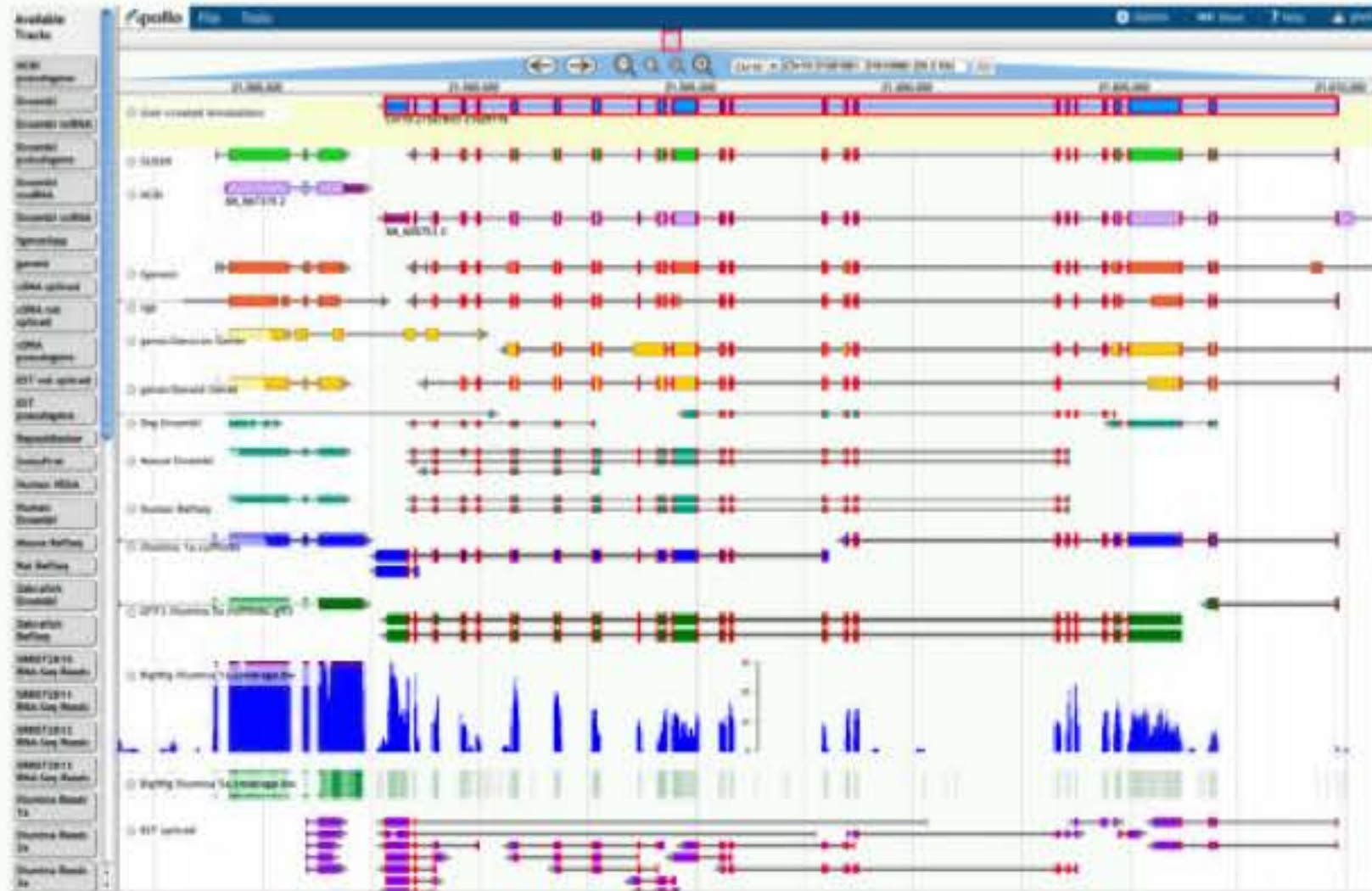


What is Web Apollo?

- Web Apollo is a web-based genomic annotation editing platform.

We need annotation editing tools to modify and refine the precise location and structure of the genome elements that predictive algorithms cannot yet resolve automatically.



Find more about Web Apollo at
<http://GenomeArchitect.org>
and
[Genome Biol 14:R93. \(2013\).](#)

Brief history of Apollo*:



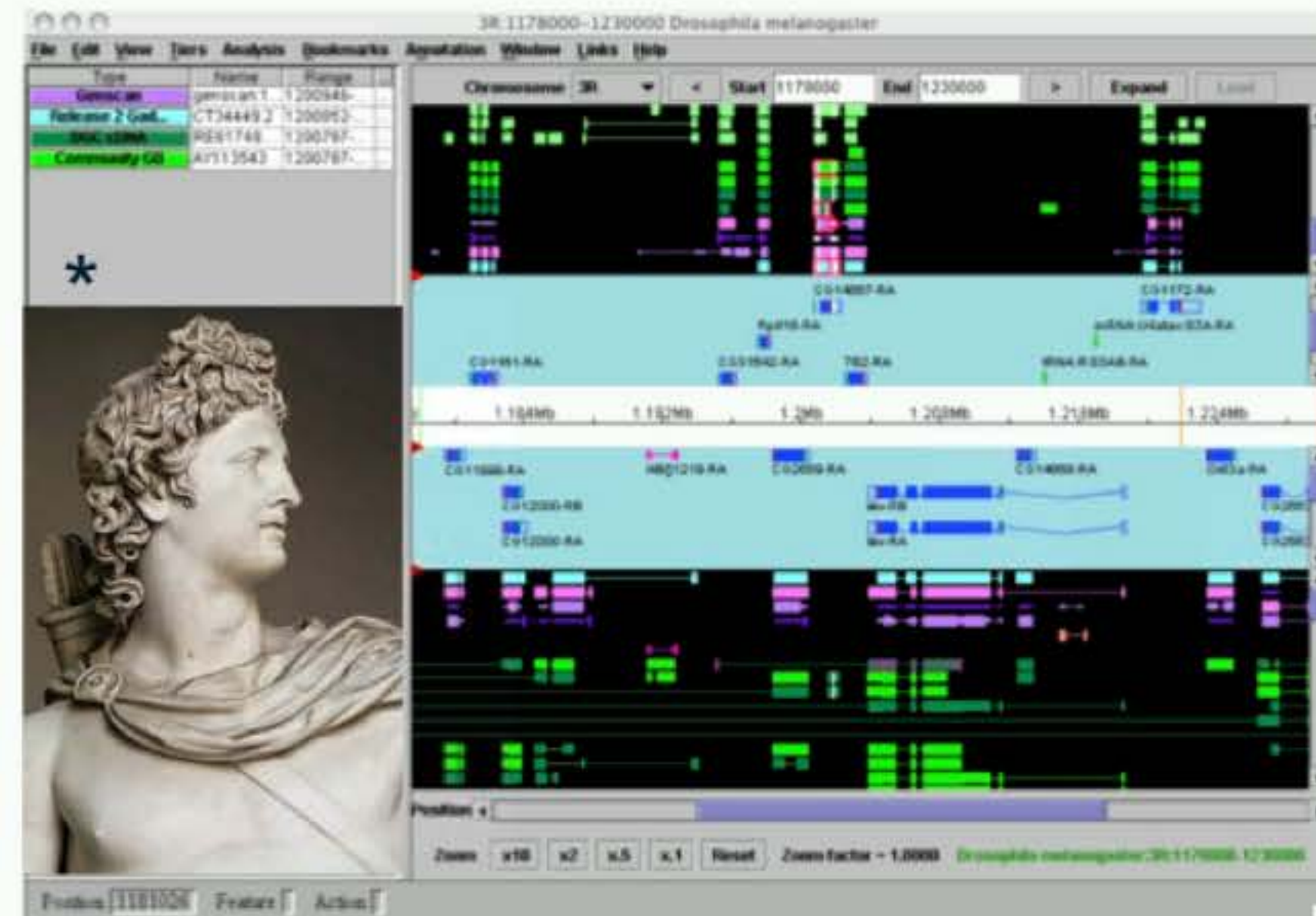
Biologists could finally visualize computational analyses and experimental evidence from genomic features and build manually-curated consensus gene structures. Apollo became a very popular, open source tool (insects, fish, mammals, birds, etc.).

a. Desktop:

one person at a time editing a specific region, annotations saved in local files; slowed down collaboration.

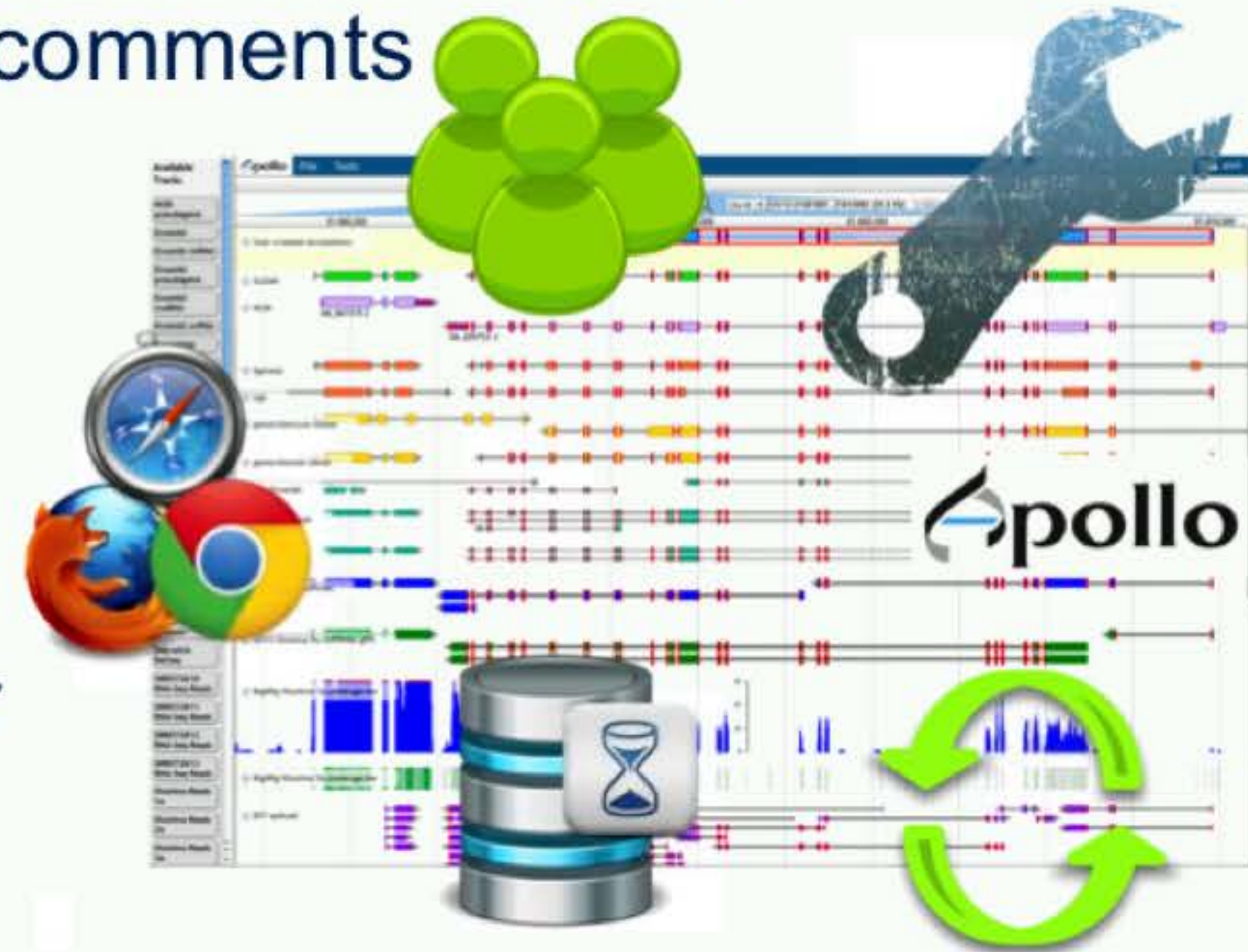
b. Java Web Start:

users saved annotations directly to a centralized database; potential issues with stale annotation data remained.



Web Apollo

- Browser-based; plugin for JBrowse.
- Allows for intuitive annotation creation and editing, with gestures and pull-down menus to create transcripts, add/delete/resize exons, merge/split exons or transcripts, insert comments (CV, freeform text), etc.
- Customizable rules and appearance.
- Edits in one client are instantly pushed to all other clients.



Dispersed, community-based gene manual annotation efforts.

Using Web Apollo, we* have trained geographically dispersed scientific communities to perform biologically supported manual annotations, and monitored their findings: ~80 institutions, 14 countries, hundreds of scientists, and **gate keepers**.

- Training workshops and geneborees.
- Tutorials with detailed instructions.
- Personalized user support.



*Collaboration with Elsik Lab,
Hymenoptera Genome
Database.

What have we learned?

Harvesting expertise from dispersed researchers who assigned functions to predicted and curated peptides, we have developed more interactive and responsive tools, as well as better visualization, editing, and analysis capabilities.

Assessment:

1. Was it helpful / productive to work together?
2. Were manual annotations improved?
3. Did the shared and distributed annotation effort help improve the quality of scientific findings?

Improved Automated Annotations*

In many cases, automated annotations have been improved.

Also, learned of the challenges of newer sequencing technologies, e.g.:

- Frameshifts and indel errors
- Split genes across scaffolds
- Highly repetitive sequences

To face these challenges, we train annotators in recovering coding sequences in agreement with all available biological evidence.

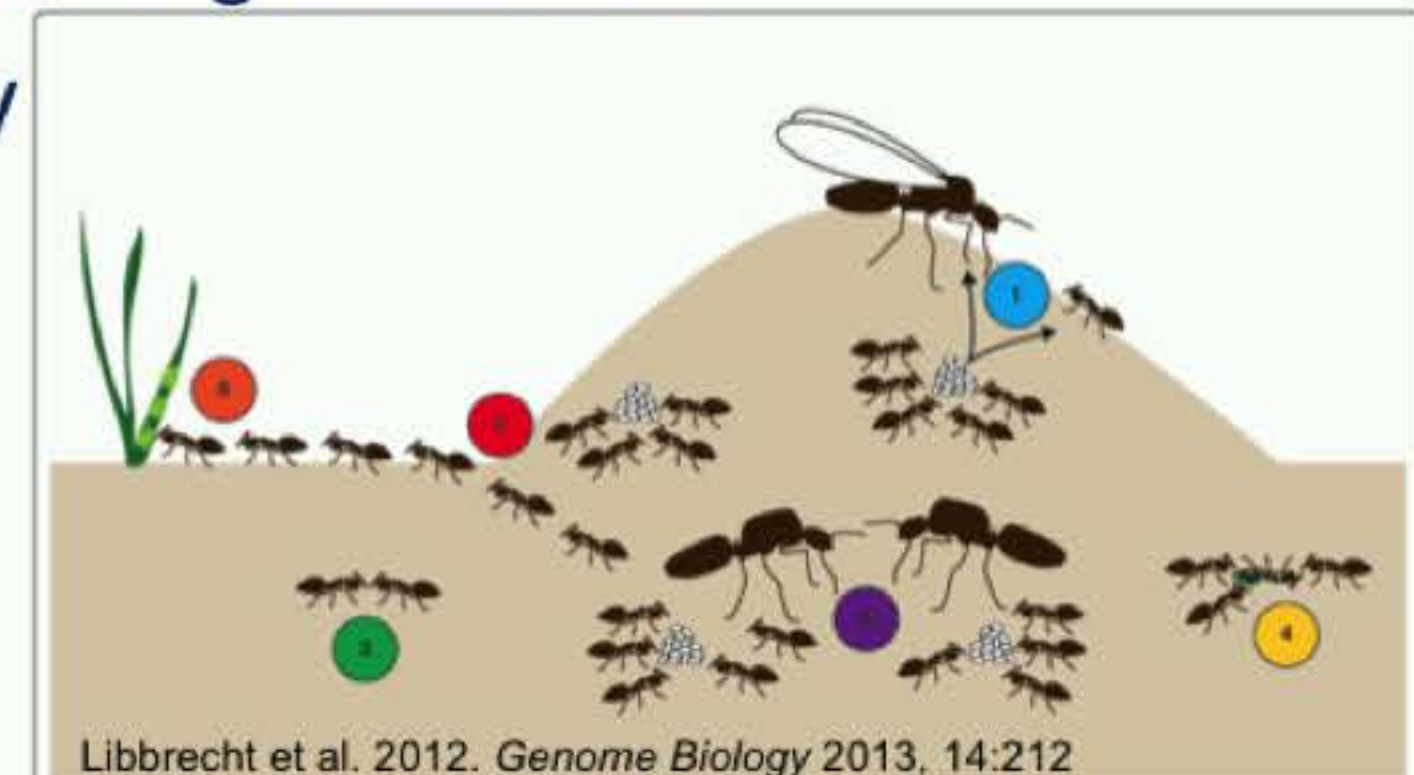
... groups of communities have taught us a lot!

Understanding the evolution of sociality.

Comparison of the genomes of 7 species of ants contributed to a better understanding of the evolution and organization of insect societies at the molecular level.

Insights drawn mainly from six core aspects of ant biology:

1. Alternative morphological castes
2. Division of labor
3. Chemical Communication
4. Alternative social organization
5. Social immunity
6. Mutualism



Web Apollo

The screenshot displays the Apollo genome browser interface. At the top, there is a navigation bar with the Apollo logo and menu items: File, View, Tools, and Help. A user profile icon labeled 'demo' is in the top right. Below the navigation bar is a coordinate scale from 20,560,000 to 22,760,000. A search bar shows 'Chr10' and a specific region 'Chr10:22209226..22215685 (6.46 Kb)'. Below the search bar are navigation icons (back, forward, zoom in, zoom out) and a 'Go' button. The main area contains several tracks:

- 'User-created Annotations' Track:** A yellow track showing blue boxes representing annotations. One annotation is labeled 'MGC139957'. Another annotation is labeled 'APEX1'.
- Evidence Tracks Area:** A track showing evidence for the 'APEX1' gene. It includes a track for 'NCBI' with a purple box labeled 'MGC139957' and another track for 'MGC14242'.

On the left side, there is a sidebar titled 'Available Tracks' with a search filter 'filter by text'. The list of available tracks includes: NCBI pseudogene, Ensembl miRNA, Ensembl pseudogene, Ensembl snoRNA, Ensembl snRNA, Fgenesh, fgeneshpp, GeneID, SGP, and cDNA spliced.

Graphical User Interface (GUI) for editing annotations

Web Apollo

'File':
Upload your own
evidence: GFF3,
BAM, BigWig, VCF*.
Add combination
and sequence search
tracks.

'Tools':
Use BLAT to query the
genome with a protein
or DNA sequence.

The screenshot displays the Web Apollo interface. At the top, there is a navigation bar with 'File', 'View', 'Tools', and 'Help' menus. Below this is a genomic coordinate scale from 20,560,000 to 22,760,000. The main track area is divided into two sections: a yellow 'User-created Annotations' track and a white 'Evidence Tracks Area'. The 'User-created Annotations' track shows a gene model for MGC139957. The 'Evidence Tracks Area' shows evidence for MGC139957 and APEX1. On the left, the 'Available Tracks' sidebar lists various track types, with an orange arrow pointing to the 'cDNA spliced' track. The 'Tools' menu at the top is also highlighted with an orange arrow.

Available Tracks

Graphical User Interface (GUI) for editing annotations

Web Apollo

'File':
Upload your own
evidence: GFF3,
BAM, BigWig, VCF*.
Add combination
and sequence search
tracks.

'View': change
color by CDS,
toggle strands,
set highlight.

'Tools':
Use BLAT to query the
genome with a protein
or DNA sequence.

The screenshot displays the Web Apollo interface with a navigation menu (File, View, Tools, Help) and a coordinate scale from 20,560,000 to 22,760,000. The main area shows several tracks: 'User-created Annotations' (yellow background) with a blue gene model for MGC139957; 'Evidence Tracks Area' (white background) with a purple gene model for MGC139957 and a red gene model for APEX1. The 'Available Tracks' sidebar on the left lists various track types, with an orange arrow pointing to 'cDNA spliced'.

