100.00	37003	MT898130.1
Vibrio parahaemolyticus strain VP1 capsule biosynthesis gene...	NA	670	30.2	30.2	78%	774	100.00	37003	MT898026.1
Bacillus altitudinis strain BIM B-263 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3763717	CP063360.1
PREDICTED: Acanthopagrus latus dynein, axonemal, heavy chain 5...	yellowf	8177	30.2	30.2	78%	774	100.00	13240	XM_037079118.1
PREDICTED: Acanthopagrus latus dynein, axonemal, heavy chain 5...	yellowf	8177	30.2	30.2	78%	774	100.00	13350	XM_037079117.1
PREDICTED: Acanthopagrus latus dynein, axonemal, heavy chain 5...	yellowf	8177	30.2	30.2	78%	774	100.00	14502	XM_037079116.1
PREDICTED: Acanthopagrus latus NACHT, LRR and PYD...	yellowf	8177	30.2	30.2	78%	774	100.00	5603	XM_037080307.1
PREDICTED: Acanthopagrus latus NACHT, LRR and PYD...	yellowf	8177	30.2	30.2	78%	774	100.00	5612	XM_037080306.1
PREDICTED: Acanthopagrus latus NACHT, LRR and PYD...	yellowf	8177	30.2	30.2	78%	774	100.00	5620	XM_037080305.1
PREDICTED: Acanthopagrus latus NACHT, LRR and PYD...	yellowf	8177	30.2	30.2	78%	774	100.00	5618	XM_037080304.1
PREDICTED: Sturnira hondurensis colony stimulating factor 2...	NA	192404	30.2	30.2	78%	774	100.00	4059	XM_037068121.1
PREDICTED: Sturnira hondurensis colony stimulating factor 2...	NA	192404	30.2	30.2	78%	774	100.00	4059	XM_037068120.1
PREDICTED: Oncorhynchus mykiss microtubule-associated protein ...	rainbow	8022	30.2	30.2	78%	774	100.00	6950	XM_021589362.2
PREDICTED: Oncorhynchus mykiss microtubule-associated protein ...	rainbow	8022	30.2	30.2	78%	774	100.00	7007	XM_036967043.1
PREDICTED: Oncorhynchus mykiss microtubule-associated protein ...	rainbow	8022	30.2	30.2	78%	774	100.00	7022	XM_036967041.1

PREDICTED: Oncorhynchus mykiss microtubule-associated protein ...	rainbow	8022	30.2	30.2	78%	774	100.00	7052	XM_036967040.1
PREDICTED: Oncorhynchus mykiss microtubule-associated protein ...	rainbow	8022	30.2	30.2	78%	774	100.00	7067	XM_021589361.2
PREDICTED: Oncorhynchus mykiss microtubule-associated protein ...	rainbow	8022	30.2	30.2	78%	774	100.00	7145	XM_021589359.2
PREDICTED: Oncorhynchus mykiss microtubule-associated protein ...	rainbow	8022	30.2	30.2	78%	774	100.00	7157	XM_036967039.1
PREDICTED: Oncorhynchus mykiss microtubule-associated protein ...	rainbow	8022	30.2	30.2	78%	774	100.00	7084	XM_036967038.1
PREDICTED: Oncorhynchus mykiss microtubule-associated protein ...	rainbow	8022	30.2	30.2	78%	774	100.00	7160	XM_036967037.1
PREDICTED: Oncorhynchus mykiss deleted in malignant brain tumo...	rainbow	8022	30.2	30.2	78%	774	100.00	1500	XM_036953911.1
PREDICTED: Oncorhynchus mykiss deleted in malignant brain tumo...	rainbow	8022	30.2	30.2	78%	774	100.00	1203	XM_036971881.1
Macrobrachium nipponense isolate FS-2020 chromosome 47	NA	159736	30.2	30.2	78%	774	100.00	36926747	CP062011.1
Macrobrachium nipponense isolate FS-2020 chromosome 42	NA	159736	30.2	30.2	78%	774	100.00	54564452	CP062051.1
Macrobrachium nipponense isolate FS-2020 chromosome 31	NA	159736	30.2	30.2	78%	774	100.00	73203386	CP062049.1
Mycobacterium tuberculosis KZN 605, complete genome	NA	478435	30.2	30.2	78%	774	100.00	4399120	CP001976.1
Mycobacterium chubuense NBB4, complete genome	NA	710421	30.2	30.2	78%	774	100.00	5583723	CP003053.1
Mycobacterium tuberculosis RGTB423, complete genome	NA	1091501	30.2	30.2	78%	774	100.00	4406587	CP003234.1
Mycobacterium tuberculosis RGTB327, complete genome	NA	1091500	30.2	30.2	78%	774	100.00	4380119	CP003233.1
Mycobacterium tuberculosis str. Erdman = ATCC 35801 DNA,...	NA	652616	30.2	30.2	78%	774	100.00	4392353	AP012340.1
Mycobacterium tuberculosis UT205 complete genome	NA	1097669	30.2	30.2	78%	774	100.00	4418088	HE608151.1
Gordonia polyisoprenivorans VH2, complete genome	NA	1112204	30.2	30.2	78%	774	100.00	5669805	CP003119.1
Dicentrarchus labrax chromosome sequence corresponding to...	Europea	13489	30.2	30.2	78%	774	100.00	18113738	FQ310506.3
Mycobacterium bovis BCG str. Mexico, complete genome	NA	717522	30.2	30.2	78%	774	100.00	4350386	CP002095.1
PREDICTED: Balaenoptera musculus chromosome 12 C6orf120 homolo...	Blue wh	9771	30.2	30.2	78%	774	100.00	1021	XM_036871355.1
Colletotrichum siamense Ophiobolin F synthase (CGCS363_v010583...	NA	690259	30.2	30.2	78%	774	100.00	2277	XM_036642432.1
PREDICTED: Trichosurus vulpecula DS cell adhesion molecule...	common	9337	30.2	30.2	78%	774	100.00	6042	XM_036744150.1
Mycobacterium tuberculosis strain 1-0006P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4419608	CP041876.1
Mycobacterium tuberculosis	NA	1773	30.2	30.2	78%	774	100.00	4432141	CP041875.1

strain 1-0007P6C4 chromosome,...									
Mycobacterium tuberculosis strain 1-0009P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4418159	CP041874.1
Mycobacterium tuberculosis strain 1-0013P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4410415	CP041873.1
Mycobacterium tuberculosis strain 1-0017P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4418318	CP041872.1
Mycobacterium tuberculosis strain 1-0021P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4429476	CP041871.1
Mycobacterium tuberculosis strain 1-0023P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4419801	CP041870.1
Mycobacterium tuberculosis strain 1-0028P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4412588	CP041869.1
Mycobacterium tuberculosis strain 1-0030P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4430047	CP041868.1
Mycobacterium tuberculosis strain 1-0031P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4419967	CP041867.1
Mycobacterium tuberculosis strain 1-0036P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4404858	CP041866.1
Mycobacterium tuberculosis strain 1-0039P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4411261	CP041865.1
Mycobacterium tuberculosis strain 1-0044P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4387956	CP041864.1
Mycobacterium tuberculosis strain 1-0045P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4416971	CP041863.1
Mycobacterium tuberculosis strain 1-0047P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4434707	CP041862.1
Mycobacterium tuberculosis strain 1-0054P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4419916	CP041861.1
Mycobacterium tuberculosis strain 1-0056P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4413638	CP041860.1
Mycobacterium tuberculosis strain 1-0061P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4413879	CP041859.1
Mycobacterium tuberculosis strain 1-0064P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4417680	CP041858.1
Mycobacterium tuberculosis strain 1-0069P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4416165	CP041857.1
Mycobacterium tuberculosis strain 1-0071P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4416231	CP041856.1
Mycobacterium tuberculosis strain 1-0084P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4419973	CP041855.1

Mycobacterium tuberculosis strain 1-0102P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4421377	CP041854.1
Mycobacterium tuberculosis strain 1-0107P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4444842	CP041853.1
Mycobacterium tuberculosis strain 1-0110P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4425422	CP041852.1
Mycobacterium tuberculosis strain 1-0112P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4413235	CP041851.1
Mycobacterium tuberculosis strain 1-0116P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4416797	CP041850.1
Mycobacterium tuberculosis strain 1-0123P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4420004	CP041849.1
Mycobacterium tuberculosis strain 1-0137P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4419694	CP041848.1
Mycobacterium tuberculosis strain 1-0149P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4418657	CP041847.1
Mycobacterium tuberculosis strain 1-0153P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4419030	CP041846.1
Mycobacterium tuberculosis strain 1-0156P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4419404	CP041845.1
Mycobacterium tuberculosis strain 1-0160P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4431494	CP041844.1
Mycobacterium tuberculosis strain 1-0168P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4405183	CP041843.1
Mycobacterium tuberculosis strain 2-0013P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4414962	CP041842.1
Mycobacterium tuberculosis strain 2-0021P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4438299	CP041841.1
Mycobacterium tuberculosis strain 2-0023P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4438366	CP041839.1
Mycobacterium tuberculosis strain 2-0022P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4438339	CP041840.1
Mycobacterium tuberculosis strain 2-0028P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4438281	CP041838.1
Mycobacterium tuberculosis strain 2-0029P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4438363	CP041837.1
Mycobacterium tuberculosis strain 2-0031P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4418552	CP041836.1
Mycobacterium tuberculosis strain 2-0034P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4410873	CP041835.1
Mycobacterium tuberculosis strain 2-0043-unknownP6C4	NA	1773	30.2	30.2	78%	774	100.00	4409038	CP041834.1

chromosom...									
Mycobacterium tuberculosis strain 2-0046P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4438223	CP041833.1
Mycobacterium tuberculosis strain 2-0052P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4404274	CP041832.1
Mycobacterium tuberculosis strain 2-0059P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4425172	CP041831.1
Mycobacterium tuberculosis strain 2-0068P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4417769	CP041830.1
Mycobacterium tuberculosis strain 3-0059P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4376753	CP041829.1
Mycobacterium tuberculosis strain 3-0090P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4433503	CP041828.1
Mycobacterium tuberculosis strain 3-0096P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4450340	CP041827.1
Mycobacterium tuberculosis strain 3-0124P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4447644	CP041826.1
Mycobacterium tuberculosis strain 4-0010P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4400007	CP041825.1
Mycobacterium tuberculosis strain 4-0012P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4401614	CP041824.1
Mycobacterium tuberculosis strain 4-0019P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4400017	CP041823.1
Mycobacterium tuberculosis strain 4-0024P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4399945	CP041822.1
Mycobacterium tuberculosis strain 4-0062P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4399842	CP041821.1
Mycobacterium tuberculosis strain 4-0073P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4414542	CP041820.1
Mycobacterium tuberculosis strain 4-0077P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4401396	CP041819.1
Mycobacterium tuberculosis strain 4-0087P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4428457	CP041818.1
Mycobacterium tuberculosis strain 4-0096P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4408117	CP041817.1
Mycobacterium tuberculosis strain SEA00042P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4424310	CP041816.1
Mycobacterium tuberculosis strain SEA02010036P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4416761	CP041815.1
Mycobacterium tuberculosis strain SEA06535P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4408176	CP041814.1

Mycobacterium tuberculosis strain SEA07010354P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4438102	CP041813.1
Mycobacterium tuberculosis strain SEA07020250P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4407077	CP041812.1
Mycobacterium tuberculosis strain SEA08151P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4413498	CP041811.1
Mycobacterium tuberculosis strain SEA08162P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4408888	CP041810.1
Mycobacterium tuberculosis strain SEA09020048P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4391433	CP041809.1
Mycobacterium tuberculosis strain SEA09167P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4368671	CP041808.1
Mycobacterium tuberculosis strain SEA11020038P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4397139	CP041807.1
Mycobacterium tuberculosis strain SEA11020057P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4402162	CP041806.1
Mycobacterium tuberculosis strain SEA11020068P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4402473	CP041805.1
Mycobacterium tuberculosis strain SEA11020092P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4406516	CP041804.1
Mycobacterium tuberculosis strain SEA11278P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4410029	CP041803.1
Mycobacterium tuberculosis strain SEA12126P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4410647	CP041802.1
Mycobacterium tuberculosis strain SEA12202P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4433058	CP041801.1
Mycobacterium tuberculosis strain SEA12334P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4427826	CP041800.1
Mycobacterium tuberculosis strain SEA13020298P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4406587	CP041799.1
Mycobacterium tuberculosis strain SEA13111P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4410956	CP041798.1
Mycobacterium tuberculosis strain SEA14117P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4397372	CP041797.1
Mycobacterium tuberculosis strain SEA14318P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4426614	CP041796.1
Mycobacterium tuberculosis strain SEA14333P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4408229	CP041795.1
Mycobacterium tuberculosis strain SEA15228P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4407803	CP041794.1
Mycobacterium tuberculosis strain SEA15229P6C4	NA	1773	30.2	30.2	78%	774	100.00	4431110	CP041793.1

chromosome,...									
Mycobacterium tuberculosis strain SEA15230P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4412837	CP041792.1
Mycobacterium tuberculosis strain SEA17020023P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4420316	CP041791.1
Mycobacterium tuberculosis strain SEA17020024P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4420315	CP041790.1
Mycobacterium tuberculosis strain SEA17020028P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4415138	CP041789.1
Mycobacterium tuberculosis strain SEA17020030P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4405198	CP041788.1
PREDICTED: Colossoma macropomum dynein, axonemal, heavy chain ...	tambaqu	42526	30.2	30.2	78%	774	100.00	14462	XM_036592645.1
PREDICTED: Megalops cyprinoides oxysterol binding protein-like...	Indo-Pa	118141	30.2	30.2	78%	774	100.00	3145	XM_036515923.1
PREDICTED: Megalops cyprinoides oxysterol binding protein-like...	Indo-Pa	118141	30.2	30.2	78%	774	100.00	3036	XM_036515922.1
PREDICTED: Megalops cyprinoides oxysterol binding protein-like...	Indo-Pa	118141	30.2	30.2	78%	774	100.00	2828	XM_036515921.1
PREDICTED: Megalops cyprinoides oxysterol binding protein-like...	Indo-Pa	118141	30.2	30.2	78%	774	100.00	2732	XM_036515920.1
PREDICTED: Megalops cyprinoides oxysterol binding protein-like...	Indo-Pa	118141	30.2	30.2	78%	774	100.00	2897	XM_036515919.1
Mycobacterium tuberculosis strain 4-0041P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4400017	CP043995.1
Mycobacterium tuberculosis strain 1-0072P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4421012	CP043996.1
Mycobacterium tuberculosis strain 1-0066P6C4 chromosome,...	NA	1773	30.2	30.2	78%	774	100.00	4416715	CP043997.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowf	8177	30.2	30.2	78%	774	100.00	28391644	LR884480.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowf	8177	30.2	30.2	78%	774	100.00	24488360	LR884479.1
Acanthopagrus latus isolate v.2019 genome assembly, chromosome...	yellowf	8177	30.2	60.5	89%	774	100.00	24955350	LR884478.1
Infirmifilum lucidum strain 3507LT chromosome, complete genome	NA	2776706	30.2	30.2	78%	774	100.00	1625846	CP062310.1
Fusarium oxysporum f. sp. koae isolate 44 chromosome 7	NA	654392	30.2	30.2	78%	774	100.00	4223514	CP052901.1
Fusarium oxysporum isolate 170 chromosome 7	NA	5507	30.2	30.2	78%	774	100.00	4350714	CP052889.1
PREDICTED: Molothrus ater grainyhead like transcription factor...	NA	84834	30.2	30.2	78%	774	100.00	4834	XM_036381341.1

PREDICTED: Molothrus ater protein tyrosine phosphatase...	NA	84834	30.2	30.2	78%	774	100.00	2127	XM_036404491.1
PREDICTED: Molothrus ater protein tyrosine phosphatase...	NA	84834	30.2	30.2	78%	774	100.00	5162	XM_036404490.1
PREDICTED: Molossus molossus WD repeat domain 53 (WDR53),...	Pallas'	27622	30.2	30.2	78%	774	100.00	865	XM_036242984.1
PREDICTED: Molossus molossus **ZINC finger** protein 7 (**ZNF7**),...	Pallas'	27622	30.2	30.2	78%	774	100.00	3894	XM_036281319.1
PREDICTED: Molossus molossus **ZINC finger** protein 7 (**ZNF7**),...	Pallas'	27622	30.2	30.2	78%	774	100.00	4223	XM_036281318.1
PREDICTED: Molossus molossus **ZINC finger** protein 7 (**ZNF7**),...	Pallas'	27622	30.2	30.2	78%	774	100.00	4412	XM_036281317.1
Bacillus amyloliquefaciens strain INH2-4b chromosome, complete...	NA	1390	30.2	30.2	78%	774	100.00	4023066	CP061852.1
PREDICTED: Rousettus aegyptiacus **ZINC finger** protein 74 (**ZNF74**...	Egyptia	9407	30.2	30.2	78%	774	100.00	5233	XM_036221079.1
PREDICTED: Rousettus aegyptiacus **ZINC finger** protein 74 (**ZNF74**...	Egyptia	9407	30.2	30.2	78%	774	100.00	5281	XM_036221078.1
PREDICTED: Rousettus aegyptiacus **ZINC finger** protein 74 (**ZNF74**...	Egyptia	9407	30.2	30.2	78%	774	100.00	5329	XM_016120200.2
PREDICTED: Rousettus aegyptiacus **ZINC finger** protein 74 (**ZNF74**...	Egyptia	9407	30.2	30.2	78%	774	100.00	5332	XM_036221077.1
Homo sapiens DNA, chromosome 16, nearly complete genome	human	9606	30.2	30.2	78%	774	100.00	94690957	AP023476.1
PREDICTED: Onychomys torridus calcium voltage-gated channel...	souther	38674	30.2	30.2	78%	774	100.00	8171	XM_036195083.1
Bacillus velezensis strain AK-0 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3969447	CP047119.1
Poecilia reticulata genome assembly, chromosome: 22	guppy	8081	30.2	30.2	78%	774	100.00	24441338	LR880666.1
Poecilia reticulata genome assembly, chromosome: 21	guppy	8081	30.2	30.2	78%	774	100.00	25956221	LR880665.1
Poecilia reticulata genome assembly, chromosome: 11	guppy	8081	30.2	30.2	78%	774	100.00	29172019	LR880655.1
Poecilia reticulata genome assembly, chromosome: 10	guppy	8081	30.2	30.2	78%	774	100.00	32921471	LR880654.1
Poecilia reticulata genome assembly, chromosome: 1	guppy	8081	30.2	30.2	78%	774	100.00	34343053	LR880645.1
PREDICTED: Fundulus heteroclitus estrogen-related receptor del...	mummich	8078	30.2	30.2	78%	774	100.00	4227	XM_036131474.1
PREDICTED: Fundulus heteroclitus estrogen-related receptor del...	mummich	8078	30.2	30.2	78%	774	100.00	4219	XM_036131472.1
PREDICTED: Fundulus heteroclitus estrogen-related receptor del...	mummich	8078	30.2	30.2	78%	774	100.00	4236	XM_036131471.1
PREDICTED: Fundulus	mummich	8078	30.2	30.2	78%	774	100.00	4218	XM_036131470.1

heteroclitus estrogen-related receptor del...									
PREDICTED: Fundulus heteroclitus estrogen-related receptor del...	mummich	8078	30.2	30.2	78%	774	100.00	4365	XM_036131469.1
PREDICTED: Fundulus heteroclitus uncharacterized LOC118558646...	mummich	8078	30.2	30.2	78%	774	100.00	425	XR_004928410.1
PREDICTED: Halichoerus grypus uncharacterized LOC118524490...	gray se	9711	30.2	30.2	78%	774	100.00	1425	XR_004911646.1
PREDICTED: Halichoerus grypus potassium two pore domain channe...	gray se	9711	30.2	30.2	78%	774	100.00	3694	XM_036074696.1
PREDICTED: Halichoerus grypus Dmx like 1 (DMXL1), transcript...	gray se	9711	30.2	30.2	78%	774	100.00	10119	XM_036123787.1
PREDICTED: Halichoerus grypus Dmx like 1 (DMXL1), transcript...	gray se	9711	30.2	30.2	78%	774	100.00	9078	XM_036123786.1
PREDICTED: Halichoerus grypus Dmx like 1 (DMXL1), transcript...	gray se	9711	30.2	30.2	78%	774	100.00	9141	XM_036123785.1
PREDICTED: Halichoerus grypus Dmx like 1 (DMXL1), transcript...	gray se	9711	30.2	30.2	78%	774	100.00	11545	XM_036123784.1
PREDICTED: Halichoerus grypus Dmx like 1 (DMXL1), transcript...	gray se	9711	30.2	30.2	78%	774	100.00	11545	XM_036123783.1
PREDICTED: Halichoerus grypus Dmx like 1 (DMXL1), transcript...	gray se	9711	30.2	30.2	78%	774	100.00	11597	XM_036123782.1
PREDICTED: Halichoerus grypus Dmx like 1 (DMXL1), transcript...	gray se	9711	30.2	30.2	78%	774	100.00	11609	XM_036123781.1
PREDICTED: Halichoerus grypus Dmx like 1 (DMXL1), transcript...	gray se	9711	30.2	30.2	78%	774	100.00	11660	XM_036123780.1
PREDICTED: Halichoerus grypus **ZINC finger** protein 7 (**ZNF7**),...	gray se	9711	30.2	30.2	78%	774	100.00	5513	XM_036105802.1
PREDICTED: Halichoerus grypus **ZINC finger** protein 7 (**ZNF7**),...	gray se	9711	30.2	30.2	78%	774	100.00	4730	XM_036105801.1
PREDICTED: Halichoerus grypus **ZINC finger** protein 7 (**ZNF7**),...	gray se	9711	30.2	30.2	78%	774	100.00	4364	XM_036105800.1
PREDICTED: Halichoerus grypus **ZINC finger** protein 7 (**ZNF7**),...	gray se	9711	30.2	30.2	78%	774	100.00	4622	XM_036105799.1
PREDICTED: Halichoerus grypus **ZINC finger** protein 7 (**ZNF7**),...	gray se	9711	30.2	30.2	78%	774	100.00	4775	XM_036105798.1
PREDICTED: Halichoerus grypus **ZINC finger** protein 7 (**ZNF7**),...	gray se	9711	30.2	30.2	78%	774	100.00	4391	XM_036105797.1
PREDICTED: Halichoerus grypus **ZINC finger** protein 7 (**ZNF7**),...	gray se	9711	30.2	30.2	78%	774	100.00	4656	XM_036105796.1

PREDICTED: Halichoerus grypus **ZINC finger** protein 7 (**ZNF7**),...	gray se	9711	30.2	30.2	78%	774	100.00	4809	XM_036105795.1
PREDICTED: Halichoerus grypus **ZINC finger** protein 7 (**ZNF7**),...	gray se	9711	30.2	30.2	78%	774	100.00	4986	XM_036105794.1
PREDICTED: Halichoerus grypus **ZINC finger** protein 7 (**ZNF7**),...	gray se	9711	30.2	30.2	78%	774	100.00	5034	XM_036105793.1
Bacillus velezensis strain CLA178 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	4068479	CP061087.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2064	XR_004883994.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2323	XR_004883993.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2315	XR_004883992.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2364	XR_004883991.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	1874	XR_004883990.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	3420	XR_004883989.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2278	XR_004883988.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	3422	XR_004883987.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2139	XR_004883986.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2145	XR_002572205.2
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2183	XR_004883985.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2322	XR_002572207.2
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2189	XR_002572208.2
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2174	XR_004883984.1
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	1877	XR_002572203.2
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	3323	XR_004883983.1

PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2360	XR_002572206.2
PREDICTED: Helianthus annuus uncharacterized LOC110903883...	common	4232	30.2	30.2	100%	774	94.74	2366	XR_002572204.2
Bacillus altitudinis strain BA06 chromosome, complete genome	NA	293387	30.2	30.2	78%	774	100.00	3755709	CP039020.1
PREDICTED: Amphiprion ocellaris interleukin-1 receptor accesso...	clown a	80972	30.2	30.2	78%	774	100.00	3298	XM_023296674.2
PREDICTED: Amphiprion ocellaris interleukin-1 receptor accesso...	clown a	80972	30.2	30.2	78%	774	100.00	3316	XM_023296673.2
Synechococcus sp. MIT S9220 chromosome, complete genome	NA	166309	30.2	30.2	78%	774	100.00	2424175	CP047958.1
PREDICTED: Amphiprion ocellaris KIAA0753 ortholog (kiaa0753),...	clown a	80972	30.2	30.2	78%	774	100.00	3631	XM_023272048.2
PREDICTED: Amphiprion ocellaris KIAA0753 ortholog (kiaa0753),...	clown a	80972	30.2	30.2	78%	774	100.00	3631	XM_023272047.2
PREDICTED: Amphiprion ocellaris KIAA0753 ortholog (kiaa0753),...	clown a	80972	30.2	30.2	78%	774	100.00	3634	XM_023272046.2
Synechococcus sp. MEDNS5 chromosome, complete genome	NA	1442554	30.2	30.2	78%	774	100.00	2435869	CP047952.1
Synechococcus sp. PROS-7-1 chromosome, complete genome	NA	1442556	30.2	30.2	78%	774	100.00	2565218	CP047945.1
Synechococcus sp. BIOS-E4-1 chromosome	NA	1400864	30.2	30.2	78%	774	100.00	3314220	CP047935.1
Acomys russatus genome assembly, chromosome: 32	golden	60746	30.2	846	89%	774	100.00	49586240	LR877243.1
Acomys russatus genome assembly, chromosome: 31	golden	60746	30.2	574	78%	774	100.00	43509854	LR877242.1
Acomys russatus genome assembly, chromosome: 30	golden	60746	30.2	362	89%	774	100.00	40934070	LR877241.1
Acomys russatus genome assembly, chromosome: 28	golden	60746	30.2	513	89%	774	100.00	43538471	LR877239.1
Acomys russatus genome assembly, chromosome: 27	golden	60746	30.2	483	89%	774	100.00	58391991	LR877238.1
Acomys russatus genome assembly, chromosome: 25	golden	60746	30.2	816	89%	774	100.00	53031086	LR877236.1
Acomys russatus genome assembly, chromosome: 23	golden	60746	30.2	483	100%	774	100.00	59861171	LR877234.1
Acomys russatus genome assembly, chromosome: 22	golden	60746	30.2	483	89%	774	100.00	59984821	LR877233.1
Acomys russatus genome assembly, chromosome: 18	golden	60746	30.2	423	94%	774	100.00	64120505	LR877229.1
Acomys russatus genome assembly, chromosome: 17	golden	60746	30.2	937	89%	774	100.00	65338851	LR877228.1
Acomys russatus genome assembly, chromosome: 15	golden	60746	30.2	725	89%	774	100.00	67302882	LR877226.1
Acomys russatus genome assembly, chromosome: 12	golden	60746	30.2	755	89%	774	100.00	61352468	LR877223.1
Acomys russatus genome assembly, chromosome: 11	golden	60746	30.2	695	94%	774	100.00	62768634	LR877222.1
Acomys russatus genome assembly, chromosome: 10	golden	60746	30.2	846	89%	774	100.00	78787447	LR877221.1
Acomys russatus genome assembly, chromosome: 7	golden	60746	30.2	816	89%	774	100.00	69034057	LR877218.1
Acomys russatus genome	golden	60746	30.2	785	100%	774	100.00	86290179	LR877214.1

assembly, chromosome: 3									
Onychomys torridus genome assembly, chromosome: 22	souther	38674	30.2	30.2	78%	774	100.00	42861602	LR877209.1
Onychomys torridus genome assembly, chromosome: 21	souther	38674	30.2	30.2	78%	774	100.00	54077118	LR877208.1
Onychomys torridus genome assembly, chromosome: 20	souther	38674	30.2	30.2	78%	774	100.00	48895294	LR877207.1
Onychomys torridus genome assembly, chromosome: 18	souther	38674	30.2	30.2	78%	774	100.00	66632817	LR877205.1
Onychomys torridus genome assembly, chromosome: 17	souther	38674	30.2	30.2	78%	774	100.00	64256681	LR877204.1
Onychomys torridus genome assembly, chromosome: 12	souther	38674	30.2	30.2	78%	774	100.00	75710165	LR877199.1
Onychomys torridus genome assembly, chromosome: 11	souther	38674	30.2	30.2	78%	774	100.00	93020901	LR877198.1
PREDICTED: Egretta garzetta protein tyrosine phosphatase...	little	188379	30.2	30.2	78%	774	100.00	1403	XM_035901628.1
PREDICTED: Egretta garzetta protein tyrosine phosphatase...	little	188379	30.2	30.2	78%	774	100.00	5764	XM_035901627.1
Mycobacterium tuberculosis strain H37Rv_IC1 chromosome	NA	1773	30.2	30.2	78%	774	100.00	4411530	CP053903.1
Mycobacterium tuberculosis strain H37Rv_IC2 chromosome	NA	1773	30.2	30.2	78%	774	100.00	4411308	CP053902.1
PREDICTED: Oncorhynchus keta translocase of outer mitochondria...	chum sa	8018	30.2	30.2	78%	774	100.00	1472	XM_035795053.1
PREDICTED: Oncorhynchus keta microtubule-associated protein...	chum sa	8018	30.2	30.2	78%	774	100.00	3717	XM_035788214.1
PREDICTED: Oncorhynchus keta microtubule-associated protein...	chum sa	8018	30.2	30.2	78%	774	100.00	3776	XM_035788213.1
PREDICTED: Oncorhynchus keta microtubule-associated protein...	chum sa	8018	30.2	30.2	78%	774	100.00	3794	XM_035788212.1
PREDICTED: Oncorhynchus keta microtubule-associated protein...	chum sa	8018	30.2	30.2	78%	774	100.00	3821	XM_035788211.1
PREDICTED: Oncorhynchus keta microtubule-associated protein...	chum sa	8018	30.2	30.2	78%	774	100.00	3838	XM_035788210.1
PREDICTED: Oncorhynchus keta microtubule-associated protein...	chum sa	8018	30.2	30.2	78%	774	100.00	3917	XM_035788209.1
PREDICTED: Oncorhynchus keta microtubule-associated protein...	chum sa	8018	30.2	30.2	78%	774	100.00	3896	XM_035788208.1
PREDICTED: Oncorhynchus keta microtubule-associated protein...	chum sa	8018	30.2	30.2	78%	774	100.00	3912	XM_035788207.1
PREDICTED: Oncorhynchus keta microtubule-associated protein...	chum sa	8018	30.2	30.2	78%	774	100.00	3927	XM_035788206.1
PREDICTED: Oncorhynchus keta microtubule-associated protein...	chum sa	8018	30.2	30.2	78%	774	100.00	3930	XM_035788205.1
Plasmodium vinckei genome assembly, chromosome: PVSEL_06	NA	5860	30.2	30.2	78%	774	100.00	1199642	LR865427.1
PREDICTED: Canis lupus dingo plexin A4 (PLXNA4), transcript...	dingo	286419	30.2	30.2	78%	774	100.00	12992	XM_025471690.2