Available Tracks

Graphical User Interface (GUI) for editing annotations

Web Apollo

'File':
Upload your own
evidence: GFF3,
BAM, BigWig, VCF*.
Add combination
and sequence search
tracks.

'View': change
color by CDS,
toggle strands,
set highlight.

'Tools':
Use BLAT to query the
genome with a protein
or DNA sequence.

Navigation tools:
pan and zoom

Search box: go
to a scaffold or a
gene model.

The screenshot displays the Web Apollo interface. At the top, there is a navigation bar with the 'pollo' logo and menu items: 'File', 'View', 'Tools', and 'Help'. Below the navigation bar is a genomic coordinate scale from 20,560,000 to 22,760,000. A search box contains 'Chr10:22209226..22213685 (6.46 Kb)' with a 'Go' button. The main area shows several tracks: 'User-created Annotations' (yellow background) with a track for 'MGC139957' and 'APEX1'; and 'Evidence Tracks Area' (white background) with tracks for 'NCBI' and 'MGC139957'. On the left, an 'Available Tracks' sidebar lists various track types: 'filter by text', 'NCBI pseudogene', 'Ensembl miRNA', 'Ensembl pseudogene', 'Ensembl snoRNA', 'Ensembl snRNA', 'Fgenesh', 'fgeneshpp', 'GeneID', 'SGP', and 'cDNA spliced'. An orange arrow points from the 'File' menu to the 'Available Tracks' sidebar. Another orange arrow points from the 'Tools' menu to the navigation tools (pan and zoom). A third orange arrow points from the search box to the search input field. A fourth orange arrow points from the 'View' menu to the 'User-created Annotations' track.

Available Tracks

Graphical User Interface (GUI) for editing annotations

Web Apollo

'File':
Upload your own
evidence: GFF3,
BAM, BigWig, VCF*.
Add combination
and sequence search
tracks.

'View': change
color by CDS,
toggle strands,
set highlight.

'Tools':
Use BLAT to query the
genome with a protein
or DNA sequence.

Navigation tools:
pan and zoom

Search box: go
to a scaffold or a
gene model.

Grey bar of coordinates
indicates location. You can
also select here in order to
zoom to a sub-region.

The screenshot displays the Web Apollo interface. At the top, a navigation bar includes the 'pollo' logo and menu items: 'File', 'View', 'Tools', and 'Help'. Below this is a coordinate bar with a grey gradient, showing genomic coordinates from 20,560,000 to 22,760,000. A search box contains 'Chr10:22209226..22213685 (6.46 Kb)' and a 'Go' button. The main area features several tracks: 'User-created Annotations' (yellow background) showing a gene model for MGC139957; 'Evidence Tracks Area' (white background) showing evidence for MGC139957 and APEX1; and 'Available Tracks' on the left side with a list of track types including NCBI pseudogene, Ensembl miRNA, Ensembl pseudogene, Ensembl snoRNA, Ensembl snRNA, Fgenesh, fgeneshpp, GeneID, SGP, and cDNA spliced. A 'Login' button is visible in the top right corner.

Available Tracks

Login

Graphical User Interface (GUI) for editing annotations

Web Apollo

- Two **new** kinds of **tracks**:
 - annotation editing
 - sequence alteration editing

The screenshot displays the Web Apollo interface for a specific genomic region. At the top, navigation icons (left and right arrows, zoom in and zoom out) are visible. Below them, a search bar shows 'Chr10' and a specific coordinate range 'Chr10:22213112..22213274 (163 b)', with a 'Go' button. The main area is divided into several tracks. The top track is labeled 'DNA Track' and contains a DNA sequence: 'P R P A L G T * A V T S T N A S Y S A T I T R P S * S C S S S P S A C I R H I G C H Q H K C V I F S H N H S A F L I M F F L T L G L H * A H R L S P A Q M R H I Q P Q S L A G L P D H V L P H L CCTCGGCCTGCATTAGG CACATAGGCTGTCACCAGCACAAAT GCGTCATATTCAGCCACAATCACTC GGCCTTCCTGATCATGTTCTTCCTCACCGGAGCCGGACGTAATCC GTGTATCCGACAGTGGTCGTGTTTACGCAGTATAAGTCGGTGTAGTGAG CCGGAAGGACTAGTACAAGAAGGAGTGG G R G A N P V Y A T V L V F A D Y E A V I V R G E Q D H E E E G R P R C * A C L S D G A C I R * I * G C D S P R G S * T R G * V E A Q M L C M P Q * W C L H T M N L W L * E A K R I M N K R V'. A red horizontal bar highlights a portion of this sequence. Below the DNA track is a yellow track labeled ''User-created Annotations' Track'. At the bottom, there is a purple track.

Web Apollo

- Annotation Information Editor

Annotation Info Editor

Gene		Transcript	
Name	Apurinic-Apyrimidinic Endonucleas	Name	Apurinic-Apyrimidinic Endonucleas
Symbol	Apex-1	Symbol	Apex-1
Description	Multifunctional DNA Repair Enzym	Description	Multifunctional DNA Repair Enzym
Status		Status	
<input checked="" type="radio"/> Approved <input type="radio"/> Needs review		<input checked="" type="radio"/> Approved <input type="radio"/> Needs review	
DBXRefs		DBXRefs	
DB	Accession	DB	Accession
		WormBase	WB_000123
		FlyBase	FB0000456
<input type="button" value="Add"/> <input type="button" value="Delete"/>		<input type="button" value="Add"/> <input type="button" value="Delete"/>	

Web Apollo

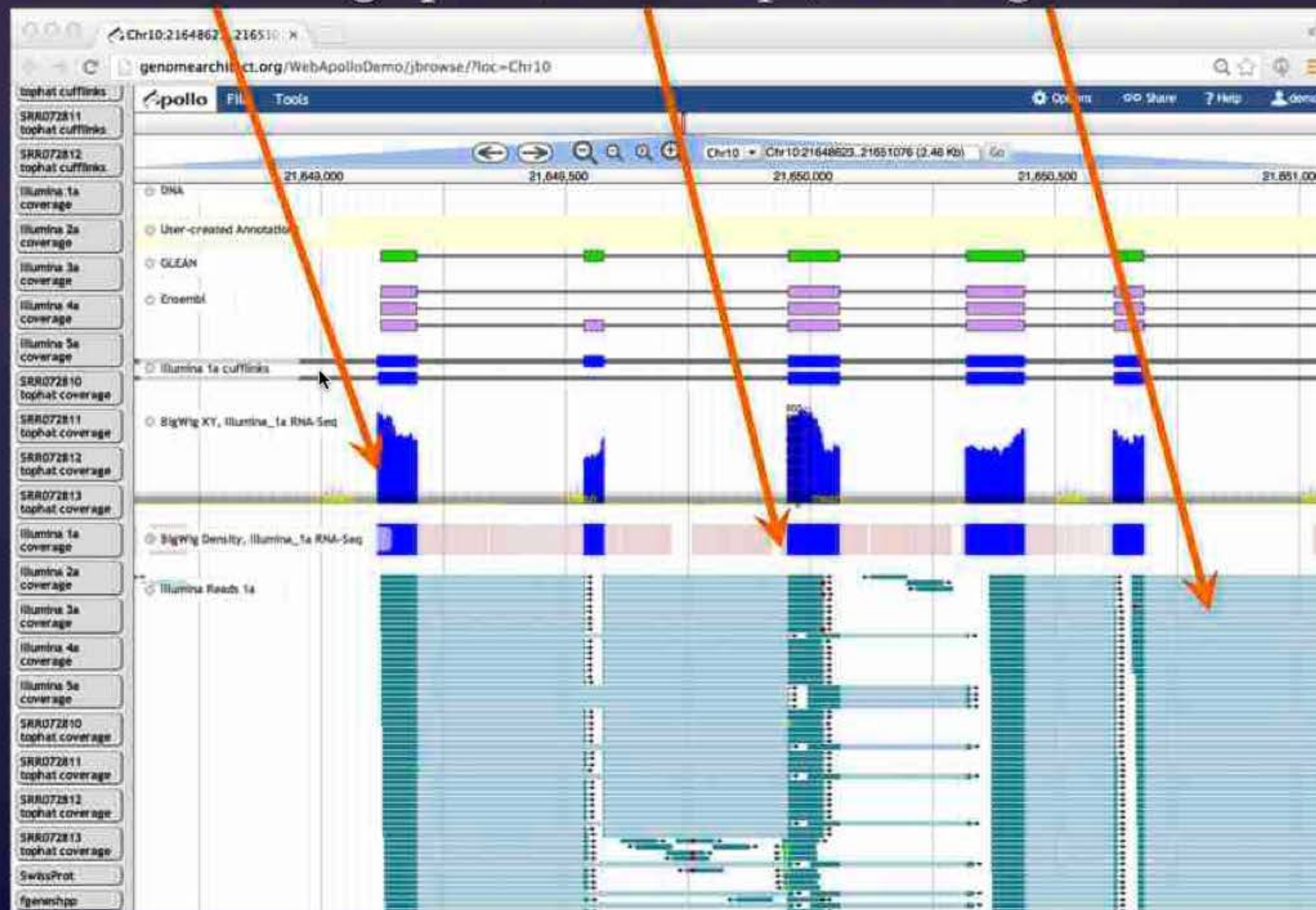
- Annotation Information Editor

The screenshot displays the 'Annotation Info Editor' interface, which is split into two panels. Each panel contains several sections for editing annotation data:

- Attributes:** A table with columns 'Tag' and 'Value'. Below the table are 'Add' and 'Delete' buttons.
- Pubmed IDs:** A list of PubMed IDs. In the left panel, '44556' is highlighted. In the right panel, '656546' is present. Below the list are 'Add' and 'Delete' buttons.
- Gene Ontology IDs:** A list of Gene Ontology IDs. In the right panel, 'GO:0000811' is present. Below the list are 'Add' and 'Delete' buttons.
- Comments:** A text area for comments. In the right panel, the comment 'Dicistronic transcript' is present, and a new entry 'ANNOTATION TYPE: Change an existing GLEAN gene model' is highlighted. Below the text area are 'Add' and 'Delete' buttons.

[Some of the] Functionality:

- Protein-coding gene annotation (that you know and love)
- Sequence alterations (less coverage = more fragmentation)
- Visualization of stage and cell-type specific transcription data as coverage plots, heat maps, and alignments



Arthropodcentric Thanks!

- ⌘ AgriPest Base
- ⌘ FlyBase
- ⌘ Hymenoptera Genome Database
- ⌘ VectorBase
- ⌘ *Apis mellifera*
- ⌘ *Tribolium castaneum*
- ⌘ *Pogonomyrmex barbatus*
- ⌘ *Manduca sexta*
- ⌘ *Bombus terrestris*
- ⌘ *Helicoverpa armigera*
- ⌘ *Nasonia vitripennis*
- ⌘ *Acyrtosiphon pisum*
- ⌘ *Mayetiola destructor*
- ⌘ *Atta cephalotes*
- ⌘ *Linepithema humile*
- ⌘ *Camponotus floridanus*
- ⌘ *Solenopsis invicta*
- ⌘ *Acromyrmex echinatior*



Thanks!

BBOP

Web Apollo

Gregg Helt

Ed Lee

Rob Buels *

Mitch Skinner *

Justin Reese §

Chris Childers §

Gene Ontology

Chris Mungall

Seth Carbon

Heiko Dietze

Web Apollo: <http://GenomeArchitect.org>

GO: <http://GeneOntology.org>

i5K: <http://arthropodgenomes.org/wiki/i5K>

- **Berkeley Bioinformatics Open-source Projects (BBOP), Berkeley Lab: Web Apollo and Gene Ontology teams. Suzanna Lewis (PI).**
- **Ian Holmes Lab (PI).** *U. of California Berkeley.
- The team at Hymenoptera Genome Database. §U. of Missouri. **Christine G. Elsik (PI).**
- Arthropod genomics community (fringy Richards, Monica Poelchau, Alexie Papanicolaou, Gene Robinson, Juergen Gadau, Chris R Smith, Owen McMillan, Owain Edwards, Kevin Hackett, and a few hundred more).
- i5K Steering Committee, NAL (USDA), HGSC-BCM, BGI, 1KITE.
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- Images used with permission: AlexanderWild.com
- **For your attention, thank you!**

Show 25 entries

Filter:

Organism	Name	Length
<input type="checkbox"/> Athalia rosae	Scaffold500	1008
<input type="checkbox"/> Athalia rosae	Scaffold464	1026
<input type="checkbox"/> Athalia rosae	Scaffold488	1037
<input type="checkbox"/> Athalia rosae	Scaffold425	1043
<input type="checkbox"/> Athalia rosae	Scaffold507	1061
<input type="checkbox"/> Athalia rosae	Scaffold433	1062
<input type="checkbox"/> Athalia rosae	Scaffold426	1067
<input type="checkbox"/> Athalia rosae	Scaffold506	1076
<input type="checkbox"/> Athalia rosae	Scaffold460	1087
<input type="checkbox"/> Athalia rosae	Scaffold510	1088
<input type="checkbox"/> Athalia rosae	Scaffold436	1091
<input type="checkbox"/> Athalia rosae	Scaffold450	1092
<input type="checkbox"/> Athalia rosae	Scaffold412	1105
<input type="checkbox"/> Athalia rosae	Scaffold490	1108
<input type="checkbox"/> Athalia rosae	Scaffold466	1114
<input type="checkbox"/> Athalia rosae	Scaffold454	1119
<input type="checkbox"/> Athalia rosae	Scaffold444	1131
<input type="checkbox"/> Athalia rosae	Scaffold482	1134
<input type="checkbox"/> Athalia rosae	Scaffold521	1138
<input type="checkbox"/> Athalia rosae	Scaffold478	1163
<input type="checkbox"/> Athalia rosae	Scaffold465	1169
<input type="checkbox"/> Athalia rosae	Scaffold498	1171
<input type="checkbox"/> Athalia rosae	Scaffold439	1178
<input type="checkbox"/> Athalia rosae	Scaffold505	1188
<input type="checkbox"/> Athalia rosae	Scaffold420	1194

Showing 1 to 25 of 522 entries

Previous Next

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

Protein Protein [dropdown] [input] Search Advanced Help

Display Settings: FASTA

Send to: [dropdown]

antennapedia-like protein [Nasonia vitripennis]

NCBI Reference Sequence: NP_001161164.1

[GenPept](#) [Graphics](#)

```
>gi|266457590|ref|NP_001161164.1| antennapedia-like protein [Nasonia vitripennis]
MSSYFANSYIPDLRNGGVEHPHQHQHYGAAVQVPQQQAVQQPQQASDPCDPSMLRQGVPGHHGYGAA
TGQQPGMPYPRFPPYDRMDIRNAAYYQQQQEHEGMDMASYRASSPSAGMAGLHMGTPTPVNGHPASTPI
VYASCKLQAAAVDHQGSVLDGPDSPPLVDAQMHQMHPQHTHMQAQQSHPQQQPQPQAPHQQAHMQPQQT
QQQHMMYQQQTQPQQPQPAAMHPQQQAQQQHQGVVASPLGQQQPGTPQSAAPTNLPSPLYPWMRSQFER
KRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMRKWKKETKTKGEPNSGDG
DTDISPQTSPQG
```

Change region shown [dropdown]

Analyze this sequence

- [Run BLAST](#)
- [Identify Conserved Domains](#)
- [Highlight Sequence Features](#)
- [Find in this Sequence](#)

Articles about the LOC100118060 gene

Functional and evolutionary insights from the genomes of three parasitoid wasps [Science, 2010] [See all...](#)

Identical proteins for NP_001161164.1

Antennapedia-like protein [Nasonia vitripennis] [ACT63883] [See all...](#)

Reference sequence information

RefSeq mRNA
See reference mRNA sequence for the LOC100118060 gene (NM_001167692.1).

mmtorres

2,200,000

000

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

- Available Tracks
- filter by text
 - augustus_masked
 - blastx_Annelida
 - blastx_Arthropoda
 - blastx_Atelocerata
 - blastx_Cephalochordata
 - blastx_Chelicerata
 - blastx_Cnidaria
 - blastx_Craniata
 - blastx_Crustacea
 - blastx_Echinodermata
 - blastx_Mollusca
 - blastx_Nemata
 - blastx_Nematomorpha
 - blastx_Onychophora
 - blastx_Parazoa
 - blastx_Placozoa
 - blastx_Platyhelminthes
 - blastx_Priapulida
 - blastx_Tardigrada
 - blastx_Tunicata
 - blastx_UNCATEGORISED
 - Cegma
 - est_gff
 - protein2genome_Annelida
 - protein2genome_Arthropoda
 - protein2genome_Atelocerata
 - protein2genome_Cephalochordata
 - protein2genome_Chelicerata
 - protein2genome_Cnidaria
 - protein2genome_Craniata

0 50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 850 900 950 1,000

Scaffold500 Scaffold500:102..856 (756 b) Go

125 250 375 500 625 750

User-created Annotations

Track	Start	End	Score	Strand	Label
augustus_masked					
blastx_Annelida					
blastx_Arthropoda					
blastx_Atelocerata					
blastx_Cephalochordata					
blastx_Chelicerata					
blastx_Cnidaria					
blastx_Craniata					
blastx_Crustacea					
blastx_Echinodermata					
blastx_Mollusca					
blastx_Nemata					
blastx_Nematomorpha					
blastx_Onychophora					
blastx_Parazoa					
blastx_Placozoa					
blastx_Platyhelminthes					
blastx_Priapulida					
blastx_Tardigrada					
blastx_Tunicata					
blastx_UNCATEGORISED					
Cegma					
est_gff					
protein2genome_Annelida					
protein2genome_Arthropoda					
protein2genome_Atelocerata					
protein2genome_Cephalochordata					
protein2genome_Chelicerata					
protein2genome_Cnidaria					
protein2genome_Craniata					

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

apollo File View Tools Help mmtorres

0 50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 850 900 950 1,000

125 375 500 625 750

User-created

filter by text

- augustus_masked
- blastx_Annelida
- blastx_Arthropoda
- blastx_Atelocerata
- blastx_Cephalochordata
- blastx_Chelicerata
- blastx_Cnidaria
- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- Cegma
- est_gff
- protein2genome_Annelida
- protein2genome_Arthropoda
- protein2genome_Atelocerata
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

Scaffold500 Scaffold500:102..856 (756 b) Go

protein2genome_Chelicerata
protein2genome_Cnidaria
protein2genome_Craniata

0 50 100 150 Search sequence 300 350 400 450 500 550 600 650 700 750 800 850 900 950 1,000

125 250 375 500 625 750

Scaffold500 Scaffold500:102..856 (756 b) Go

User-created Annotations

Track Name	Start	End	Score	Strand	Color
augustus_masked					
blastx_Annelida					
blastx_Arthropoda					
blastx_Atelocerata					
blastx_Cephalochordata					
blastx_Chelicerata					
blastx_Cnidaria					
blastx_Craniata					
blastx_Crustacea					
blastx_Echinodermata					
blastx_Mollusca					
blastx_Nemata					
blastx_Nematomorpha					
blastx_Onychophora					
blastx_Parazoa					
blastx_Placozoa					
blastx_Platyhelminthes					
blastx_Priapulida					
blastx_Tardigrada					
blastx_Tunicata					
blastx_UNCATEGORISED					
Cegma					
est_gff					
protein2genome_Annelida					
protein2genome_Arthropoda					
protein2genome_Atelocerata					
protein2genome_Cephalochordata					
protein2genome_Chelicerata					
protein2genome_Cnidaria					
protein2genome_Craniata					

User-created Annotations

Available Tracks

- filter by text
- augustus_masked
- blastx_Annelida
- blastx_Arthropoda
- blastx_Atelocerata
- blastx_Cephalochordata
- blastx_Chelicerata
- blastx_Cnidaria
- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
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- est_gff
- protein2genome_Annelida
- protein2genome_Arthropoda
- protein2genome_Atelocerata
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

Search sequence [X]

BLAT protein [v]

Enter sequence

Search all genomic sequences

Search

Available Tracks
X filter by text
augustus_masked
blastx_Annelida
blastx_Arthropoda
blastx_Atelocerata
blastx_Cephalochordata
blastx_Chelicerata
blastx_Cnidaria
blastx_Craniata
blastx_Crustacea
blastx_Echinodermata
blastx_Mollusca
blastx_Nemata
blastx_Nematomorpha
blastx_Onychophora
blastx_Parazoa
blastx_Placozoa
blastx_Platyhelminthes
blastx_Priapulida
blastx_Tardigrada
blastx_Tunicata
blastx_UNCATEGORISED
Cegma
est_gff
protein2genome_Annel
protein2genome_Arthr
protein2genome_Atelo
protein2genome_Cepha
protein2genome_Chelli
protein2genome_Cnida
protein2genome_Crani

Search sequence
BLAT protein
Enter sequence
MSSYFANSYIPDLRNGGVEHPHQHQHYGAAVQVPQQQAVQQQPQQASDPCDPSMLRQGVPGHHGYGAA
TGQQPGMPYPRFPPYDRMDIRNAAYYQQQQEHGMDMASYRASSPSAGMAGLHMGHTPTPVNGHPASTPI
VYASCKLQAAAVDHQGSVLDGPDSPPLVDAQMHHQMHPQHTHMQAQQSHPPQQPQAPHQQAHMQPQQT
QQQHMMYQQQTQPQQPQPAAMHPQQAQQQQHQGVVASPLGQQQPGTPQSAAPTNLPSPLYPWMRSQFER
KRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKETKTKGEPNSGDG
DTDISPQTSPPG
Search all genomic sequences
Search

Available Tracks

- filter by text
- augustus_masked
- blastx_Annelida
- blastx_Arthropoda
- blastx_Atelocerata
- blastx_Cephalochordata
- blastx_Chelicerata
- blastx_Cnidaria
- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- Cegma
- est_gff
- protein2genome_Annelida
- protein2genome_Arthropoda
- protein2genome_Atelocerata
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

Search sequence

BLAT protein

Enter sequence

```
MSSYFANSYIPDLRNGGVEHPHQHQHYGAAVQVPQQQAVQQQPQQASDPCDPSMLRQGVPGHHGYGAA
TGQQPGMPYPRFPPYDRMDIRNAAYYQQQQEHGMDMASYRASSPSAGMAGLHMGTPTPVNGHPASTPI
VYASCKLQAAAVDHQGSVLDGPDSPPLVDAQMHHQMHPQHTHMQAQQSHPPQQPQAPHQQAHMQPQQT
QQQHMMYQQQTQPQQPQPAAMHPQQAQQQQHQQGVVASPLGQQQPGTPQSAAPTNLPSPLYPWMRSQFER
KRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKETKTKGEPNSGDG
DTDISPQTSPQG
```

Search all genomic sequences

Search

- Available Tracks
- filter by text
 - augustus_masked
 - blastx_Annelida
 - blastx_Arthropoda
 - blastx_Atelocerata
 - blastx_Cephalochordata
 - blastx_Chelicerata
 - blastx_Cnidaria
 - blastx_Craniata
 - blastx_Crustacea
 - blastx_Echinodermata
 - blastx_Mollusca
 - blastx_Nemata
 - blastx_Nematomorpha
 - blastx_Onychophora
 - blastx_Parazoa
 - blastx_Placozoa
 - blastx_Platyhelminthes
 - blastx_Priapulida
 - blastx_Tardigrada
 - blastx_Tunicata
 - blastx_UNCATEGORISED
 - Cegma
 - est_gff
 - protein2genome_Annelida
 - protein2genome_Arthropoda
 - protein2genome_Atelocerata
 - protein2genome_Cephalochordata
 - protein2genome_Chelicerata
 - protein2genome_Cnidaria
 - protein2genome_Craniata

apollo File View Tools Help mmtorres

0 50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 850 900 950 1,000

Scaffold500 Scaffold500:102..856 (756 b) Go

125 250 375 500 625 750

User-created Annotations

AROS_v0.5.2-Models

Search sequence

BLAT protein

Enter sequence

```

QQQHMMYQQQTQPQQPQAAMHPQQQAQQQHGGVVASPLGQQQPGTPQSAAPTNLPSPLYPWMRSQFER
KRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMRMKWKKETKTKGEPNSGDG
DTDISPQTSPPG
  
```

Search all genomic sequences

Search

ID	Start	End	Score	Significance	Identity
Scaffold38	1032382	1032188	129	3.5e-30	87.69
Scaffold38	892933	892748	118	1.2e-26	91.94
Scaffold12	344367	344191	114	1.3e-25	93.22
Scaffold12	118262	118086	111	8.8e-25	91.53
Scaffold38	919430	919260	110	2.6e-24	94.74
Scaffold38	1025519	1025364	108	1e-23	100
Scaffold38	842584	842408	101	9.8e-22	83.05
Scaffold38	1031986	1031831	96	4.3e-20	87.04
Scaffold38	791001	790828	85	8.2e-17	74.14
Scaffold38	671606	671442	79	4.7e-15	72.73
Scaffold161	254525	254352	70	1.8e-12	63.79
Scaffold38	1032181	1032071	67	2.7e-11	83.78
Scaffold12	529459	529316	67	2.7e-11	68.75
Scaffold38	1031698	1031585	63	2.3e-10	78.95

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

- Available Tracks
- filter by text
 - augustus_masked
 - blastx_Annelida
 - blastx_Arthropoda
 - blastx_Atelocerata
 - blastx_Cephalochordata
 - blastx_Chelicerata
 - blastx_Cnidaria
 - blastx_Craniata
 - blastx_Crustacea
 - blastx_Echinodermata
 - blastx_Mollusca
 - blastx_Nemata
 - blastx_Nematomorpha
 - blastx_Onychophora
 - blastx_Parazoa
 - blastx_Placozoa
 - blastx_Platyhelminthes
 - blastx_Priapulida
 - blastx_Tardigrada
 - blastx_Tunicata
 - blastx_UNCATEGORISED
 - Cegma
 - est_gff
 - protein2genome_Annelida
 - protein2genome_Arthropoda
 - protein2genome_Atelocerata
 - protein2genome_Cephalochordata
 - protein2genome_Chelicerata
 - protein2genome_Cnidaria
 - protein2genome_Craniata

apollo File View Tools Help mmtorres

0 50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 850 900 950 1,000

Scaffold500 Scaffold500:102..856 (756 b) Go

125 250 375 500 625 750

User-created Annotations

AROS_v0.5.2-Models

Search sequence

BLAT protein

Enter sequence

QQQHMMYQQQTQPQQPQAAMHPQQQAQQQHGGVVASPLGQQQPGTPQSAAPTNLPSPLYPWMSQFER
KRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMMKWKKETKTKGEPNSGDG
DTDISPQTSPPG

Search all genomic sequences

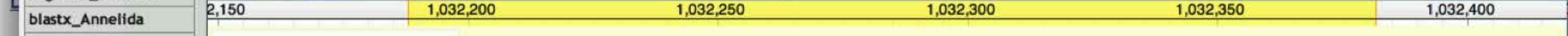
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Scaffold12	118262	118086	111	8.8e-25	91.53
Scaffold38	919430	919260	110	2.6e-24	94.74
Scaffold38	1025519	1025364	108	1e-23	100
Scaffold38	842584	842408	101	9.8e-22	83.05
Scaffold38	1031986	1031831	96	4.3e-20	87.04
Scaffold38	791001	790828	85	8.2e-17	74.14
Scaffold38	671606	671442	79	4.7e-15	72.73
Scaffold161	254525	254352	70	1.8e-12	63.79
Scaffold38	1032181	1032071	67	2.7e-11	83.78
Scaffold12	529459	529316	67	2.7e-11	68.75
Scaffold38	1031698	1031585	63	2.3e-10	78.95

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata



Scaffold38 Scaffold38:1032149..1032420 (273 b) Go



User-created Annotations

AROS_v0.5.2-Models ArosTmpB006329-RA

Available Tracks

- filter by text
- augustus_masked
- blastx_Annelida
- blastx_Arthropoda
- blastx_Atelocerata
- blastx_Cephalochordata
- blastx_Chelicerata
- blastx_Cnidaria
- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- Cegma
- est_gff
- protein2genome_Annelida
- protein2genome_Arthropoda
- protein2genome_Atelocerata
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

protein2genome_Chelicerata
protein2genome_Cnidaria
protein2genome_Craniata



User-created Annotations

Available Tracks

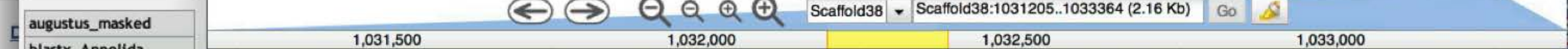
- filter by text
- augustus_masked
- blastx_Annelida
- blastx_Arthropoda
- blastx_Atelocerata
- blastx_Cephalochordata
- blastx_Chelicerata
- blastx_Cnidaria
- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- Cegma
- est_gff
- protein2genome_Annelida
- protein2genome_Arthropoda
- protein2genome_Atelocerata
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

AROS_v0.5.2-Models ArosTmpB006329-RA

protein2genome_Chelicerata

protein2genome_Cnidaria

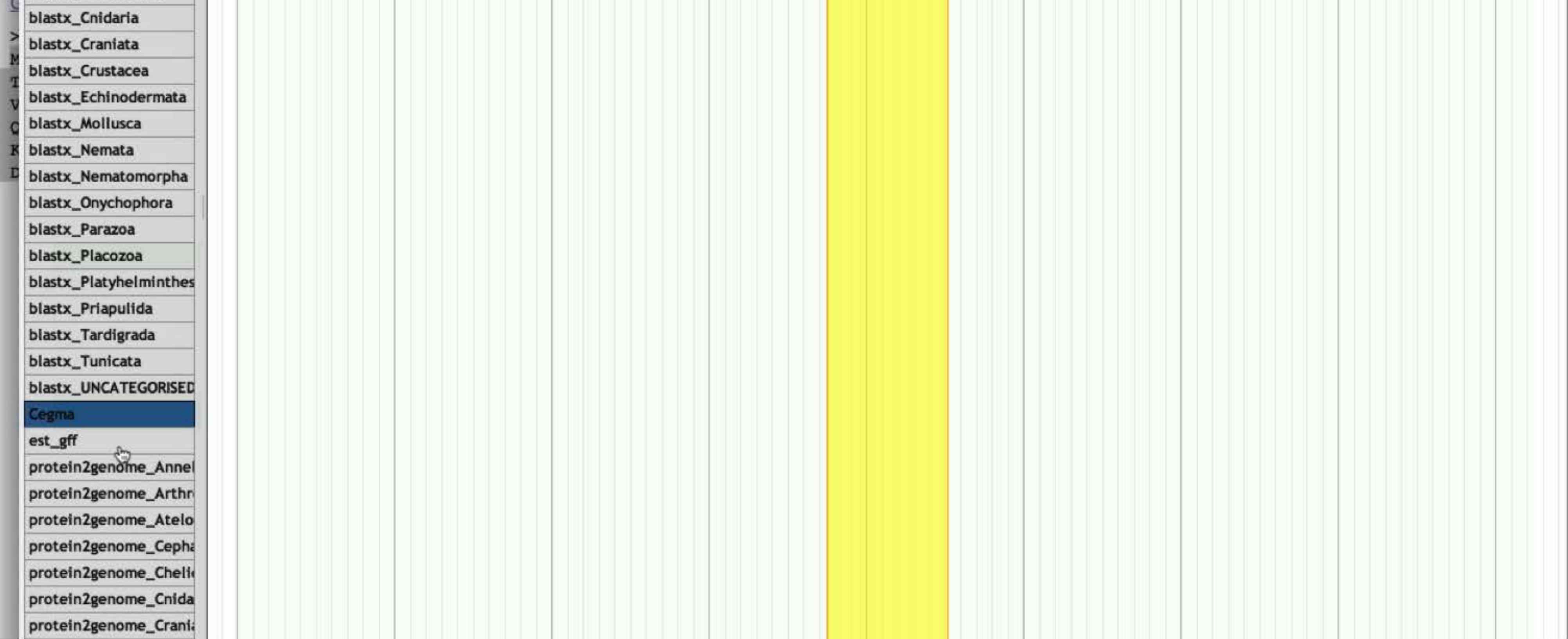
protein2genome_Craniata



User-created Annotations

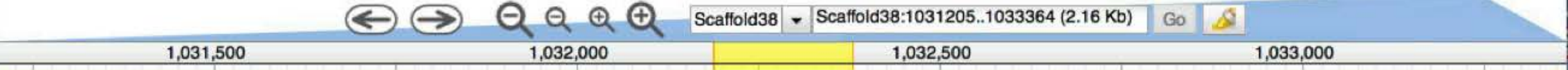
AROS_v0.5.2-Models

ArosTmpB006329-RA ArosTmpM006330-RA



- protein2genome_Annelida
- protein2genome_Arthropoda
- protein2genome_Atelerata
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

- Available Tracks
- filter by text
 - augustus_masked
 - blastx_Annelida
 - blastx_Atelocerata
 - blastx_Cephalochordata
 - blastx_Chelicerata
 - blastx_Cnidaria
 - blastx_Craniata
 - blastx_Crustacea
 - blastx_Echinodermata
 - blastx_Mollusca
 - blastx_Nemata
 - blastx_Nematomorpha
 - blastx_Onychophora
 - blastx_Parazoa
 - blastx_Placozoa
 - blastx_Platyhelminthes
 - blastx_Priapulida
 - blastx_Tardigrada
 - blastx_Tunicata
 - blastx_UNCATEGORISED
 - Cegma
 - est_gff
 - protein2genome_Annelida
 - protein2genome_Arthropoda
 - protein2genome_Atelocerata
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 - protein2genome_Cnidaria
 - protein2genome_Craniata
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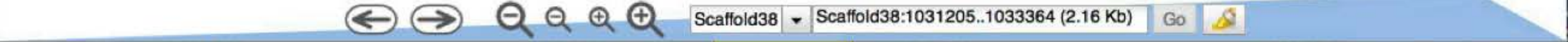


User-created Annotations

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 - ArosTmpB006329-RA
 - ArosTmpM006330-RA
- blastx_Arthropoda
 - tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae
 - tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis
 - tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera
 - tr|E2AHC7|E2AHC7_CAMFO:Camponotus_floridanus
 - tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum
 - tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum
 - tr|G6CQ59|G6CQ59_DANPL:Danaus_plexippus
 - tr|Q26469|Q26469_SCHAM:Schistocerca_americana
 - tr|E0VKJ8|E0VKJ8_PEDHC:Pediculus_humanus_subsp_corporis
 - tr|E2B5W1|E2B5W1_HARSA:Harpegnathos_saltator

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- Cegma
- est_gff
- protein2genome_Annel
- protein2genome_Anthr
- protein2genome_Atelo
- protein2genome_Cepha
- protein2genome_Cheli
- protein2genome_Cnida
- protein2genome_Crani
- protein2genome_Crust
- protein2genome_Echin
- protein2genome_Mollu
- protein2genome_Nema
- protein2genome_Nema
- protein2genome_Onych
- protein2genome_Paraz
- protein2genome_Placo
- protein2genome_Platyl
- protein2genome_Priap
- protein2genome_Tardigr
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata



User-created Annotations

AROS_v0.5.2-Models

ArosTmpB006329-RA

ArosTmpM006330-RA

blastx_Arthropoda

- tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae
- tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis
- tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera
- tr|E2AHC7|E2AHC7_CAMFO:Camponotus_floridanus
- tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum
- tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum
- tr|G6CQ59|G6CQ59_DANPL:Danaus_plexippus
- tr|Q26469|Q26469_SCHAM:Schistocerca_americana
- tr|E0VKJ8|E0VKJ8_PEDHC:Pediculus_humanus_subsp_corporis
- tr|E2B5W1|E2B5W1_HARSA:Harpegnathos_saltator

CoGeBlast

New here? [Get a CoGe account.](#)

Welcome to the **new beta version** of CoGeBlast.
If you experience any difficulties or prefer to use the old version, please [click here](#).

CoGe Blast NCBI Blast

Run CoGe Blast

Specify Target Genomes

Organism:

Matching Organisms (1)

- Athalia rosae

+ Add

Selected Genomes

- None

Genome Info + Add all

Import List Clear

BLAST Parameters

Type: Nucleotide Sequence (blastn) ... [more](#)

Query Sequence(s)

Enter FASTA sequence(s) here

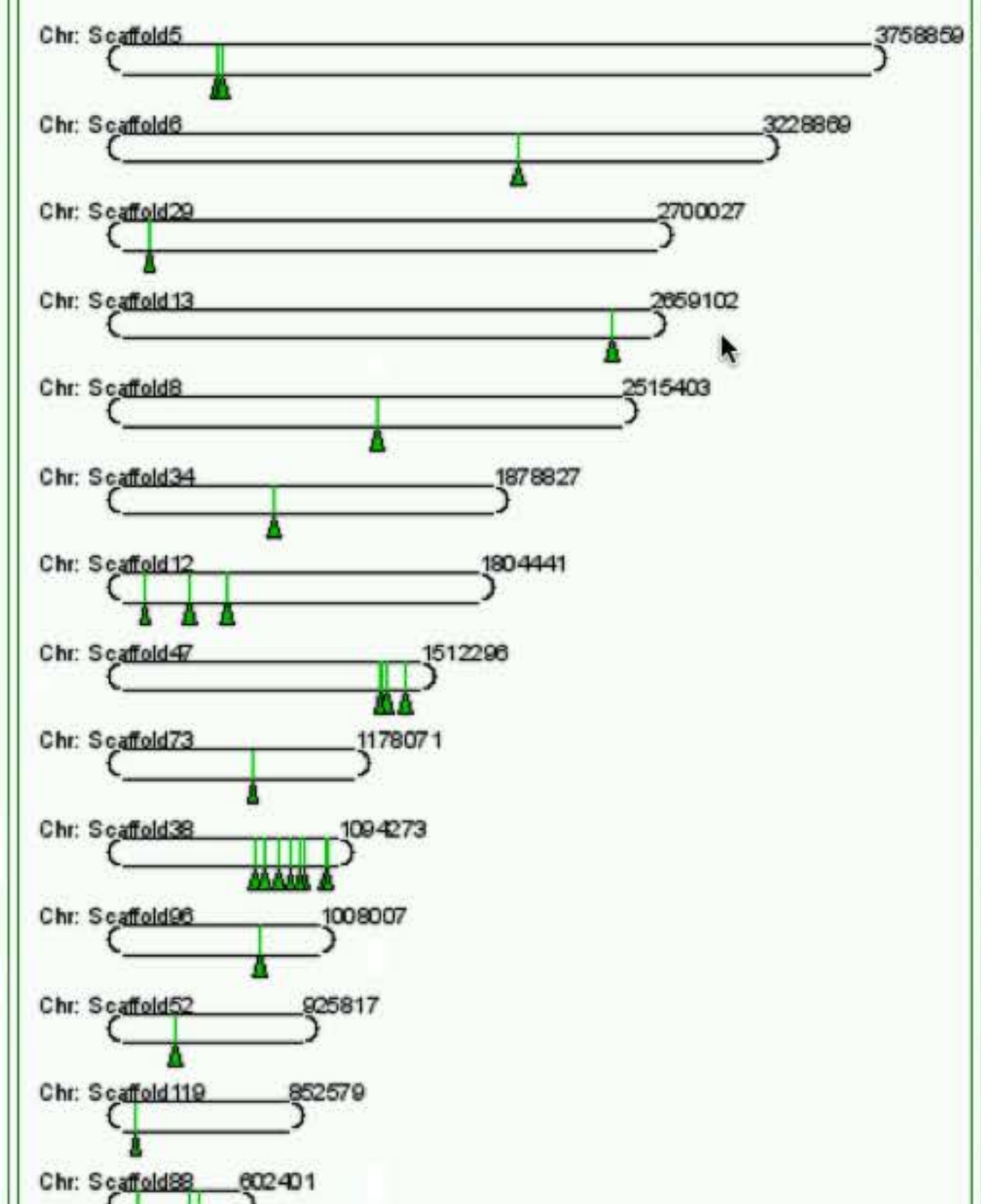
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata



Genomic HSP Visualization [hide](#)

[Generate List of Matching Genomes](#)

Athalia rosae (Baylor i5k pilot unmasked v1)
[Blast Report](#)
[Enlarge](#)



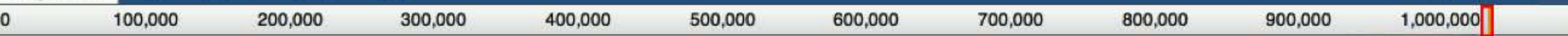
HSP Table [hide](#)

[Change Viewable Columns](#) Click column headers to sort

Query Seq	Org	Chr	Position	HSP#	E-value	Quality	Close Genom Feat
<input type="checkbox"/> Nvit_antp	Athalia rosae (Baylor i5k pilot unmasked v1)	Scaffold12	529498	10	5e-14	9.9%	None
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<input type="checkbox"/> Nvit_antp	Athalia rosae (Baylor i5k pilot unmasked v1)	Scaffold123	382540	12	2e-11	9.1%	None
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protein2genome_Chelicerata
protein2genome_Cnidaria
protein2genome_Craniata

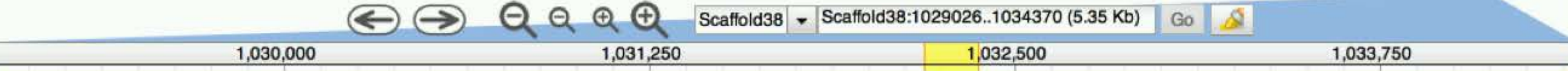
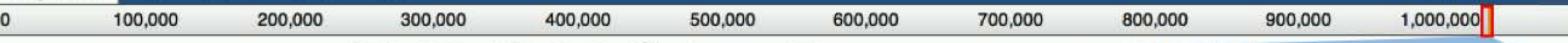
- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
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- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annel
- protein2genome_Atelo
- protein2genome_Cepha
- protein2genome_Chelk
- protein2genome_Cnida
- protein2genome_Crani
- protein2genome_Crust
- protein2genome_Echin
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- protein2genome_Nema
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- protein2genome_Onych
- protein2genome_Paraz
- protein2genome_Placo
- protein2genome_Platyf
- protein2genome_Priap
- protein2genome_Tardi
- protein2genome_Tunic
- protein2genome_UNCA
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata



User-created Annotations

- AROS_v0.5.2-Models
 - ArosTmpB006329-RA
 - ArosTmpM006330-RA
- protein2genome_Arthropoda
 - tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae
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 - tr|E2AHC7|E2AHC7_CAMFO:Camponotus_floridanus
 - tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum
 - tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum
 - tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis
 - tr|E2B5W1|E2B5W1_HARSA:Harpegnathos_saltator
- Cegma
 - BUSC3033.19
- blastx_Arthropoda
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 - tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis
 - tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera
 - tr|E2AHC7|E2AHC7_CAMFO:Camponotus_floridanus
 - tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum
 - tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
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- protein2genome_Annel
- protein2genome_Atelo
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- protein2genome_Echin
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- protein2genome_Nema
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- protein2genome_Placo
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- protein2genome_Tardi
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- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata



User-created Annotations

AROS_v0.5.2-Models

ArosTmpB006329-RA

ArosTmpM006330-RA

protein2genome_Arthropoda

tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae

tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera

tr|E2AHC7|E2AHC7_CAMFO:Camponotus_floridanus

tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum

tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis

tr|E2B5W1|E2B5W1_HARSA:Harpegnathos_saltator

Cegma

BUSC3033.19

blastx_Arthropoda

tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis

tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera

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tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum

tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annel
- protein2genome_Atelo
- protein2genome_Cepha
- protein2genome_Chelk
- protein2genome_Cnida
- protein2genome_Crani
- protein2genome_Crust
- protein2genome_Echin
- protein2genome_Mollu
- protein2genome_Nema
- protein2genome_Nema
- protein2genome_Onych
- protein2genome_Paraz
- protein2genome_Placo
- protein2genome_Platyf
- protein2genome_Priap
- protein2genome_Tardi
- protein2genome_Tunic
- protein2genome_UNCA
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

apollo File View Tools Help mmtorres

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1,030,000 1,031,250 1,032,500 1,033,750

User-created Annotations
ArosTmpB006329-RA

AROS_v0.5.2-Models
ArosTmpB006329-RA ArosTmpM006330-RA

protein2genome_Arthropoda

- tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae
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BUSC3033.19

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- blastx_Placozoa
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- protein2genome_Nema
- protein2genome_Onych
- protein2genome_Paraz
- protein2genome_Placo
- protein2genome_Platyf
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- protein2genome_Tardi
- protein2genome_Tunic
- protein2genome_UNCA
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

apollo File View Tools Help mmtorres

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User-created Annotations

ArosTmpB006329-RA

AROS_v0.5.2-Models

protein2genome_Arthropoda

Cegma

blastx_Arthropoda

ArosTmpB006329-RA

ArosTmpM006330-RA

tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae

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- protein2genome_Tunic
- protein2genome_UNCA
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

apollo File View Tools Help mmtorres

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1,028,750 1,030,000 1,031,250 1,032,500 1,033,750

Scaffold38 Scaffold38:1028616..1033960 (5.35 Kb) Go

User-created Annotations

ArosTmpB006329-RA

Information

- Get sequence
- Zoom to base level
- Delete
- Merge
- Split
- Duplicate
- Make intron
- Set translation start
- Set longest ORF
- Set readthrough stop codon
- Flip strand
- Set as 5' end
- Set as 3' end
- Set both ends
- Annotation Info Editor
- Undo
- Redo
- History

AROS_v0.5.2-Models

ArosTmpB006329-RA

protein2genome_Arthropoda

ArosTmpM006330-RA

59_9CUCU:Dendroctonus_ponderosae

V0_APIME:Apis_mellifera

C7_CAMFO:Camponotus_floridanus

A7_TRICA:Tribolium_castaneum

R2_TRICA:Tribolium_castaneum

8_NASVI:Nasonia_vitripennis

Annotation Info Editor

2B5W1|E2B5W1_HARSA:Harpegnathos_saltator

Cegma

BUSC3033.19

blastx_Arthropoda

- tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae
- tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis
- tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera
- tr|E2AHC7|E2AHC7_CAMFO:Camponotus_floridanus
- tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum
- tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

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- blastx_Parazoa
- blastx_Placozoa
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- protein2genome_Cnidaria
- protein2genome_Craniata

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1,028,750 1,030,000 1,031,250 1,032,500 1,033,750

User-created Annotations ArosTmpB006329-RA

Information Get sequence Zoom to base level

Delete Merge Split Duplicate Make intron Set translation start Set longest ORF Set readthrough stop codon Flip strand

Set as 5' end Set as 3' end Set both ends

Annotation Info Editor Undo Redo History

AROS_v0.5.2-Models ArosTmpB006329-RA ArosTmpM006330-RA

protein2genome_Arthropoda 59_9CUCU:Dendroctonus_ponderosae

7V0_APIME:Apis_mellifera

C7_CAMFO:Camponotus_floridanus

HA7_TRICA:Tribolium_castaneum

R2_TRICA:Tribolium_castaneum

8_NASVI:Nasonia_vitripennis

2B5W1|E2B5W1_HARSA:Harpegnathos_saltator

Cegma BUSC3033.19

blastx_Arthropoda tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis

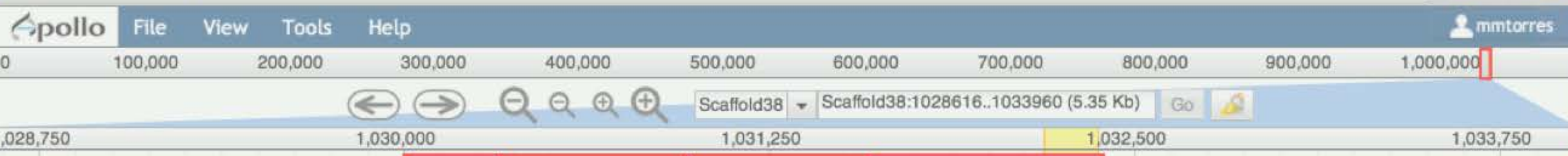
tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera

tr|E2AHC7|E2AHC7_CAMFO:Camponotus_floridanus

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- blastx_Placozoa
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- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata



User-created Annotations

Sequence

>FBE08E6BAA47147DDBE4C554BC9DCB7C (sequence:mRNA) 380 residues [peptide]

```

MSSYFANQFVPLRNGGVEHPHQHQHYGAAVQVPQQTQGMQQPQQAADPCDPSLLRQGVPGHHYGATA
GQQGMPYPRFPPYDRMDIRNAAYYQQQEHGGMDGMAGYRSSSPSSAMGGHMGHTPTPNGIPSTPIVYAS
CKLQAAAVDHDQGGVLDGPDSPDPLVESQMHHQMHPQHPMQAQQPPLQQHQHMQQQHMMYQQQQGTT
QQQQQATMHPQQQQPPQHGGVVTSPGLPQQGAPQGTAGANLPSPLYPWMRSQFARQFERSWILPNES
HLEIGAKVGGRLRYTVSNFSQQFQVTSLVVRSRLRAEISQTRVSENEKISFAFPPIILRREIVIGAKEKV
LSISRVSIRPGLTSLGKSFTSFYEPKNTSG
  
```

Peptide sequence
 cDNA sequence
 CDS sequence
 Genomic sequence
 Genomic sequence +/- 500 bases

- tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera
- tr|E2AHC7|E2AHC7_CAMFO:Camponotus_floridanus
- tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum
- tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

NCBI/BLAST Home
BLAST finds regions of similarity between biological sequences. [more...](#)

New DELTA-BLAST, a more sensitive protein-protein search

BLAST Assembled RefSeq Genomes

Choose a species genome to search, or [list all genomic BLAST databases.](#)

- [Human](#)
- [Mouse](#)
- [Rat](#)
- [Arabidopsis thaliana](#)
- [Oryza sativa](#)
- [Bos taurus](#)
- [Danio rerio](#)
- [Drosophila melanogaster](#)
- [Gallus gallus](#)
- [Pan troglodytes](#)
- [Microbes](#)
- [Apis mellifera](#)

Basic BLAST

Choose a BLAST program to run.

- [nucleotide blast](#) Search a **nucleotide** database using a **nucleotide** query
Algorithms: blastn, megablast, discontinuous megablast
- [protein blast](#) Search **protein** database using a **protein** query
Algorithms: blastp, psi-blast, phi-blast, delta-blast
- [blastx](#) Search **protein** database using a **translated nucleotide** query
- [tblastn](#) Search **translated nucleotide** database using a **protein** query
- [tblastx](#) Search **translated nucleotide** database using a **translated nucleotide** query

Specialized BLAST

Choose a type of specialized search (or database name in parentheses.)

- Make specific primers with [Primer-BLAST](#)

Your Recent Results **New!**

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News

[BLAST 2.2.29+ released](#)

A new version of the stand-alone BLAST+ applications is available. Mon, 06 Jan 2014 12:00:00 EST

[More BLAST news...](#)

Tip of the Day

[More tips...](#)

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Waiting for blast.ncbi.nlm.nih.gov...

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

NCBI/BLAST/blastp suite **Standard Protein BLAST**
blastn blastp blastx tblastn tblastx

Enter Query Sequence BLASTP programs search protein databases using a protein query. [more...](#) [Reset page](#) [Bookmark](#)

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) Query subrange

From

To

Or, upload file No file chosen

Job Title
Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database

Organism Exclude
Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude Models (XM/XP) Uncultured/environmental sample sequences

Entrez Query
Enter an Entrez query to limit search

Program Selection

Algorithm

- blastp (protein-protein BLAST)
- PSI-BLAST (Position-Specific Iterated BLAST)
- PHI-BLAST (Pattern Hit Initiated BLAST)
- DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

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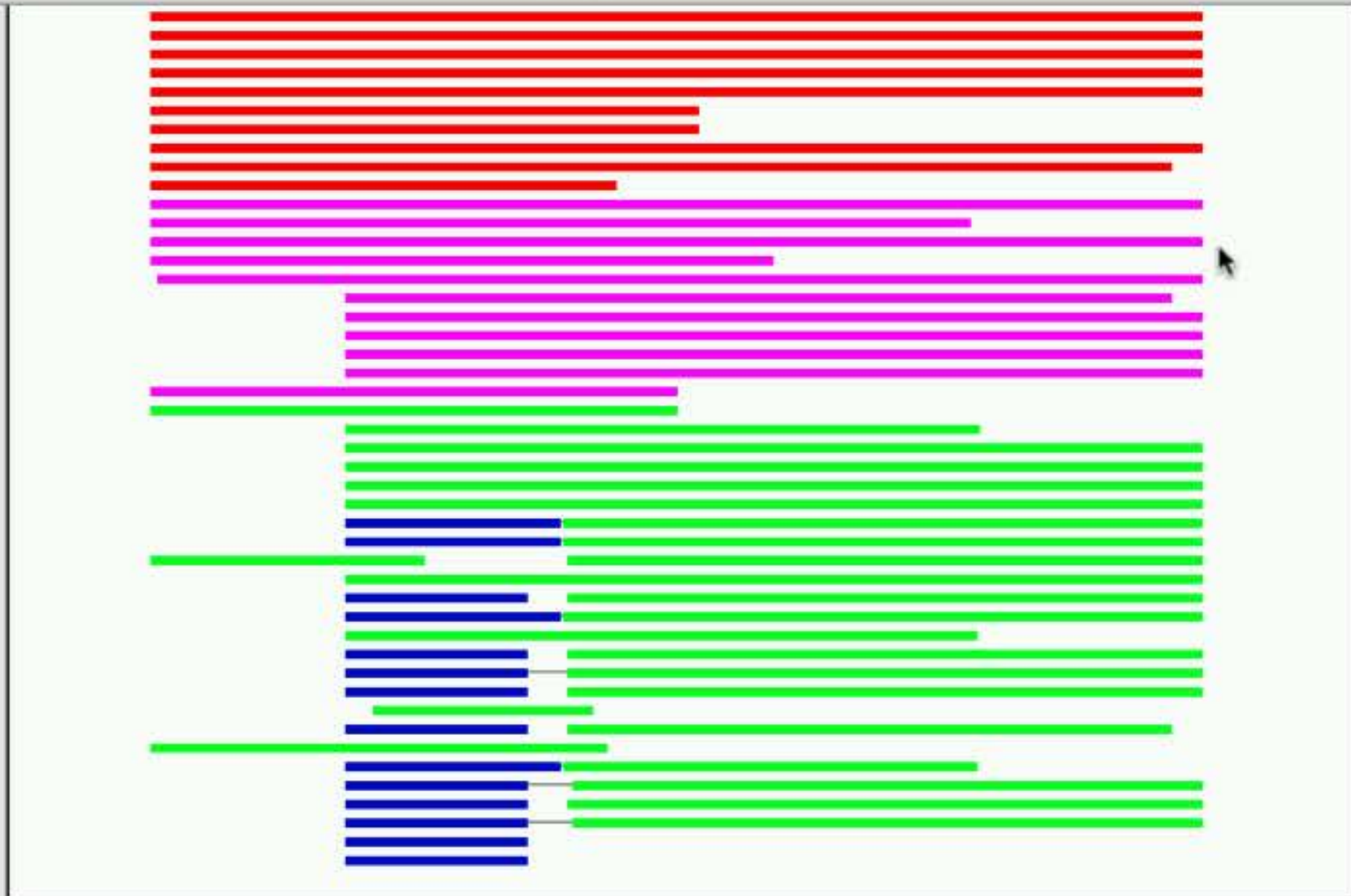
2,200,0

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protein2genome_Chelicerata

protein2genome_Cnidaria

protein2genome_Craniata



Descriptions

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Homeotic protein antennapedia [Camponotus floridanus]	335	335	89%	3e-109	65%	EFN67244.1
<input type="checkbox"/> PREDICTED: homeotic protein antennapedia-like [Megachile rotundata]	331	331	89%	2e-107	62%	XP_003700435.1
<input type="checkbox"/> homeobox protein H90 [Apis mellifera] >emb CAC06383.1 Antennapedia protein [Apis mellifera]	325	325	89%	4e-105	65%	NP_001011571.1
<input type="checkbox"/> PREDICTED: homeotic protein antennapedia-like [Apis florea]	313	313	89%	2e-100	63%	XP_003691231.1
<input type="checkbox"/> Homeotic protein antennapedia [Acromyrmex echinator]	308	308	89%	1e-98	61%	EGI64366.1

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

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000

Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Homeotic protein antennapedia [Camponotus floridanus]	335	335	89%	3e-109	65%	EFN67244.1
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<input type="checkbox"/> PREDICTED: homeotic protein antennapedia-like [Apis florea]	313	313	89%	2e-100	63%	XP_003691231.1
<input type="checkbox"/> Homeotic protein antennapedia [Acromyrmex echinator]	308	308	89%	1e-98	61%	EGI64366.1
<input type="checkbox"/> PREDICTED: homeotic protein antennapedia [Bombus terrestris] >gb ADZ11103.1 antennapedia-like protein [Bombus ter	307	307	46%	3e-98	84%	XP_003402194.1
<input type="checkbox"/> PREDICTED: homeotic protein antennapedia-like [Bombus impatiens]	307	307	46%	4e-98	84%	XP_003487458.1
<input type="checkbox"/> PREDICTED: LOW QUALITY PROTEIN: homeotic protein antennapedia-like [Apis dorsata]	300	300	89%	2e-95	61%	XP_006615925.1
<input type="checkbox"/> antennapedia-like protein [Nasonia vitripennis] >gb ACT63883.1 Antennapedia-like protein [Nasonia vitripennis]	286	286	87%	6e-90	63%	NP_001161164.1
<input type="checkbox"/> Homeotic protein antennapedia [Harpegnathos saltator]	231	231	39%	4e-70	81%	EFN88930.1
<input type="checkbox"/> homeodomain transcription factor Prothoraxless [Tribolium castaneum] >gb EEZ99250.1 antennapedia [Tribolium castane	167	167	89%	7e-45	42%	AAK96031.1
<input type="checkbox"/> hypothetical protein YQE_06892, partial [Dendroctonus ponderosae] >gb ERL93092.1 hypothetical protein D910_10394,	156	156	70%	2e-41	47%	ENN76593.1
<input type="checkbox"/> prothoraxless [Tribolium castaneum] >gb AAF69136.1 AF228509_1 prothoraxless [Tribolium castaneum]	137	137	89%	9e-34	38%	NP_001034505.1
<input type="checkbox"/> conserved hypothetical protein [Pediculus humanus corporis] >gb EEB13904.1 conserved hypothetical protein [Pediculus	127	127	53%	6e-30	46%	XP_002426642.1
<input type="checkbox"/> antennapedia-like proteinue protein [Danaus plexippus]	122	122	89%	1e-28	35%	EHJ76618.1
<input type="checkbox"/> antennapedia homologue protein [Bombyx mori] >db BAA04087.1 Antennapedia homologue protein [Bombyx mori] >gb /	102	102	70%	8e-22	36%	NP_001037319.1
<input type="checkbox"/> AGAP004660-PA [Anopheles gambiae str. PEST] >gb AAC31945.1 Antennapedia homeotic protein [Anopheles gambiae]	93.6	93.6	73%	2e-18	35%	XP_311618.2
<input type="checkbox"/> homeotic antennapedia protein [Culex quinquefasciatus] >gb EDS27380.1 homeotic antennapedia protein [Culex quinqu	85.5	85.5	73%	2e-15	33%	XP_001842678.1
<input type="checkbox"/> homeotic antennapedia protein, putative [Aedes aegypti] >gb EAT38125.1 AAEL009947-PA [Aedes aegypti]	85.1	85.1	73%	2e-15	33%	XP_001660496.1
<input type="checkbox"/> PREDICTED: homeotic protein antennapedia-like isoform X3 [Ceratitis capitata]	80.9	80.9	73%	8e-14	33%	XP_004524344.1
<input type="checkbox"/> PREDICTED: homeotic protein antennapedia-like isoform X1 [Ceratitis capitata]	80.4	80.4	45%	0e-12	35%	XP_001017197.1