PREDICTED: Canis lupus dingo plexin A4 (PLXNA4), transcript...	dingo	286419	30.2	30.2	78%	774	100.00	12898	XM_035698599.1
PREDICTED: Canis lupus dingo plexin A4 (PLXNA4), transcript...	dingo	286419	30.2	30.2	78%	774	100.00	12990	XM_035698598.1
PREDICTED: Canis lupus dingo plexin A4 (PLXNA4), transcript...	dingo	286419	30.2	30.2	78%	774	100.00	13013	XM_035698597.1
PREDICTED: Zalophus californianus potassium two pore domain...	Califor	9704	30.2	30.2	78%	774	100.00	5189	XM_027603933.2
Pipistrellus Pipistrellus genome assembly, chromosome: 19	common	59474	30.2	30.2	78%	774	100.00	24193083	LR862375.1
Pipistrellus Pipistrellus genome assembly, chromosome: 16	common	59474	30.2	30.2	78%	774	100.00	46231460	LR862372.1
Pipistrellus Pipistrellus genome assembly, chromosome: 8	common	59474	30.2	60.5	89%	774	100.00	83522093	LR862364.1
Pipistrellus Pipistrellus genome assembly, chromosome: 7	common	59474	30.2	60.5	89%	774	100.00	84548104	LR862363.1
Pipistrellus Pipistrellus genome assembly, chromosome: 5	common	59474	30.2	30.2	78%	774	100.00	94929986	LR862361.1
Ovis aries isolate contig_4496 chromosome Y genomic sequence	sheep	9940	30.2	30.2	78%	774	100.00	888	MT768564.1
Micromonospora sp. 28ISP2-46 chromosome	NA	2749844	30.2	30.2	78%	774	100.00	6644909	CP059322.1
Bacillus velezensis strain BIOMA BV10 chromosome, complete genome	NA	492670	30.2	30.2	78%	774	100.00	3917533	CP059318.1
Metarhizium brunneum strain 4556 chromosome 5, complete sequence	NA	500148	30.2	30.2	78%	774	100.00	4290503	CP058936.1
PREDICTED: Cygnus atratus protein tyrosine phosphatase...	black s	8868	30.2	30.2	78%	774	100.00	3331	XM_035565337.1
PREDICTED: Cygnus atratus protein tyrosine phosphatase...	black s	8868	30.2	30.2	78%	774	100.00	1985	XM_035565336.1
PREDICTED: Cygnus atratus protein tyrosine phosphatase...	black s	8868	30.2	30.2	78%	774	100.00	4645	XM_035565334.1
PREDICTED: Cygnus atratus DS cell adhesion molecule (**DSCAM**), mRNA	black s	8868	30.2	30.2	78%	774	100.00	6009	XM_035546056.1
Bacillus pumilus strain UAMX chromosome, complete genome	NA	1408	30.2	30.2	78%	774	100.00	3854893	CP058951.1
Cyclobacteriaceae bacterium isolate SSA6 chromosome	NA	2099675	30.2	30.2	78%	774	100.00	4262804	CP058703.1
PREDICTED: Oxyura jamaicensis protein tyrosine phosphatase...	ruddy d	8884	30.2	30.2	78%	774	100.00	2124	XM_035316892.1
PREDICTED: Oxyura jamaicensis protein tyrosine phosphatase...	ruddy d	8884	30.2	30.2	78%	774	100.00	2289	XM_035316891.1
PREDICTED: Callithrix jacchus F-box protein 25 (FBXO25),...	white-t	9483	30.2	30.2	78%	774	100.00	5973	XR_004732560.1
PREDICTED: Callithrix jacchus F-box protein 25 (FBXO25),...	white-t	9483	30.2	30.2	78%	774	100.00	6015	XR_004732559.1
PREDICTED: Callithrix jacchus F-box protein 25 (FBXO25),...	white-t	9483	30.2	30.2	78%	774	100.00	6152	XR_004732558.1

Mycobacterium tuberculosis variant bovis strain 3/86Rv chromosome	NA	1765	30.2	30.2	78%	774	100.00	4350102	CP023708.2
PREDICTED: Callithrix jacchus F-box protein 25 (FBXO25),...	white-t	9483	30.2	30.2	78%	774	100.00	4976	XR_004732566.1
PREDICTED: Callithrix jacchus F-box protein 25 (FBXO25),...	white-t	9483	30.2	30.2	78%	774	100.00	5146	XR_004732563.1
PREDICTED: Hippoglossus stenolepis transcription initiation...	Pacific	195615	30.2	30.2	78%	774	100.00	5543	XM_035154662.1
PREDICTED: Hippoglossus stenolepis transcription initiation...	Pacific	195615	30.2	30.2	78%	774	100.00	5687	XM_035154652.1
Danio rerio genome assembly, chromosome: 1	zebrafi	7955	30.2	30.2	78%	774	100.00	59568845	LR812063.1
Danio rerio genome assembly, chromosome: 7	zebrafi	7955	30.2	60.5	84%	774	100.00	32288296	LR812044.1
Anas platyrhynchos genome assembly, chromosome: Z	mallard	8839	30.2	30.2	78%	774	100.00	74035964	LS423640.1
Anas platyrhynchos genome assembly, chromosome: 21	mallard	8839	30.2	30.2	78%	774	100.00	15673935	LS423631.1
Anas platyrhynchos genome assembly, chromosome: 11	mallard	8839	30.2	30.2	78%	774	100.00	21688649	LS423621.1
Danio rerio genome assembly, chromosome: 7	zebrafi	7955	30.2	60.5	84%	774	100.00	68646688	LR812600.1
Danio rerio strain Nadia (NA) genome assembly, chromosome: 7	zebrafi	7955	30.2	30.2	78%	774	100.00	71468568	LR812575.1
Danio rerio strain Nadia (NA) genome assembly, chromosome: 1	zebrafi	7955	30.2	30.2	78%	774	100.00	58221445	LR812569.1
Danio rerio strain Cooch Behar (CB) genome assembly, chromosom...	zebrafi	7955	30.2	30.2	78%	774	100.00	65279001	LR812550.1
Danio rerio strain Cooch Behar (CB) genome assembly, chromosom...	zebrafi	7955	30.2	60.5	78%	774	100.00	54094920	LR812544.1
Danio kyathit genome assembly, chromosome: 7	NA	242068	30.2	30.2	78%	774	100.00	89469171	LR812525.1
Danio aesculapii genome assembly, chromosome: 7	NA	1142201	30.2	30.2	78%	774	100.00	74246351	LR812512.1
Danio aesculapii genome assembly, chromosome: 2	NA	1142201	30.2	30.2	78%	774	100.00	60050756	LR812511.1
Mus musculus targeted non-conditional, lacZ-tagged mutant alle...	house m	10090	30.2	30.2	78%	774	100.00	36447	JN959500.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged...	house m	10090	30.2	30.2	78%	774	100.00	37938	JN954292.1
Mus musculus targeted non-conditional, lacZ-tagged mutant alle...	house m	10090	30.2	30.2	78%	774	100.00	39384	JN953268.1
Mus musculus targeted non-conditional, lacZ-tagged mutant alle...	house m	10090	30.2	30.2	78%	774	100.00	38426	JN952837.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged...	house m	10090	30.2	30.2	78%	774	100.00	38484	JN948503.1
Mus musculus targeted non-conditional, lacZ-tagged mutant alle...	house m	10090	30.2	30.2	78%	774	100.00	37937	JN946427.1
Mus musculus targeted KO-first, conditional ready, lacZ-tagged...	house m	10090	30.2	30.2	78%	774	100.00	39387	JN945386.1
Mycobacterium tuberculosis	NA	707235	30.2	30.2	78%	774	100.00	4398525	CP002992.1

CTRI-2, complete genome									
Mycobacterium bovis BCG str. Moreau RDJ complete genome	NA	413996	30.2	30.2	78%	774	100.00	4340116	AM412059.2
Mycobacterium canettii CIPT 140010059 complete genome	NA	1048245	30.2	30.2	78%	774	100.00	4482059	HE572590.1
Mycobacterium africanum GM041182 complete genome	NA	572418	30.2	30.2	78%	774	100.00	4389314	FR878060.1
Mycobacterium tuberculosis CCDC5180, complete genome	NA	443150	30.2	30.2	78%	774	100.00	4405981	CP001642.1
Mycobacterium tuberculosis CCDC5079, complete genome	NA	443149	30.2	30.2	78%	774	100.00	4398812	CP001641.1
Hoyosella subflava DQS3-9A1 chromosome, complete genome	NA	443218	30.2	30.2	78%	774	100.00	4738809	CP002786.1
Homo sapiens CXXC **finger** protein 1 pseudogene 1 (CXXC1P1),...	human	9606	30.2	30.2	78%	774	100.00	36438	NG_028296.1
Mycobacterium tuberculosis KZN 4207, complete genome	NA	478433	30.2	30.2	78%	774	100.00	4394985	CP001662.1
Neospora caninum Liverpool complete genome, chromosome VIII	NA	572307	30.2	30.2	78%	774	100.00	6723156	FR823390.1
Homo sapiens FOSMID clone ABC24-970F8 from chromosome 1,...	human	9606	30.2	30.2	78%	774	100.00	41179	AC243921.1
Cryptococcus gattii WM276 Exocyst protein, putative partial mRNA	NA	367775	30.2	30.2	78%	774	100.00	3504	XM_003196682.1
Cryptococcus gattii WM276 chromosome K, complete sequence	NA	367775	30.2	30.2	78%	774	100.00	1040760	CP000296.1
Micromonospora sp. L5, complete genome	NA	648999	30.2	30.2	100%	774	94.74	6962533	CP002399.1
Caenorhabditis remanei hypothetical protein (CRE_12530) mRNA,...	NA	31234	30.2	30.2	78%	774	100.00	1632	XM_003107745.1
Crassostrea gigas clone CG_Ba58D2, complete sequence	Pacific	29159	30.2	30.2	78%	774	100.00	133199	GU207433.1
Crassostrea gigas clone CG_Ba106O6, complete sequence	Pacific	29159	30.2	30.2	78%	774	100.00	158090	GU207429.1
Crassostrea gigas clone CG_Ba67A11, complete sequence	Pacific	29159	30.2	30.2	78%	774	100.00	203422	GU207422.1
Crassostrea gigas clone CG_Ba21O17, complete sequence	Pacific	29159	30.2	30.2	78%	774	100.00	164533	GU207421.1
Crassostrea gigas clone CG_Ba33M18, complete sequence	Pacific	29159	30.2	30.2	78%	774	100.00	136953	GU207416.1
Crassostrea gigas clone CG_Ba3I17, complete sequence	Pacific	29159	30.2	30.2	78%	774	100.00	172567	GU207407.1
Sus scrofa clone CH242-222K18 fatty acid desaturase 2 (FADS2)...	pig	9823	30.2	30.2	78%	774	100.00	44968	FJ263685.1
Picea glauca clone GQ03202_A11 mRNA sequence	white s	3330	30.2	30.2	78%	774	100.00	752	BT108877.1
Nakamurella multipartita DSM 44233 chromosome, complete genome	NA	479431	30.2	30.2	78%	774	100.00	6060298	CP001737.1
Mycobacterium tuberculosis KZN	NA	478434	30.2	30.2	78%	774	100.00	4398250	CP001658.1

1435, complete genome									
Latimeria menadoensis, clone VMRC4-121C4, complete sequence	Menado	106881	30.2	30.2	78%	774	100.00	166048	AC215495.4
Oncorhynchus mykiss clone omyk-evo-511-197 Transcription...	rainbow	8022	30.2	30.2	78%	774	100.00	1476	BT073991.1
Homo sapiens chromosome 13q34 schizophrenia region contig 1...	human	9606	30.2	30.2	78%	774	100.00	3112181	AE014294.1
Mycobacterium bovis BCG str. Tokyo 172 DNA, complete genome	NA	561275	30.2	30.2	78%	774	100.00	4371711	AP010918.1
Pan troglodytes BAC clone CH251-547J18 from chromosome 14,...	chimpan	9598	30.2	30.2	78%	774	100.00	208484	AC193895.4
Homo sapiens FOSMID clone ABC9-43824800B13 from chromosome 1,...	human	9606	30.2	30.2	78%	774	100.00	40181	AC212261.3
Pig DNA sequence from clone CH242-127H16 on chromosome 18,...	pig	9823	30.2	30.2	78%	774	100.00	253879	CU467666.11
Karlodinium micrum strain CCMP1975 isolate Kmi-cDNAN18-2 cold...	NA	407301	30.2	30.2	78%	774	100.00	816	EF134113.1
Karlodinium micrum strain CCMP1975 isolate Kmi-cDNAN18-1 cold...	NA	407301	30.2	30.2	78%	774	100.00	813	EF134112.1
Macaca mulatta BAC CH250-339C18 (Children's Hospital Oakland...	Rhesus	9544	30.2	30.2	78%	774	100.00	176229	AC203225.4
Mycobacterium tuberculosis F11, complete genome	NA	336982	30.2	30.2	78%	774	100.00	4424435	CP000717.1
Mycobacterium tuberculosis H37Ra, complete genome	NA	419947	30.2	30.2	78%	774	100.00	4419977	CP000611.1
Aspergillus niger contig An12c0300, genomic contig	NA	5061	30.2	30.2	78%	774	100.00	25396	AM270286.1
Mycobacterium bovis BCG Pasteur 1173P2, complete genome	NA	410289	30.2	30.2	78%	774	100.00	4374522	AM408590.1
Mycobacterium vanbaalenii PYR-1, complete genome	NA	350058	30.2	30.2	100%	774	94.74	6491865	CP000511.1
Myxococcus xanthus DK 1622, complete genome	NA	246197	30.2	60.5	78%	774	100.00	9139763	CP000113.1
Magnaporthe grisea 70-15 clone 61J04 telomere region, partial...	NA	242507	30.2	30.2	78%	774	100.00	34460	DQ493955.1
Oryza sativa chromosome 3 BAC OSJNBa0090P23 genomic sequence,...	Japanes	39947	30.2	30.2	78%	774	100.00	126163	AC084380.9
Mus musculus chromosome 5, clone RP23-170E15, complete sequence	house m	10090	30.2	30.2	78%	774	100.00	193480	AC115786.8
Oryza sativa Japonica Group cultivar Nipponbare chromosome 3...	Japanes	39947	30.2	30.2	78%	774	100.00	89172	AC084295.10
Mus musculus chromosome 5, clone RP23-451E8, complete sequence	house m	10090	30.2	30.2	78%	774	100.00	184672	AC118010.11
Mycobacterium tuberculosis CDC1551, complete genome	NA	83331	30.2	30.2	78%	774	100.00	4403837	AE000516.2
Mus musculus chromosome 7, clone RP24-397O2, complete	house m	10090	30.2	30.2	78%	774	100.00	167677	AC102299.11

sequence									
Mus musculus chromosome 17, clone RP24-301I14, complete sequence	house m	10090	30.2	30.2	78%	774	100.00	209975	AC132910.8
Mus musculus chromosome 15, clone RP23-256A2, complete sequence	house m	10090	30.2	30.2	78%	774	100.00	204704	AC099704.7
Mus musculus BAC clone RP23-283O7 from chromosome 19, complete...	house m	10090	30.2	30.2	78%	774	100.00	134644	AC141437.4
Mus musculus BAC clone RP24-308A19 from chromosome 15, complet...	house m	10090	30.2	30.2	78%	774	100.00	168423	AC131773.3
Homo sapiens chromosome 8, clone RP11-91J19, complete sequence	human	9606	30.2	30.2	78%	774	100.00	161160	AC083964.3
Homo sapiens cDNA FLJ44863 fis, clone BRALZ2011337	human	9606	30.2	30.2	78%	774	100.00	2396	AK126813.1
Homo sapiens 3 BAC RP11-274J15 (Roswell Park Cancer Institute...	human	9606	30.2	30.2	78%	774	100.00	170330	AC092896.9
Mus musculus chromosome 3, clone RP24-324K2, complete sequence	house m	10090	30.2	30.2	78%	774	100.00	161596	AC162036.4
Pan troglodytes clone rp43-111m15, complete sequence	chimpan	9598	30.2	30.2	78%	774	100.00	175281	AC092859.26
Zebrafish DNA sequence from clone DKEYP-78B3 in linkage group ...	zebrafi	7955	30.2	30.2	78%	774	100.00	186965	BX664612.15
Tetraodon nigroviridis full-length cDNA	spotted	99883	30.2	30.2	78%	774	100.00	576	CR714081.2
Human DNA sequence from clone RP5-832C2 on chromosome 1,...	human	9606	30.2	30.2	78%	774	100.00	87105	AL645728.31
Homo sapiens chromosome 11, clone RP11-889I17, complete sequence	human	9606	30.2	30.2	78%	774	100.00	170027	AC132217.15
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length...	house m	10090	30.2	30.2	78%	774	100.00	1888	AK041477.1
Human DNA sequence from clone RP5-1160K1 on chromosome 1,...	human	9606	30.2	30.2	78%	774	100.00	112911	AL355310.20
Homo sapiens chromosome 5 clone RP11-880E14, complete sequence	human	9606	30.2	30.2	78%	774	100.00	94993	AC117534.2
Homo sapiens chromosome 5 clone CTD-2131I18, complete sequence	human	9606	30.2	30.2	78%	774	100.00	112967	AC025177.6
Homo sapiens chromosome 5 clone CTC-276P9, complete sequence	human	9606	30.2	30.2	78%	774	100.00	178030	AC008406.7
Homo sapiens 13q14 chronic lymphocytic leukemia suppressor loc...	human	9606	30.2	30.2	78%	774	100.00	440917	AF440620.1
Human DNA sequence from clone RP11-78L19 on chromosome...	human	9606	30.2	30.2	78%	774	100.00	181541	AL136524.24
Human DNA sequence from clone RP11-554F11 on chromosome 10,...	human	9606	30.2	30.2	78%	774	100.00	43958	AL159172.16

Human DNA sequence from clone RP11-22L13 on chromosome 1,...	human	9606	30.2	30.2	78%	774	100.00	99477	AL590438.12
Drosophila melanogaster, chromosome 2R, region 54B-54B, BAC...	fruit f	7227	30.2	30.2	78%	774	100.00	161244	AC009535.9
Human DNA sequence from clone RP11-175B12 on chromosome 13,...	human	9606	30.2	30.2	78%	774	100.00	126427	AL161424.13
Human DNA sequence from clone RP1-127C7 on chromosome...	human	9606	30.2	30.2	78%	774	100.00	185832	AL137800.12
Human DNA sequence from clone RP3-384F21 on chromosome 1q24,...	human	9606	30.2	30.2	78%	774	100.00	96879	AL022171.1
Human DNA sequence from clone RP1-212G6 on chromosome...	human	9606	30.2	30.2	78%	774	100.00	156601	AL009172.1
Zebrafish DNA sequence from clone RP71-1O24 in linkage group 1...	zebrafi	7955	30.2	30.2	78%	774	100.00	133325	AL627423.27
Oryza sativa Japonica Group genomic DNA, chromosome 7, PAC...	Japanes	39947	30.2	30.2	78%	774	100.00	159980	AP005452.5
Zebrafish DNA sequence from clone CH211-214C7 in linkage group...	zebrafi	7955	30.2	30.2	78%	774	100.00	204893	BX511120.8
Homo sapiens chromosome 16 clone CTD-2519M14, complete sequence	human	9606	30.2	30.2	78%	774	100.00	185158	AC008732.9
Streptomyces coelicolor A3(2) complete genome; segment 7/29	NA	100226	30.2	30.2	78%	774	100.00	283100	AL939110.1
Mouse DNA sequence from clone RP23-414F19 on chromosome 13,...	house m	10090	30.2	30.2	78%	774	100.00	150424	AL645704.9
Homo sapiens chromosome 5 clone CTB-184C17, complete sequence	human	9606	30.2	30.2	78%	774	100.00	72259	AC027305.4
Mus musculus chromosome 3, clone RP24-283P8, complete sequence	house m	10090	30.2	30.2	78%	774	100.00	161178	AC102272.20
Mus musculus chromosome 3, clone RP23-86I19, complete sequence	house m	10090	30.2	30.2	78%	774	100.00	130155	AC165416.12
Mus musculus chromosome 3, clone RP24-434E24, complete sequence	house m	10090	30.2	30.2	78%	774	100.00	176948	AC123634.10
Mus musculus chromosome 19, clone RP24-210C4, complete sequence	house m	10090	30.2	30.2	78%	774	100.00	168235	AC137148.14
Mus musculus BAC clone RP23-397C5 from 5, complete sequence	house m	10090	30.2	30.2	78%	774	100.00	212387	AC132397.4
Zebrafish DNA sequence from clone DKEY-77F17 in linkage group...	zebrafi	7955	30.2	30.2	78%	774	100.00	139084	AL935332.12
Homo sapiens chromosome 8, clone RP11-18D5, complete sequence	human	9606	30.2	30.2	78%	774	100.00	103709	AC090135.13
Mouse DNA sequence from clone RP23-228L24 on chromosome X,...	house m	10090	30.2	30.2	78%	774	100.00	186645	AL807773.7

Mouse DNA sequence from clone RP23-163J20 on chromosome 2,...	house m	10090	30.2	30.2	78%	774	100.00	248940	AL669828.13
Human chromosome 14 DNA sequence BAC R-260M19 of library RPCI-...	human	9606	30.2	30.2	78%	774	100.00	174612	AL512357.4
Mouse DNA sequence from clone RP23-434F13 on chromosome 11,...	house m	10090	30.2	30.2	78%	774	100.00	187006	AL591436.8
Homo sapiens genomic DNA, chromosome 11q, clone:RP11-626H12,...	human	9606	30.2	30.2	78%	774	100.00	121600	AP003555.2
Homo sapiens genomic DNA, chromosome 11q, clone:RP11-805J14,...	human	9606	30.2	30.2	78%	774	100.00	169725	AP000879.4
Homo sapiens chromosome 4 clone C0236G06 map 4p16, complete...	human	9606	30.2	30.2	100%	774	94.74	189805	AC004169.3
Homo sapiens (subclone 1_b11 from P1 H54) DNA sequence, comple...	human	9606	30.2	30.2	78%	774	100.00	3660	L81688.1
Mycobacterium tuberculosis sequence from clone y348	NA	1773	30.2	30.2	78%	774	100.00	40056	AD000020.1

SELEZIONE DI ALLINEAMENTI SIGNIFICATIVI

PREDICTED: Canis lupus familiaris zinc finger protein 7 (ZNF7), transcript variant X10, mRNA
Sequence ID: XM_038685417.1Length: 4695Number of Matches: 1
Range 1: 3286 to 3302 GenBank Graphics

```
Score           Expect  Identities        Gaps        Strand


34.2 bits(17)  50     17/17(100%)  0/17(0%)  Plus/Plus


Query  2      CGTCCTGGACTCACCAC  18

              |||||||||||||||||

Sbjct  3286  CGTCCTGGACTCACCAC  3302
```

Zinc finger protein 7 (ZNF7)

La **proteina 7 del dito di zinco** è una proteina che nell'**uomo** è codificata dal **gene ZNF7**. **ZNF7** ha dimostrato di interagire con **RPL7** (**Proteina ribosomiale L7** o **Proteina ribosomiale 60S L7**) (https://en.wikipedia.org/wiki/ZNF7). I **ribosomi**, gli organelli che catalizzano la sintesi proteica, sono costituiti da una **piccola subunità 40S** e da una **grande subunità 60S**. **Insieme queste subunità** sono composte da **4 specie di RNA e circa 80 proteine strutturalmente distinte**. **Questo gene codifica per una proteina ribosomiale che è un componente della subunità 60S**. La proteina appartiene alla famiglia delle **proteine ribosomiali L30P**. Contiene un dominio simile alla **cerniera della leucina** della regione di base N-terminale (BZIP) e il sottomotivo di consenso RNP RNP2. In vitro il dominio simile a BZIP media l'omodimerizzazione e il legame stabile al DNA e all'RNA, con una preferenza per l'rRNA 28S e l'mRNA (https://en.wikipedia.org/wiki/60S_ribosomal_protein_L7; https://www.genecards.org/cgi-bin/carddisp.pl?gene=RPL7). *La proteina può inibire la **traduzione senza cellule degli mRNA*** (https://www.promega.com/-/media/files/resources/product-guides/proteomics/cell-free-protein-expression-systems.pdf?la=en#:~:text=Cell%2Dfree%20translation%20systems%20are,such%20as%20display%20tech%2D%20nologies), *suggerendo che svolge un ruolo regolatore nell'apparato di traduzione*. **Si trova nel citoplasma**. La proteina ha dimostrato di essere un **autoantigene in pazienti con malattie autoimmuni sistemiche, come il lupus eritematoso sistemico**. Come è tipico per i geni che codificano per proteine ribosomiali, ci sono più **pseudogeni** elaborati di questo gene dispersi attraverso il genoma. **Le malattie associate a RPL7 includono la malattia del collagene** e la **malattia autoimmune sistemica**. Tra i suoi ***percorsi correlati*** vi sono il **metabolismo delle proteine** e il **ciclo di vita dell'HIV** (https://en.wikipedia.org/wiki/60S_ribosomal_protein_L7; https://www.genecards.org/cgi-bin/carddisp.pl?gene=RPL7). Un importante **paralogo** di questo gene è **RPL7L1** (*Ribosomal Protein L7 Like 1* è un gene che codifica per proteine. **Le malattie associate a RPL7L1 includono la malattia di Charcot-Marie-Tooth, Axonal, di tipo 2N** (https://www.malacards.org/card/charcot_marie_tooth_disease_axonal_type_2n).