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protein2genome_Chelicerata

protein2genome_Cnidaria

protein2genome_Craniata

Alignments

Download v GenPept Graphics Next Previous Descriptions

Homeotic protein antennapedia [Camponotus floridanus]

Sequence ID: gb|EFN67244.1| Length: 353 Number of Matches: 1

Range 1: 1 to 329 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
335 bits(860)	3e-109	Compositional matrix adjust.	225/347(65%)	247/347(71%)	24/347(6%)

Query	1	MSSYFANQFVPLDRNGGVEHPHQHQQHYGAAVQVPQQTQGMQQQPQQAADPCDPSLLRQG	60
Sbjct	1	MSSYFAN ++PDLRNGGVEHPHQHQQHYGAAVQVPQQTQ +QQQ QQA DPCDPSLLRQG	60
Query	61	VPGHHYGAT-AGQQGMPYPRFPYDRMDIRNAAYYQQQEHGGMDGMAGYRSSSPSSAMG	119
Sbjct	61	VSAHHYGTGGQQDMPYPRFPYDRMDIRNAAYYQHQQEHGSMAGYRSTSPNPSMG	120
Query	120	GHMGTPTPNPSTPIVYASCKLQAAAVDHQGGVLDGPDSPDPLVESQMHHQMHQHPH	179
Sbjct	121	GHMGTPTPNPSTPIVYASCKLQAAAVDHQGGVLDGPDSP-PLVESQMHHQMHQHPH	179
Query	180	M----QAQQPPLQHQHQQHMQQQHMMYQQQQGTTQQQQQATMHPQQQQQPPPHQGVVT	235
Sbjct	180	MQTQQSQHAQQQPQHQLQAQQHMMYQQQQSQTTSQQGQSAMHPQQQQQ-TQQHGVVA	238
Query	236	SPLGPPQQGAPQGTAGANLPSPLYPWMSQFARQFERSWILPNESHLEIGAKVGLRLYT	295
Sbjct	239	SLSLQQGAPQSAASSNLPSPLYPWMSQFARQFERSWILPNESHLEIGAKVGLRLYT	282
Query	296	VSNFSQQFQVTSLVVRSRLRAEISQTRVVSENE-KISFAFPPIILRRE	341
Sbjct	283	TLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMRKWKKE	329

Related Information

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PREDICTED: homeotic protein antennapedia-like [Megachile rotundata]

Sequence ID: ref|XP_003700435.1| Length: 352 Number of Matches: 1

Range 1: 1 to 328 GenPept Graphics Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
331 bits(848)	2e-107	Compositional matrix adjust.	214/346(62%)	232/346(67%)	23/346(6%)

Query	1	MSSYFANQFVPLDRNGGVEHPHQHQQHYGAAVQVPQQTQGMQQQPQQAADPCDPSLLRQG	60
Sbjct	1	MSSYFAN ++PDLRNGGVEHPHQHQQHYGAAVQVPQQTQ +QQQ QQA DPCDPSLLRQG	60
Query	61	VPGHHYGATAGQQGMPYPRFPYDRMDIRNAAYYQQQEHGGMDGMAGYRSSSPSSAMGG	120

Related Information

Gene - associated gene details

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

mmortres

033,750

2,200,000

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Alignments Result Summary Guide Tree Phylogenetic Tree Submission Details

Download Alignment File Hide Colors Send to ClustalW2_Phylogeny

CLUSTAL 2.1 multiple sequence alignment

```
Antp_Nvit          MSSFYFANSYIPDLRNGGVEHPHQHQHYGAAVQVPQQQAVQQQPQQASDPCDPSMLRQG 60
Athros_putative_seq MSSFYANQFVPPDLRNGGVEHPHQHQHYGAAVQVPQQTQGMQQQPQQAADPCDPSLLRQG 60
*****.:*****:*****:*****:*****

Antp_Nvit          VPGHHGYGAATGQQPGMPYPRFPPYDRMDIRNAAYYQQQQQEHGMD-MASYRASSPSAGM 119
Athros_putative_seq VPGHH-YGATAGQQ-GMPYPRFPPYDRMDIRNAAYYQQQQEHGGMDGMAGYRSSSPSSAM 118
***** ***:***:*****:*** ***:***:*****:.*

Antp_Nvit          AGLHMGHTPTPVNGHPASTPIVYASCKLQAAAVDHQGSVLDGPDSP-PLVDAQMHQMHP 178
Athros_putative_seq GG-HMGHTPTP-NGIP-STPIVYASCKLQAAAVDHQGGVLDGPDSPDPLVESQMHHQMHP 175
.* ***** ** * *****:***** ***:*****

Antp_Nvit          QHTHMQAQQSHPQQQPQAPHQQAHMQPQQTQQQHMMYQQQTQ--PQQPQPAAMHPQQQ 236
Athros_putative_seq QHPHMQAQQ-----PPLQQHQHMQ----QQQHMMYQQQQGTQQQQQATMHPQQQ 223
**.* ***** * ::* *** ***** * .** * *:*****

Antp_Nvit          AQQQ-QHQGVVASPLGQQQPGTPQSAAPTNLPSPLYPWMRSQFERKRGR----- 284
Athros_putative_seq QQPPPQHQGVVTSPLGPPQQGAPQGTAGANLPSPLYPWMRSQFARQFERSWILPNESHLE 283
* *****:***** ** *:***:*****:***** *: *

Antp_Nvit          -----QTYTRYQTLLELEKEFHFNRYLTRRRRIEIAHALCLTE-----RQIK 325
Athros_putative_seq IGAKVGGRLRLYTVSNFSQQFQVTSLVVRSRLRAEISQTRVVSENEKISFAFPPPIILRREIV 343
* . :*:***:*** ** * ***:***:*** ***:***

Antp_Nvit          IWFQNRMRKWKKETKTKGEPNSGDGDTDISPQTSPQG 362
Athros_putative_seq IGAKEKVLISIRVSIKPLTSLGKSFYEPKNTSG 380
* :*:***:*** ** * ***:***:*** ***:***
```

PLEASE NOTE: Showing colors on large alignments is slow.

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protein2genome_Chelicerata

protein2genome_Cnidaria

protein2genome_Craniata

Alignments Result Summary Guide Tree Phylogenetic Tree Submission Details

Download Alignment File Hide Colors Send to ClustalW2_Phylogeny

CLUSTAL 2.1 multiple sequence alignment

```
Antp_Nvit          MSSFYFANSYIPDLRNGGVEHPHQHQHYGAAVQVPQQQAVQQQPQQASDPCDPSMLRQG 60
Athros_putative_seq MSSFYANQFVFDLRNGGVEHPHQHQHYGAAVQVPQQTQGMQQQPQQAADPCDPSLLRQG 60
*****.:*****:*****:*****:*****

Antp_Nvit          VPGHHGYGAATGQQPGMPYPRFPPYDRMDIRNAAYYQQQQQEHGMD-MASYRASSPSAGM 119
Athros_putative_seq VPGHH-YGATAGQQ-GMPYPRFPPYDRMDIRNAAYYQQQQEHGGMDGMAGYRSSSPSSAM 118
***** ***:***:*****:*** ***:***:*****:.*

Antp_Nvit          AGLHMGHTPTPVNGHPASTPIVYASCKLQAAAVDHQGSVLDGPDSP-PLVDAQMHQMHP 178
Athros_putative_seq GG-HMGHTPTP-NGIP-STPIVYASCKLQAAAVDHQGGVLDGPDSPDPLVESQMHHQMHP 175
.* ***** ** * *****:***** ***:*****

Antp_Nvit          QHTHMQAQQSHPQQQPQAPHQQAHMQPQQTQQQHMMYQQQTQ--PQQPQPAAMHPQQQ 236
Athros_putative_seq QHPHMQAQQ-----PPLQQHQHMQ----QQQHMMYQQQQGTQQQQQATMHPQQQ 223
**.:***** * :.* ** ***** * .** * *:*****

Antp_Nvit          AQQQ-QHQGVVASPLGQQQPGTPQSAAPTNLPSPLYPWMRSQFERKRGR----- 284
Athros_putative_seq QQPPPQHQGVVTSPLGPQQQAPQGTAGANLPSPLYPWMRSQFARQFERSWILPNESHLE 283
* *****:***** ** *:***.:* :***** ***: *

Antp_Nvit          -----QTYTRYQTLLELEKEFHFNRYLTRRRRIEIAHALCLTE-----RQIK 325
Athros_putative_seq IGAKVGGRLRLYTVSNFSQQFQVTSLVVRSRLRAEISQTRVVSENEKISFAFPPPIILRREIV 343
* .:***:***.:** * ***:***:***

Antp_Nvit          IWFQNRMRKWKKETKTKGEPNSGDGDTDISPQTSPQG 362
Athros_putative_seq IGAKEKVLISIRVSIKPLTSLGKSFYEPKNTSG 380
* :***:***.:** * ***:***:***
```

PLEASE NOTE: Showing colors on large alignments is slow.

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mmortres

protein2genome_Chelicerata

protein2genome_Cnidaria

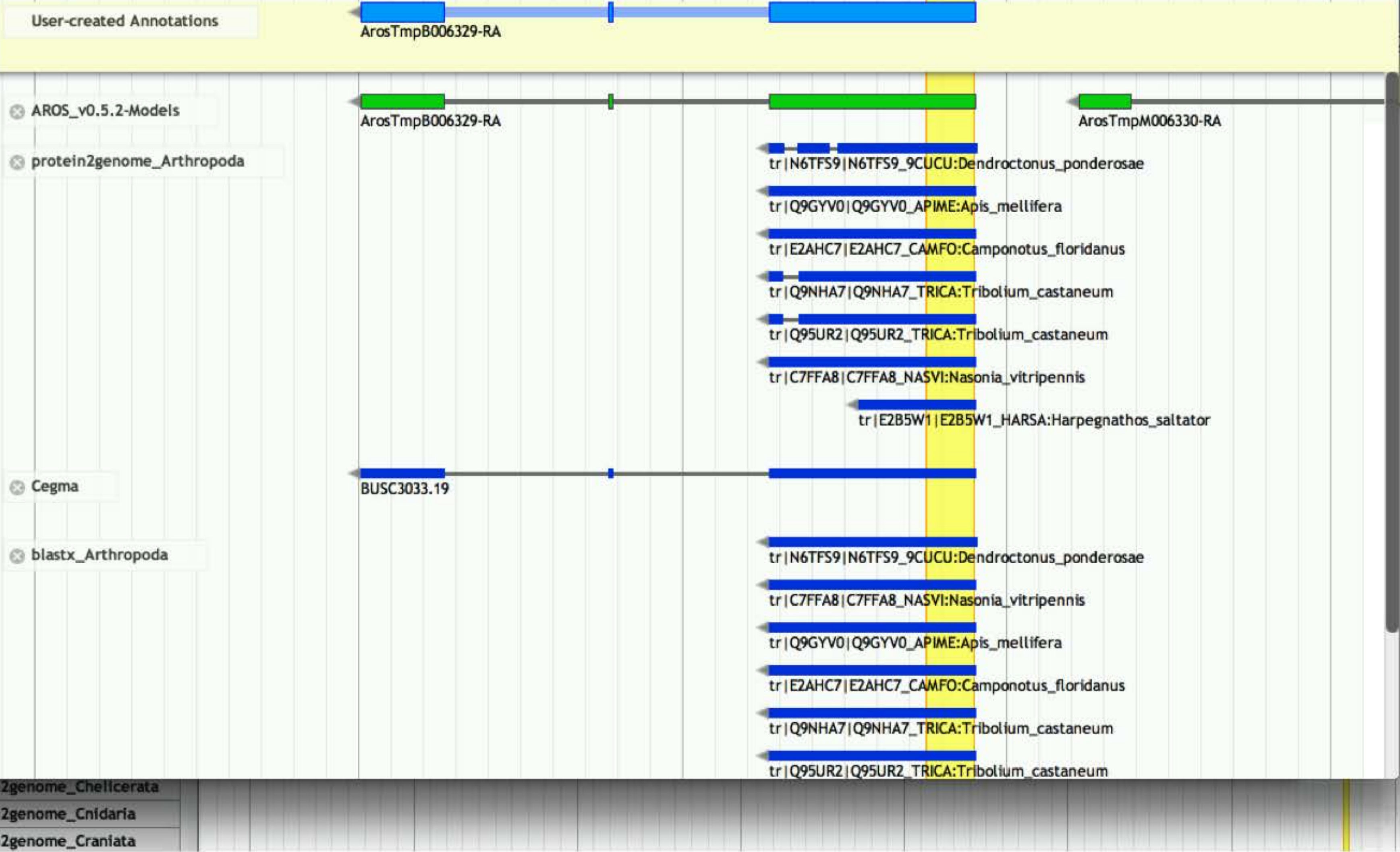
protein2genome_Craniata

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annel
- protein2genome_Atelo
- protein2genome_Cepha
- protein2genome_Chelk
- protein2genome_Cnida
- protein2genome_Crani
- protein2genome_Crust
- protein2genome_Echin
- protein2genome_Mollu
- protein2genome_Nema
- protein2genome_Nema
- protein2genome_Onych
- protein2genome_Paraz
- protein2genome_Placo
- protein2genome_Platyf
- protein2genome_Priap
- protein2genome_Tardi
- protein2genome_Tunic
- protein2genome_UNCA
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

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Scaffold38 Scaffold38:1028616..1033960 (5.35 Kb) Go

1,028,750 1,030,000 1,031,250 1,032,500 1,033,750



- blastx_Cranifata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annel
- protein2genome_Atelo
- protein2genome_Cepha
- protein2genome_Chelli
- protein2genome_Cnida
- protein2genome_Crani
- protein2genome_Crusta
- protein2genome_Echin
- protein2genome_Mollu
- protein2genome_Nema
- protein2genome_Nema
- protein2genome_Onych
- protein2genome_Paraz
- protein2genome_Placo
- protein2genome_Platyf
- protein2genome_Priap
- protein2genome_Tardigr
- protein2genome_Tunic
- protein2genome_UNCA
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Cranifata

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User-created Annotations

AROS_v0.5.2-Models

protein2genome_Arthropoda

tr|F8J2L5|F8J2L5_9HEMI:Pachygrontha_nigriventris

tr|Q6IT84|Q6IT84_ONCFA:Oncopeltus_fasciatus

tr|E0VKK0|E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis

tr|H9JA47|H9JA47_BOMMO:Bombyx_mori

tr|D2A356|D2A356_TRICA:Tribolium_castaneum

tr|Q6IT83|Q6IT83_ONCFA:Oncopeltus_fasciatus

tr|Q16EL3|Q16EL3_AEDAE:Aedes_aegypti

tr|Q26498|Q26498_SCHGR:Schistocerca_gregaria

tr|N6TEF7|N6TEF7_9CUCU:Dendroctonus_ponderosae

tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes

tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata

tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica

tr|Q0H299|Q0H299_9HEXA:Folsomia_candida

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

ArosTmpB006329-RA

ArosTmpB006329-RA

ArosTmpM0

tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae

tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera

tr|E2AHC7|E2AHC7_CAMFO:Camponotus_rufus

tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum

tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis

tr|E2B5W1|E2B5W1_HARSA:Haemaphysalis_schlegelii

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
- protein2genome_Atelocerata
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata
- protein2genome_Crustacea
- protein2genome_Echinodermata
- protein2genome_Mollusca
- protein2genome_Nematomorpha
- protein2genome_Nematomorpha
- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

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Scaffold38 Scaffold38:1022861..1033550 (10.69 Kb) Go

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User-created Annotations

Scaffold38:1025117-1025513

ArosTmpB006329-RA

AROS_v0.5.2-Models

ArosTmpB006329-RA

ArosTmpM006329-RA

protein2genome_Athropoda

tr|F8J2L5|F8J2L5_9HEMI:Pachygrontha_nigriventris

tr|Q6IT84|Q6IT84_ONCFA:Oncopeltus_fasciatus

tr|E0VKK0|E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis

tr|H9JA47|H9JA47_BOMMO:Bombyx_mori

tr|D2A356|D2A356_TRICA:Tribolium_castaneum

tr|Q6IT83|Q6IT83_ONCFA:Oncopeltus_fasciatus

tr|Q16EL3|Q16EL3_AEDAE:Aedes_aegypti

tr|Q26498|Q26498_SCHGR:Schistocerca_gregaria

tr|N6TEF7|N6TEF7_9CUCU:Dendroctonus_ponderosae

tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes

tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata

tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica

tr|Q0H299|Q0H299_9HEXA:Folsomia_candida

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

tr|N6TF59|N6TF59_9CUCU:Dendroctonus_ponderosae

tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera

tr|E2AHC7|E2AHC7_CAMFO:Camponotus_rufus

tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum

tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis

tr|E2B5W1|E2B5W1_HARSA:Harpalus_fuscicornis

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annel
- protein2genome_Atelo
- protein2genome_Cepha
- protein2genome_Cheli
- protein2genome_Cnida
- protein2genome_Crani
- protein2genome_Crust
- protein2genome_Echin
- protein2genome_Mollu
- protein2genome_Nema
- protein2genome_Nema
- protein2genome_Onych
- protein2genome_Paraz
- protein2genome_Placo
- protein2genome_Platy
- protein2genome_Priap
- protein2genome_Tardi
- protein2genome_Tunic
- protein2genome_UNCA
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

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User-created Annotations Scaffold38:1025117-1025513

AROS_v0.5.2-Models

protein2genome_Athropoda

tr|F8J2L5|F8J2L5_9HEMI:Pachygrontha_nigriventris

tr|Q6IT84|Q6IT84_ONCFA:Oncopeltus_fasciatus

tr|E0VKK0|E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis

tr|H9JA47|H9JA47_BOMMO:Bombyx_mori

tr|D2A356|D2A356_TRICA:Tribolium_castaneum

tr|Q6IT83|Q6IT83_ONCFA:Oncopeltus_fasciatus

tr|Q16EL3|Q16EL3_AEDAE:Aedes_aegypti

tr|Q26498|Q26498_SCHGR:Schistocerca_gregaria

tr|N6TEF7|N6TEF7_9CUCU:Dendroctonus_ponderosae

tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes

tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata

tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica

tr|Q0H299|Q0H299_9HEXA:Folsomia_candida

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

ArosTmpB006329-RA

ArosTmpM006329-RA

tr|N6TF59|N6TF59_9CUCU:Dendroctonus_ponderosae

tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera

tr|E2AHC7|E2AHC7_CAMFO:Camponotus_rufus

tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum

tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis

tr|E2B5W1|E2B5W1_HARSA:Harpalus_carpophilus

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
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- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata
- protein2genome_Crustacea
- protein2genome_Echinodermata
- protein2genome_Mollusca
- protein2genome_Nematomorpha
- protein2genome_Nemata
- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

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Scaffold38 Scaffold38:1022861..1033550 (10.69 Kb) Go

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User-created Annotations Scaffold38:1025117-1025513

AROS_v0.5.2-Models ArosTmpB006329-RA ArosTmpM006329-RA

protein2genome_Athropoda

tr F8J2L5 F8J2L5_9HEMI:Pachygrontha_nigriventris	
tr Q6IT84 Q6IT84_ONCFA:Oncopeltus_fasciatus	
tr E0VKK0 E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis	
tr H9JA47 H9JA47_BOMMO:Bombyx_mori	
tr D2A356 D2A356_TRICA:Tribolium_castaneum	
tr Q6IT83 Q6IT83_ONCFA:Oncopeltus_fasciatus	
tr Q16EL3 Q16EL3_AEDAE:Aedes_aegypti	
tr Q26498 Q26498_SCHGR:Schistocerca_gregaria	
tr N6TEF7 N6TEF7_9CUCU:Dendroctonus_ponderosae	
tr H9HPZ8 H9HPZ8_ATTCE:Atta_cephalotes	
tr N6UIC4 N6UIC4_9CUCU:Dendroctonus_ponderosae	
tr Q0H2A2 Q0H2A2_9INSE:Ephemera_vulgata	
tr Q9UA50 Q9UA50_9INSE:Thermobia_domestica	
tr Q0H299 Q0H299_9HEXA:Folsomia_candida	
tr Q7PN76 Q7PN76_ANOGA:Anopheles_gambiae	
tr N6TF59 N6TF59_9CUCU:Dendroctonus_ponderosae	
tr Q9GYV0 Q9GYV0_APIME:Apis_mellifera	
tr E2AHC7 E2AHC7_CAMFO:Camponotus_rufus	
tr Q9NHA7 Q9NHA7_TRICA:Tribolium_castaneum	
tr Q95UR2 Q95UR2_TRICA:Tribolium_castaneum	
tr C7FFA8 C7FFA8_NASVI:Nasonia_vitripennis	
tr E2B5W1 E2B5W1_HARSA:Harpalus_carpophilus	

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1,025,000 1,027,500 1,030,000 1,032,500

User-created Annotations: Scaffold38:1025117-1025513

AROS_v0.5.2-Models

protein2genome_Arthropoda

tr|F8J2L5|F8J2L5_9HEMI:Pachygrontha_nigriventris

tr|Q6IT84|Q6IT84_ONCFA:Oncopeltus_fasciatus

tr|E0VKK0|E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis

tr|H9JA47|H9JA47_BOMMO:Bombyx_mori

tr|D2A356|D2A356_TRICA:Tribolium_castaneum

tr|Q6IT83|Q6IT83_ONCFA:Oncopeltus_fasciatus

tr|Q16EL3|Q16EL3_AEDAE:Aedes_aegypti

tr|Q26498|Q26498_SCHGR:Schistocerca_gregaria

tr|N6TEF7|N6TEF7_9CUCU:Dendroctonus_ponderosae

tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes

tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata

tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica

tr|Q0H299|Q0H299_9HEXA:Folsomia_candida

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

ArosTmpB006329-RA

ArosTmpM006329-RA

tr|N6TF59|N6TF59_9CUCU:Dendroctonus_ponderosae

tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera

tr|E2AHC7|E2AHC7_CAMFO:Camponotus_rufus

tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum

tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis

tr|E2B5W1|E2B5W1_HARSA:Harpegnathos saltator

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
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- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
- protein2genome_Ateleta
- protein2genome_Cephalopoda
- protein2genome_Chelicerata
- protein2genome_Cnidaria
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- protein2genome_Echinodermata
- protein2genome_Mollusca
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- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
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- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

0 100,000 200,000 300,000 400,000 500,000 600,000 700,000 800,000 900,000 1,000,000

Scaffold38 Scaffold38:1022861..1033550 (10.69 Kb) Go

1,025,000 1,027,500 1,030,000 1,032,500

User-created Annotations Scaffold

Information Get sequence Zoom to base level

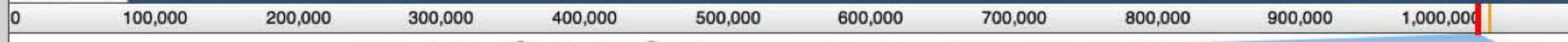
Delete Merge Split Duplicate Make intron Set translation start Set longest ORF Set readthrough stop codon Flip strand Set as 5' end Set as 3' end Set both ends Annotation Info Editor Undo Redo History

AROS_v0.5.2-Models protein2genome_Arthropoda

Annotations and tracks visible in the JBrowse interface:

- AROS_v0.5.2-Models**: A track showing gene models with green bars and arrows.
- protein2genome_Arthropoda**: A track showing protein-coding genes with blue bars and arrows. Visible entries include:
 - tr|F8...a_nigriventris
 - tr|...us_fasciatus
 - tr|...us_humanus_subsp_corporis
 - tr|...x_mori
 - tr|...h_castaneum
 - tr|...us_fasciatus
 - tr|...egypti
 - tr|...cerca_gregaria
 - tr|N6TEF7|N6TEF7_9CUCU:Dendroctonus_ponderosae
 - tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes
 - tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae
 - tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata
 - tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica
 - tr|Q0H299|Q0H299_9HEXA:Folsomia_candida
 - tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae
- ArosTmpB006329-RA**: A gene model represented by a green bar with a vertical line.
- ArosTmpM0063...**: Another gene model represented by a green bar with a vertical line.
- tr|N6TF59|N6TF59_9CUCU:Dendroct...**: A protein-coding gene with a blue bar and arrow.
- tr|Q9GYV0|Q9GYV0_APIME:Apis_mel...**: A protein-coding gene with a blue bar and arrow.
- tr|E2AHC7|E2AHC7_CAMFO:Camponc...**: A protein-coding gene with a blue bar and arrow.
- tr|Q9NHA7|Q9NHA7_TRICA:Tribolium...**: A protein-coding gene with a blue bar and arrow.
- tr|Q95UR2|Q95UR2_TRICA:Tribolium...**: A protein-coding gene with a blue bar and arrow.
- tr|C7FFA8|C7FFA8_NASVI:Nasonia_vit...**: A protein-coding gene with a blue bar and arrow.
- tr|E2B5W1|E2B5W1_HARSA:Harp...**: A protein-coding gene with a blue bar and arrow.

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
- protein2genome_Ateleta
- protein2genome_Cephalopoda
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata
- protein2genome_Crustacea
- protein2genome_Echinodermata
- protein2genome_Mollusca
- protein2genome_Nematoda
- protein2genome_Nematomorpha
- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata



Reference sequence

S F F Y F G T K F L F A S R * G R G H G R F L C V A A S L G T D * N G T L S R V P T F G

F I L L F W N Q I F I C L S V R Q R A W A I S M R R R L V R Y R L K W N S F S S S N V W Y

TTTCATTCTTCTATTTTGGAAACC AAATTTTATTTGCTCTCGGTGAG GCAGAGGGCATGGGCGATTTCTATG CGTCGCCGCTCGTTAGGTACCGAT TGAATGGAACCTCTTTCTCGAGTTC CAACGTTTGGT

AAAGTAAGAAGATAAAACCTTGG TTTAAAAATAAACGGAGAGCCACTC CGTCTCCCGTACCCGCTAAAGATAC GCAGCGCGGAGCAATCCATGGCTTACTTTACCTTGAGAAAGAGCTCAAG GTTGCAAACCA

N * E E I K S G F K * K G R P S A S P M P S K * A D G G R * T G I S I S S K R S N W R K T

K M R R R N Q F W I K I Q R E T L C L A H A I E I R R R R R T L Y R N F H F E K E L E L T Q

M E N K * K P V L N K N A E R H P L P C P R N R H T A A E N P V S Q F P V R E R T G V N P

User-created Annotations Scaffold38:1025117-1025513

Track	Annotation
AROS_v0.5.2-Models	
protein2genome_Arthropoda	tr F8J2L5 F8J2L5_9HEMI:Pachygrontha_nigriventris
protein2genome_Ateleta	tr E0VKK0 E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis
protein2genome_Chelicerata	tr H9JA47 H9JA47_BOMMO:Bombyx_mori
protein2genome_Cnidaria	
protein2genome_Craniata	tr D2A356 D2A356_TRICA:Tribolium_castaneum
protein2genome_Crustacea	tr Q16EL3 Q16EL3_AEDAE:Aedes_aegypti
protein2genome_Echinodermata	
protein2genome_Mollusca	tr Q26498 Q26498_SCHGR:Schistocerca_gregaria
protein2genome_Nematoda	tr N6TEF7 N6TEF7_9CUCU:Dendroctonus_ponderosae
protein2genome_Nematomorpha	tr H9HPZ8 H9HPZ8_ATTCE:Atta_cephalotes
protein2genome_Onychophora	
protein2genome_Parazoa	
protein2genome_Placozoa	tr N6UIC4 N6UIC4_9CUCU:Dendroctonus_ponderosae
protein2genome_Platyhelminthes	tr Q0H2A2 Q0H2A2_9INSE:Ephemera_vulgata
protein2genome_Priapulida	
protein2genome_Tardigrada	tr Q9UA50 Q9UA50_9INSE:Thermobia_domestica
protein2genome_Tunicata	
protein2genome_UNCATEGORISED	tr Q0H299 Q0H299_9HEXA:Folsomia_candida

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
- protein2genome_Ateolozoa
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata
- protein2genome_Crustacea
- protein2genome_Echinodermata
- protein2genome_Mollusca
- protein2genome_Nematoda
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- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

apollo File View Tools Help mmtorres

0 100,000 200,000 300,000 400,000 500,000 600,000 700,000 800,000 900,000 1,000,000

Scaffold38 Scaffold38:1025432..1025564 (133 b) Go

1,025,450 1,025,475 1,025,500 1,025,525 1,025,550

Reference sequence
 E M E L F L E F Q R L V S R V R L P T P P P F * N R K Y K M D M G I N F R S
 A S L G T D * N G T L S R V P T F G I A C T F A Y P V S F L K Q K I Q N G Y G D K F S L V
 R L V R Y R L K W N S F S S S N V W Y R V Y V C L P R F L S E T E N T K W I W G * I F A R
 CCGCCTCGTTAGGTACCGAT TGAAATGGAAC TCTTCTCGAGTTC CAACGTTTGGTATCGCGTGTACGTT TGCCTACCCCGTTTCTCTTCTGAAA CAGAAAATACAAAATGGATATGGGG ATAAATTTTCGCTCG
 GCGGAGCAATCCATGGCTA ACTTTACCTTGAGAAAAGAGCTCAAG GTTGCAAACCATAGCGCACATGCAA ACGGATGGGGCAAAGGAAAGACTTTGTCTTTTATGTTTTACCTATACCCCTATTTAAAAGCGGAGC
 G G R * T G I S I S S K R S N W R K T D R T R K G V G N G K Q F L F Y L I S I P I F K R E
 R R T L Y R N F H F E K E L E L T Q Y R T Y T Q R G R K R E S V S F V F H I H P Y I K A R
 A A E N P V S Q F P V R E R T G V N P I A H V N A * G T E K R F C F I C F P Y P S L N E S

User-created Annotations
 Scaffold38:1025117-1025513

AROS_v0.5.2-Models

protein2genome_Arthropoda tr|F8J2L5|F8J2L5_9HEMI:Pachygrontha_nigriventris

tr|E0VKK0|E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis

tr|H9JA47|H9JA47_BOMMO:Bombyx_mori

tr|D2A356|D2A356_TRICA:Tribolium_castaneum

tr|Q16EL3|Q16EL3_AEDAE:Aedes_aegypti

tr|Q26498|Q26498_SCHGR:Schistocerca_gregaria

tr|N6TEF7|N6TEF7_9CUCU:Dendroctonus_ponderosae

tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes

tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata

tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica

tr|Q0H299|Q0H299_9HEXA:Folsomia_candida

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
- protein2genome_Ateolozoa
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata
- protein2genome_Crustacea
- protein2genome_Echinodermata
- protein2genome_Mollusca
- protein2genome_Nematomorpha
- protein2genome_Nemata
- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

apollo File View Tools Help mmtorres

0 100,000 200,000 300,000 400,000 500,000 600,000 700,000 800,000 900,000 1,000,000

Scaffold38 Scaffold38:1025432..1025564 (133 b) Go

1,025,450 1,025,475 1,025,500 1,025,525 1,025,550

Reference sequence
 E M E L F L E F Q R L V S R V R L P T P P P F * N R K Y K M D M G I N F R S
 A S L G T D * N G T L S R V P T F G I A C T F A Y P V S F L K Q K I Q N G Y G D K F S L V
 R L V R Y R L K W N S F S S S N V W Y R V Y V C L P R F L S E T E N T K W I W G * I F A R
 CCGCCTCGTTAGGTACCGAT TGAAATGGAAC TCTTCTCGAGTTC CAACGTTTGGTATCGCGTGTACGTT TGCCTACCCCGTTTCTCTGAAA CAGAAAATACAAAATGGATATGGGG ATAAATTTTCGCTCG
 GCGGAGCAATCCATGGCTA ACTTTACCTTGAGAAAAGAGCTCAAG GTTGCAAACCATAGCGCACATGCAA ACGGATGGGGCAAAGGAAAGACTTTGTCTTTTATGTTTTACCTATACCCCTATTTAAAAGCGGAGC
 G G R * T G I S I S S K R S N W R K T D R T R K G V G N G K Q F L F Y L I S I P I F K R E
 R R T L Y R N F H F E K E L E L T Q Y R T Y T Q R G R K R E S V S F V F H I H P Y I K A R
 A A E N P V S Q F P V R E R T G V N P I A H V N A * G T E K R F C F I C F P Y P S L N E S

User-created Annotations Scaffold38:1025117-1025513

AROS_v0.5.2-Models

protein2genome_Arthropoda tr|F8J2L5|F8J2L5_9HEMI:Pachygrontha_nigriventris

tr|E0VKK0|E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis

tr|H9JA47|H9JA47_BOMMO:Bombyx_mori

tr|D2A356|D2A356_TRICA:Tribolium_castaneum

tr|Q16EL3|Q16EL3_AEDAE:Aedes_aegypti

tr|Q26498|Q26498_SCHGR:Schistocerca_gregaria

tr|N6TEF7|N6TEF7_9CUCU:Dendroctonus_ponderosae

tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes

tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata

tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica

tr|Q0H299|Q0H299_9HEXA:Folsomia_candida

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
- protein2genome_Ateleta
- protein2genome_Cephalopoda
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Crustacea
- protein2genome_Echinodermata
- protein2genome_Mollusca
- protein2genome_Nematoda
- protein2genome_Nematomorpha
- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

0 100,000 200,000 300,000 400,000 500,000 600,000 700,000 800,000 900,000 1,000,000

Scaffold38 Scaffold38:1025432..1025564 (133 b) Go

1,025,450 1,025,475 1,025,500 1,025,525 1,025,550

Reference sequence

```

E M E L F L E F Q R L V S R V R L P T P P P F * N R K Y K M D M G I N F R S
A S L G T D * N G T L S R V P T F G I A C T F A Y P V S F L K Q K I Q N G Y G D K F S L V
R L V R Y R L K W N S F S S S N V W Y R V Y V C L P R F L S E T E N T K W I W G * I F A R
CCGCCTCGTTAGGTACCGATTGAAATGGAACCTTTCTCGAGTTCCAACGTTTGGTATCGCGTGTACGTTTGCCTACCCCGTTTCTTTCTGAAAACAGAAAATACAAAATGGATATGGGGATAAATTTTCGCTCG
CGCGGAGCAATCCATGGCTAACCTTACCTTGAGAAAAGAGCTCAAGGTTGCAAACCATAGCGCACATGCAAACGGATGGGGCAAAGGAAAGACTTTGTCTTTTATGTTTTACCTATACCCCTATTTAAAAGCGGAGC
G G R * T G I S I S S K R S N W R K T D R T R K G V G N G K Q F L F Y L I S I P I F K R E
R R T L Y R N F H F E K E L E L T Q Y R T Y T Q R G R K R E S V S F V F H I H P Y I K A R
A A E N P V S Q F P V R E R T G V N P I A H V N A * G T E K R F C F I C F P Y P S L N E S

```

User-created Annotations Scaffold38:1025117-1025513

Track	Annotation
AROS_v0.5.2-Models	
protein2genome_Arthropoda	tr F8J2L5 F8J2L5_9HEMI:Pachygrontha_nigriventris
	tr E0VKK0 E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis
	tr H9JA47 H9JA47_BOMMO:Bombyx_mori
	tr D2A356 D2A356_TRICA:Tribolium_castaneum
	tr Q16EL3 Q16EL3_AEDAE:Aedes_aegypti
	tr Q26498 Q26498_SCHGR:Schistocerca_gregaria
	tr N6TEF7 N6TEF7_9CUCU:Dendroctonus_ponderosae
	tr H9HPZ8 H9HPZ8_ATTCE:Atta_cephalotes
	tr N6UIC4 N6UIC4_9CUCU:Dendroctonus_ponderosae
	tr Q0H2A2 Q0H2A2_9INSE:Ephemera_vulgata
	tr Q9UA50 Q9UA50_9INSE:Thermobia_domestica
	tr Q0H299 Q0H299_9HEXA:Folsomia_candida

- Information
- Get sequence
- Zoom back out**
- Delete
- Merge
- Split
- Duplicate
- Make intron
- Set translation start
- Set longest ORF
- Set readthrough stop codon
- Flip strand
- Set as 5' end
- Set as 3' end
- Set both ends
- Annotation Info Editor
- Undo
- Redo
- History

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annel
- protein2genome_Atelo
- protein2genome_Cepha
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata
- protein2genome_Crustacea
- protein2genome_Echinodermata
- protein2genome_Mollusca
- protein2genome_Nematomorpha
- protein2genome_Nematomorpha
- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

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0 100,000 200,000 300,000 400,000 500,000 600,000 700,000 800,000 900,000 1,000,000

Scaffold38 Scaffold38:1022866..1033555 (10.69 Kb) Go

1,024,450 1,026,930 1,029,400 1,031,880

User-created Annotations Scaffold38:1025117-1025513

AROS_v0.5.2-Models

protein2genome_Athropoda

tr|F8J2L5|F8J2L5_9HEMI:Pachygrontha_nigriventris

tr|Q6IT84|Q6IT84_ONCFA:Oncopeltus_fasciatus

tr|E0VKK0|E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis

tr|H9JA47|H9JA47_BOMMO:Bombyx_mori

tr|D2A356|D2A356_TRICA:Tribolium_castaneum

tr|Q6IT83|Q6IT83_ONCFA:Oncopeltus_fasciatus

tr|Q16EL3|Q16EL3_AEDAE:Aedes_aegypti

tr|Q26498|Q26498_SCHGR:Schistocerca_gregaria

tr|N6TEF7|N6TEF7_9CUCU:Dendroctonus_ponderosae

tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes

tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata

tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica

tr|Q0H299|Q0H299_9HEXA:Folsomia_candida

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

ArosTmpB006329-RA

ArosTmpM00

tr|N6TF59|N6TF59_9CUCU:Dendroctonus_ponderosae

tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera

tr|E2AHC7|E2AHC7_CAMFO:Camponotus_rufus

tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum

tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis

tr|E2B5W1|E2B5W1_HARSA:Haemaphysalis_schlegelii

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
- protein2genome_Atelocerata
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata
- protein2genome_Crustacea
- protein2genome_Echinodermata
- protein2genome_Mollusca
- protein2genome_Nemata
- protein2genome_Nematomorpha
- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

apollo File View Tools Help

mmortres

0 100,000 200,000 300,000 400,000 500,000 600,000 700,000 800,000 900,000 1,000,000

Scaffold38 Scaffold38:1022866..1033555 (10.69 Kb) Go

1,024,450 1,026,930 1,029,400 1,031,880

User-created Annotations Scaffold38:1025117-1025513

Information

- Go to sequence
- Zoom to base level
- Delete
- Merge
- Split
- Duplicate
- Make intron
- Set translation start
- Set longest ORF
- Set readthrough stop codon
- Flip strand
- Set as 5' end
- Set as 3' end
- Set both ends
- Annotation Info Editor
- Undo
- Redo
- History

AROS_v0.5.2-Models

protein2genome_Athropoda

tr|F8J2L5|F8J2L5_9HEMI:Pachygrontha_nigr

tr|Q6IT84|Q6IT84_ONCFA:Oncopeltus_fasc

tr|E0VKK0|E0VKK0_PEDHC:Pediculus_hun

tr|H9JA47|H9JA47_BOMMO:Bombyx_mori

tr|D2A356|D2A356_TRICA:Tribolium_casta

tr|Q6IT83|Q6IT83_ONCFA:Oncopeltus_fasc

tr|Q16EL3|Q16EL3_AEDAE:Aedes_aegypti

tr|Q26498|Q26498_SCHGR:Schistocerca

tr|N6TEF7|N6TEF7_9CUCU:Dendroctonus_ponderosae

tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes

tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata

tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica

tr|Q0H299|Q0H299_9HEXA:Folsomia_candida

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

ArosTmpB006329-RA

ArosTmpM00

tr|N6TF59|N6TF59_9CUCU:Dendroctonus_ponderosae

tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera

tr|E2AHC7|E2AHC7_CAMFO:Camponotus_pennsylvanicus

tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum

tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis

tr|E2B5W1|E2B5W1_HARSA:Haemaphysalis_schlegelii

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
- protein2genome_Atela
- protein2genome_Cephalopoda
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Crustacea
- protein2genome_Echinodermata
- protein2genome_Mollusca
- protein2genome_Nematoda
- protein2genome_Nematomorpha
- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata



Sequence

>AC41F65CADB9B7BF355D550438868959 (sequence:mRNA) 350 residues [peptide]
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 GQQGMPYPRFPYDRMDIRNAAYYQQQEHGGMDGMAGYRSSSPSSAMGGHMGHTPTPNGIPSTPIVYAS
 CKLQAAAVDHDQGGVLDGPDSPDPLVESQMHHQMHPQHPHMQAQQPPLQQHQHMQQQHMMYQQQQGTT
 QQQQATMHPQQQQPPPHQGVVTSPLGPQQGAPQGTAGANLPSPLYPWMRSQFERKRGRQTYTRYQT
 LELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMRKWKKENKTKGEPGSGDGDTDISPQTSPPQ

Peptide sequence
 cDNA sequence
 CDS sequence
 Genomic sequence
 Genomic sequence +/- 500 bases

- tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata
- tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica
- tr|Q0H299|Q0H299_9HEXA:Folsomia_candida
- tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

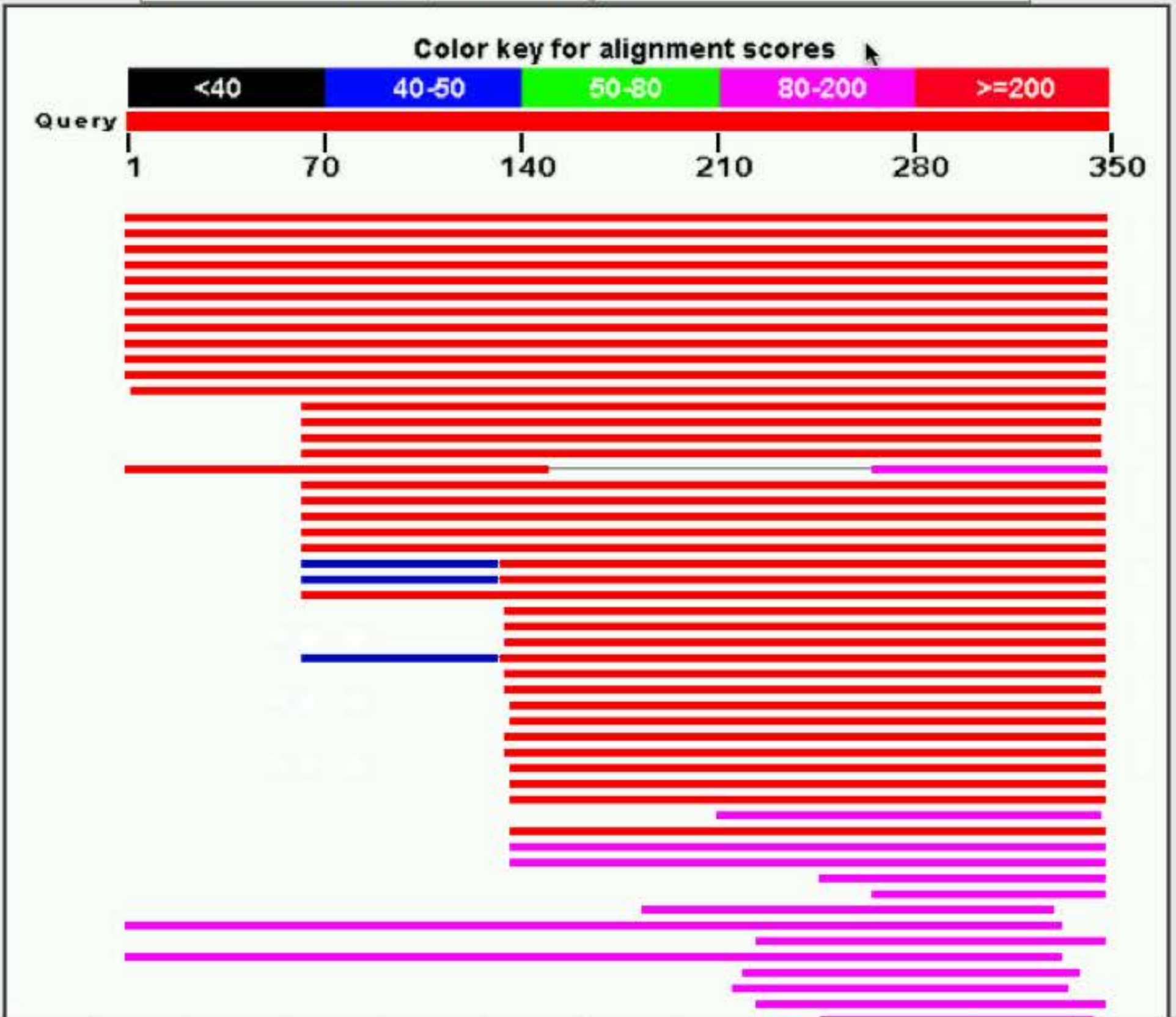
Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 105 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



mmtorres

mmtorres

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ArosTmpM00

JCU:Dendro

PIME:Apis_m

MFO:Campor

RICA:Tribolium

RICA:Tribolium

SVI:Nasonia_m

WT_HARSA:Ho

Alignments Result Summary Guide Tree Phylogenetic Tree Submission Details

Download Alignment File Hide Colors Send to ClustalW2_Phylogeny

CLUSTAL 2.1 multiple sequence alignment

```

Athros_putative_scf38_2  MSSYFANQFVPDLRNGGVEHPHQHQHYGAAVQVPQQTQGMQQQPQQAAD 50
Amel_antp                MSSYFANSYIPDLRNGGVEHPHQHQHYGAAVQVPQQTQSVQQQSQQAGD 50
Nvit_antp                MSSYFANSYIPDLRNGGVEHPHQHQHYGAAVQVPQQQAVQQQPQQASD 50
*****.:*****

Athros_putative_scf38_2  PCDPSLLRQGVPGHH-YGATAGQQ-GMPYPRFPPYDRMDIRNAAYYQQQ- 97
Amel_antp                PCDPSLLRQGVPGHH-YGAAGSQQ-DMPYPRFPPYNRMDMRNATYYQHQ- 97
Nvit_antp                PCDPSMLRQGVPGHHGYGAATGQQPGMPYPRFPPYDRMDIRNAAYYQQQQ 100
*****:*****

Athros_putative_scf38_2  QEHG-GMDGMAGYRSSSPSSAMGG-HMGHTPTP-NGIP-STPIVYASCKL 143
Amel_antp                QDHGSGMDGMGGYRSASPSGMMG--HMGHTPTP-NGHP-STPIVYASCKL 143
Nvit_antp                QEHG--MD-MASYRASSPSAGMAGLHMGHTPTPVNGHPASTPIVYASCKL 147
*:* * * . . . . .

Athros_putative_scf38_2  QAAAVDHQGGVLDGPDSPDPLVESQMHHQMHPQHHPMQAQQ--PPLQQH- 190
Amel_antp                QAAAVDHQGSVLDGPDSP-PLVESQMHHQMHTQHHPMQPQQGQHQSQAQ- 191
Nvit_antp                QAAAVDHQGSVLDGPDSP-PLVDAQMHHQMHPQHHTMQAQQSHPQQQPQP 196
*****.*****

Athros_putative_scf38_2  -----QQHMQ-----QQQHMMYQQQQQG-TTQQQQQATMHPQQQQQPPPQH 230
Amel_antp                -----QQHLQA----HEQHMMYQQQQQSQAASQSQPGMHPRQQQQ-AQQH 232
Nvit_antp                QAPHQQAHPQVPQQTQQQHMMYQQQTQP---QQPQPAAMHPQQQAQ-QQQH 242
*:* * . . . . .

Athros_putative_scf38_2  QGVVTSPLGPQQQGAPQGTAGANLPSPLYPWMRSQFERKRGRQTYTRYQT 280
Amel_antp                QGVVTSPLSQQQQAAPQGAASANLPSPLYPWMRSQFERKRGRQTYTRYQT 282
Nvit_antp                QGVVASPLGQQQPGTPQSAAPTNLPSPLYPWMRSQFERKRGRQTYTRYQT 292
****:***. * .:*. .: * :*****

Athros_putative_scf38_2  LELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMRKWKKENKTK 330
Amel_antp                LELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRMRKWKKENKSK 332

```

mmtorres

mmtorres

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ArosTmpM00

JCU:Dendroc

PIME:Apis_m

MFO:Campor

RICA:Tribolium

ICA:Tribolium

SVI:Nasonia_yit

W1_HARSA:Ha

protein2genome_Chelicerata

protein2genome_Cnidaria

protein2genome_Craniata

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
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- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
- protein2genome_Atelocerata
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Crustacea
- protein2genome_Echinodermata
- protein2genome_Mollusca
- protein2genome_Nematoda
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- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED

Annotation Info Editor

gene

Name

Symbol

Description

Status

Approved Needs review

DBXRefs

DB	Accession

Add Delete

Attributes

Tag	Value

Add Delete

Pubmed IDs

mRNA

Name

Symbol

Description

Status

Approved Needs review

DBXRefs

DB	Accession

Add Delete

Attributes

Tag	Value

Add Delete

Pubmed IDs

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

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1,031,880

ArosTmpM00

tr|N6TFS9|N6TFS9_9CUCU:Dendro

tr|Q9GYV0|Q9GYV0_APIME:Apis_m

tr|E2AHC7|E2AHC7_CAMFO:Campor

tr|Q9NHA7|Q9NHA7_TRICA:Tribolium

tr|Q95UR2|Q95UR2_TRICA:Tribolium

tr|C7FFA8|C7FFA8_NASVI:Nasonia_yit

tr|E2B5W1|E2B5W1_HARSA:Ha

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
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- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED

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Annotation Info Editor

gene

Name:

Symbol:

Description:

Status: Approved Needs review

DB	Accession

Tag	Value

Pubmed IDs:

mRNA

Name:

Symbol:

Description:

Status: Approved Needs review

DB	Accession

Tag	Value

Pubmed IDs:

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

- blastx_Craniata
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- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
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- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
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- protein2genome_Ateleta
- protein2genome_Cephalochordata
- protein2genome_Chelicerata
- protein2genome_Cnidaria
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- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED

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Annotation Info Editor

gene

Name: similar to antennapedia
 Symbol: antp
 Description:

Status

Approved Needs review

DBXRefs

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Add Delete

Attributes

Tag	Value

Add Delete

Pubmed IDs

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Name: Scaffold38:1025117-1025513
 Symbol:
 Description:

Status

Approved Needs review

DBXRefs

DB	Accession

Add Delete

Attributes

Tag	Value

Add Delete

Pubmed IDs

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
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- blastx_Nematomorpha
- blastx_Onychophora
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- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

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Annotation Info Editor

gene

Name:

Symbol:

Description:

Status: Approved Needs review

DBXRefs:

DB	Accession

Attributes:

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Pubmed IDs:

mRNA

Name:

Symbol:

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Status: Approved Needs review

DBXRefs:

DB	Accession

Attributes:

Tag	Value

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tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
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- blastx_Nematomorpha
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- protein2genome_Cnidaria
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- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

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Annotation Info Editor

Tag	Value

Add Delete

Pubmed IDs

Tag	Value

Add Delete

Gene Ontology IDs

Enter new Gene Ontology ID

Tag	Value

Add Delete

Comments

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

900,000 1,000,000

1,031,880

ArosTmpM00

tr|N6TFS9|N6TFS9_9CUCU:Dendro

tr|Q9GYV0|Q9GYV0_APIME:Apis_m

tr|E2AHC7|E2AHC7_CAMFO:Campor

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tr|Q95UR2|Q95UR2_TRICA:Tribolium

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vit

tr|E2B5W1|E2B5W1_HARSA:Ha

- blastx_Craniata
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- protein2genome_Onychophora
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- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

Annotation Info Editor

Tag	Value

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Pubmed IDs

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Add Delete

Gene Ontology IDs

GO:

Add Delete

Comments

Tag	Value

Add Delete

Pubmed IDs

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Add Delete

Gene Ontology IDs

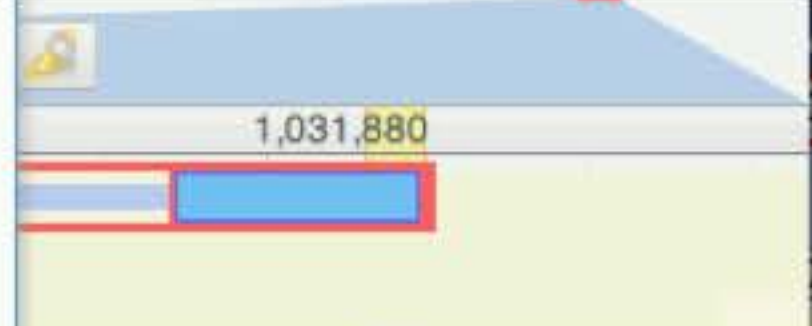
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Comments

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

900,000 1,000,000



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- tr|N6TFS9|N6TFS9_9CUCU:Dendro
- tr|Q9GYV0|Q9GYV0_APIME:Apis_m
- tr|E2AHC7|E2AHC7_CAMFO:Campor
- tr|Q9NHA7|Q9NHA7_TRICA:Tribolium
- tr|Q95UR2|Q95UR2_TRICA:Tribolium
- tr|C7FFA8|C7FFA8_NASVI:Nasonia_vit
- tr|E2B5W1|E2B5W1_HARSA:Ha

You are using an AmiGO Labs prototype. See here for more information.

DNA binding

Term Information

Accession GO:0003677
Name DNA binding
Ontology molecular_function
Synonyms microtubule/chromatin interaction
 plasmid binding
Definition Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid). *Source:* GOC:tb, GOC:vw, GOC:dph, GOC:jl
Comment None
Subset gosubset_prok
 goslim_yeast
 goslim_plant
 goslim_aspergillus
 goslim_candida
 goslim_generic
Related [Search for bioentities](#) that have been annotated with this term.
Commun... [GN Add](#) usage comments for this term on the [GONUTS wiki](#).

Associations

[Graph Views](#) [Inferred Tree View](#) [Ancestors and Children](#) [Mappings](#)

Free-text filtering

Your search is pinned to these filters

- + document_category: annotation
- + regulates_closure: GO:0003677

No current user filters.

Found entities

Total: 64655; showing 1-10 Results count

<input type="checkbox"/>	Gene/Product name	Qualifier	Direct annotation	Annotation extension	Source	Taxon	Evidence	Evidence with	PANTHER family
<input type="checkbox"/>	TLE1	Uncharacterized protein	negative regulation of	l-kappaB	UniProtKB	Bos taurus	IEA	Ensembl:ENSP00000365682	transducing enhancer protein

mmortorres

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ArosTmpM00

JCU:Dendro

PIME:Apis_m

MFO:Campor

RICA:Tribolium

RICA:Tribolium

SVI:Nasonia

WT_HARSA:Ha

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

DNA binding

Term Information

Accession [GO:0003677](#)
Name DNA binding
Ontology molecular_function
Synonyms microtubule/chromatin interaction
 plasmid binding
Definition Any molecular function by which a gene product interacts selectively and non-covalently with DNA (deoxyribonucleic acid). *Source:* GOC:tb, GOC:vw, GOC:dph, GOC:jl
Comment None
Subset gosubset_prok
 goslim_yeast
 goslim_plant
 goslim_aspergillus
 goslim_candida
 goslim_generic
Related [Search](#) for *bioentities* that have been annotated with this term.
Commun... [GN Add](#) usage comments for this term on the [GONUTS](#) wiki.

Associations [Graph Views](#) [Inferred Tree View](#) [Ancestors and Children](#) [Mappings](#)

Free-text filtering

- Your search is pinned to these filters
- + document_category: annotation
 - + regulates_closure: GO:0003677
- No current user filters.
- [Source](#)

Found entities

Total: 64655; showing 1-10 **Results count**

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<input type="checkbox"/>	TLE1	Uncharacterized protein	negative regulation of I-kappaB kinase/NF-		UniProtKB	Bos taurus	IEA	Ensembl:ENSP00000365682	transducing enhancer protein pthr10814