Nell'articolo intitolato "***Specific Interactions of the Autoantigen L7 with Multi-zinc Finger Protein ZNF7 and Ribosomal Protein S7***" (Interazioni specifiche dell'autoantigene L7 con la proteina multizinco Finger ZNF7 e la proteina ribosomiale S7), **Stephan Witte** e **Ulrich Krawinkel** spiegano che "***ZNF7 è una proteina multi-zinco simile a un fattore di trascrizione** composta da 687 amminoacidi e ha una massa molecolare prevista di 78 kDa. È ampiamente espresso in varie linee cellulari. La proteina è costituita da 15 C_2H_2 domini a dita di zinco che comprendono quasi il 70% della proteina. I domini delle dita condividono il 70% di somiglianza di sequenza e si conformano quasi esattamente alla sequenza consenso delle dita di zinco che legano il DNA e l'RNA. Oltre alle proprietà di legame degli acidi nucleici dei domini a dita di zinco, sono state riportate interazioni proteiche mediate dalle dita di zinco, compresa l'interazione di un dominio a dita di zinco con un motivo a cerniera di leucina. Tuttavia, restano da specificare le interfacce responsabili dell'interazione di L7 e ZNF7. **La localizzazione cellulare di ZNF7 è sconosciuta, sebbene sia stata suggerita una localizzazione nucleare**. Tuttavia, non è stata esclusa una* *localizzazione nel citoplasma e mostriamo in questo studio che* ***ZNF7 co-purifica con ribosomi eucariotici***. ***Ciò suggerisce una localizzazione ribosomiale di ZNF7, dove può agire come regolatore traslazionale***. *Inoltre, è stato recentemente dimostrato che ZNF7 è un substrato della proteina chinasi attivata da mitogeni* in vitro, *suggerendo un* ***ruolo nelle vie di trasduzione del segnale***. *Tuttavia, non è noto se la fosforilazione di ZNF7 mediata dalla proteina chinasi attivata da mitogeni influenzi il legame di ZNF7 a L7* in vivo.” (https://www.jbc.org/article/S0021-9258(19)65686-3/fulltext). Il gene **ZNF7** è conservato nell’**uomo**, nello scimpanzé, nella scimmia Rhesus, nella mucca, nel topo e nel ratto. 125 organismi hanno ortologhi con il gene umano ZNF7. Nell’**Homo Sapiens**, il gene **ZNF7** ha un’espressione ubiquitaria nei **testicoli**, nell’**endometrio** e in **altri 25 tessuti** (https://www.ncbi.nlm.nih.gov/gene/475129).

Le **nucleasi a dita di zinco (ZFN)** sono enzimi di restrizione artificiali generati dalla fusione di un *dominio di legame del DNA a dita di zinco* con un *dominio di scissione del DNA*. I domini a dita di zinco possono essere progettati per mirare a specifiche sequenze di DNA desiderate e ciò consente alle nucleasi a dita di zinco di indirizzare sequenze uniche all’interno di genomi complessi. *Sfruttando i macchinari endogeni per la riparazione del DNA,* ***questi reagenti possono essere utilizzati per alterare con precisione i genomi di organismi superiori***. *Insieme a CRISPR/Cas9 e TALEN, ZFN è uno strumento importante nel campo dell’editing del genoma* (https://en.wikipedia.org/wiki/Zinc_finger_nuclease). *Le nucleasi a dita di zinco sono utili per manipolare i genomi di molte piante e animali e vari tipi di cellule di mammifero*. Le nucleasi a dito di zinco sono state utilizzate anche in un ***modello murino di emofilia*** e uno studio clinico ha rilevato che ***le cellule T umane CD4+ con il gene CCR5 interrotto dalle nucleasi a dita di zinco sono sicure come potenziale trattamento per l’HIV/AIDS***. **Gli ZFN sono utilizzati anche per creare una nuova generazione di modelli di malattie genetiche chiamati modelli isogeni di malattie umane** e per riscrivere la sequenza di un allele invocando il **meccanismo di ricombinazione omologa (HR)** per riparare il DSB usando il frammento di DNA fornito come stampo. Il macchinario HR ricerca l’omologia tra il cromosoma danneggiato e il frammento extra-cromosomico e copia la sequenza del frammento tra le due estremità rotte del cromosoma, *indipendentemente dal fatto che il frammento contenga la sequenza originale*. Se il soggetto è omozigote per l’allele bersaglio, l’efficienza della tecnica è ridotta poiché la copia non danneggiata dell’allele può essere utilizzata come modello per la riparazione invece del frammento fornito (https://en.wikipedia.org/wiki/Zinc_finger_nuclease). *Gli* ***ZFN*** *possono essere utilizzati per disabilitare le mutazioni dominanti in individui eterozigoti producendo rotture del doppio filamento (DSB) nel DNA nell’allele mutante, che, in assenza di uno stampo di* ***unione delle estremità non omologhe (NHEJ)****, sarà riparato da cellule non omologhe*. **Se i domini a dita di zinco non sono sufficientemente specifici per il loro sito bersaglio** o **non mirano a un sito univoco all’interno del genoma di interesse**, **può verificarsi una scissione fuori bersaglio**. Tale scissione fuori bersaglio può portare alla produzione di ***sufficienti rotture del doppio filamento da sopraffare il meccanismo di riparazione*** e, di conseguenza, produrre **riarrangiamenti cromosomici e/o morte cellulare**. **Eventi di scissione fuori bersaglio possono anche promuovere l’integrazione casuale del DNA del donatore** (https://en.wikipedia.org/wiki/Zinc_finger_nuclease). In alcuni casi, tuttavia, la riparazione è imperfetta, con conseguente cancellazione o inserimento di coppie di basi, producendo un frame-shift e impedendo la produzione della proteina dannosa. *È anche possibile utilizzare più coppie di ZFN per rimuovere completamente interi grandi segmenti di sequenza genomica*. Gli ZFN sono stati utilizzati anche per **modificare gli alleli che causano malattie nei disordini ripetuti di triplette**. Sono stati progettati specifici motivi a dita di zinco per riconoscere sequenze di DNA distinte. L’mRNA codificante ZFN è stato iniettato in embrioni unicellulari e un’alta percentuale di animali portava le mutazioni e i fenotipi desiderati. Gli ZFN possono creare in modo specifico ed efficiente **alleli mutanti ereditabili nei loci di interesse nella linea germinale e gli alleli indotti da ZFN possono essere propagati nelle generazioni successive** (https://en.wikipedia.org/wiki/Zinc_finger_nuclease). **Il gene kdr nel pesce zebra codifica per il recettore del fattore di crescita endoteliale vascolare-2**. Le *lesioni mutagene in questo sito bersaglio sono state indotte utilizzando la tecnica ZFN*. La tecnica ZFN consente la generazione diretta di *una serie allelica mirata di mutanti*; *non si basa sull’esistenza di linee di cellule staminali embrionali specie-specifiche ed è applicabile ad altri vertebrati*, in particolare quelli i cui

embrioni sono facilmente disponibili; infine, è anche possibile **ottenere knock-in mirati in zebrafish, quindi è possibile creare modelli di malattie umane finora inaccessibili** (https://en.wikipedia.org/wiki/Zinc_finger_nuclease). Riguardo l'uso degli ***ZFN nella terapia genica***, **il successo dipende dall'efficace inserimento di geni terapeutici in un appropriato sito bersaglio cromosomico all'interno del genoma umano**, **senza causare danno cellulare, mutazioni oncogene o una risposta immunitaria**. La costruzione di **vettori plasmidici** è semplice e diretta. L'approccio basato sul plasmide che codifica ZFN ha il potenziale per *aggirare tutti i problemi associati alla* ***somministrazione virale di geni terapeutici***. **Come per molte proteine estranee inserite nel corpo umano, esiste il rischio di una risposta immunologica contro l'agente terapeutico e le cellule in cui è attivo. Poiché la proteina deve essere espressa solo transitoriamente, tuttavia, il tempo in cui può svilupparsi una risposta è breve** (https://en.wikipedia.org/wiki/Zinc_finger_nuclease). Gli **ZNF** potrebbero anche agire come *reclutatori di modificatori della cromatina*, come *cofattori* o come *proteine strutturali coinvolte nella migrazione e invasione cellulare*. In particolare, **il ruolo degli ZNF nello sviluppo, nella progressione e nelle metastasi del cancro** sta diventando un argomento di ricerca interessante (https://www.nature.com/articles/cddiscovery201771). La natura modulare del motivo del dito di zinco consente di legare un gran numero di **combinazioni di sequenze di DNA e RNA con un alto grado di affinità e specificità**, ed è quindi **ideale per proteine di ingegneria che possono essere mirate e legare sequenze di DNA specifiche** (https://en.wikipedia.org/wiki/Zinc_finger).
Lo **ione Zinco** e le **proteine Zinc Finger** sono state già citate rispettivamente nel Capitolo III e IV di questo documento. Allo stesso modo, le **proteine Zinc Finger** sono state oggetto approfondito di studio in "I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis" (Si vedano le pagine 189, 230, 232, 238, 248 e 255). A tal proposito, i motivi a **dito di zinco**, sono stati identificati anche tra gli *allineamenti significativi* [*Egretta garzetta zinc finger protein 639 (ZNF639), transcript variant X1, X2 and X3, mRNA*] della sequenza di RNA "**GTGAAATGGTTATGTGTGGCGG**" del *RdRp Gene del "Bat coronavirus BM48-31/BGR/2008, complete genome"*. La sequenza "**GTGAAATGGTTATGTGTGGCGG**" è una delle due sequenze del **gene RdRp** (*RNA polimerasi RNA dipendente*, il motore del processo di **trascrizione** del *SARS-CoV-2*) i cui allineamenti significativi delle ricerche BLAST idenficano il ***Pipistrello*** e il ***Pangolino*** (***Malese*** e ***Cinese***). Questa sequenza è importante perché essa è quasi totalmente identica alla sequenza "**GTGAAATGGTCATGTGTGGCGG**", la sequenza di RNA oggetto di studio del documento "**I Misteri del Dna** (**Parte Prima)**".

PREDICTED: Condylura cristata zinc finger with KRAB and SCAN domains 8 (ZKSCAN8), mRNA

Sequence ID: XM_012734646.1Length: 6917Number of Matches: 1

Related Information
Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 860 to 875 GenBank Graphics

```
Score          Expect  Identities      Gaps        Strand


32.2 bits(16)  196     16/16(100%)  0/16(0%)  Plus/Minus


CDS: Putative 1       5        R   S   E   G   G

Query                 4      TCCTGGACTCACCACC   19

                             ||||||||||||||||

Sbjct                 875    TCCTGGACTCACCACC   860

CDS:PREDICTED: zinc   263      R   S   E   G   G
```

/prodotto="zinc finger protein with KRAB and SCAN domains 8"

Il **dominio SCAN è un motivo di 84 residui** altamente conservato che si trova vicino all'N-terminale di una sottofamiglia di **proteine a dita di zinco C_2H_2**. Il dominio SCAN, noto anche come **regione ricca di leucina (LeR)**, funziona come dominio di interazione proteica, mediando l'autoassociazione o l'associazione selettiva con altre proteine (https://www.ncbi.nlm.nih.gov/books/NBK6264/; https://www.uniprot.org/uniprot/Q15776; https://www.nextprot.org/entry/NX_Q15776/; https://pubmed.ncbi.nlm.nih.gov/19887448/). **Urrutia**, nel riassunto del suo articolo intitolato *R. KRAB-containing zinc-finger repressor proteins* [Genome Biol 4, 231 (2003). https://doi.org/10.1186/gb-2003-4-10-231], afferma: "**La più grande famiglia di fattori di trascrizione a dita di zinco comprende quelli contenenti la scatola associata a Krüppel (o dominio KRAB)**, che sono presenti solo nei vertebrati tetrapodi…...Il dominio KRAB, che si trova nella *regione ammino-terminale delle proteine*, si comporta come un **dominio repressore trascrizionale legandosi alle proteine corepressori**, mentre il **dominio motivi a dita di zinco C_2H_2 legano il DNA**. Le funzioni attualmente note per i **membri della famiglia di proteine contenenti KRAB includono la repressione trascrizionale dei promotori della RNA polimerasi I, II e III, il legame e lo splicing dell'RNA e il controllo della funzione del nucleolo**. **I membri della famiglia sono coinvolti nel mantenimento del nucleolo, nella differenziazione cellulare, nella proliferazione cellulare, nell'apoptosi e nella trasformazione neoplastica** (https://genomebiology.biomedcentral.com/articles/10.1186/gb-2003-4-10-231).

PREDICTED: Glycine soja zinc finger CCCH domain-containing protein 38-like (LOC114415771), transcript variant X2, mRNA

Sequence ID: XM_028380610.1Length: 5420Number of Matches: 1

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Range 1: 2170 to 2184 GenBank Graphics

```
Score            Expect  Identities       Gaps        Strand


30.2 bits(15)  774    15/15(100%)  0/15(0%)  Plus/Minus


Query  5     CCTGGACTCACCACC  19
             |||||||||||||||
Sbjct  2184  CCTGGACTCACCACC  2170
```

Zinc finger CCCH domain-containing protein 38-like

PREDICTED: Pteropus vampyrus zinc finger protein 74 (ZNF74), transcript variant X6, mRNA

Sequence ID: XM_023528269.1Length: 2995Number of Matches: 1

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Range 1: 2434 to 2448 GenBank Graphics

```
Score            Expect  Identities       Gaps        Strand


30.2 bits(15)  774    15/15(100%)  0/15(0%)  Plus/Plus


Query  4     TCCTGGACTCACCAC  18
             |||||||||||||||
Sbjct  2434  TCCTGGACTCACCAC  2448
```

Zinc finger protein 74 (ZNF74)

Zinc finger protein 74 è una proteina che nell'uomo è codificata dal gene **ZNF74**. La **suscettibilità alla schizofrenia** è stata associata a una mutazione in questa proteina. ZNF74 ha dimostrato di interagire con **POLR2A** (https://en.wikipedia.org/wiki/ZNF74). **La subunità RPB1 della RNA polimerasi II diretta dal DNA** , nota anche come **RPB1** , è un enzima che nell'uomo è codificato dal **gene *POLR2A***. Questo gene codifica per la **subunità più grande della RNA polimerasi II**, la polimerasi responsabile della sintesi dell'RNA messaggero negli eucarioti (https://en.wikipedia.org/wiki/POLR2A). **Urrutia** in *R. KRAB-containing zinc-finger repressor proteins* [Genome Biol 4, 231 (2003). https://doi.org/10.1186/gb-2003-4-10-231], afferma: "Lo **Znf74 umano** si trova in strutture granulari discrete nel nucleo, è strettamente associato alla matrice nucleare, si lega all'RNA e interagisce con l'RNA polimerasi II. Questa proteina contenente KRAB contiene un dominio KRAB A troncato e 12 diversi C_2H_2 motivi a dita di zinco che sono sufficienti per indirizzare la proteina alla matrice nucleare e per il legame dell'RNA. Inoltre, Znf74 interagisce con la forma iperfosforilata della RNA polimerasi II e colocalizza con essa in domini nucleari che sono arricchiti in fattori di splicing. Questi risultati suggeriscono che Znf74 può regolare l'espressione genica attraverso meccanismi sia trascrizionali che post-trascrizionali. KS1, che ha dieci domini zinc-finger ed entrambi i box KRAB A e B, è un forte repressore dell'attività della RNA polimerasi mediante il meccanismo mediato da Kap1 descritto di seguito. **KS1 è anche un soppressore della trasformazione neoplastica che è mediata da diversi oncogeni.**".

PREDICTED: Chenopodium quinoa zinc finger MYM-type protein 1-like (LOC110713585), mRNA
Sequence ID: XM_021892034.1Length: 1350Number of Matches: 1

Related Information

Gene-associated gene details
Genome Data Viewer-aligned genomic context
Range 1: 1295 to 1309 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	774	15/15(100%)	0/15(0%)	Plus/Plus

```
CDS: Putative 1        1         P   G   L   T
Query                  3      GTCCTGGACTCACCA   17
                              |||||||||||||||
Sbjct                  1295   GTCCTGGACTCACCA   1309
CDS:zinc finger MYM-   432    G   P   G   L   T
```

/prodotto="zinc finger MYM-type protein 1-like"

Zinc Finger MYM-type protein 1-like

Le **dita di zinco di tipo MYM** sono state identificate nelle **proteine della famiglia MYM**. La proteina umana Q14202 è coinvolta in una traslocazione cromosomica e può essere responsabile del ritardo legato all'X in XQ13.1 . Q9UBW7 è anche coinvolto nella malattia. Nelle **malattie mieloproliferative** è fuso al *recettore 1 dell'FGF*; nelle **malattie mieloproliferative atipiche** è riarrangiato. I membri della famiglia in genere sono coinvolti nello sviluppo. Questo **dominio Zn-finger** funziona come un **trans-attivatore trascrizionale dei geni virali tardivi del vaccino** e **gli ortologhi si trovano anche in tutti i grandi virus a DNA nucleocitoplasmatico, NCLDV**. Questo dominio si trova anche fuso ai terminali C delle ricombinasi da alcuni trasposoni procarioti (https://www.ebi.ac.uk/interpro/entry/InterPro/IPR010507/).

PREDICTED: Chinchilla lanigera zinc finger protein 3 (Znf3), transcript variant X5, mRNA

Sequence ID: XM_005413761.2Length: 2573Number of Matches: 1

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Range 1: 370 to 384 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	774	15/15(100%)	0/15(0%)	Plus/Minus

```
CDS: Putative 1        4       R   S   E   G
Query                  3     GTCCTGGACTCACCA   17
                             |||||||||||||||
Sbjct                  384   GTCCTGGACTCACCA   370
CDS:PREDICTED: zinc    60    T   R   S   E   G
```

/prodotto="zinc finger protein 3 isoform X2"

PREDICTED: Lepeophtheirus salmonis zinc finger protein ubi-d4 A-like (LOC121121892), transcript variant X1, mRNA

Sequence ID: XM_040716884.1Length: 1831Number of Matches: 1

Range 1: 884 to 898 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	774	15/15(100%)	0/15(0%)	Plus/Plus

```
CDS: Putative 1        1      R   P   G   L   T
Query                  2     CGTCCTGGACTCACC   16
                             |||||||||||||||
Sbjct                  884   CGTCCTGGACTCACC   898
CDS:zinc finger prot   256    R   P   G   L   T
```

/prodotto="zinc finger protein ubi-d4 A-like isoform X1"

PREDICTED: Rousettus aegyptiacus zinc finger protein 74 (ZNF74), transcript variant X4, mRNA

Sequence ID: XM_036221079.1Length: 5233Number of Matches: 1

Range 1: 2892 to 2906 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	774	15/15(100%)	0/15(0%)	Plus/Plus

```
Query  4      TCCTGGACTCACCAC  18
              |||||||||||||||
Sbjct  2892   TCCTGGACTCACCAC  2906
```

Homo sapiens CXXC finger protein 1 pseudogene 1 (CXXC1P1), RefSeqGene on chromosome X
Sequence ID: NG_028296.1Length: 36438Number of Matches: 1

Range 1: 20086 to 20100 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	774	15/15(100%)	0/15(0%)	Plus/Minus

```
Query  3      GTCCTGGACTCACCA  17
              |||||||||||||||
Sbjct  20100  GTCCTGGACTCACCA  20086
```

CXXC finger protein 1 pseudogene 1 (CXXC1P1)

Questo gene è sovraespresso nell'**Ovaio** e nei **Testicoli**.

This gene is overexpressed in **Ovary** and **Testis**.

https://www.gtexportal.org/home/gene/CXXC1P1

https://www.ncbi.nlm.nih.gov/gene/392459

https://www.genecards.org/cgi-bin/carddisp.pl?gene=CXXC1P1

https://www.genenames.org/data/gene-symbol-report/#!/hgnc_id/HGNC:27864

http://atlasgeneticsoncology.org/Genes/GC_CXXC1P1.html

https://en.wikipedia.org/wiki/Msh_homeobox_2 ? guarda anche le interazioni

https://www.genecards.org/cgi-bin/carddisp.pl?gene=RAB43

6.2 LA SEQUENZA "AES (3)" E I RISULTATI DELLA RICERCA BLAST

Quella mostrata qui di seguito è la sequenza totale del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*.

C TCGAGCTGGT ACTGCATGCA 3900
CGCAATGCTA GCTGCCCCTT TC**CCGTCCTG GGTACCCCGA GTCTCCCCCG 3950**
ACCTCGGGTC CCAGGTATGC TCCCACCTCC ACCTGCCCCA CTCACCACCT 4000
CTGCTAGTTC CAGACACCTC CCAAGCACGC AGCAATGCAG CTCAAAACGC 4050
TTAGCCTAGC CACACCCCCA CGGGAAACAG CAGTGATTAA CCTTTAGCAA 4100
TAAACGAAAG TTTAACTAAG CTATACTAAC CCCAGGGTTG GTCAATTTCG 4150
TGCCAGCCAC ACCCTGGAGC TAGC

Le **lettere nere in grassetto** sono le lettere poste tra i **DUE spezzoni di sequenza** che costituiscono la **Sequenza "ZINC FINGER"** (la sequenza discussa nel paragrafo precedente). La sequenza **Query** (**CCGTCCTGGGTACCCCGAGTCTCCCCC GACCTCGGGTCCCAGGTATGCTCCCACCTCCACCTGCCCCACTCACCACC**) mostrata sotto è formata dai due segmenti della **Sequenza "ZINC FINGER"** e dalle lettere che li dividono. Questa nuova sequenza è stata definita **Sequenza "AES(3)"** (***A**mino-terminal **E**nhancer of **S**plit* *o potenziatore ammino-terminale dell'mRNA diviso*. Per il significato di **AES** si rimanda allo studio del Capitolo II di questo documento). Questa sequenza è stata sottoposta ad una ricerca BLAST e nelle pagine seguenti sono mostrati gli *allineamenti significativi* ottenuti e gli "**organismi**" e i "**prodotti**" a cui tali allineamenti si riferiscono. **I risultati dei "prodotti" identificati dalla ricerca BLAST sono coerenti** (ovvero l'atteso ***A**mino-terminal **E**nhancer of **S**plit*, uno dei componenti principali del *3'-UTR del Vaccino Sars-Cov-2 mRNA BioNTech/Pfizer*) **con quanto dichiarato nel documento scaricato dalla WHO** (https://berthub.eu/articles/11889.doc), documento relativo al "codice sorgente" integrale del Vaccino mRNA Sars-Cov-2 BioNTech/Pfizer (BNT162b2). In altri termini, le **sorprese** mostrate nel paragrafo precedente dalla ricerca BLAST su alcune parti costituenti la **Sequenza "AES(3)"** (le parti corrispondenti alla **Sequenza "ZINC FINGER"**) emergono **SOLO** se alcuni elementi costitutivi della stessa (le **lettere in grassetto**) vengono omessi, ottenendo così la **Sequenza "ZINC FINGER"**.

QUERY: **CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCA
CCTCCACCTGCCCCACTCACCACC**

Search Parameters

Program	blastn
Word size	28
Expect value	0.05
Hitlist size	**5000**
Match/Mismatch scores	1,-2
Gapcosts	0,2.5
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

SEQUENCES SELECTED: 39

Description	Name	Taxid	Score	Score	cover	Value	Ident	Len	Accession
Homo sapiens gp130 associated protein GAM mRNA, complete cds	human	9606	134	134	100%	9,00E-28	97.40	1317	AF072902.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	132	132	100%	3,00E-27	97.40	1805	XM_034945921.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	132	132	100%	3,00E-27	97.40	1808	XM_034945920.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	132	132	100%	3,00E-27	97.40	1731	XM_034945919.1
PREDICTED: Pan paniscus TLE family member 5, transcriptional...	pygmy chimpa...	9597	132	132	100%	3,00E-27	97.40	1891	XM_034945918.1
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	132	132	100%	3,00E-27	97.40	1798	NM_001130.6
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	132	132	100%	3,00E-27	97.40	1795	NM_198970.2
Eukaryotic synthetic construct chromosome 19	NA	111789	132	264	100%	3,00E-27	97.40	64242768	CP034522.1
Eukaryotic synthetic construct chromosome 19	NA	111789	132	264	100%	3,00E-27	97.40	64242768	CP034497.1
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	132	132	100%	3,00E-27	97.40	1512	XM_016937029.2
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	132	132	100%	3,00E-27	97.40	1683	XM_016937028.2
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	132	132	100%	3,00E-27	97.40	1693	XM_016937027.2
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	132	132	100%	3,00E-27	97.40	1888	XM_024351913.1
PREDICTED: Pan troglodytes amino-terminal enhancer of split...	chimpanzee	9598	132	132	100%	3,00E-27	97.40	1891	XM_024351912.1
PREDICTED: Homo sapiens TLE family member 5, transcriptional...	human	9606	132	132	100%	3,00E-27	97.40	1881	XM_006722664.1
Homo sapiens DNA, chromosome 19, nearly complete genome	human	9606	132	132	100%	3,00E-27	97.40	59105444	AP023479.1
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	132	132	100%	3,00E-27	97.40	17057	NG_029870.1
Homo sapiens cDNA clone IMAGE:3464459, **** WARNING: chimeric...	human	9606	132	132	100%	3,00E-27	97.40	2395	BC040415.1
Homo sapiens cDNA clone IMAGE:4120426, **** WARNING: chimeric...	human	9606	132	132	100%	3,00E-27	97.40	3387	BC007797.1
Homo sapiens TLE family member 5, transcriptional modulator...	human	9606	132	132	100%	3,00E-27	97.40	1754	NM_198969.1
Homo sapiens cDNA FLJ37835 fis, clone BRSSN2010110, weakly...	human	9606	132	132	100%	3,00E-27	97.40	3276	AK095154.1

Homo sapiens cDNA FLJ37272 fis, clone BRAMY2012091, highly...	human	9606	132	132	100%	3,00E-27	97.40	1884	AK094591.1
Homo sapiens PP2150 mRNA, complete cds	human	9606	132	132	100%	3,00E-27	97.40	1035	AF269289.1
Homo sapiens chromosome 19, cosmid F23613, complete sequence	human	9606	132	132	100%	3,00E-27	97.40	42301	AC005944.1
Human homolog of Drosophila enhancer of split m9/m10 mRNA,...	human	9606	132	132	100%	3,00E-27	97.40	1288	U04241.1
PREDICTED: Hylobates moloch TLE family member 5, transcription...	silvery gibbon	81572	126	126	100%	2,00E-25	96.10	1672	XM_032176817.1
PREDICTED: Gorilla gorilla gorilla TLE family member 5,...	western lowl...	9595	126	126	100%	2,00E-25	96.10	1586	XM_031007483.1
PREDICTED: Gorilla gorilla gorilla TLE family member 5,...	western lowl...	9595	126	126	100%	2,00E-25	96.10	1804	XM_031007481.1
PREDICTED: Gorilla gorilla gorilla TLE family member 5,...	western lowl...	9595	126	126	100%	2,00E-25	96.10	1807	XM_031007480.1
PREDICTED: Nomascus leucogenys TLE family member 5,...	northern whi...	61853	126	126	100%	2,00E-25	96.10	1839	XM_030795556.1
Homo sapiens chromosome 19 groucho protein homolog (AES) gene,...	human	9606	126	126	100%	2,00E-25	96.10	12683	AH007143.2
Homo sapiens isolate CHM13 chromosome 19	human	9606	126	126	100%	2,00E-25	96.10	61707364	CP068259.2
PREDICTED: Piliocolobus tephrosceles TLE family member 5,...	Ugandan red ...	591936	111	111	100%	4,00E-21	92.50	1796	XM_026455495.2
PREDICTED: Trachypithecus francoisi TLE family member 5,...	Francois's l...	54180	100	100	100%	9,00E-18	90.00	1752	XM_033199976.1
PREDICTED: Trachypithecus francoisi TLE family member 5,...	Francois's l...	54180	100	100	100%	9,00E-18	90.00	1877	XM_033199975.1
PREDICTED: Trachypithecus francoisi TLE family member 5,...	Francois's l...	54180	100	100	100%	9,00E-18	90.00	1876	XM_033199974.1
PREDICTED: Trachypithecus francoisi TLE family member 5-like...	Francois's l...	54180	95.3	95.3	100%	4,00E-16	88.75	1344	XM_033189604.1
PREDICTED: Rhinopithecus bieti amino-terminal enhancer of spli...	black snub-n...	61621	95.3	95.3	100%	4,00E-16	88.75	1747	XM_017847996.1
PREDICTED: Rhinopithecus bieti amino-terminal enhancer of spli...	black snub-n...	61621	95.3	95.3	100%	4,00E-16	88.75	1653	XM_017847995.1

SELEZIONE DI ALLINEAMENTI SIGNIFICATIVI

Homo sapiens gp130 associated protein GAM mRNA, complete cds

Sequence ID: AF072902.1Length: 1317Number of Matches: 1

Related Information Gene-associated gene details GEO Profiles-microarray expression data
PubChem BioAssay-bioactivity screening
Range 1: 1094 to 1170 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
134 bits(72)	9e-28	75/77(97%)	0/77(0%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1094  CCGTCCTGGGNACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1153

Query  61    CTGCCCCACTCACCACC  77
             |||||||||||||||||
Sbjct  1154  CTGCCCCACTCACCACC  1170
```

PREDICTED: Pan paniscus TLE family member 5, transcriptional modulator (TLE5), transcript variant X4, mRNA

Sequence ID: XM_034945921.1Length: 1805Number of Matches: 1

Range 1: 1321 to 1397 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1321  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1380

Query  61    CTGCCCCACTCACCACC  77
             |||||||||||||||||
Sbjct  1381  CTGCCCCACTCACCACC  1397
```

Homo sapiens TLE family member 5, transcriptional modulator (TLE5), transcript variant 2, mRNA

Sequence ID: NM_001130.6Length: 1798Number of Matches: 1

Related Information Gene-associated gene details PubChem BioAssay-bioactivity screening
Genome Data Viewer-aligned genomic context
Range 1: 1313 to 1389 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1313  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1372
```

```
Query  61    CTGCCCCACTCACCACC  77
             |||||||||||||||||
Sbjct  1373  CTGCCCCACTCACCACC  1389
```

Eukaryotic synthetic construct chromosome 19

Sequence ID: CP034522.1Length: 64242768Number of Matches: 2

Range 1: 2993317 to 2993393 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Minus

```
Query  1        CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
                |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  2993393  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  2993334

Query  61       CTGCCCCACTCACCACC  77
                |||||||||||||||||
Sbjct  2993333  CTGCCCCACTCACCACC  2993317
```

Range 2: 61383187 to 61383263 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Minus

```
Query  1         CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
                 |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  61383263  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  61383204

Query  61        CTGCCCCACTCACCACC  77
                 |||||||||||||||||
Sbjct  61383203  CTGCCCCACTCACCACC  61383187
```

PREDICTED: Pan troglodytes amino-terminal enhancer of split (AES), transcript variant X6, mRNA

Sequence ID: XM_016937029.2Length: 1512Number of Matches: 1

Related Information Gene-associated gene details Genome Data Viewer-aligned genomic context
Range 1: 1028 to 1104 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1028  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1087
```

```
Query  61    CTGCCCCACTCACCACC  77
             |||||||||||||||||
Sbjct  1088  CTGCCCCACTCACCACC  1104
```

Homo sapiens DNA, chromosome 19, nearly complete genome

Sequence ID: AP023479.1Length: 59105444Number of Matches: 1

Range 1: 2910579 to 2910655 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Minus

```
Query  1        CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
                |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  2910655  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  2910596

Query  61       CTGCCCCACTCACCACC  77
                |||||||||||||||||
Sbjct  2910595  CTGCCCCACTCACCACC  2910579
```

Homo sapiens cDNA clone IMAGE:3464459, **** WARNING: chimeric clone ****

Sequence ID: BC040415.1Length: 2395Number of Matches: 1

Related Information GEO Profiles-microarray expression data
Range 1: 1232 to 1308 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Minus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1308  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1249

Query  61    CTGCCCCACTCACCACC  77
             |||||||||||||||||
Sbjct  1248  CTGCCCCACTCACCACC  1232
```

Homo sapiens cDNA clone IMAGE:4120426, **** WARNING: chimeric clone ****

Sequence ID: BC007797.1Length: 3387Number of Matches: 1

Related Information
GEO Profiles-microarray expression data
Range 1: 3133 to 3209 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  3133  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  3192
```

```
Query  61    CTGCCCCACTCACCACC  77
             |||||||||||||||||
Sbjct  3193  CTGCCCCACTCACCACC  3209
```

Homo sapiens cDNA FLJ37835 fis, clone BRSSN2010110, weakly similar to GRG PROTEIN

Sequence ID: AK095154.1Length: 3276Number of Matches: 1

Related Information Gene-associated gene details PubChem BioAssay-bioactivity screening
Range 1: 2791 to 2867 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  2791  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  2850

Query  61    CTGCCCCACTCACCACC  77
             |||||||||||||||||
Sbjct  2851  CTGCCCCACTCACCACC  2867
```

Weakly similar to GRG PROTEIN (debolmente simile alla PROTEINA GRG)

(https://www.prospecbio.com/aes_human)

Homo sapiens cDNA FLJ37272 fis, clone BRAMY2012091, highly similar to Homo sapiens amino-terminal enhancer of split (AES), transcript variant 1, mRNA

Sequence ID: AK094591.1Length: 1884Number of Matches: 1

Related Information Gene-associated gene details PubChem BioAssay-bioactivity screening
Range 1: 1400 to 1476 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1400  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1459

Query  61    CTGCCCCACTCACCACC  77
             |||||||||||||||||
Sbjct  1460  CTGCCCCACTCACCACC  1476
```

Homo sapiens PP2150 mRNA, complete cds

Sequence ID: AF269289.1Length: 1035Number of Matches: 1

Related Information Gene-associated gene details GEO Profiles-microarray expression data
PubChem BioAssay-bioactivity screening
Range 1: 707 to 783 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Plus

```
CDS: Putative 1        1      P  S  W  V  P  R  V  S  P  D  L  G  S  Q  V  C  S  H  L  H
Query                  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
                             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct                  707   CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  766
CDS:unknown [Homo sa   51     P  S  W  A  P  R  V  S  P  D  P  G  S  Q  V  C  S  H  L  H

CDS: Putative 1        21     L  P  H  S  P  P
Query                  61    CTGCCCCACTCACCACC  77
                             |||||||||||||||||
Sbjct                  767   CTGCCCCACTCACCACC  783
CDS:unknown [Homo sa   71     L  P  H  S  P  P
```

Homo sapiens chromosome 19, cosmid F23613, complete sequence

Sequence ID: AC005944.1Length: 42301Number of Matches: 1

Related Information
Genome Data Viewer-aligned genomic context
Range 1: 4567 to 4643 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Minus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  4643  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  4584

Query  61    CTGCCCCACTCACCACC  77
             |||||||||||||||||
Sbjct  4583  CTGCCCCACTCACCACC  4567
```

Human homolog of Drosophila enhancer of split m9/m10 mRNA, complete cds

Sequence ID: U04241.1Length: 1288Number of Matches: 1

Related Information
Gene-associated gene details
GEO Profiles-microarray expression data
PubChem BioAssay-bioactivity screening
Range 1: 1055 to 1131 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(71)	3e-27	75/77(97%)	0/77(0%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1055  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1114

Query  61    CTGCCCCACTCACCACC  77
             |||||||||||||||||
Sbjct  1115  CTGCCCCACTCACCACC  1131
```

PREDICTED: Hylobates moloch TLE family member 5, transcriptional modulator (TLE5), mRNA

Sequence ID: XM_032176817.1Length: 1672Number of Matches: 1

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Range 1: 1184 to 1260 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
126 bits(68)	2e-25	74/77(96%)	0/77(0%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1184  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1243

Query  61    CTGCCCCACTCACCACC  77
             ||||||||||| |||||
Sbjct  1244  CTGCCCCACTCGCCACC  1260
```

PREDICTED: Gorilla gorilla gorilla TLE family member 5, transcriptional modulator (TLE5), transcript variant X3, mRNA

Sequence ID: XM_031007483.1Length: 1586Number of Matches: 1

Related Information

Gene-associated gene details

Genome Data Viewer-aligned genomic context

Range 1: 1103 to 1179 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
126 bits(68)	2e-25	74/77(96%)	0/77(0%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| ||||||||||||||||||||  |||||||||||||||||||||||||||
Sbjct  1103  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCTGGGTCCCAGGTATGCTCCCACCTCCAC  1162

Query  61    CTGCCCCACTCACCACC  77
             |||||||||||||||||
Sbjct  1163  CTGCCCCACTCACCACC  1179
```

PREDICTED: Nomascus leucogenys TLE family member 5, transcriptional modulator (TLE5), mRNA

Sequence ID: XM_030795556.1Length: 1839Number of Matches: 1

Related Information Gene-associated gene details Genome Data Viewer-aligned genomic context
Range 1: 1352 to 1428 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
126 bits(68)	2e-25	74/77(96%)	0/77(0%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
             |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1352  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1411

Query  61    CTGCCCCACTCACCACC  77
             ||||||||||| |||||
Sbjct  1412  CTGCCCCACTCGCCACC  1428
```

Homo sapiens chromosome 19 groucho protein homolog (AES) gene, complete cds

Sequence ID: AH007143.2Length: 12683Number of Matches: 1

Related Information Gene-associated gene details GEO Profiles-microarray expression data
Range 1: 11869 to 11945 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
126 bits(68)	2e-25	74/77(96%)	0/77(0%)	Plus/Plus

```
Query  1      CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
              |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  11869  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  11928

Query  61     CTGCCCCACTCACCACC  77
              ||| |||||||||||||
Sbjct  11929  CTGGCCCACTCACCACC  11945
```

Homo sapiens isolate CHM13 chromosome 19

Sequence ID: CP068259.2Length: 61707364Number of Matches: 1

Range 1: 3026772 to 3026848 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
126 bits(68)	2e-25	74/77(96%)	0/77(0%)	Plus/Minus

```
Query  1        CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCAC  60
                |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  3026848  CCGTCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  3026789

Query  61       CTGCCCCACTCACCACC  77
                ||||||| |||||||||
Sbjct  3026788  CTGCCCCCCTCACCACC  3026772
```

PREDICTED: Piliocolobus tephrosceles TLE family member 5, transcriptional modulator (TLE5), mRNA

Sequence ID: XM_026455495.2Length: 1796Number of Matches: 1

Related Information Gene-associated gene details Genome Data Viewer-aligned genomic context
Range 1: 1308 to 1387 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
111 bits(60)	4e-21	74/80(93%)	3/80(3%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCA-  59
             || ||||||| |||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  1308  CCATCCTGGGCACCCCGAGTCTCCCCCGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1367

Query  60    --CCTGCCCCACTCACCACC  77
               ||||||||||||||||||
Sbjct  1368  CTCCTGCCCCACTCACCACC  1387
```

PREDICTED: Trachypithecus francoisi TLE family member 5, transcriptional modulator (TLE5), transcript variant X3, mRNA

Sequence ID: XM_033199976.1Length: 1752Number of Matches: 1

Range 1: 1266 to 1345 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
100 bits(54)	9e-18	72/80(90%)	3/80(3%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCA-  59
             || ||||||| ||||||||||||||| |||| |||||||||||||||||||||||||||
Sbjct  1266  CCATCCTGGGCACCCCGAGTCTCCCCAGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1325

Query  60    --CCTGCCCCACTCACCACC  77
               |||||||| |||||||||
Sbjct  1326  CTCCTGCCCCGCTCACCACC  1345
```

PREDICTED: Rhinopithecus bieti amino-terminal enhancer of split (AES), transcript variant X2, mRNA

Sequence ID: XM_017847996.1Length: 1747Number of Matches: 1

Related Information Gene-associated gene details Genome Data Viewer-aligned genomic context
Range 1: 1263 to 1342 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
95.3 bits(51)	4e-16	71/80(89%)	3/80(3%)	Plus/Plus

```
Query  1     CCGTCCTGGGTACCCCGAGTCTCCCCCGACCTCGGGTCCCAGGTATGCTCCCACCTCCA-  59
             || ||||||| ||||||||||||||  |||| |||||||||||||||||||||||||||
Sbjct  1263  CCATCCTGGGCACCCCGAGTCTCCCTAGACCCCGGGTCCCAGGTATGCTCCCACCTCCAC  1322

Query  60    --CCTGCCCCACTCACCACC  77
               |||||||| |||||||||
Sbjct  1323  CTCCTGCCCCGCTCACCACC  1342
```

CAPITOLO VII

LA SEQUENZA DI RNA “GTGAAATGGTCATGTGTGGCGG” DEL SARS-COV-2 UTILIZZATA PER L’ANALISI DEL 3’-UTR DEL VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER

OBIETTIVI DEL CAPITOLO VII

In questo capitolo è spiegato il motivo per cui è stata utilizzata la sequenza di **RNA “GTGAAATGGTCATGTGTGGCGG”** per l’analisi del ***3’-UTR del Vaccino mRNA SARS-CoV-2 Biontech/Pfizer***. A questo scopo, sono state riassunte alcune informazioni del capitolo III del documento intitolato “I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis”. Queste informazioni sono relative alla sequenza sopra citata del **gene RdRp** o ***R***_NA-_***d***_ependent_ ***R***_NA_ ***p***_olymerase_ (in italiano ***R***_NA_ ***p***_olimerasi_ ***R***_NA-_***d***_ipendente_) *del SARS-CoV-2*. Nel nostro precedente lavoro, questa sequenza è stata oggetto di molteplici modificazioni [si rimanda a “Misteri del Dna (Parte Prima)” per i necessari approfondimenti].

7.1 IL GENE RdRp E LA SEQUENZA DI RNA “GTGAAATGGTCATGTGTGGCGG” DEL SARS-COV-2

Il **gene RdRp** [o *__R__NA-__d__ependent __R__NA __p__olymerase* (in italiano *__R__NA __p__olimerasi __R__NA-__d__ipendente*) *del SARS-CoV-2*, è parte di ***ORF1ab*** (**O**pen **R**eading **F**rame, *quadro* o *cornice di lettura aperto*, fase di lettura che consente di codificare un’intera proteina, senza incontrare codoni di stop prematuri e quindi formare una proteina tronca - https://it.wikipedia.org/wiki/Open_reading_frame) **è specifico del SARS-CoV-2** (https://it.wikipedia.org/wiki/SARS-CoV-2).

Nella Figura 7.1 (presentata nella pagina successiva) sono mostrate **sei sequenze ottenute dal 2019-nCoV** che vengono utilizzate come controllo positivo del tampone rinofaringeo (https://www.eurosurveillance.org/content/table/10.2807/1560-7917.ES.2020.25.3.2000045.t1?fmt=ahah&fullscreen=true).

Il **Gene RdRp** è importante perché mediante la sua azione il virus (il *SARS-CoV-2*) responsabile della **Covid-19** realizza la sua replicazione (copia di se stesso).

Del **Gene RdRp** (*pSARS-F*), è stata selezionata la sequenza di **22 basi di RNA “GTGAAATGGTCATGTGTGGCGG”** (indicata dalla freccia verde in **Fig. 7.1**), attualmente utilizzata, assieme ad altre sequenze, come controllo positivo (nel tampone rinofaringeo) della presenza dell’infezione da *SARS-CoV-2*.

Su questa sequenza è stata eseguita una ***Ricerca Blast* completa**. Della lista dei primi **100** *allineamenti significativi* riscontrati, è stata selezionata la prima sequenza (la **Sequenza ID: MW411920.1** riportata qui di seguito).

DCLS-2538/2020, complete genome.
Sequence ID: MW411920.1 Length: 29899 Number of Matches: 1
Range 1: 15427 to 15448 GenBank Graphics

```
Score              Expect     Identities           Gaps          Strand

44.1 bits(22)      0.037      22/22(100%)          0/22(0%)      Plus/Plus

CDS: Putative 1        1          E   M   V   M   C   G   G
Query                  1      GTGAAATGGTCATGTGTGGCGG  22
                              ||||||||||||||||||||||
Sbjct                  15427  GTGAAATGGTCATGTGTGGCGG  15448
CDS:ORF1ab polyprote   5056   S   E   M   V   M   C   G   G
```

Tutto il lavoro di approfondimento presentato nel documento “I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis” **riguarda SOLO la sequenza “GTGAAATGGTCATGTGTGGCGG”** (definita **Sequenza Originara**) **e le sue molteplici modificazioni**.

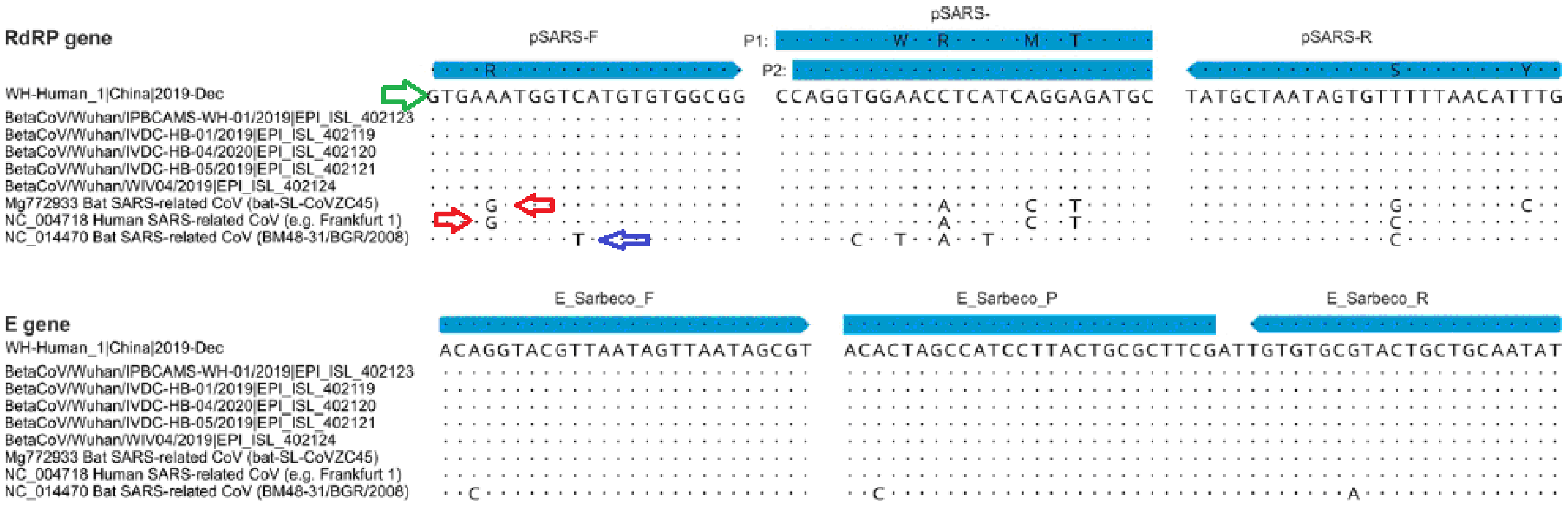


Figure 2 Partial alignments of oligonucleotide binding regions. Panels show six available sequences of 2019-nCoV, aligned to the corresponding partial sequences of SARS-CoV strain Frankfurt 1, which can be used as a positive control for all three RT-PCR assays. The alignment also contains the most closely-related bat virus (Bat SARS-related CoV isolate bat-SL-CoVZC45, GenBank Acc.No. MG772933.1) as well as the most distant member within the SARS-related bat CoV clade, detected in Bulgaria (GenBank Acc. No. NC_014470). Dots represent identical nucleotides compared to sequence Wuhan-Hu 1. Substitutions are specified. More comprehensive alignments in the Appendix.

Fig. 7.1

https://www.who.int/docs/default-source/coronaviruse/protocol-v2-1.pdf

7.2 IL MOTIVO PER CUI È STATA UTILIZZATA LA SEQUENZA "GTGAAATGGTCATGTGTGGCGG" PER L'ANALISI DEL 3'-UTR DEL VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER

Avvalendoci della **Teoria Tricromatica dell'Equilibrio dei Sistemi** (**T.T.E.S.**) e del suo programma computerizzato, la **Sequenza Originara** ha subito molteplici modificazioni. Nel documento intitolato "I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis" sono mostrati i risultati di queste modificazioni.

Per rendere possibile la replicazione dei risultati ottenuti, il capitolo VII e il capitolo VIII del documento sopracitato (**capitoli ai quali si rimanda per gli indispensabili approfondimenti**) sono stati dedicati all'insegnamento della procedura utilizzata per generare numerose e diverse **nuove sequenze** di DNA o di RNA che rispettano fedelmente i numerosi e diversi **"*trend non manifesti*"** della **sequenza originaria**.

I "**trend non manifesti**" sono *andamenti*, non chiaramente identificabili, presenti in tutte le sequenze di DNA e di RNA. A partire da **ognuno** dei **possibili** "**Trend Non Manifesti**" della **sequenza originaria** è possibile generare un numero indeterminato di "nuove sequenze".

L'identificazione dei "**trend non manifesti**" costituisce il presupposto fondamentale per le modificazioni delle sequenze di DNA e RNA eseguite con il software della **T.T.E.S.** . Per la **MODIFICAZIONE COMPLETA DELLA SEQUENZA ORIGINARIA** e la generazione di **TUTTE LE NUOVE SEQUENZE** è necessario **identificare tutti i possibili TREND NON MANIFESTI** della **sequenza originaria**. I principali "**TREND NON MANIFESTI**" sono **VENTIQUATTRO**. Essi sono stati identificati attribuendo un numero compreso da **0** a **3** alle **quattro basi azotate** (**T, C, G** e **A**) [per esempio, **Trend n° 1 (T=0; C=1; G=2; A=3)**].

E' fondamentale sottolineare che la **sequenza originaria** differisce da **tutte le nuove sequenze generate** per almeno il **70% di basi** (si tratta quindi di **materiale biologico molto differente**) e che i **"24 *trend non manifesti*"** delle sequenze di Dna o Rna aumentano notevolmente la **complessità del codice genetico** ed ***evidenziano somiglianze e differenze attualmente ignote tra le sequenze***.

Alla luce di queste considerazioni e per scopi puramente teorici (evidenziare eventuali "**affinità**" tra la **Sequenza Originaria** e il **VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER**), abbiamo utilizzato i **"24 *trend non manifesti*"** generati dalla **sequenza "GTGAAATGGTCATGTGTGGCGG"** e con essi analizzato il **3'-UTR DEL VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER**. Abbiamo scelto il **3'-UTR** per due motivi: 1) perché costituito da un numero di basi limitato (295); 2) perché, essendo *materiale genetico Non Tradotto*, stimolava la nostra curiosità. Come è facile immaginare dalla lettura dei capitoli precedenti, *i risultati ottenuti sono stati inattesi, sorprendenti e necessariamente bisognosi di altre spiegazioni e chiarimenti*.

CAPITOLO VIII

PROCEDURA PER L’IDENTIFICAZIONE E L’UNIONE DI SEGMENTI DI SEQUENZA SIGNIFICATIVI NON CONTIGUI DEL 3’-UTR DEL VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER

OBIETTIVI DEL CAPITOLO VIII

In questo capitolo, è spiegata sinteticamente la procedura utilizzata per identificare e unire tra loro i piccoli segmenti di sequenza significativi non contigui del ***3'-UTR del Vaccino mRNA SARS-CoV-2 Biontech/Pfizer***.
A tale scopo è necessario spiegare preliminarmente la **procedura per l'identificazione delle Triplette dei Trends (I i D d) e degli 8 Colori/Note corrispondenti**.
La comprensione piena dei due paragrafi di questo capitolo non può però prescidere dallo studio propedeutico del Capitolo VII e del Capitolo VIII del documento intitolato "I Misteri del Dna (Parte Prima). Relazioni tra Sars-Cov-2, Pipistrello, Pangolino, Influenzavirus A, HIV-1 e i Bacilli Paranthracis e Anthracis".

8.1 PROCEDURA PER L'IDENTIFICAZIONE DELLE TRIPLETTE DEI TRENDS (I i D d) E DEGLI 8 COLORI/NOTE

In questo paragrafo è spiegata la **procedura per l'identificazione delle Triplette dei Trends (I i D d) e degli 8 Colori/Note corrispondenti**.
La procedura spiegata qui di seguito è generalizzabile a qualsiasi altra condizione di indagine simile.

Data la **Sequenza Originaria** **"GTGAAATGGTCATGTGTGGCGG"**

(la ***sequenza di RNA del Gene RdRp del SARS-CoV-2*** della quale abbiamo già ampiamente discusso nel capitolo precedente) **identifichiamo i 24 Trends principali**. La spiegazione che segue riguarda *solo uno dei 24 trends*, il **Trend n° 1** (la procedura è identica e va ripetuta anche per gli altri Trends):

1) Identifichiamo il Trend n° 1 sostituendo alle
lettere i numeri specifici corrispondenti al **Trend n° 1** (**T=0; C=1; G=2; A=3**).

Identificazione del Trend n° 1 (T=0; C=1; G=2; A=3)

Sequenza Originaria	**G**	**T**	**G**	**A**	**A**	**A**	**T**	**G**	**G**	**T**	**C**	**A**	**T**	**G**	**T**	**G**	**T**	**G**	**G**	**C**	**G**	**G**
Trend n° 1 (T=0; C=1; G=2; A=3)	**2**	**0**	**2**	**3**	**3**	**3**	**0**	**2**	**2**	**0**	**1**	**3**	**0**	**2**	**0**	**2**	**0**	**2**	**2**	**1**	**2**	**2**

2) Identifichiamo il Trend n° 1 (I i D d) attribuendo ad ogni numero specifico (in funzione dell'*Incremento*, del *Decremento* o della *mancanza di variazione* rispetto al numero precedente) *una delle quattro lettere* presentate qui di seguito:

I = **Increase** (Incremento rispetto al precedente **numero specifico** assegnato)
i = **repeated increase** (incremento ripetuto rispetto al precedente **numero specifico** assegnato)
D = **Decrease** (Decremento rispetto al precedente **numero specifico** assegnato)
d = **repeated decrease** (decremento ripetuto rispetto al precedente **numero specifico** assegnato)

Identificazione del Trend n° 1 (I i D d)

Sequenza Originaria	**G**	**T**	**G**	**A**	**A**	**A**	**T**	**G**	**G**	**T**	**C**	**A**	**T**	**G**	**T**	**G**	**T**	**G**	**G**	**C**	**G**	**G**
Trend n° 1 (T=0; C=1; G=2; A=3)	**2**	**0**	**2**	**3**	**3**	**3**	**0**	**2**	**2**	**0**	**1**	**3**	**0**	**2**	**0**	**2**	**0**	**2**	**2**	**1**	**2**	**2**
Trend n° 1 (I i D d)	**-**	**D**	**I**	**I**	**i**	**i**	**D**	**I**	**i**	**D**	**I**	**I**	**D**	**I**	**D**	**I**	**D**	**I**	**i**	**D**	**I**	**i**

3) Identifichiamo le Triplette del Trend n° 1 (I i D d) leggendo a scorrere (da sinistra verso destra) le singole ***lettere*** del **Trend n° 1 (I i D d)** e unendole a **gruppi di tre**:

Identificazione delle Triplette del Trend n° 1 (I i D d)

Sequenza Originaria	G	T	G	A	A	A	T	G	G	T	C	A	T	G	T	G	T	G	G	C	G	G
Trend n° 1 (T=0; C=1; G=2; A=3)	2	0	2	3	3	3	0	2	2	0	1	3	0	2	0	2	0	2	2	1	2	2
Trend n° 1 (I i D d)	-	D	I	I	i	i	D	I	i	D	I	I	D	I	D	I	D	I	i	D	I	i
Triplette del Trend n° 1 (I i D d)				D	I	I	i	i	D	I	i	D	I	I	D	I	D	I	D	I	i	D
				I	I	i	i	D	I	i	D	I	I	D	I	D	I	D	I	i	D	I
				I	i	i	D	I	i	D	I	I	D	I	D	I	D	I	i	D	I	i

4) Infine, **identifichiamo gli 8 Colori/Note** delle singole **Triplette del Trend n° 1 (I i D d)** attribuendo ad ogni tripletta il **Colore/Nota** stabilito nello schema seguente [*attenzione, in questa fase della procedura, le lettere delle triplette del* **Trend n° 1 (I i D d)** *si leggono come se fossero tutte scritte in maiuscolo*]:

DDD = DO3 **DID = MI** **IID = SOL** **DII = SI**

IDD = RE **DDI = FA** **IDI = LA** **III = DO4**

Identificazione dei Colori/Note

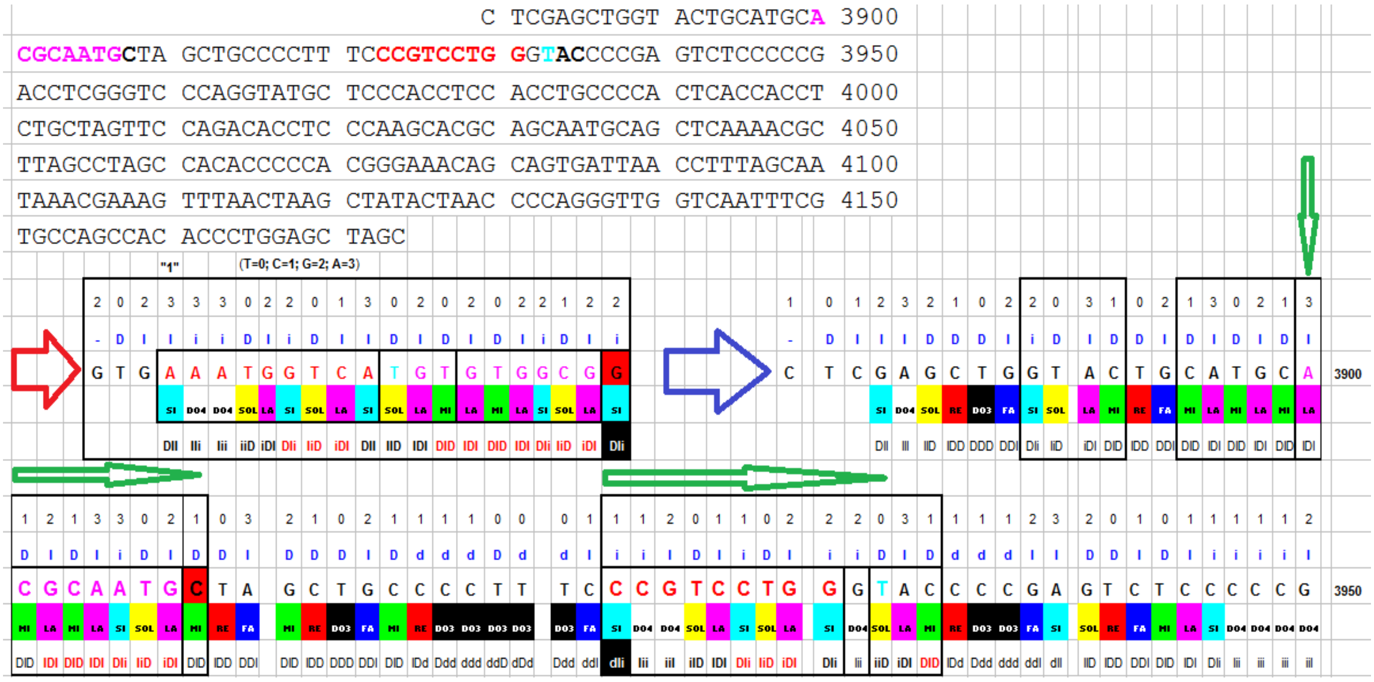
Sequenza Originaria	G	T	G	A	A	A	T	G	G	T	C	A	T	G	T	G	T	G	G	C	G	G
Trend n° 1 (T=0; C=1; G=2; A=3)	2	0	2	3	3	3	0	2	2	0	1	3	0	2	0	2	0	2	2	1	2	2
Trend n° 1 (I i D d)	-	D	I	I	i	i	D	I	i	D	I	I	D	I	D	I	D	I	i	D	I	i
Triplette del Trend n° 1 (I i D d)				D	I	I	i	i	D	I	i	D	I	I	D	I	D	I	D	I	i	D
				I	I	i	i	D	I	i	D	I	I	D	I	D	I	D	I	i	D	I
				I	i	i	D	I	i	D	I	I	D	I	D	I	D	I	i	D	I	i
Colori e Note Musicali delle singole Triplette del Trend n° 1 (I i D d)				S I	D O 4	D O 4	S O L	L A	S I	S O L	L A	S I	S O L	L A	M I	L A	M I	L A	S I	S O L	L A	S I

8.2 PROCEDURA PER L'IDENTIFICAZIONE E L'UNIONE DI SEGMENTI DI SEQUENZA SIGNIFICATIVI NON CONTIGUI DEL 3'-UTR DEL VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER

In questo paragrafo è spiegata (in modo molto sintetico) la **procedura per identificare e unire i segmenti di sequenza significativi non contigui del 3'-UTR DEL VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER**.

Come è stato accennato alla fine del capitolo precedente, per evidenziare eventuali "**affinità**" tra la **Sequenza Originaria** (la sequenza "**GTGAAATGGTCATGTGTGGCGG**" del Gene RdRp del SARS-CoV-2) e il **VACCINO mRNA SARS-COV-2 BIONTECH/PFIZER**, abbiamo utilizzato i **"24 *trend non manifesti*"** generati dalla **Sequenza Originaria** e con essi analizzato la **Sequenza 3'-UTR**.

In Fig. 8.1 (in alto a sinistra) è mostrata la sequenza **3'-UTR** [in essa, come vedremo, le lettere colorate costituiranno i TRE SEGMENTI della **Sequenza "HIV-1"** (sequenza ampiamente discussa nel capitolo III di questo documento)]. Nella stessa figura (indicata dalla **freccia rossa**, nel riquadro più in basso a sinistra) è mostrata la sequenza "**GTGAAATGGTCATGTGTGGCGG**" del Gene RdRp del SARS-CoV-2, della quale sono stati identificati (seguendo la procedura spiegata nel paragrafo precedente) il **Trend n° 1 (T=0; C=1; G=2; A=3)**, il **Trend n° 1 (I i D d)**, le **Triplette del Trend n° 1 (I i D d)** e gli **8 Colori/Note** delle singole **Triplette**. La stessa procedura è stata eseguita sulla **Sequenza 3'-UTR** (indicata dalla **freccia blu**, mostrata al centro della Fig. 8.1). Ottenuti questi dati, è necessario identificare gli **8 Colori/Note** (per semplificare, *evidenziati minimo a gruppi di quattro*) della **Sequenza Originaria** (indicata dalla **freccia rossa**) nella **Sequenza 3'-UTR** (indicata dalla **freccia blu**).



C TCGAGCTGGT ACTGCATGCA 3900
CGCAATGCTA GCTGCCCCTT TCCCGTCCTG GGTACCCCGA GTCTCCCCCG 3950
ACCTCGGGTC CCAGGTATGC TCCCACCTCC ACCTGCCCCA CTCACCACCT 4000
CTGCTAGTTC CAGACACCTC CCAAGCACGC AGCAATGCAG CTCAAAACGC 4050
TTAGCCTAGC CACACCCCCA CGGGAAACAG CAGTGATTAA CCTTTAGCAA 4100
TAAACGAAAG TTTAACTAAG CTATACTAAC CCCAGGGTTG GTCAATTTCG 4150
TGCCAGCCAC ACCCTGGAGC TAGC

"1" (T=0; C=1; G=2; A=3)

2 0 2 3 3 3 0 2 2 0 1 3 0 2 0 2 0 2 2 1 2 2
- D I I i i D I i D I I D I D I D I i D I i
G T G A A A T G G T C A T G T G T G G C G G
SI DO4 DO4 SOL LA SI SOL LA SI SOL LA MI LA MI LA SI SOL LA SI
DII IIi Iii iiD iDI DIi IiD iDI DII IID IDI DID IDI DID IDI DIi IiD iDI DIi

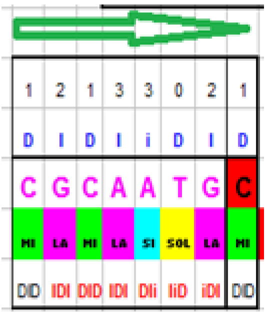
1 0 1 2 3 2 1 0 2 2 0 3 1 0 2 1 3 0 2 1 3
- D I I I D D D I i D I D D I D I D I D I
C T C G A G C T G G T A C T G C A T G C A 3900
SI DO4 SOL RE DO3 FA SI SOL LA MI RE FA MI LA MI LA MI LA
DII III IID IDD DDD DDI DIi IiD iDI DID IDD DDI DID IDI DID IDI DID IDI

1 2 1 3 3 0 2 1 0 3 2 1 0 2 1 1 1 1 0 0 0 1 1 1 2 0 1 1 0 2 2 2 0 3 1 1 1 1 2 3 2 0 1 0 1 1 1 1 1 2
D I D I i D I D D I D D D I D d d d D d d I i i I D I i D I i i D I D d d d I I D D I D I i i i i I
C G C A A T G C T A G C T G C C C C T T T C C C G T C C T G G G T A C C C C G A G T C T C C C C C G 3950
MI LA MI LA SI SOL LA MI RE FA MI RE DO3 FA MI RE DO3 DO3 DO3 DO3 DO3 FA SI DO4 DO4 SOL LA SI SOL LA SI DO4 SOL LA MI RE DO3 DO3 FA SI SOL RE FA MI LA SI DO4 DO4 DO4 DO4
DID IDI DID IDI DIi IiD iDI DID IDD DDI DID IDD DDD DDI DID IDd Ddd ddd ddD dDd Ddd ddI dIi Iii iiI iID IDI DIi IiD iDI DIi Iii iiD iDI DID IDd Ddd ddd ddI dII IID IDD DDI DID IDI DIi Iii iii iii iiI

Fig. 8.1

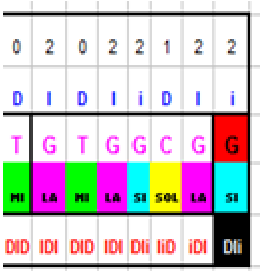
ATTENZIONE: *non sempre è possibile identificare l'intera sequenza degli* ***8 Colori/Note*** *della* ***Sequenza Originaria*** *nella* ***Sequenza 3'-UTR****, a volte è possibile identificarne solo dei segmenti, oppure i segmenti identificati sono tutti, ma il loro ordine è invertito, si presenta prima la parte finale e poi quella iniziale*.
Questa ultima evenienza è mostrata proprio in Fig. 8.1 . La **freccia verticale verde** indica l'inizio della parte finale di uno dei TRE SEGMENTI che costituiscono la **Sequenza "HIV-1"**. Gli altri *due segmenti mancanti* sono rintracciabili poco più avanti (si veda sotto la seconda **freccia orizzontale verde**, mostrata al centro della Fig. 8.1), interrotti da una *base di Guanina* (**G**).

ATTENZIONE: alcune volte bisogna fare dei particolari aggiustamenti. E' il caso della *base di Citosina* (**C**) che è stata mantenuta nella **Sequenza "HIV-1"** nonostante corrispondesse ad un **MI** invece che ad un **SI**, come ci si sarebbe dovuti attendere (si vedano le Fig. 8.2 e 8.3).



1	2	1	3	3	0	2	1
D	I	D	I	i	D	I	D
C	G	C	A	A	T	G	C
MI	LA	MI	LA	SI	SOL	LA	MI
DID	IDI	DID	IDI	DIi	IiD	iDI	DID

Fig. 8.2

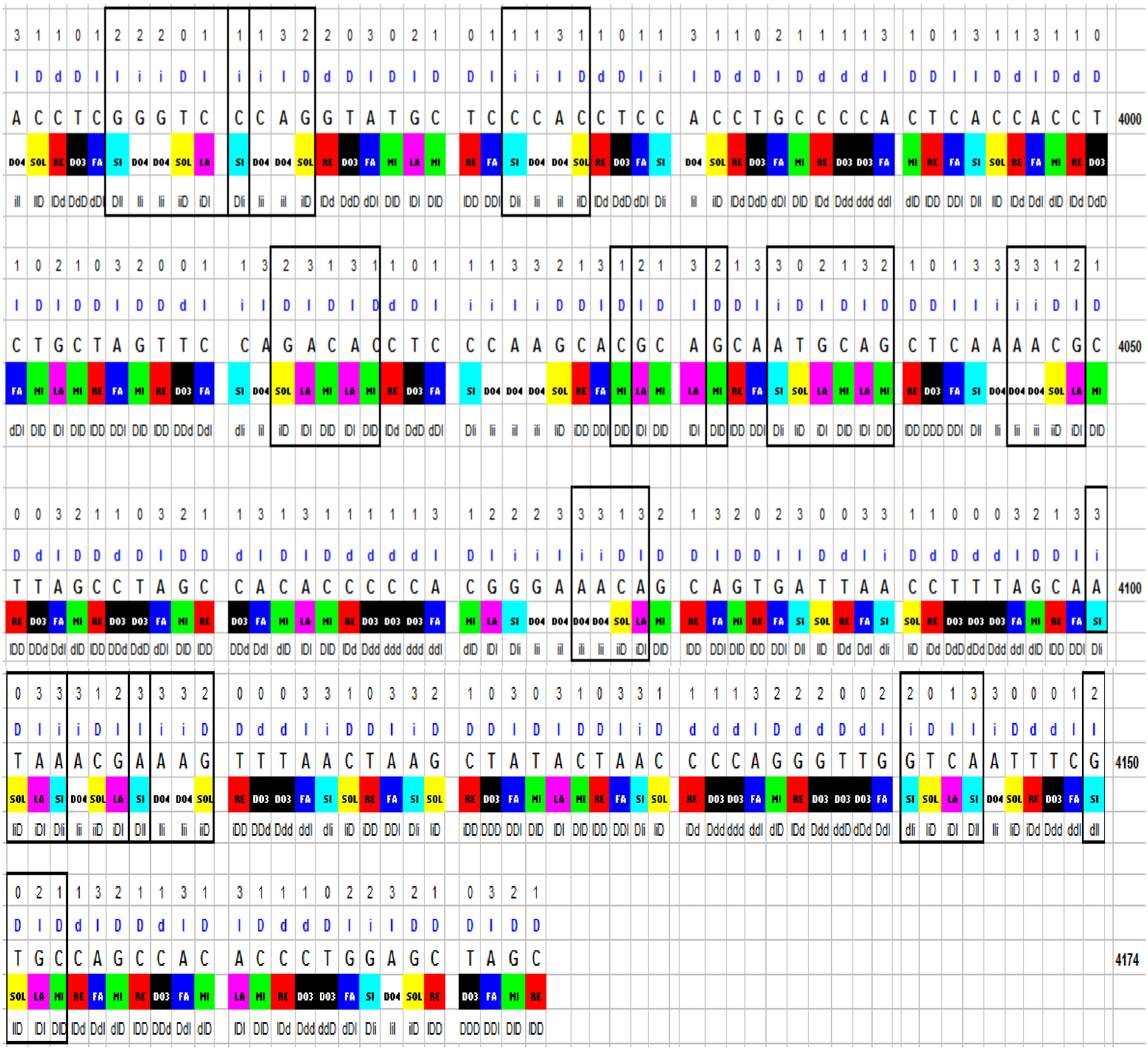


0	2	0	2	2	1	2	2
D	I	D	I	i	D	I	i
T	G	T	G	G	C	G	G
MI	LA	MI	LA	SI	SOL	LA	SI
DID	IDI	DID	IDI	DIi	IiD	iDI	DIi

Fig. 8.3

In Fig. 8.4 (si veda la pagina successiva) è mostrata la parte restante dell'analisi della **Sequenza 3'-UTR** [**Trend n° 1 (T=0; C=1; G=2; A=3)**].

ATTENZIONE: *Per un'analisi completa della* ***Sequenza 3'-UTR****, tutte le procedure appena descritte devono essere eseguite considerando anche* ***gli altri 23 Trends*** (per ragioni di spazio i dati completi riferiti agli altri Trends non sono mostrati in questo documento).



3	1	1	0	1	2	2	2	0	1	1	1	3	2	2	0	3	0	2	1	0	1	1	1	3	1	1	0	1	1	3	1	1	0	2	1	1	1	1	3	1	0	1	3	1	1	3	1	1	0	
I	D	d	D	I	I	i	i	D	I	i	i	I	D	d	D	I	D	I	D	D	I	i	i	I	D	d	D	I	i	I	D	d	D	I	D	d	d	d	I	D	D	I	I	D	d	I	D	d	D	
A	C	C	T	C	G	G	G	T	C	C	C	A	G	G	T	A	T	G	C	T	C	C	C	A	C	C	T	C	C	A	C	C	T	G	C	C	C	C	A	C	T	C	A	C	C	A	C	C	T	4000
D04	SOL	RE	D03	FA	SI	D04	D04	SOL	LA	SI	D04	D04	SOL	RE	D03	FA	MI	LA	MI	RE	FA	SI	D04	D04	SOL	RE	D03	FA	SI	D04	SOL	RE	D03	FA	MI	RE	D03	D03	FA	MI	RE	FA	SI	SOL	RE	FA	MI	RE	D03	
iII	IID	IDd	DdD	dDI	DII	IIi	Iii	iiD	iDI	DIi	Iii	iiI	iID	IDd	DdD	dDI	DID	IDI	DID	IDD	DDI	DIi	Iii	iiI	iID	IDd	DdD	dDI	DIi	IiI	iID	IDd	DdD	dDI	DID	IDd	Ddd	ddd	ddI	dID	IDD	DDI	DII	IID	IDd	DdI	dID	IDd	DdD	

1	0	2	1	0	3	2	0	0	1	1	3	2	3	1	3	1	1	0	1	1	1	3	3	2	1	3	1	2	1	3	2	1	3	3	0	2	1	3	2	1	0	1	3	3	3	3	1	2	1	
I	D	I	D	D	I	D	D	d	I	i	I	D	I	D	I	D	d	D	I	i	i	I	i	D	D	I	D	I	D	I	D	D	I	i	D	I	D	I	D	D	D	I	I	i	i	i	D	I	D	
C	T	G	C	T	A	G	T	T	C	C	A	G	A	C	A	C	C	T	C	C	C	A	A	G	C	A	C	G	C	A	G	C	A	A	T	G	C	A	G	C	T	C	A	A	A	A	C	G	C	4050
FA	MI	LA	MI	RE	FA	MI	RE	D03	FA	SI	D04	SOL	LA	MI	LA	MI	RE	D03	FA	SI	D04	D04	D04	SOL	RE	FA	MI	LA	MI	LA	MI	RE	FA	SI	SOL	LA	MI	LA	MI	RE	D03	FA	SI	D04	D04	D04	SOL	LA	MI	
dDI	DID	IDI	DID	IDD	DDI	DID	IDD	DDd	DdI	dIi	IiI	iID	IDI	DID	IDI	DID	IDd	DdD	dDI	DIi	Iii	iiI	iIi	IiD	iDD	DDI	DID	IDI	DID	IDI	DID	IDD	DDI	DIi	IiD	iDI	DID	IDI	DID	IDD	DDD	DDI	DII	IIi	Iii	iii	iiD	iDI	DID	

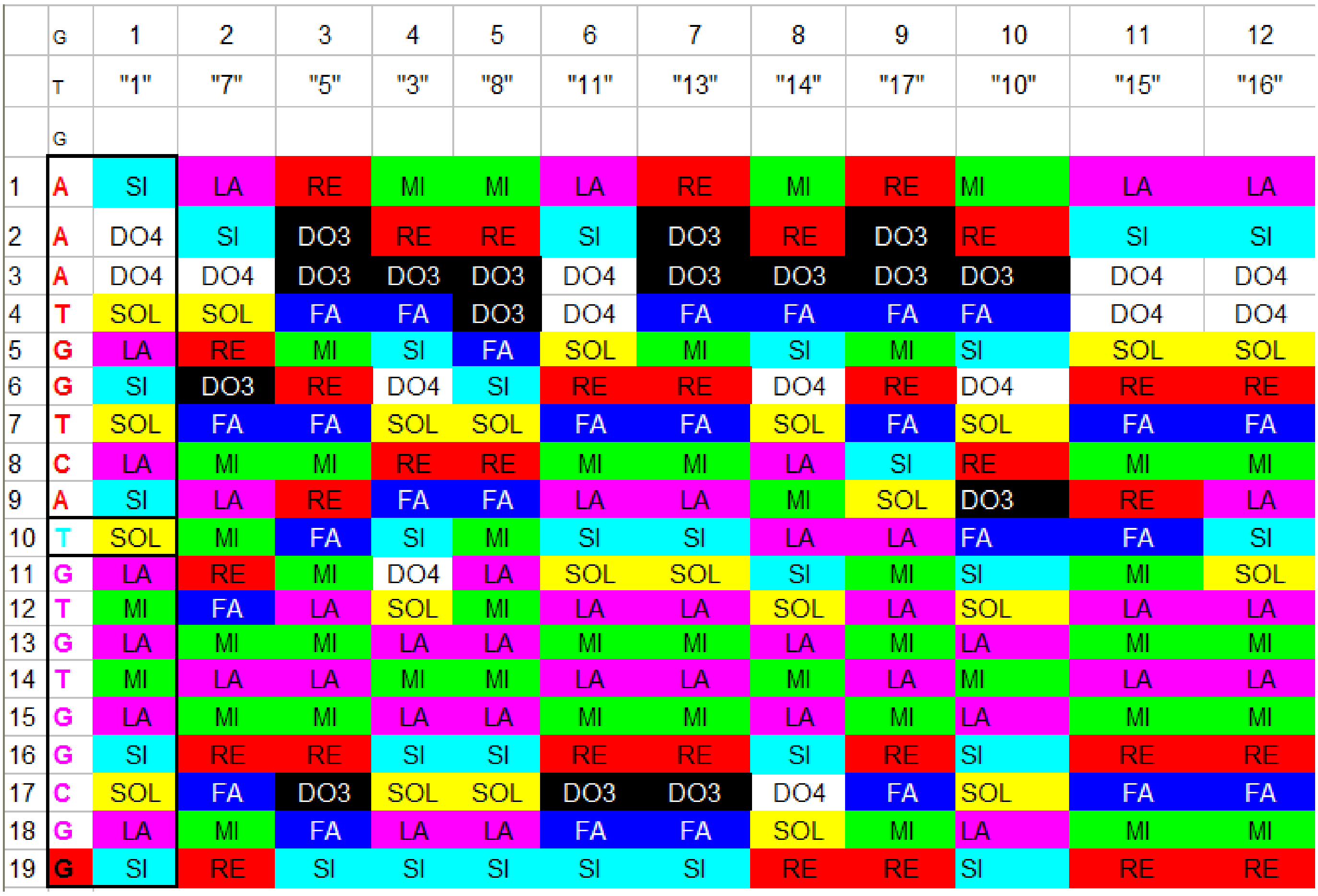
0	0	3	2	1	1	0	3	2	1	1	3	1	3	1	1	1	1	1	3	1	2	2	2	3	3	3	1	3	2	1	3	2	0	2	3	0	0	3	3	1	1	0	0	0	3	2	1	3	3	
D	d	I	D	D	d	D	I	D	D	d	I	D	I	D	d	d	d	d	I	D	I	i	i	I	i	i	D	I	D	D	I	D	D	I	I	D	d	I	i	D	d	D	d	d	I	D	D	I	i	
T	T	A	G	C	C	T	A	G	C	C	A	C	A	C	C	C	C	C	A	C	G	G	G	A	A	A	C	A	G	C	A	G	T	G	A	T	T	A	A	C	C	T	T	T	A	G	C	A	A	4100
RE	D03	FA	MI	RE	D03	D03	FA	MI	RE	D03	FA	MI	LA	MI	RE	D03	D03	D03	FA	MI	LA	SI	D04	D04	D04	D04	SOL	LA	MI	RE	FA	MI	RE	FA	SI	SOL	RE	FA	SI	SOL	RE	D03	D03	D03	FA	MI	RE	FA	SI	
IDD	DDd	DdI	dID	IDD	DDd	DdD	dDI	DID	IDD	DDd	DdI	dID	IDI	DID	IDd	Ddd	ddd	ddd	ddI	dID	IDI	DIi	Iii	iiI	iIi	Iii	iiD	iDI	DID	IDD	DDI	DID	IDD	DDI	DII	IID	IDd	DdI	dIi	IiD	iDd	DdD	dDd	Ddd	ddI	dID	IDD	DDI	DIi	

0	3	3	3	1	2	3	3	3	2	0	0	0	3	3	1	0	3	3	2	1	0	3	0	3	1	0	3	3	1	1	1	1	3	2	2	2	0	0	2	2	0	1	3	3	0	0	0	1	2	
D	I	i	i	D	I	I	i	i	D	D	d	d	I	i	D	D	I	i	D	D	D	I	D	I	D	D	I	i	D	d	d	d	I	D	d	d	D	d	I	i	D	I	I	i	D	d	d	I	I	
T	A	A	A	C	G	A	A	A	G	T	T	T	A	A	C	T	A	A	G	C	T	A	T	A	C	T	A	A	C	C	C	C	A	G	G	G	T	T	G	G	T	C	A	A	T	T	T	C	G	4150
SOL	LA	SI	D04	SOL	LA	SI	D04	D04	SOL	RE	D03	D03	FA	SI	SOL	RE	FA	SI	SOL	RE	D03	FA	MI	LA	MI	RE	FA	SI	SOL	RE	D03	D03	FA	MI	RE	D03	D03	D03	FA	SI	SOL	LA	SI	D04	SOL	RE	D03	FA	SI	
IiD	iDI	DIi	Iii	iiD	iDI	DII	IIi	Iii	iiD	iDD	DDd	Ddd	ddI	dIi	IiD	iDD	DDI	DIi	IiD	iDD	DDD	DDI	DID	IDI	DID	IDD	DDI	DIi	IiD	iDd	Ddd	ddd	ddI	dID	IDd	Ddd	ddD	dDd	DdI	dIi	IiD	iDI	DII	IIi	IiD	iDd	Ddd	ddI	dII	

0	2	1	1	3	2	1	1	3	1	3	1	1	1	0	2	2	3	2	1	0	3	2	1																											
D	I	D	d	I	D	D	d	I	D	I	D	d	d	D	I	i	I	D	D	D	I	D	D																											
T	G	C	C	A	G	C	C	A	C	A	C	C	C	T	G	G	A	G	C	T	A	G	C																											4174
SOL	LA	MI	RE	FA	MI	RE	D03	FA	MI	LA	MI	RE	D03	D03	FA	SI	D04	SOL	RE	D03	FA	MI	RE																											
IID	IDI	DID	IDd	DdI	dID	IDD	DDd	DdI	dID	IDI	DID	IDd	Ddd	ddD	dDI	DIi	IiI	iID	IDD	DDD	DDI	DID	IDD																											

Fig. 8.4

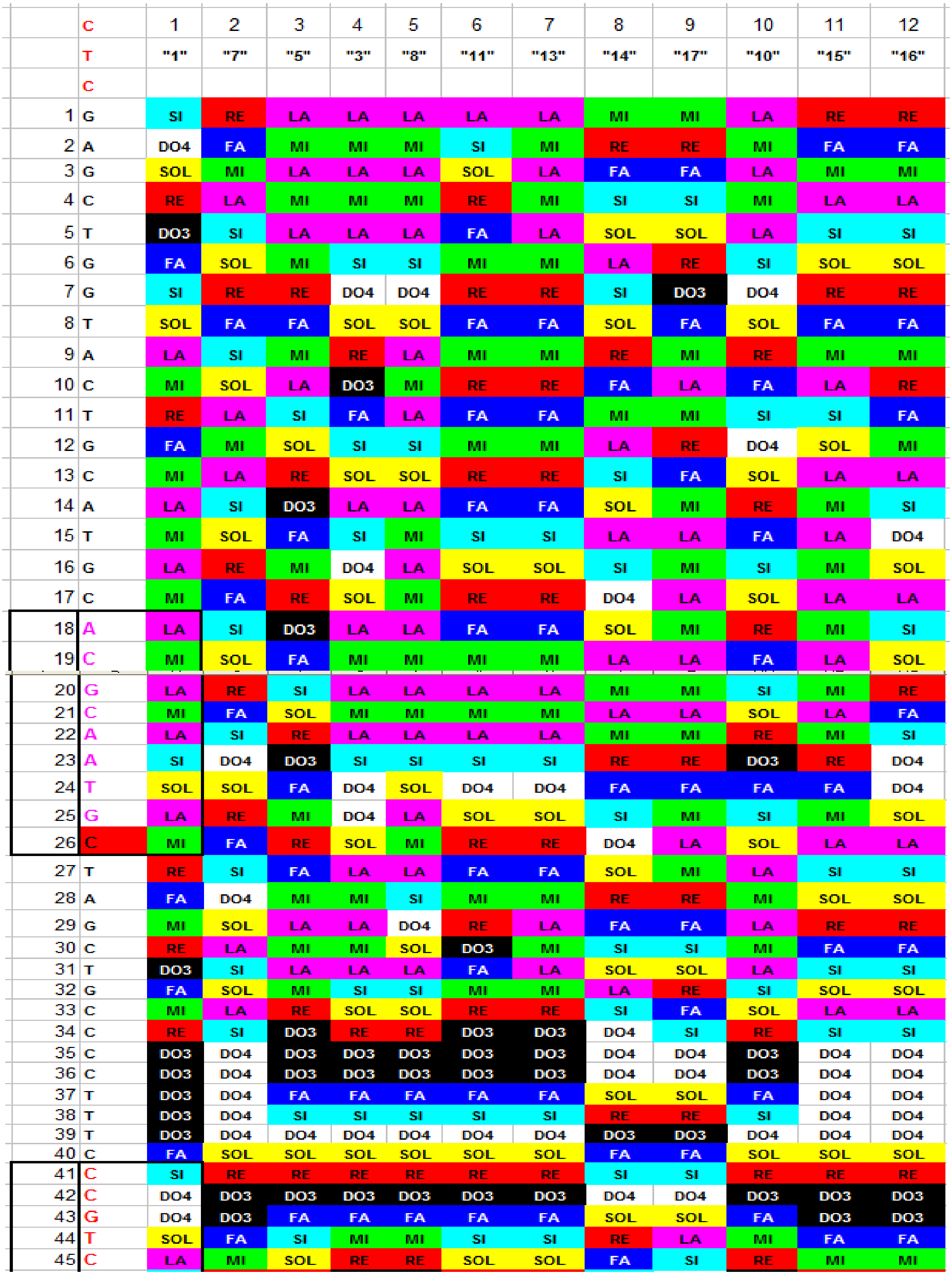
Nella pagina successiva (Fig. 8.5) è mostrata una tabella con i **Colori/Note** attribuiti alla **Sequenza Originaria** (la sequenza “**GTGAAATGGTCATGTGTGGCGG**” del Gene RdRp del SARS-CoV-2). In tabella sono mostrati solo i **Colori/Note** di **12 Trends** (Trend n° “1”, “7”, “5”, “3”, “8”, “11”, “13”, “14”, “17”, “10”, “15” e “16”) dei **24 Trends** principali. Il **Trend n° 1 (T=0; C=1; G=2; A=3)** è quello identificato nel paragrafo 8.1 .



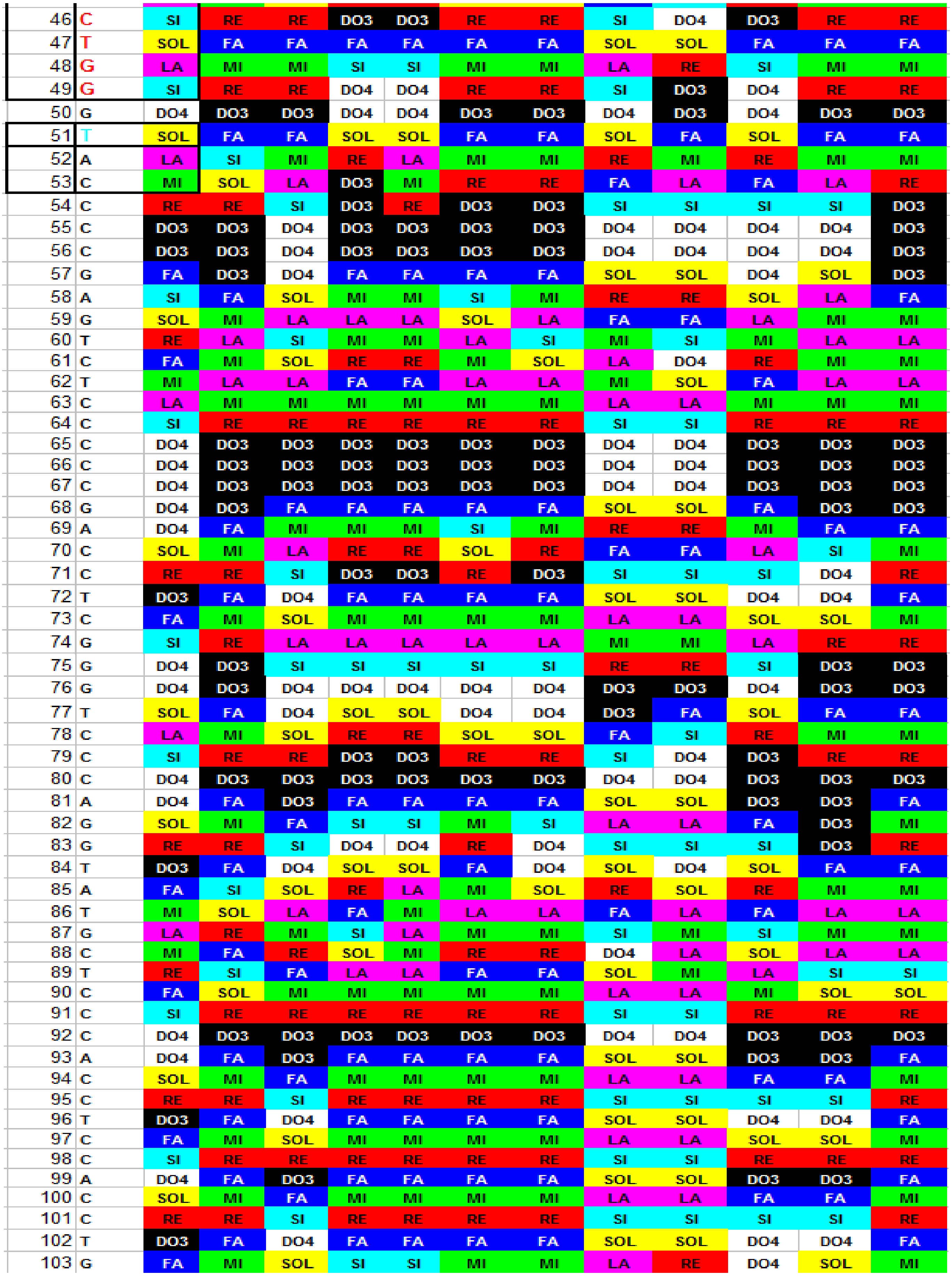
	G	1	2	3	4	5	6	7	8	9	10	11	12
	T	"1"	"7"	"5"	"3"	"8"	"11"	"13"	"14"	"17"	"10"	"15"	"16"
	G												
1	A	SI	LA	RE	MI	MI	LA	RE	MI	RE	MI	LA	LA
2	A	DO4	SI	DO3	RE	RE	SI	DO3	RE	DO3	RE	SI	SI
3	A	DO4	DO4	DO3	DO3	DO3	DO4	DO3	DO3	DO3	DO3	DO4	DO4
4	T	SOL	SOL	FA	FA	DO3	DO4	FA	FA	FA	FA	DO4	DO4
5	G	LA	RE	MI	SI	FA	SOL	MI	SI	MI	SI	SOL	SOL
6	G	SI	DO3	RE	DO4	SI	RE	RE	DO4	RE	DO4	RE	RE
7	T	SOL	FA	FA	SOL	SOL	FA	FA	SOL	FA	SOL	FA	FA
8	C	LA	MI	MI	RE	RE	MI	MI	LA	SI	RE	MI	MI
9	A	SI	LA	RE	FA	FA	LA	LA	MI	SOL	DO3	RE	LA
10	T	SOL	MI	FA	SI	MI	SI	SI	LA	LA	FA	FA	SI
11	G	LA	RE	MI	DO4	LA	SOL	SOL	SI	MI	SI	MI	SOL
12	T	MI	FA	LA	SOL	MI	LA	LA	SOL	LA	SOL	LA	LA
13	G	LA	MI	MI	LA	LA	MI	MI	LA	MI	LA	MI	MI
14	T	MI	LA	LA	MI	MI	LA	LA	MI	LA	MI	LA	LA
15	G	LA	MI	MI	LA	LA	MI	MI	LA	MI	LA	MI	MI
16	G	SI	RE	RE	SI	SI	RE	RE	SI	RE	SI	RE	RE
17	C	SOL	FA	DO3	SOL	SOL	DO3	DO3	DO4	FA	SOL	FA	FA
18	G	LA	MI	FA	LA	LA	FA	FA	SOL	MI	LA	MI	MI
19	G	SI	RE	SI	SI	SI	SI	SI	RE	RE	SI	RE	RE

Fig. 8.5

Nella pagina successiva e in quelle che seguono (Fig. 8.6) sono mostrate (unite insieme) le tabelle con i **Colori/Note** attribuiti alla **Sequenza del 3'-UTR**. In tabella sono mostrati solo i **Colori/Note** di **12 Trends** (Trend n° "1", "7", "5", "3", "8", "11", "13", "14", "17", "10", "15" e "16") dei **24 Trends** principali. Il **Trend n° 1 (T=0; C=1; G=2; A=3)** è quello identificato nel paragrafo 8.1 .



	C	1	2	3	4	5	6	7	8	9	10	11	12
	T	"1"	"7"	"5"	"3"	"8"	"11"	"13"	"14"	"17"	"10"	"15"	"16"
	C												
1	G	SI	RE	LA	LA	LA	LA	LA	MI	MI	LA	RE	RE
2	A	DO4	FA	MI	MI	MI	SI	MI	RE	RE	MI	FA	FA
3	G	SOL	MI	LA	LA	LA	SOL	LA	FA	FA	LA	MI	MI
4	C	RE	LA	MI	MI	MI	RE	MI	SI	SI	MI	LA	LA
5	T	DO3	SI	LA	LA	LA	FA	LA	SOL	SOL	LA	SI	SI
6	G	FA	SOL	MI	SI	SI	MI	MI	LA	RE	SI	SOL	SOL
7	G	SI	RE	RE	DO4	DO4	RE	RE	SI	DO3	DO4	RE	RE
8	T	SOL	FA	FA	SOL	SOL	FA	FA	SOL	FA	SOL	FA	FA
9	A	LA	SI	MI	RE	LA	MI	MI	RE	MI	RE	MI	MI
10	C	MI	SOL	LA	DO3	MI	RE	RE	FA	LA	FA	LA	RE
11	T	RE	LA	SI	FA	LA	FA	FA	MI	MI	SI	SI	FA
12	G	FA	MI	SOL	SI	SI	MI	MI	LA	RE	DO4	SOL	MI
13	C	MI	LA	RE	SOL	SOL	RE	RE	SI	FA	SOL	LA	LA
14	A	LA	SI	DO3	LA	LA	FA	FA	SOL	MI	RE	MI	SI
15	T	MI	SOL	FA	SI	MI	SI	SI	LA	LA	FA	LA	DO4
16	G	LA	RE	MI	DO4	LA	SOL	SOL	SI	MI	SI	MI	SOL
17	C	MI	FA	RE	SOL	MI	RE	RE	DO4	LA	SOL	LA	LA
18	A	LA	SI	DO3	LA	LA	FA	FA	SOL	MI	RE	MI	SI
19	C	MI	SOL	FA	MI	MI	MI	MI	LA	LA	FA	LA	SOL
20	G	LA	RE	SI	LA	LA	LA	LA	MI	MI	SI	MI	RE
21	C	MI	FA	SOL	MI	MI	MI	MI	LA	LA	SOL	LA	FA
22	A	LA	SI	RE	LA	LA	LA	LA	MI	MI	RE	MI	SI
23	A	SI	DO4	DO3	SI	SI	SI	SI	RE	RE	DO3	RE	DO4
24	T	SOL	SOL	FA	DO4	SOL	DO4	DO4	FA	FA	FA	FA	DO4
25	G	LA	RE	MI	DO4	LA	SOL	SOL	SI	MI	SI	MI	SOL
26	C	MI	FA	RE	SOL	MI	RE	RE	DO4	LA	SOL	LA	LA
27	T	RE	SI	FA	LA	LA	FA	FA	SOL	MI	LA	SI	SI
28	A	FA	DO4	MI	MI	SI	MI	MI	RE	RE	MI	SOL	SOL
29	G	MI	SOL	LA	LA	DO4	RE	LA	FA	FA	LA	RE	RE
30	C	RE	LA	MI	MI	SOL	DO3	MI	SI	SI	MI	FA	FA
31	T	DO3	SI	LA	LA	LA	FA	LA	SOL	SOL	LA	SI	SI
32	G	FA	SOL	MI	SI	SI	MI	MI	LA	RE	SI	SOL	SOL
33	C	MI	LA	RE	SOL	SOL	RE	RE	SI	FA	SOL	LA	LA
34	C	RE	SI	DO3	RE	RE	DO3	DO3	DO4	SI	RE	SI	SI
35	C	DO3	DO4	DO3	DO3	DO3	DO3	DO3	DO4	DO4	DO3	DO4	DO4
36	C	DO3	DO4	DO3	DO3	DO3	DO3	DO3	DO4	DO4	DO3	DO4	DO4
37	T	DO3	DO4	FA	FA	FA	FA	FA	SOL	SOL	FA	DO4	DO4
38	T	DO3	DO4	SI	SI	SI	SI	SI	RE	RE	SI	DO4	DO4
39	T	DO3	DO4	DO4	DO4	DO4	DO4	DO4	DO3	DO3	DO4	DO4	DO4
40	C	FA	SOL	SOL	SOL	SOL	SOL	SOL	FA	FA	SOL	SOL	SOL
41	C	SI	RE	RE	RE	RE	RE	RE	SI	SI	RE	RE	RE
42	C	DO4	DO3	DO3	DO3	DO3	DO3	DO3	DO4	DO4	DO3	DO3	DO3
43	G	DO4	DO3	FA	FA	FA	FA	FA	SOL	SOL	FA	DO3	DO3
44	T	SOL	FA	SI	MI	MI	SI	SI	RE	LA	MI	FA	FA
45	C	LA	MI	SOL	RE	RE	SOL	SOL	FA	SI	RE	MI	MI



46	C	SI	RE	RE	DO3	DO3	RE	RE	SI	DO4	DO3	RE	RE
47	T	SOL	FA	FA	FA	FA	FA	FA	SOL	SOL	FA	FA	FA
48	G	LA	MI	MI	SI	SI	MI	MI	LA	RE	SI	MI	MI
49	G	SI	RE	RE	DO4	DO4	RE	RE	SI	DO3	DO4	RE	RE
50	G	DO4	DO3	DO3	DO4	DO4	DO3	DO3	DO4	DO3	DO4	DO3	DO3
51	T	SOL	FA	FA	SOL	SOL	FA	FA	SOL	FA	SOL	FA	FA
52	A	LA	SI	MI	RE	LA	MI	MI	RE	MI	RE	MI	MI
53	C	MI	SOL	LA	DO3	MI	RE	RE	FA	LA	FA	LA	RE
54	C	RE	RE	SI	DO3	RE	DO3	DO3	SI	SI	SI	SI	DO3
55	C	DO3	DO3	DO4	DO3	DO3	DO3	DO3	DO4	DO4	DO4	DO4	DO3
56	C	DO3	DO3	DO4	DO3	DO3	DO3	DO3	DO4	DO4	DO4	DO4	DO3
57	G	FA	DO3	DO4	FA	FA	FA	FA	SOL	SOL	DO4	SOL	DO3
58	A	SI	FA	SOL	MI	MI	SI	MI	RE	RE	SOL	LA	FA
59	G	SOL	MI	LA	LA	LA	SOL	LA	FA	FA	LA	MI	MI
60	T	RE	LA	SI	MI	MI	LA	SI	MI	SI	MI	LA	LA
61	C	FA	MI	SOL	RE	RE	MI	SOL	LA	DO4	RE	MI	MI
62	T	MI	LA	LA	FA	FA	LA	LA	MI	SOL	FA	LA	LA
63	C	LA	MI	MI	MI	MI	MI	MI	LA	LA	MI	MI	MI
64	C	SI	RE	RE	RE	RE	RE	RE	SI	SI	RE	RE	RE
65	C	DO4	DO3	DO3	DO3	DO3	DO3	DO3	DO4	DO4	DO3	DO3	DO3
66	C	DO4	DO3	DO3	DO3	DO3	DO3	DO3	DO4	DO4	DO3	DO3	DO3
67	C	DO4	DO3	DO3	DO3	DO3	DO3	DO3	DO4	DO4	DO3	DO3	DO3
68	G	DO4	DO3	FA	FA	FA	FA	FA	SOL	SOL	FA	DO3	DO3
69	A	DO4	FA	MI	MI	MI	SI	MI	RE	RE	MI	FA	FA
70	C	SOL	MI	LA	RE	RE	SOL	RE	FA	FA	LA	SI	MI
71	C	RE	RE	SI	DO3	DO3	RE	DO3	SI	SI	SI	DO4	RE
72	T	DO3	FA	DO4	FA	FA	FA	FA	SOL	SOL	DO4	DO4	FA
73	C	FA	MI	SOL	MI	MI	MI	MI	LA	LA	SOL	SOL	MI
74	G	SI	RE	LA	LA	LA	LA	LA	MI	MI	LA	RE	RE
75	G	DO4	DO3	SI	SI	SI	SI	SI	RE	RE	SI	DO3	DO3
76	G	DO4	DO3	DO4	DO4	DO4	DO4	DO4	DO3	DO3	DO4	DO3	DO3
77	T	SOL	FA	DO4	SOL	SOL	DO4	DO4	DO3	FA	SOL	FA	FA
78	C	LA	MI	SOL	RE	RE	SOL	SOL	FA	SI	RE	MI	MI
79	C	SI	RE	RE	DO3	DO3	RE	RE	SI	DO4	DO3	RE	RE
80	C	DO4	DO3	DO3	DO3	DO3	DO3	DO3	DO4	DO4	DO3	DO3	DO3
81	A	DO4	FA	DO3	FA	FA	FA	FA	SOL	SOL	DO3	DO3	FA
82	G	SOL	MI	FA	SI	SI	MI	SI	LA	LA	FA	DO3	MI
83	G	RE	RE	SI	DO4	DO4	RE	DO4	SI	SI	SI	DO3	RE
84	T	DO3	FA	DO4	SOL	SOL	FA	DO4	SOL	DO4	SOL	FA	FA
85	A	FA	SI	SOL	RE	LA	MI	SOL	RE	SOL	RE	MI	MI
86	T	MI	SOL	LA	FA	MI	LA	LA	FA	LA	FA	LA	LA
87	G	LA	RE	MI	SI	LA	MI	MI	SI	MI	SI	MI	MI
88	C	MI	FA	RE	SOL	MI	RE	RE	DO4	LA	SOL	LA	LA
89	T	RE	SI	FA	LA	LA	FA	FA	SOL	MI	LA	SI	SI
90	C	FA	SOL	MI	MI	MI	MI	MI	LA	LA	MI	SOL	SOL
91	C	SI	RE	RE	RE	RE	RE	RE	SI	SI	RE	RE	RE
92	C	DO4	DO3	DO3	DO3	DO3	DO3	DO3	DO4	DO4	DO3	DO3	DO3
93	A	DO4	FA	DO3	FA	FA	FA	FA	SOL	SOL	DO3	DO3	FA
94	C	SOL	MI	FA	MI	MI	MI	MI	LA	LA	FA	FA	MI
95	C	RE	RE	SI	RE	RE	RE	RE	SI	SI	SI	SI	RE
96	T	DO3	FA	DO4	FA	FA	FA	FA	SOL	SOL	DO4	DO4	FA
97	C	FA	MI	SOL	MI	MI	MI	MI	LA	LA	SOL	SOL	MI
98	C	SI	RE	RE	RE	RE	RE	RE	SI	SI	RE	RE	RE
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100	C	SOL	MI	FA	MI	MI	MI	MI	LA	LA	FA	FA	MI
101	C	RE	RE	SI	RE	RE	RE	RE	SI	SI	SI	SI	RE
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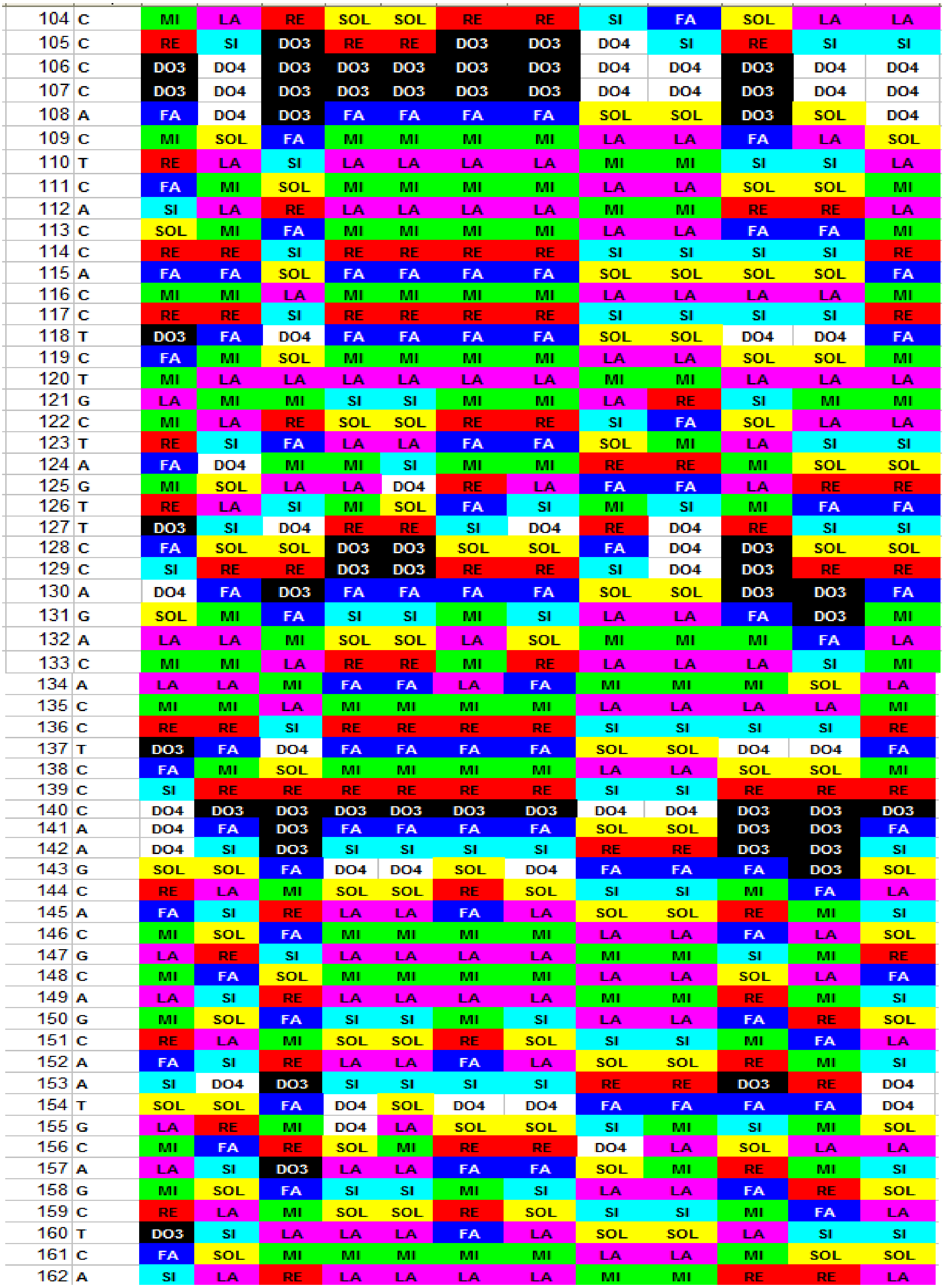

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117	C	RE	RE	SI	RE	RE	RE	RE	SI	SI	SI	SI	RE
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143	G	SOL	SOL	FA	DO4	DO4	SOL	DO4	FA	FA	FA	DO3	SOL
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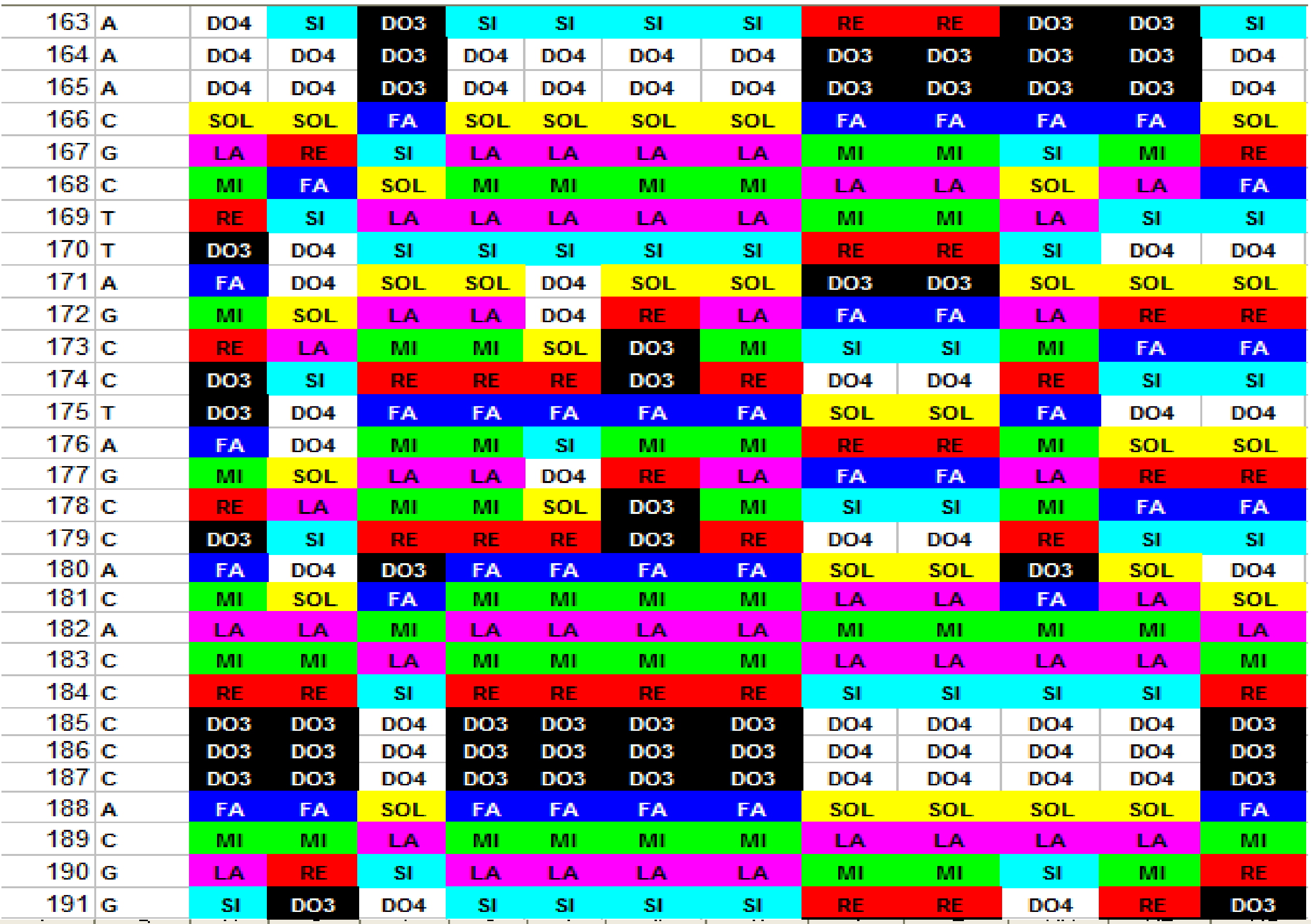

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167	G	LA	RE	SI	LA	LA	LA	LA	MI	MI	SI	MI	RE
168	C	MI	FA	SOL	MI	MI	MI	MI	LA	LA	SOL	LA	FA
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177	G	MI	SOL	LA	LA	DO4	RE	LA	FA	FA	LA	RE	RE
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185	C	DO3	DO3	DO4	DO3	DO3	DO3	DO3	DO4	DO4	DO4	DO4	DO3
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188	A	FA	FA	SOL	FA	FA	FA	FA	SOL	SOL	SOL	SOL	FA
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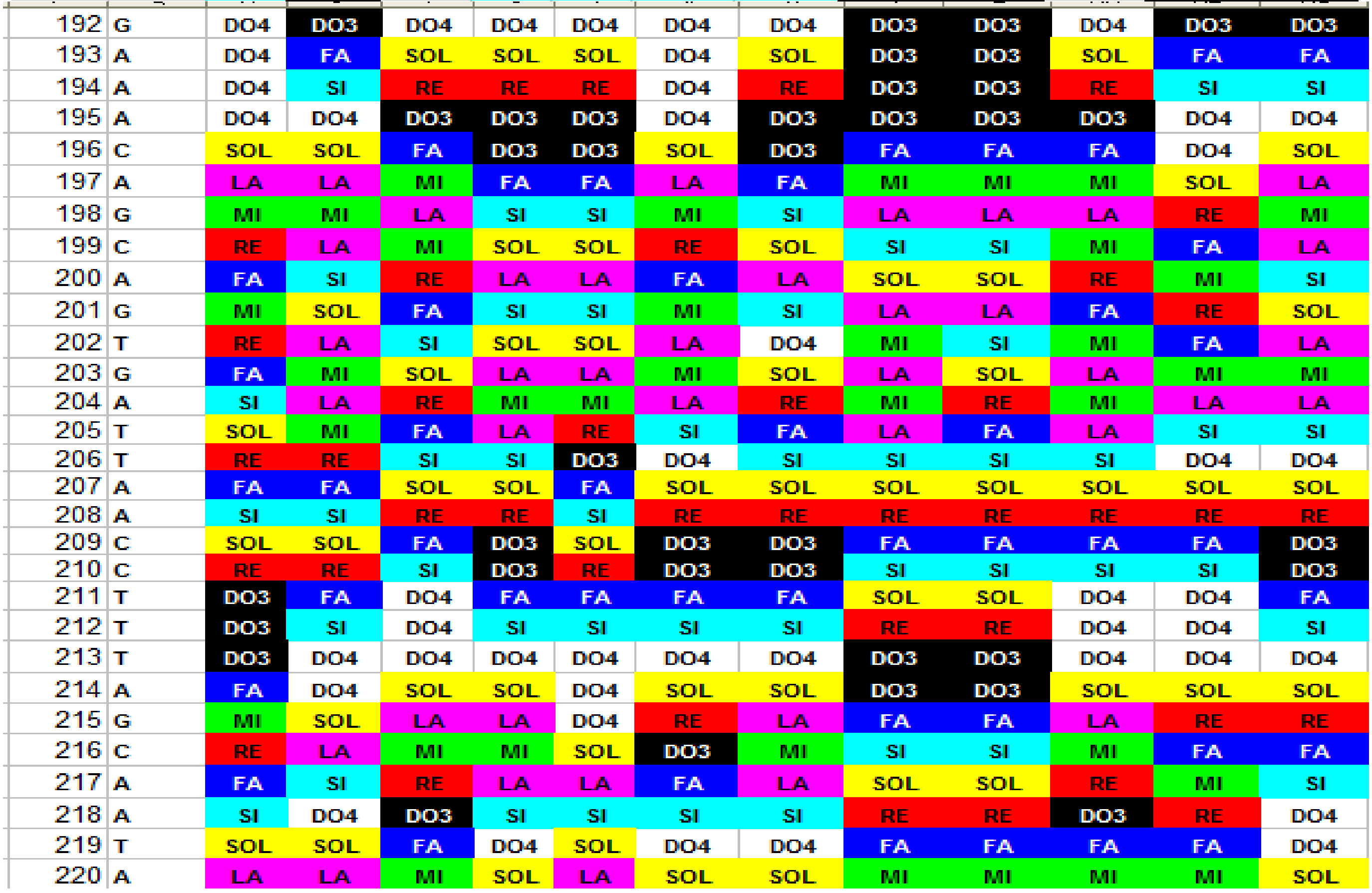

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196	C	SOL	SOL	FA	DO3	DO3	SOL	DO3	FA	FA	FA	DO4	SOL
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214	A	FA	DO4	SOL	SOL	DO4	SOL	SOL	DO3	DO3	SOL	SOL	SOL
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217	A	FA	SI	RE	LA	LA	FA	LA	SOL	SOL	RE	MI	SI
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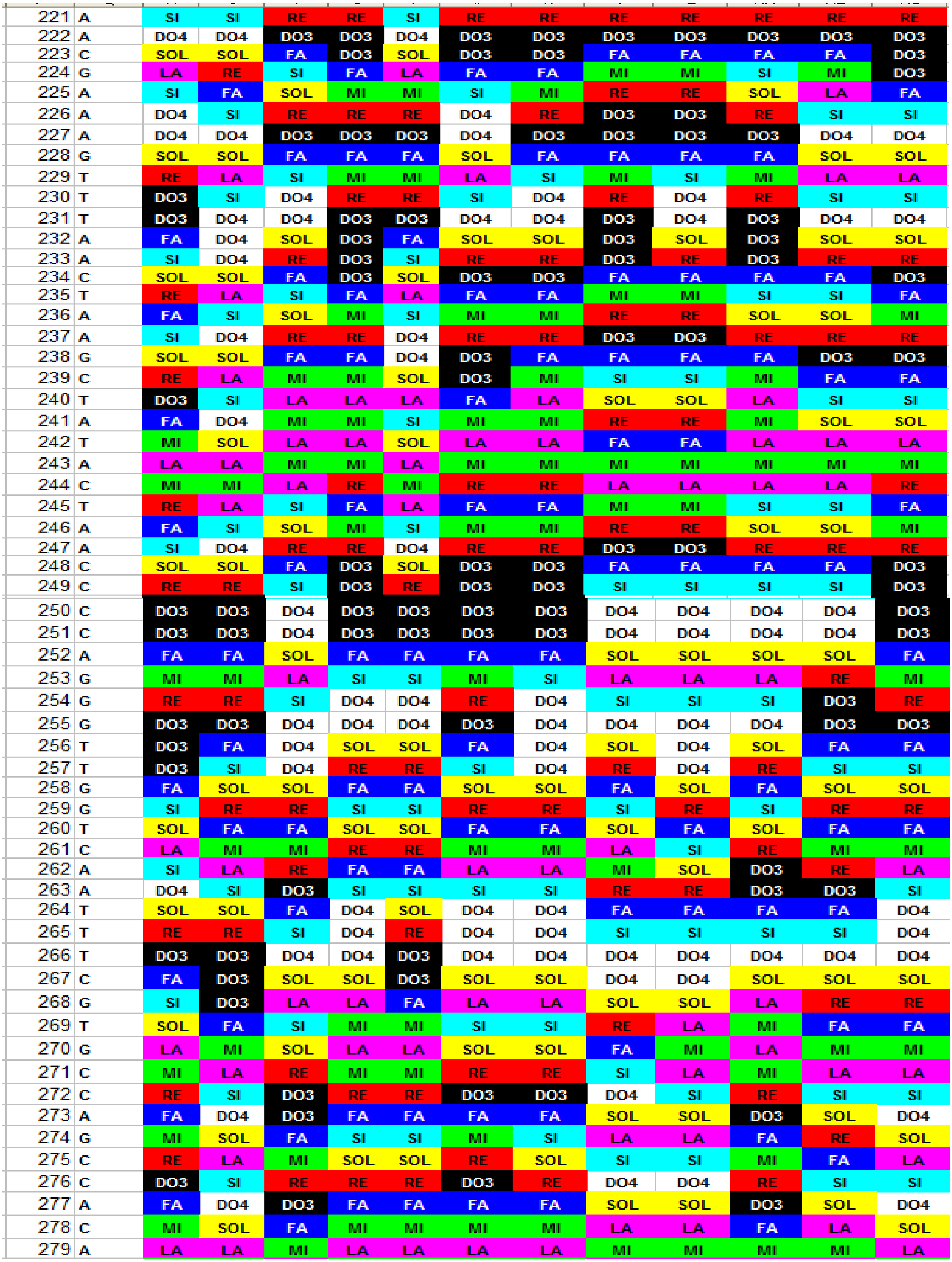

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260	T	SOL	FA	FA	SOL	SOL	FA	FA	SOL	FA	SOL	FA	FA
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267	C	FA	DO3	SOL	SOL	DO3	SOL	SOL	DO4	DO4	SOL	SOL	SOL
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271	C	MI	LA	RE	MI	MI	RE	RE	SI	LA	MI	LA	LA
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273	A	FA	DO4	DO3	FA	FA	FA	FA	SOL	SOL	DO3	SOL	DO4
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275	C	RE	LA	MI	SOL	SOL	RE	SOL	SI	SI	MI	FA	LA
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277	A	FA	DO4	DO3	FA	FA	FA	FA	SOL	SOL	DO3	SOL	DO4
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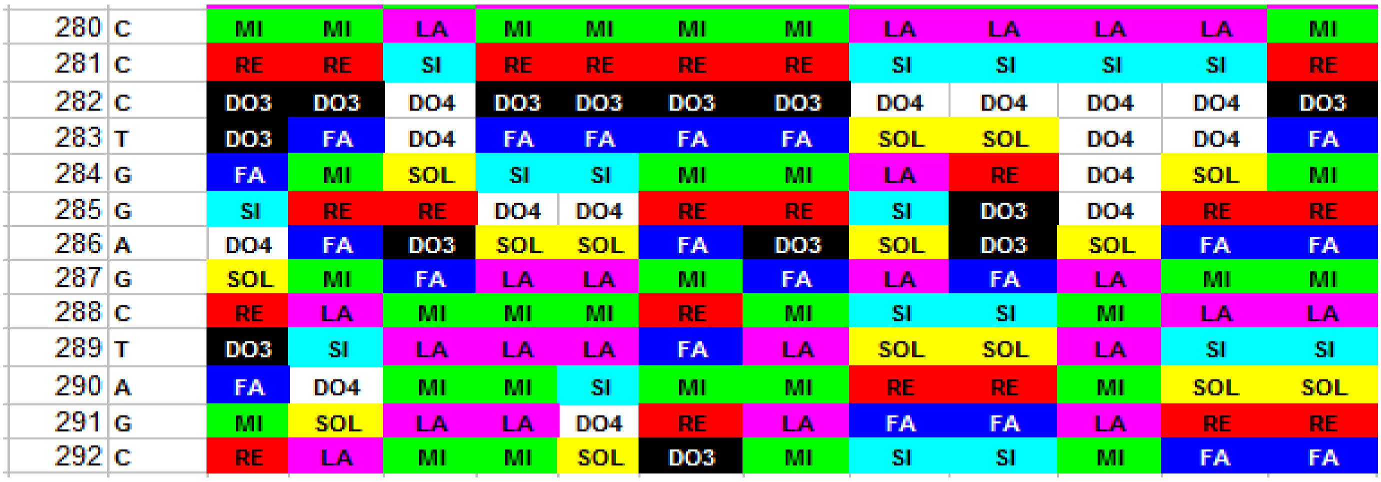

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286	A	DO4	FA	DO3	SOL	SOL	FA	DO3	SOL	DO3	SOL	FA	FA
287	G	SOL	MI	FA	LA	LA	MI	FA	LA	FA	LA	MI	MI
288	C	RE	LA	MI	MI	MI	RE	MI	SI	SI	MI	LA	LA
289	T	DO3	SI	LA	LA	LA	FA	LA	SOL	SOL	LA	SI	SI
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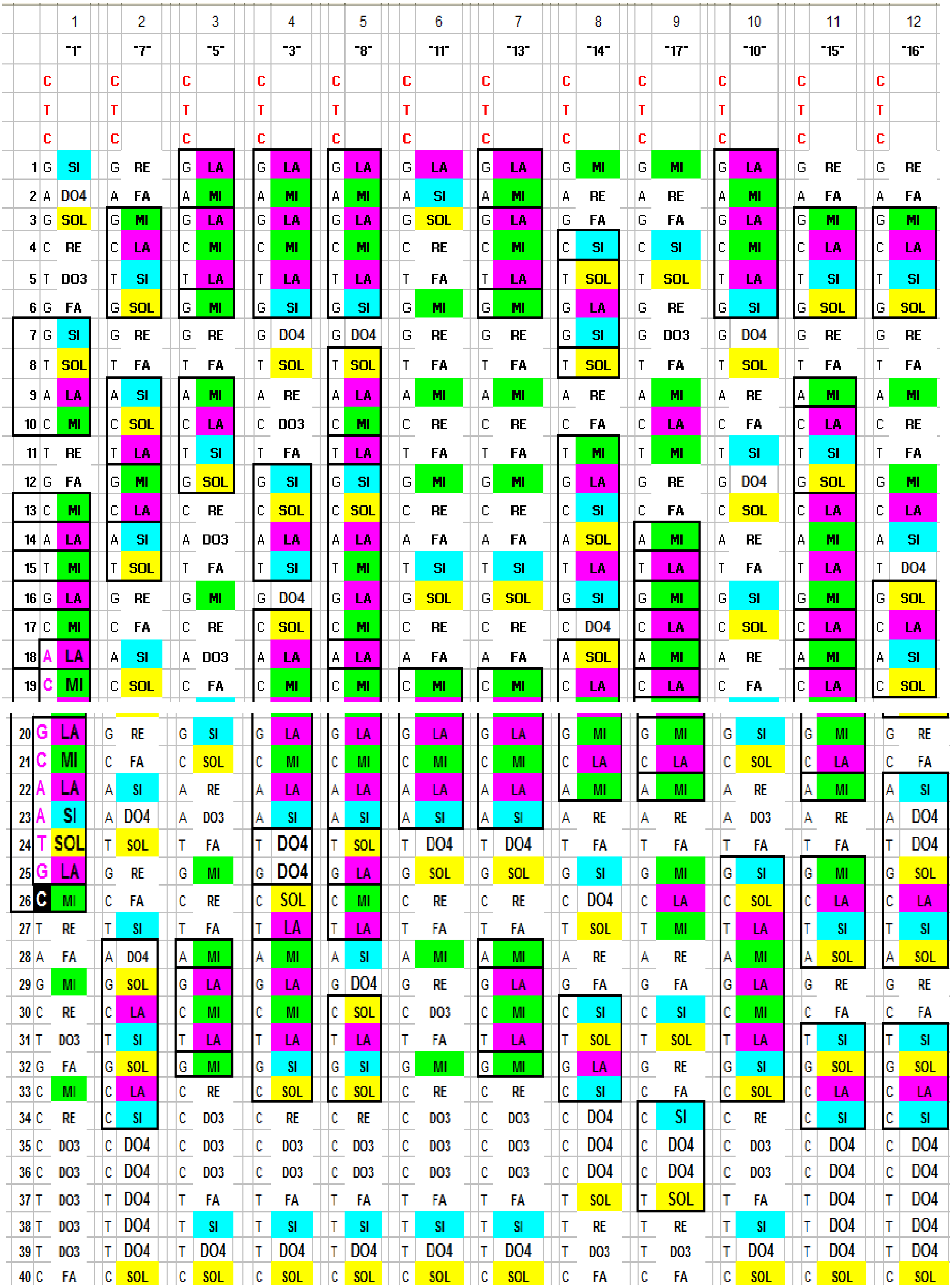
291	G	MI	SOL	LA	LA	DO4	RE	LA	FA	FA	LA	RE	RE
292	C	RE	LA	MI	MI	SOL	DO3	MI	SI	SI	MI	FA	FA

Fig. 8.6

Nella pagina successiva e in quelle che seguono (Fig. 8.7) sono mostrate (unite insieme) le tabelle nelle quali sono evidenziati **SOLO** i **Colori/Note** del **Trend n° 1 (T=0; C=1; G=2; A=3)** che sono stati attribuiti alla **Sequenza 3'-UTR**.

ATTENZIONE: *Per un'analisi completa della **sequenza 3'-UTR**, la procedure appena descritta deve essere eseguita considerando anche **gli altri 23 Trends***.



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	C		C		C		C		C		C		C		C		C		C		C		C	
	T		T		T		T		T		T		T		T		T		T		T		T	
	C		C		C		C		C		C		C		C		C		C		C		C	
1	G	SI	G	RE	G	LA	G	LA	G	LA	G	LA	G	LA	G	MI	G	MI	G	LA	G	RE	G	RE
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3	G	SOL	G	MI	G	LA	G	LA	G	LA	G	SOL	G	LA	G	FA	G	FA	G	LA	G	MI	G	MI
4	C	RE	C	LA	C	MI	C	MI	C	MI	C	RE	C	MI	C	SI	C	SI	C	MI	C	LA	C	LA
5	T	DO3	T	SI	T	LA	T	LA	T	LA	T	FA	T	LA	T	SOL	T	SOL	T	LA	T	SI	T	SI
6	G	FA	G	SOL	G	MI	G	SI	G	SI	G	MI	G	MI	G	LA	G	RE	G	SI	G	SOL	G	SOL
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18	A	LA	A	SI	A	DO3	A	LA	A	LA	A	FA	A	FA	A	SOL	A	MI	A	RE	A	MI	A	SI
19	C	MI	C	SOL	C	FA	C	MI	C	MI	C	MI	C	MI	C	LA	C	LA	C	FA	C	LA	C	SOL
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27	T	RE	T	SI	T	FA	T	LA	T	LA	T	FA	T	FA	T	SOL	T	MI	T	LA	T	SI	T	SI
28	A	FA	A	DO4	A	MI	A	MI	A	SI	A	MI	A	MI	A	RE	A	RE	A	MI	A	SOL	A	SOL
29	G	MI	G	SOL	G	LA	G	LA	G	DO4	G	RE	G	LA	G	FA	G	FA	G	LA	G	RE	G	RE
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32	G	FA	G	SOL	G	MI	G	SI	G	SI	G	MI	G	MI	G	LA	G	RE	G	SI	G	SOL	G	SOL
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37	T	DO3	T	DO4	T	FA	T	FA	T	FA	T	FA	T	FA	T	SOL	T	SOL	T	FA	T	DO4	T	DO4
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39	T	DO3	T	DO4	T	DO4	T	DO4	T	DO4	T	DO4	T	DO4	T	DO3	T	DO3	T	DO4	T	DO4	T	DO4
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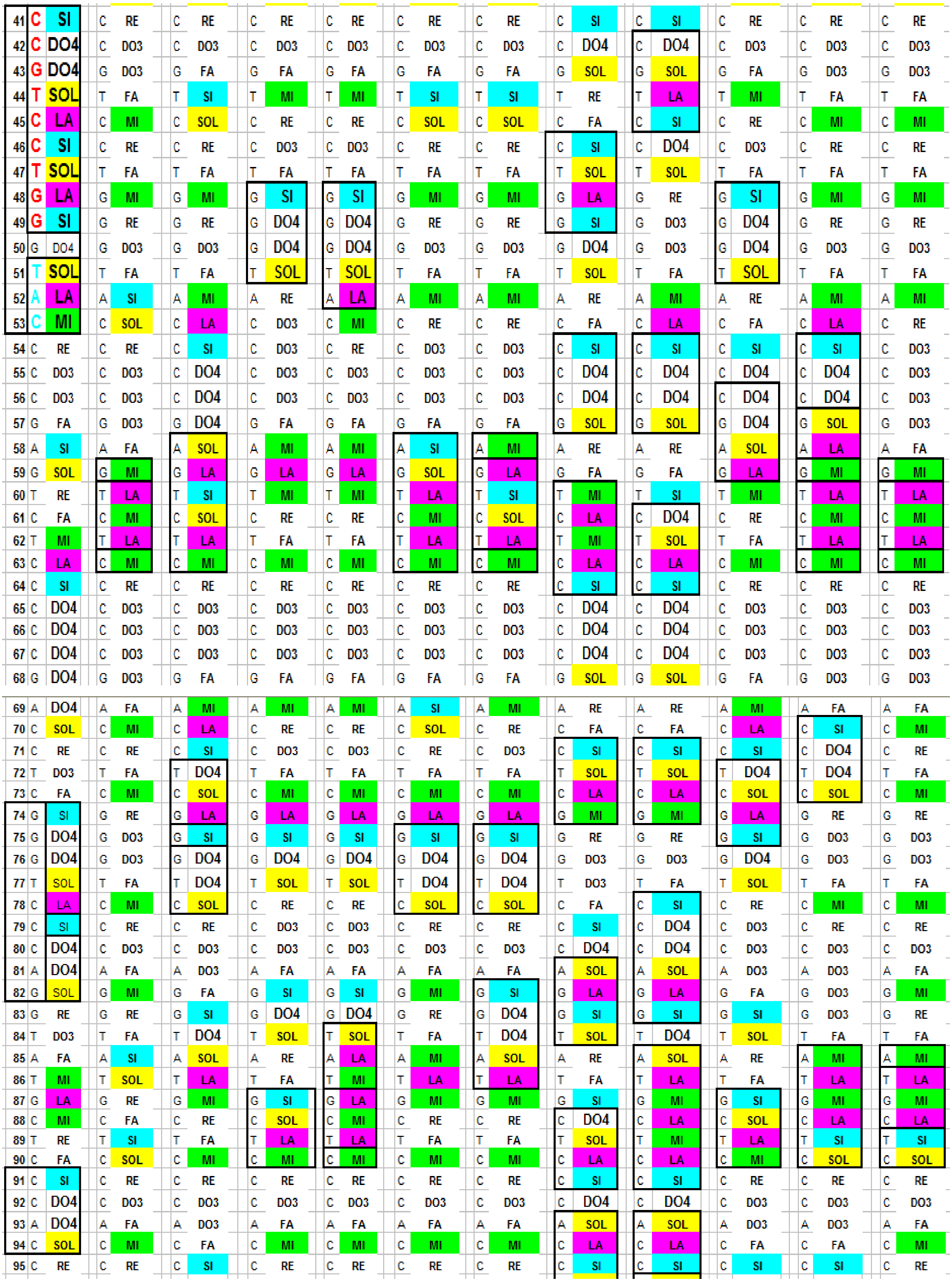

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48	G	LA	G	MI	G	MI	G	SI	G	SI	G	MI	G	MI	G	LA	G	RE	G	SI	G	MI	G	MI
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50	G	DO4	G	DO3	G	DO3	G	DO4	G	DO4	G	DO3	G	DO3	G	DO4	G	DO3	G	DO4	G	DO3	G	DO3
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57	G	FA	G	DO3	G	DO4	G	FA	G	FA	G	FA	G	FA	G	SOL	G	SOL	G	DO4	G	SOL	G	DO3
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67	C	DO4	C	DO3	C	DO3	C	DO3	C	DO3	C	DO3	C	DO3	C	DO4	C	DO4	C	DO3	C	DO3	C	DO3
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74	G	SI	G	RE	G	LA	G	LA	G	LA	G	LA	G	LA	G	MI	G	MI	G	LA	G	RE	G	RE
75	G	DO4	G	DO3	G	SI	G	SI	G	SI	G	SI	G	SI	G	RE	G	RE	G	SI	G	DO3	G	DO3
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82	G	SOL	G	MI	G	FA	G	SI	G	SI	G	MI	G	SI	G	LA	G	LA	G	FA	G	DO3	G	MI
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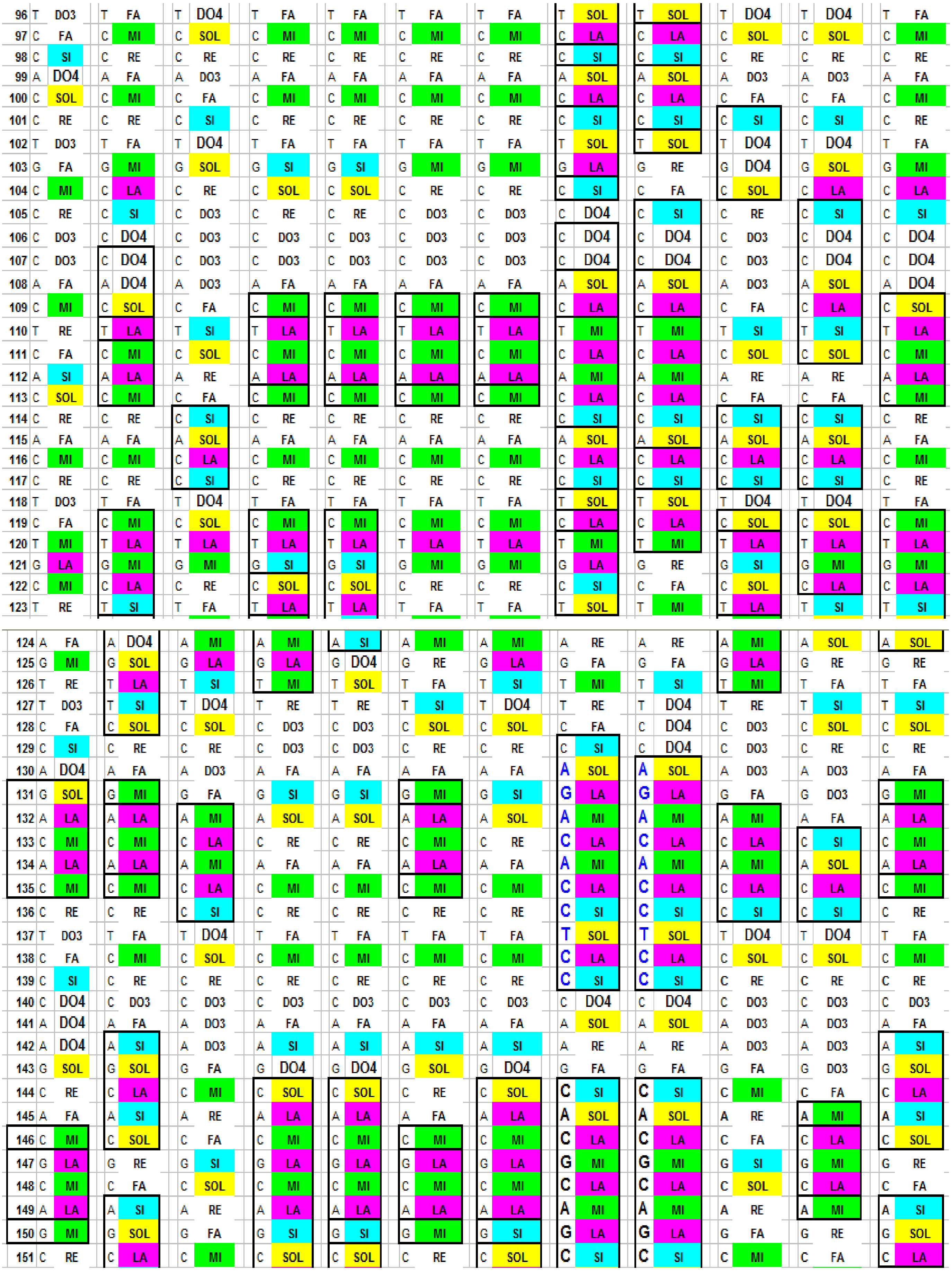

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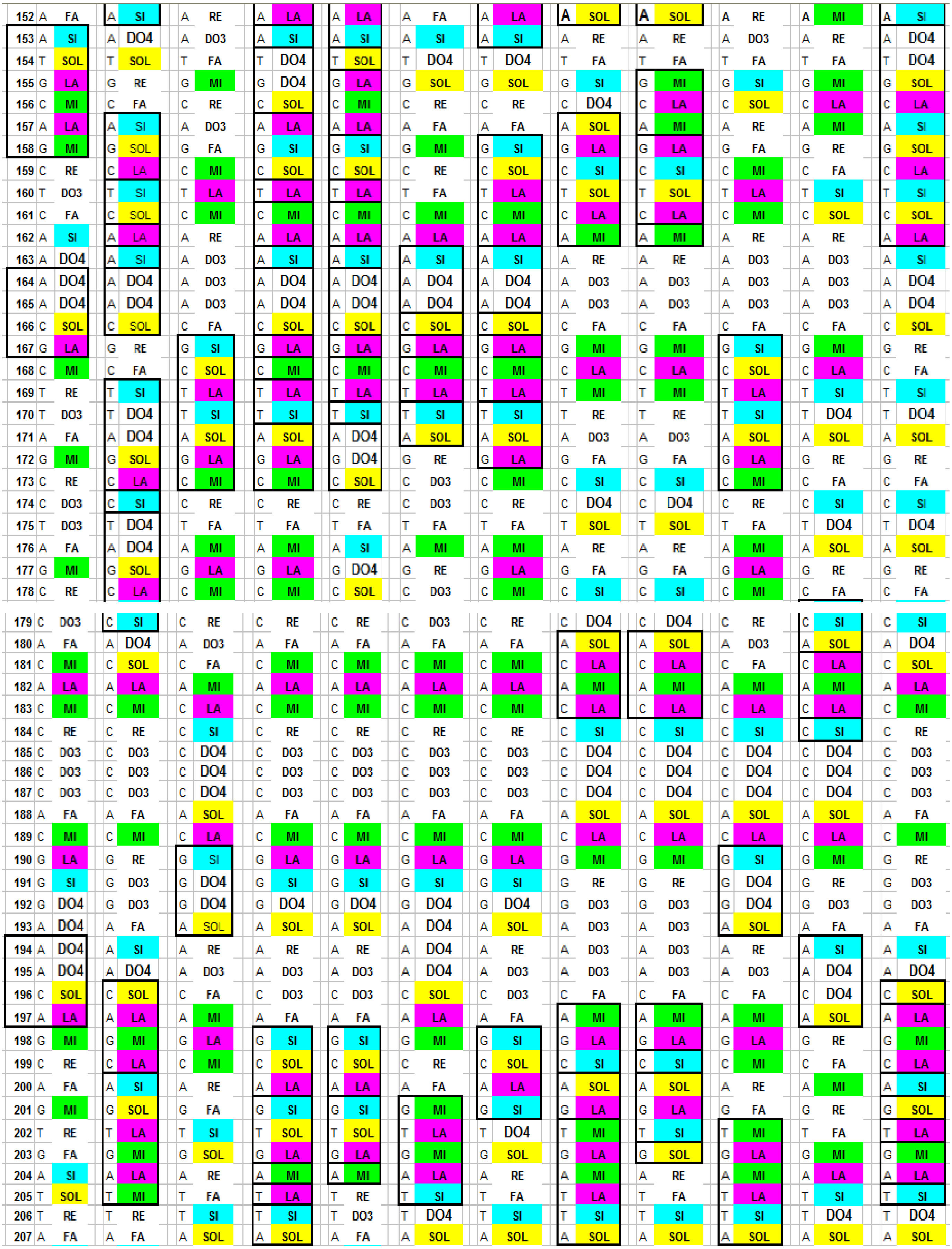

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165	A DO4	A DO4	A DO3	A DO4	A DO4	A DO4	A DO4	A DO3	A DO3	A DO3	A DO3	A DO4
166	C SOL	C SOL	C FA	C SOL	C SOL	C SOL	C SOL	C FA	C FA	C FA	C FA	C SOL
167	G LA	G RE	G SI	G LA	G LA	G LA	G LA	G MI	G MI	G SI	G MI	G RE
168	C MI	C FA	C SOL	C MI	C MI	C MI	C MI	C LA	C LA	C SOL	C LA	C FA
169	T RE	T SI	T LA	T LA	T LA	T LA	T LA	T MI	T MI	T LA	T SI	T SI
170	T DO3	T DO4	T SI	T SI	T SI	T SI	T SI	T RE	T RE	T SI	T DO4	T DO4
171	A FA	A DO4	A SOL	A SOL	A DO4	A SOL	A SOL	A DO3	A DO3	A SOL	A SOL	A SOL
172	G MI	G SOL	G LA	G LA	G DO4	G RE	G LA	G FA	G FA	G LA	G RE	G RE
173	C RE	C LA	C MI	C MI	C SOL	C DO3	C MI	C SI	C SI	C MI	C FA	C FA
174	C DO3	C SI	C RE	C RE	C RE	C DO3	C RE	C DO4	C DO4	C RE	C SI	C SI
175	T DO3	T DO4	T FA	T FA	T FA	T FA	T FA	T SOL	T SOL	T FA	T DO4	T DO4
176	A FA	A DO4	A MI	A MI	A SI	A MI	A MI	A RE	A RE	A MI	A SOL	A SOL
177	G MI	G SOL	G LA	G LA	G DO4	G RE	G LA	G FA	G FA	G LA	G RE	G RE
178	C RE	C LA	C MI	C MI	C SOL	C DO3	C MI	C SI	C SI	C MI	C FA	C FA
179	C DO3	C SI	C RE	C RE	C RE	C DO3	C RE	C DO4	C DO4	C RE	C SI	C SI
180	A FA	A DO4	A DO3	A FA	A FA	A FA	A FA	A SOL	A SOL	A DO3	A SOL	A DO4
181	C MI	C SOL	C FA	C MI	C MI	C MI	C MI	C LA	C LA	C FA	C LA	C SOL
182	A LA	A LA	A MI	A LA	A LA	A LA	A LA	A MI	A MI	A MI	A MI	A LA
183	C MI	C MI	C LA	C MI	C MI	C MI	C MI	C LA	C LA	C LA	C LA	C MI
184	C RE	C RE	C SI	C RE	C RE	C RE	C RE	C SI	C SI	C SI	C SI	C RE
185	C DO3	C DO3	C DO4	C DO3	C DO3	C DO3	C DO3	C DO4	C DO4	C DO4	C DO4	C DO3
186	C DO3	C DO3	C DO4	C DO3	C DO3	C DO3	C DO3	C DO4	C DO4	C DO4	C DO4	C DO3
187	C DO3	C DO3	C DO4	C DO3	C DO3	C DO3	C DO3	C DO4	C DO4	C DO4	C DO4	C DO3
188	A FA	A FA	A SOL	A FA	A FA	A FA	A FA	A SOL	A SOL	A SOL	A SOL	A FA
189	C MI	C MI	C LA	C MI	C MI	C MI	C MI	C LA	C LA	C LA	C LA	C MI
190	G LA	G RE	G SI	G LA	G LA	G LA	G LA	G MI	G MI	G SI	G MI	G RE
191	G SI	G DO3	G DO4	G SI	G SI	G SI	G SI	G RE	G RE	G DO4	G RE	G DO3
192	G DO4	G DO3	G DO4	G DO4	G DO4	G DO4	G DO4	G DO3	G DO3	G DO4	G DO3	G DO3
193	A DO4	A FA	A SOL	A SOL	A SOL	A DO4	A SOL	A DO3	A DO3	A SOL	A FA	A FA
194	A DO4	A SI	A RE	A RE	A RE	A DO4	A RE	A DO3	A DO3	A RE	A SI	A SI
195	A DO4	A DO4	A DO3	A DO3	A DO3	A DO4	A DO3	A DO3	A DO3	A DO3	A DO4	A DO4
196	C SOL	C SOL	C FA	C DO3	C DO3	C SOL	C DO3	C FA	C FA	C FA	C DO4	C SOL
197	A LA	A LA	A MI	A FA	A FA	A LA	A FA	A MI	A MI	A MI	A SOL	A LA
198	G MI	G MI	G LA	G SI	G SI	G MI	G SI	G LA	G LA	G LA	G RE	G MI
199	C RE	C LA	C MI	C SOL	C SOL	C RE	C SOL	C SI	C SI	C MI	C FA	C LA
200	A FA	A SI	A RE	A LA	A LA	A FA	A LA	A SOL	A SOL	A RE	A MI	A SI
201	G MI	G SOL	G FA	G SI	G SI	G MI	G SI	G LA	G LA	G FA	G RE	G SOL
202	T RE	T LA	T SI	T SOL	T SOL	T LA	T DO4	T MI	T SI	T MI	T FA	T LA
203	G FA	G MI	G SOL	G LA	G LA	G MI	G SOL	G LA	G SOL	G LA	G MI	G MI
204	A SI	A LA	A RE	A MI	A MI	A LA	A RE	A MI	A RE	A MI	A LA	A LA
205	T SOL	T MI	T FA	T LA	T RE	T SI	T FA	T LA	T FA	T LA	T SI	T SI
206	T RE	T RE	T SI	T SI	T DO3	T DO4	T SI	T SI	T SI	T SI	T DO4	T DO4
207	A FA	A FA	A SOL	A SOL	A FA	A SOL	A SOL	A SOL	A SOL	A SOL	A SOL	A SOL

208	A	SI	A	SI	A	RE	A	RE	A	SI	A	RE	A	RE	A	RE	A	RE	A	RE	A	RE	A	RE
209	C	SOL	C	SOL	C	FA	C	DO3	C	SOL	C	DO3	C	DO3	C	FA	C	FA	C	FA	C	FA	C	DO3
210	C	RE	C	RE	C	SI	C	DO3	C	RE	C	DO3	C	DO3	C	SI	C	SI	C	SI	C	SI	C	DO3
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212	T	DO3	T	SI	T	DO4	T	SI	T	SI	T	SI	T	SI	T	RE	T	RE	T	DO4	T	DO4	T	SI
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214	A	FA	A	DO4	A	SOL	A	SOL	A	DO4	A	SOL	A	SOL	A	DO3	A	DO3	A	SOL	A	SOL	A	SOL
215	G	MI	G	SOL	G	LA	G	LA	G	DO4	G	RE	G	LA	G	FA	G	FA	G	LA	G	RE	G	RE
216	C	RE	C	LA	C	MI	C	MI	C	SOL	C	DO3	C	MI	C	SI	C	SI	C	MI	C	FA	C	FA
217	A	FA	A	SI	A	RE	A	LA	A	LA	A	FA	A	LA	A	SOL	A	SOL	A	RE	A	MI	A	SI
218	A	SI	A	DO4	A	DO3	A	SI	A	SI	A	SI	A	SI	A	RE	A	RE	A	DO3	A	RE	A	DO4
219	T	SOL	T	SOL	T	FA	T	DO4	T	SOL	T	DO4	T	DO4	T	FA	T	FA	T	FA	T	FA	T	DO4
220	A	LA	A	LA	A	MI	A	SOL	A	LA	A	SOL	A	SOL	A	MI	A	MI	A	MI	A	MI	A	SOL
221	A	SI	A	SI	A	RE	A	RE	A	SI	A	RE	A	RE	A	RE	A	RE	A	RE	A	RE	A	RE
222	A	DO4	A	DO4	A	DO3	A	DO3	A	DO4	A	DO3	A	DO3	A	DO3	A	DO3	A	DO3	A	DO3	A	DO3
223	C	SOL	C	SOL	C	FA	C	DO3	C	SOL	C	DO3	C	DO3	C	FA	C	FA	C	FA	C	FA	C	DO3
224	G	LA	G	RE	G	SI	G	FA	G	LA	G	FA	G	FA	G	MI	G	MI	G	SI	G	MI	G	DO3
225	A	SI	A	FA	A	SOL	A	MI	A	MI	A	SI	A	MI	A	RE	A	RE	A	SOL	A	LA	A	FA
226	A	DO4	A	SI	A	RE	A	RE	A	RE	A	DO4	A	RE	A	DO3	A	DO3	A	RE	A	SI	A	SI
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228	G	SOL	G	SOL	G	FA	G	FA	G	FA	G	SOL	G	FA	G	FA	G	FA	G	FA	G	SOL	G	SOL
229	T	RE	T	LA	T	SI	T	MI	T	MI	T	LA	T	SI	T	MI	T	SI	T	MI	T	LA	T	LA
230	T	DO3	T	SI	T	DO4	T	RE	T	RE	T	SI	T	DO4	T	RE	T	DO4	T	RE	T	SI	T	SI
231	T	DO3	T	DO4	T	DO4	T	DO3	T	DO3	T	DO4	T	DO4	T	DO3	T	DO4	T	DO3	T	DO4	T	DO4
232	A	FA	A	DO4	A	SOL	A	DO3	A	FA	A	SOL	A	SOL	A	DO3	A	SOL	A	DO3	A	SOL	A	SOL
233	A	SI	A	DO4	A	RE	A	DO3	A	SI	A	RE	A	RE	A	DO3	A	RE	A	DO3	A	RE	A	RE
234	C	SOL	C	SOL	C	FA	C	DO3	C	SOL	C	DO3	C	DO3	C	FA	C	FA	C	FA	C	FA	C	DO3
235	T	RE	T	LA	T	SI	T	FA	T	LA	T	FA	T	FA	T	MI	T	MI	T	SI	T	SI	T	FA
236	A	FA	A	SI	A	SOL	A	MI	A	SI	A	MI	A	MI	A	RE	A	RE	A	SOL	A	SOL	A	MI
237	A	SI	A	DO4	A	RE	A	RE	A	DO4	A	RE	A	RE	A	DO3	A	DO3	A	RE	A	RE	A	RE
238	G	SOL	G	SOL	G	FA	G	FA	G	DO4	G	DO3	G	FA	G	FA	G	FA	G	FA	G	DO3	G	DO3
239	C	RE	C	LA	C	MI	C	MI	C	SOL	C	DO3	C	MI	C	SI	C	SI	C	MI	C	FA	C	FA
240	T	DO3	T	SI	T	LA	T	LA	T	LA	T	FA	T	LA	T	SOL	T	SOL	T	LA	T	SI	T	SI
241	A	FA	A	DO4	A	MI	A	MI	A	SI	A	MI	A	MI	A	RE	A	RE	A	MI	A	SOL	A	SOL
242	T	MI	T	SOL	T	LA	T	LA	T	SOL	T	LA	T	LA	T	FA	T	FA	T	LA	T	LA	T	LA
243	A	LA	A	LA	A	MI	A	MI	A	LA	A	MI	A	MI	A	MI	A	MI	A	MI	A	MI	A	MI
244	C	MI	C	MI	C	LA	C	RE	C	MI	C	RE	C	RE	C	LA	C	LA	C	LA	C	LA	C	RE
245	T	RE	T	LA	T	SI	T	FA	T	LA	T	FA	T	FA	T	MI	T	MI	T	SI	T	SI	T	FA
246	A	FA	A	SI	A	SOL	A	MI	A	SI	A	MI	A	MI	A	RE	A	RE	A	SOL	A	SOL	A	MI
247	A	SI	A	DO4	A	RE	A	RE	A	DO4	A	RE	A	RE	A	DO3	A	DO3	A	RE	A	RE	A	RE
248	C	SOL	C	SOL	C	FA	C	DO3	C	SOL	C	DO3	C	DO3	C	FA	C	FA	C	FA	C	FA	C	DO3
249	C	RE	C	RE	C	SI	C	DO3	C	RE	C	DO3	C	DO3	C	SI	C	SI	C	SI	C	SI	C	DO3
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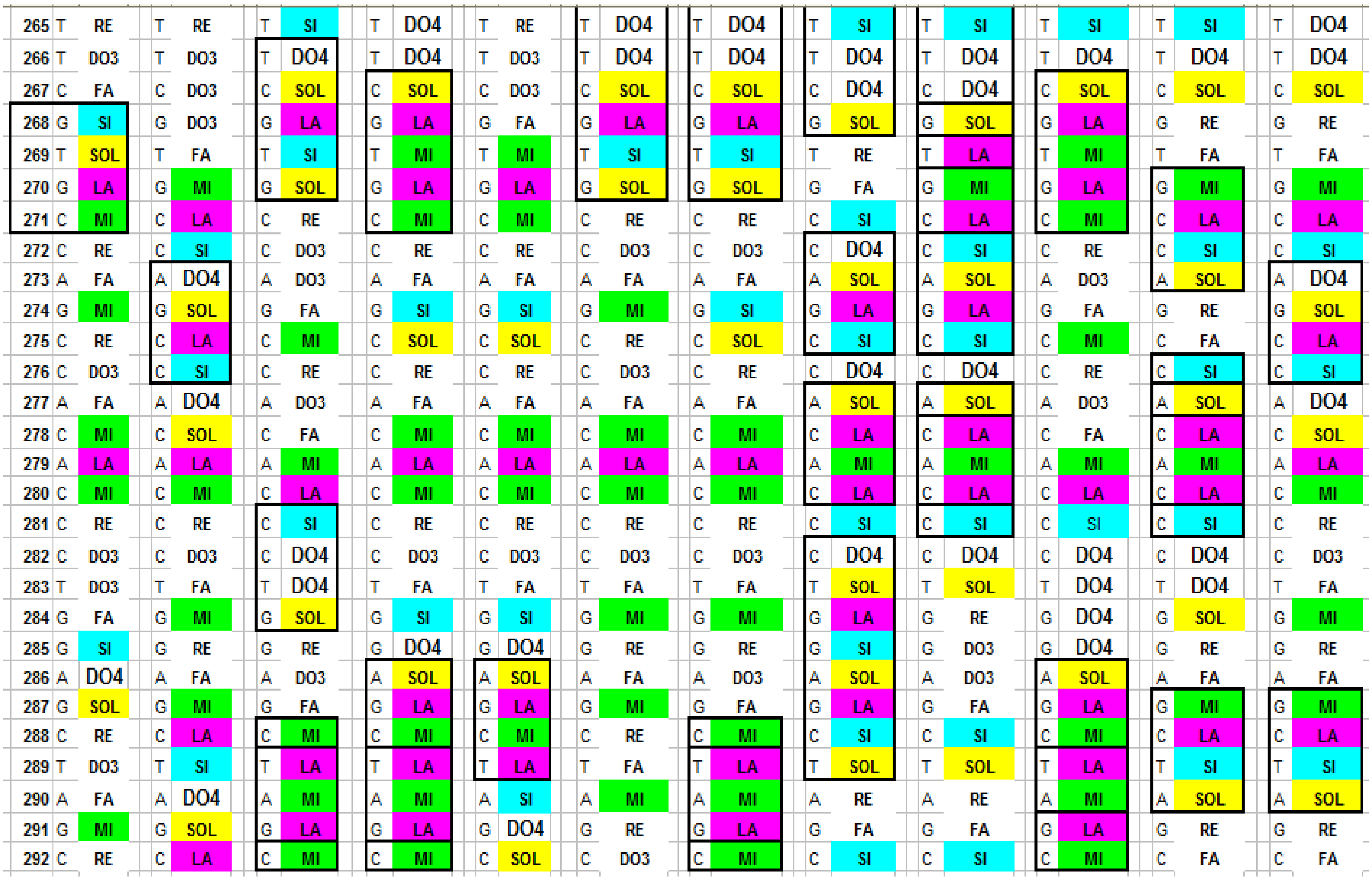
252	A	FA	A	FA	A	SOL	A	FA	A	FA	A	FA	A	FA	A	SOL	A	SOL	A	SOL	A	SOL	A	FA
253	G	MI	G	MI	G	LA	G	SI	G	SI	G	MI	G	SI	G	LA	G	LA	G	LA	G	RE	G	MI
254	G	RE	G	RE	G	SI	G	DO4	G	DO4	G	RE	G	DO4	G	SI	G	SI	G	SI	G	DO3	G	RE
255	G	DO3	G	DO3	G	DO4	G	DO4	G	DO4	G	DO3	G	DO4	G	DO4	G	DO4	G	DO4	G	DO3	G	DO3
256	T	DO3	T	FA	T	DO4	T	SOL	T	SOL	T	FA	T	DO4	T	SOL	T	DO4	T	SOL	T	FA	T	FA
257	T	DO3	T	SI	T	DO4	T	RE	T	RE	T	SI	T	DO4	T	RE	T	DO4	T	RE	T	SI	T	SI
258	G	FA	G	SOL	G	SOL	G	FA	G	FA	G	SOL	G	SOL	G	FA	G	SOL	G	FA	G	SOL	G	SOL
259	G	SI	G	RE	G	RE	G	SI	G	SI	G	RE	G	RE	G	SI	G	RE	G	SI	G	RE	G	RE
260	T	SOL	T	FA	T	FA	T	SOL	T	SOL	T	FA	T	FA	T	SOL	T	FA	T	SOL	T	FA	T	FA
261	C	LA	C	MI	C	MI	C	RE	C	RE	C	MI	C	MI	C	LA	C	SI	C	RE	C	MI	C	MI
262	A	SI	A	LA	A	RE	A	FA	A	FA	A	LA	A	LA	A	MI	A	SOL	A	DO3	A	RE	A	LA
263	A	DO4	A	SI	A	DO3	A	SI	A	SI	A	SI	A	SI	A	RE	A	RE	A	DO3	A	DO3	A	SI
264	T	SOL	T	SOL	T	FA	T	DO4	T	SOL	T	DO4	T	DO4	T	FA	T	FA	T	FA	T	FA	T	DO4



265	T	RE	T	RE	T	SI	T	DO4	T	RE	T	DO4	T	DO4	T	SI	T	SI	T	SI	T	SI	T	DO4
266	T	DO3	T	DO3	T	DO4	T	DO4	T	DO3	T	DO4	T	DO4	T	DO4	T	DO4	T	DO4	T	DO4	T	DO4
267	C	FA	C	DO3	C	SOL	C	SOL	C	DO3	C	SOL	C	SOL	C	DO4	C	DO4	C	SOL	C	SOL	C	SOL
268	G	SI	G	DO3	G	LA	G	LA	G	FA	G	LA	G	LA	G	SOL	G	SOL	G	LA	G	RE	G	RE
269	T	SOL	T	FA	T	SI	T	MI	T	MI	T	SI	T	SI	T	RE	T	LA	T	MI	T	FA	T	FA
270	G	LA	G	MI	G	SOL	G	LA	G	LA	G	SOL	G	SOL	G	FA	G	MI	G	LA	G	MI	G	MI
271	C	MI	C	LA	C	RE	C	MI	C	MI	C	RE	C	RE	C	SI	C	LA	C	MI	C	LA	C	LA
272	C	RE	C	SI	C	DO3	C	RE	C	RE	C	DO3	C	DO3	C	DO4	C	SI	C	RE	C	SI	C	SI
273	A	FA	A	DO4	A	DO3	A	FA	A	FA	A	FA	A	FA	A	SOL	A	SOL	A	DO3	A	SOL	A	DO4
274	G	MI	G	SOL	G	FA	G	SI	G	SI	G	MI	G	SI	G	LA	G	LA	G	FA	G	RE	G	SOL
275	C	RE	C	LA	C	MI	C	SOL	C	SOL	C	RE	C	SOL	C	SI	C	SI	C	MI	C	FA	C	LA
276	C	DO3	C	SI	C	RE	C	RE	C	RE	C	DO3	C	RE	C	DO4	C	DO4	C	RE	C	SI	C	SI
277	A	FA	A	DO4	A	DO3	A	FA	A	FA	A	FA	A	FA	A	SOL	A	SOL	A	DO3	A	SOL	A	DO4
278	C	MI	C	SOL	C	FA	C	MI	C	MI	C	MI	C	MI	C	LA	C	LA	C	FA	C	LA	C	SOL
279	A	LA	A	LA	A	MI	A	LA	A	LA	A	LA	A	LA	A	MI	A	MI	A	MI	A	MI	A	LA
280	C	MI	C	MI	C	LA	C	MI	C	MI	C	MI	C	MI	C	LA	C	LA	C	LA	C	LA	C	MI
281	C	RE	C	RE	C	SI	C	RE	C	RE	C	RE	C	RE	C	SI	C	SI	C	SI	C	SI	C	RE
282	C	DO3	C	DO3	C	DO4	C	DO3	C	DO3	C	DO3	C	DO3	C	DO4	C	DO4	C	DO4	C	DO4	C	DO3
283	T	DO3	T	FA	T	DO4	T	FA	T	FA	T	FA	T	FA	T	SOL	T	SOL	T	DO4	T	DO4	T	FA
284	G	FA	G	MI	G	SOL	G	SI	G	SI	G	MI	G	MI	G	LA	G	RE	G	DO4	G	SOL	G	MI
285	G	SI	G	RE	G	RE	G	DO4	G	DO4	G	RE	G	RE	G	SI	G	DO3	G	DO4	G	RE	G	RE
286	A	DO4	A	FA	A	DO3	A	SOL	A	SOL	A	FA	A	DO3	A	SOL	A	DO3	A	SOL	A	FA	A	FA
287	G	SOL	G	MI	G	FA	G	LA	G	LA	G	MI	G	FA	G	LA	G	FA	G	LA	G	MI	G	MI
288	C	RE	C	LA	C	MI	C	MI	C	MI	C	RE	C	MI	C	SI	C	SI	C	MI	C	LA	C	LA
289	T	DO3	T	SI	T	LA	T	LA	T	LA	T	FA	T	LA	T	SOL	T	SOL	T	LA	T	SI	T	SI
290	A	FA	A	DO4	A	MI	A	MI	A	SI	A	MI	A	MI	A	RE	A	RE	A	MI	A	SOL	A	SOL
291	G	MI	G	SOL	G	LA	G	LA	G	DO4	G	RE	G	LA	G	FA	G	FA	G	LA	G	RE	G	RE
292	C	RE	C	LA	C	MI	C	MI	C	SOL	C	DO3	C	MI	C	SI	C	SI	C	MI	C	FA	C	FA

Fig. 8.7

Per ragioni di spazio, in questo documento sono stati mostrati i **dati completi <u>SOLO</u>** del **Trend n°1**. Seguendo le istruzioni descritte in questo capitolo è però possibile replicare la procedura considerando tutti gli altri **23 Trends** principali.

CONCLUSIONI

CONSIDERAZIONI FINALI

I risultati presentati in questo lavoro si armonizzano incredibilmente con quelli ottenuti nel documento “I Misteri del Dna (Parte Prima)”. Essi confermano alcuni importanti e sconcertanti allineamenti significativi di sequenze di DNA e RNA. Partendo da una sequenza di 22 basi di *RNA* del *Gene RdRp* del *SARS-CoV-2* (una delle sequenze di RNA utilizzate come controllo positivo del tampone rinofaringeo), sono stati identificati “organismi” attesi, come il ***Pipistrello*** e il ***Pangolino***, e altri assolutamente inaspettati, come il ***Virus dell’Immunodeficienza Umana*** (***HIV-1)*** e i ***Bacilli del Parantrace (Bacillus Paranthracis)*** e dell’***Antrace (Bacillus Anthracis)***. Successivamente, attraverso l’analisi comparata tra la sequenza sopracitata e il 3’-UTR del Vaccino sono stati identificati nel 3’-UTR piccoli segmenti di sequenza significativi non contigui. Simulando una **trascrizione “saltante” dell’RNA (Jumping RNA Transcription)**, questi segmenti sono stati scrupolosamente collegati tra loro. Le **sequenze** ottenute da questi assemblaggi hanno confermato **la presenza di segmenti di sequenza di questi stessi “organismi”** nel 3’-UTR del Vaccino mRNA SARS-CoV-2 Biontech/Pfizer. Questi risultati meritano un urgente e approfondito dibattito internazionale.

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2 Agosto 2021