mmortorres

2,200,000

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ArosTmpM00

JCU:Dendro

PIME:Apis_m

MFO:Campor

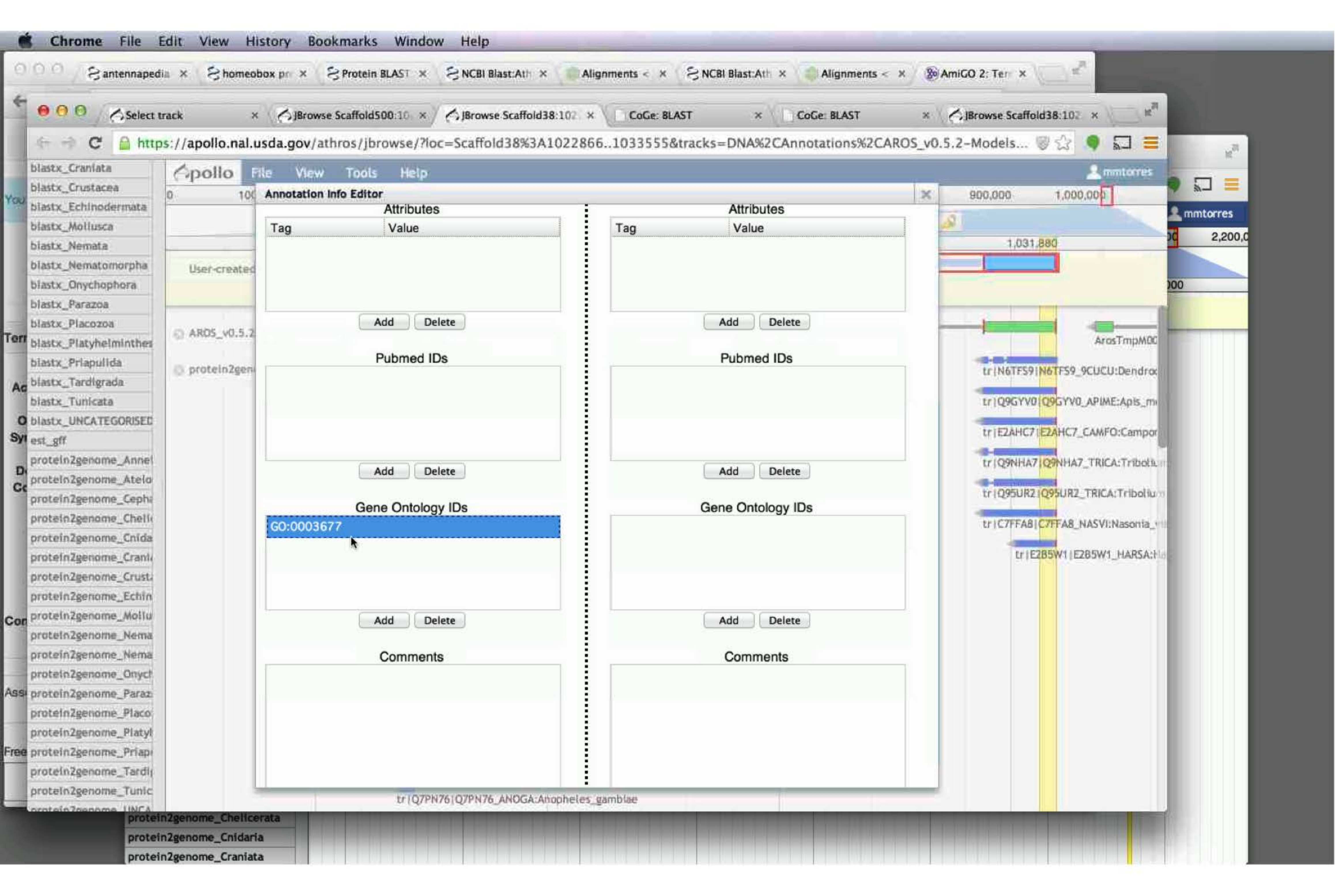
RICA:Tribolium

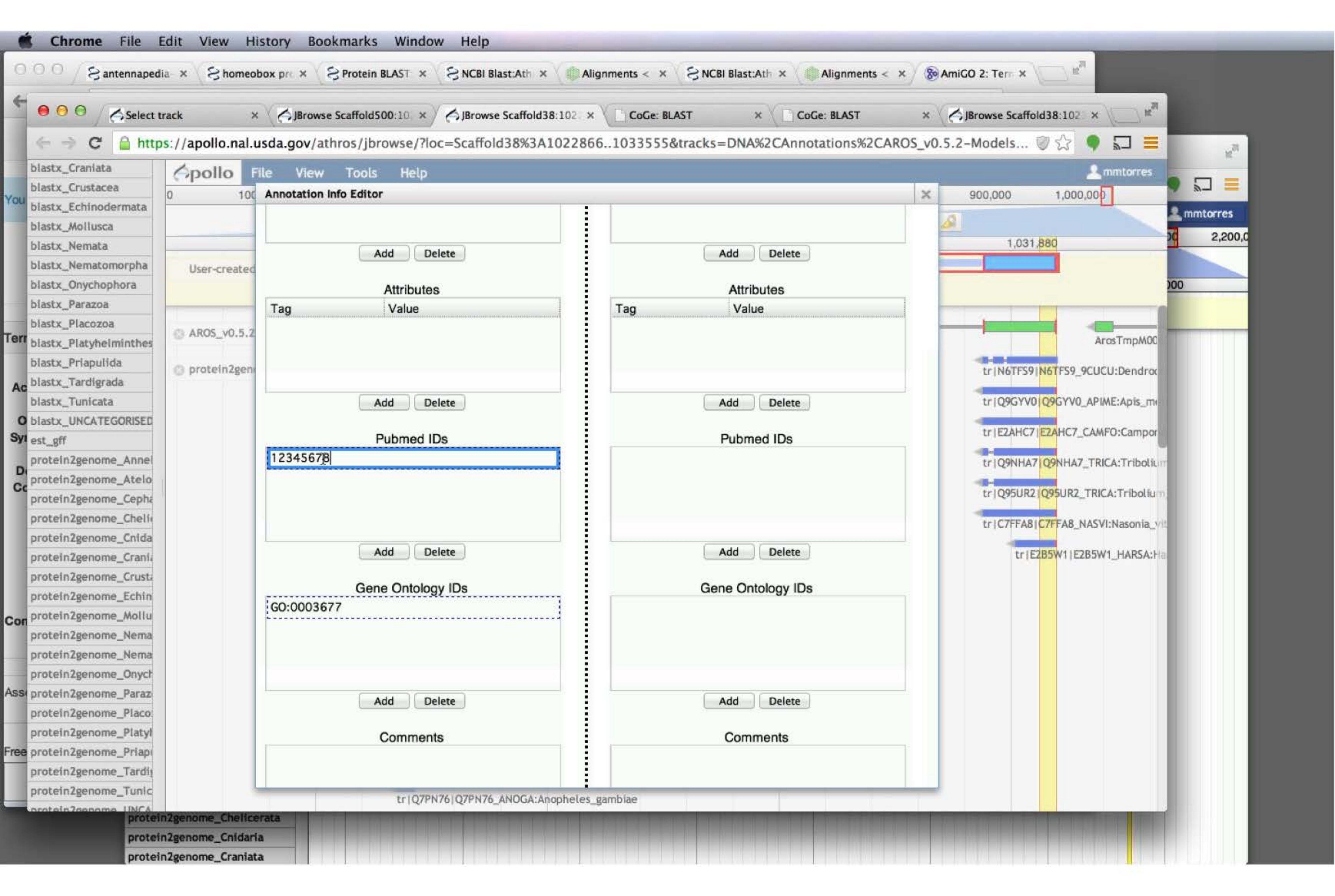
RICA:Tribolium

SVI:Nasonia_yit

W1_HARSA:Ha

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata





apollo

File View Tools Help

mmtorres

Annotation Info Editor

Add Delete

Attributes

Tag	Value

Add Delete

Pubmed IDs

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Add Delete

Gene Ontology IDs

GO:0003677

Add Delete

Comments

Add Delete

Attributes

Tag	Value

Add Delete

Pubmed IDs

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Add Delete

Gene Ontology IDs

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Add Delete

Comments

tr|Q7PN76|Q7PN76_ANOGA:Anopheles gambiae

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1,031,880

ArosTmpM00

tr|N6TF59|N6TF59_9CUCU:Dendroica

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tr|E2AHC7|E2AHC7_CAMFO:Camponotus pennsylvanicus

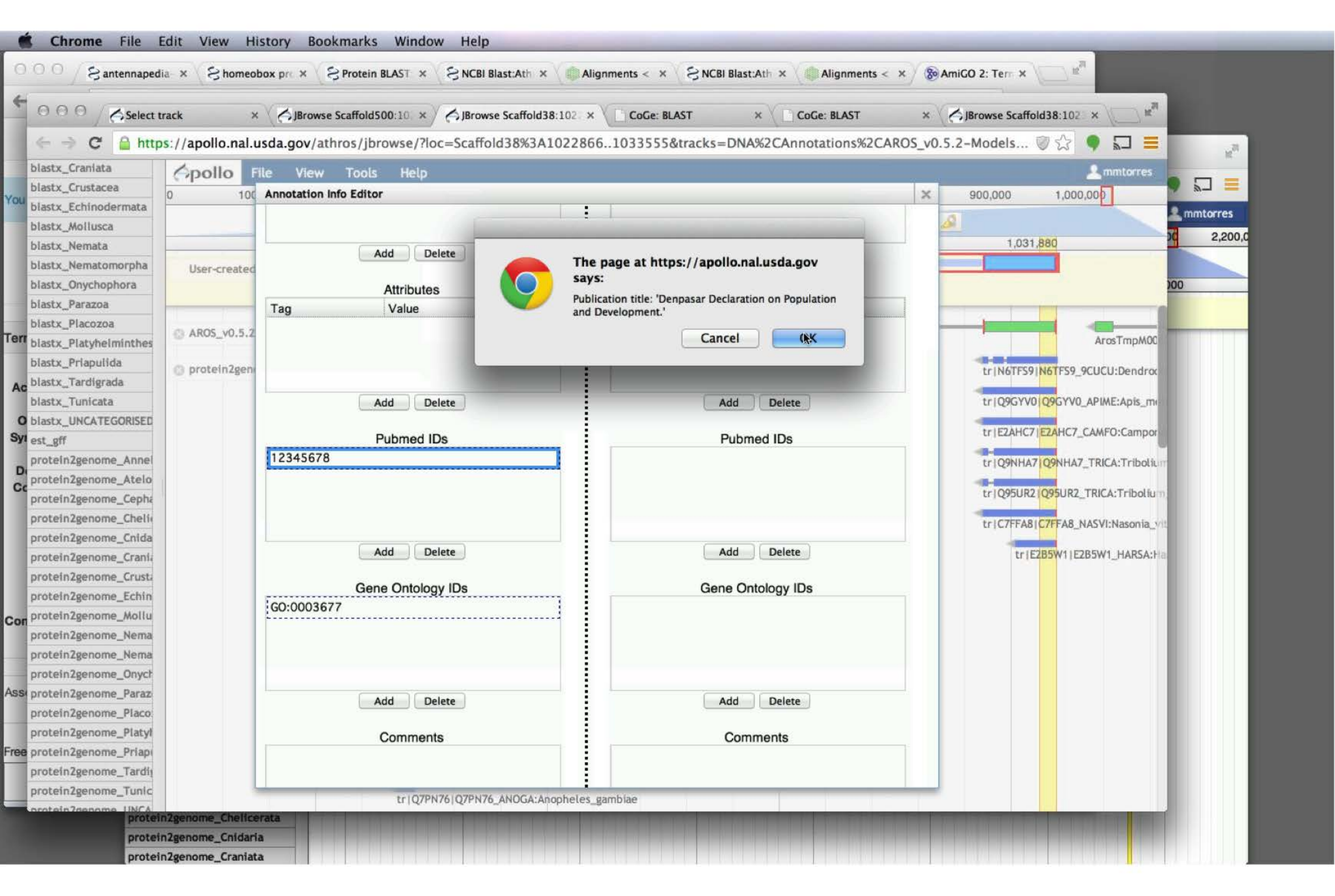
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tr|Q95UR2|Q95UR2_TRICA:Tribolium castaneum

tr|C7FFA8|C7FFA8_NASVI:Nasonia vitripennis

tr|E2B5W1|E2B5W1_HARSA:Haemaphysalis salicicola

protein2genome_Chelicerata
protein2genome_Cnidaria
protein2genome_Craniata



- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
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- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

apollo File View Tools Help

User-created

AROS_v0.5.2

protein2genome

Annotation type: Modify an existing gene model

Annotation type: Approve an existing gene model

Annotation type: Add a new gene model not existing in gene set

Annotation type: Delete an existing gene model

Annotation type: Existing gene model is a pseudogene

Annotation type: Add a gene symbol

Annotation type: Add a gene description

Annotation type: Add a comment

Annotation type: Flag incorrect gene model

Result of: Merging of two or more gene models across scaffolds. Gene involved in merge:

Result of: Merging of two or more gene models. Gene involved in merge:

Result of: Splitting a gene model. Original gene model ID:

Result of: Adding an exon to the gene model

Result of: Removing an exon from the gene model

Result of:

Data source for annotation:

Note to curator:

Selenocysteine insertion sequence at coordinates:

CDS edit: Stop codon readthrough due to selenocysteine insertion

CDS edit: sequencing error

Added 5'UTR

Added 3'UTR

Add Delete

Add Delete

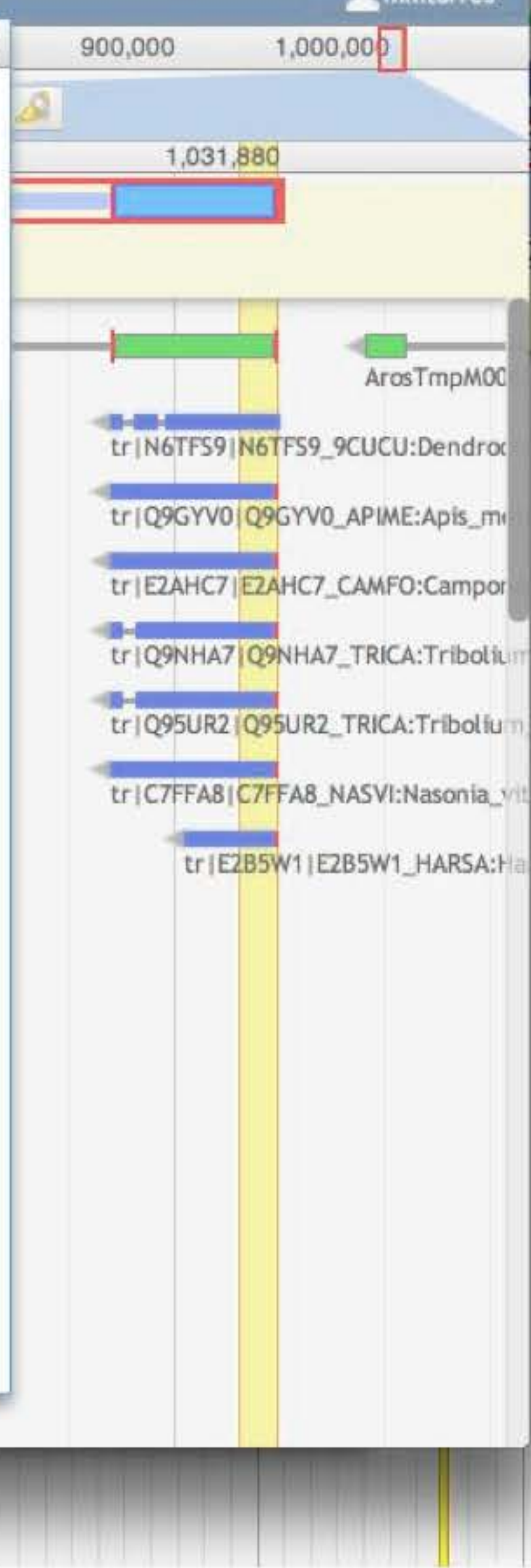
PubMed IDs

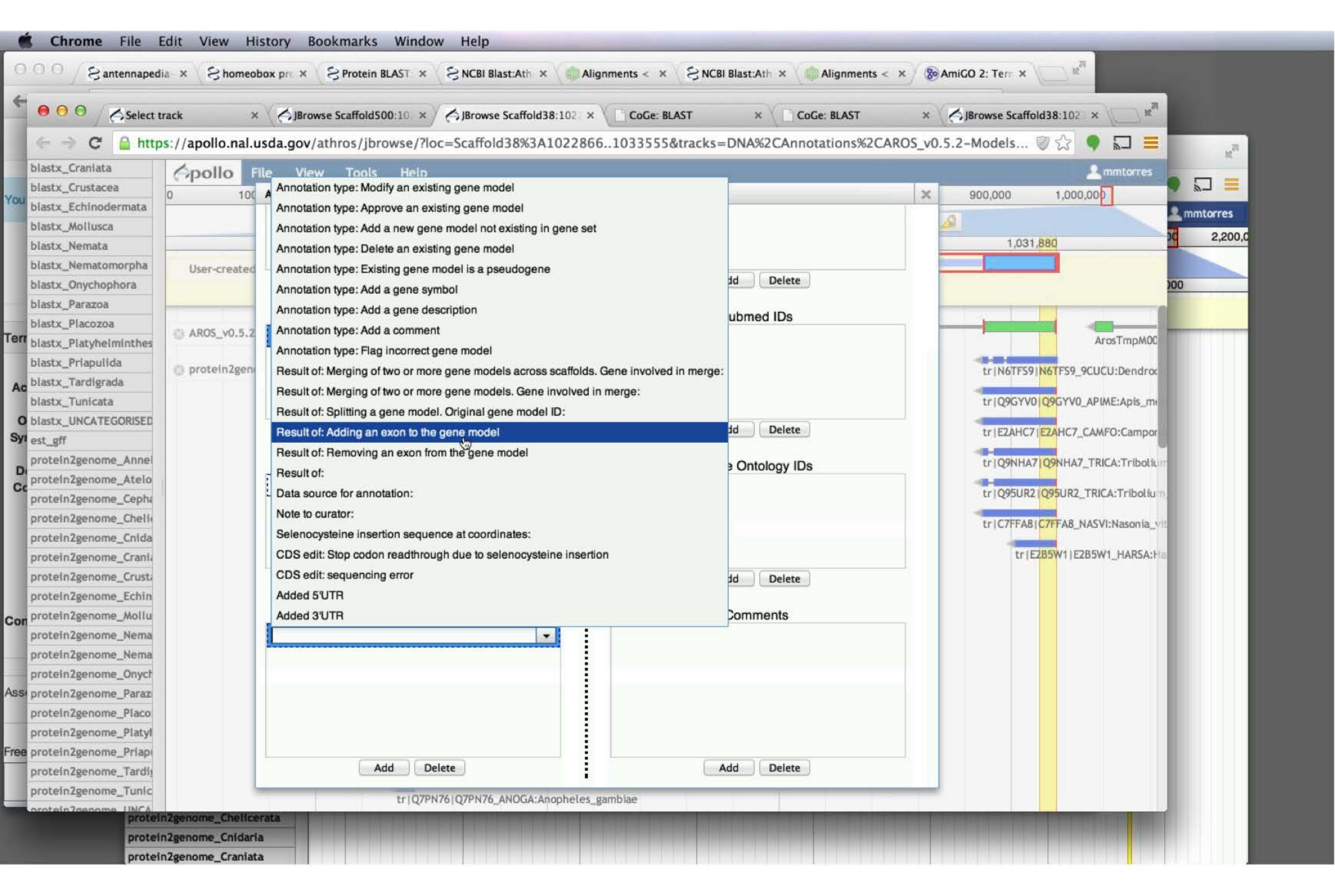
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Ontology IDs

Add Delete

Comments



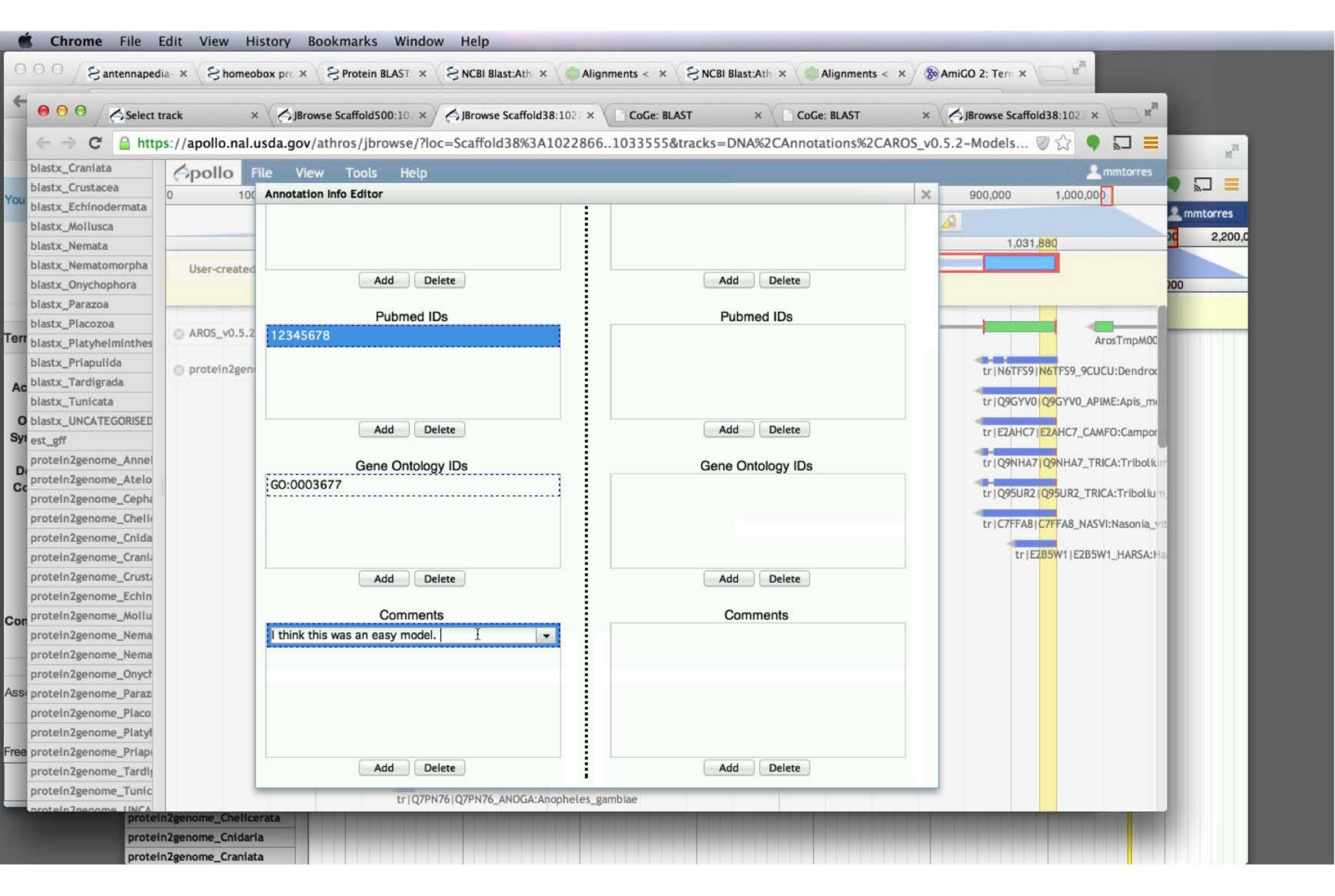


- Annotation type: Modify an existing gene model
- Annotation type: Approve an existing gene model
- Annotation type: Add a new gene model not existing in gene set
- Annotation type: Delete an existing gene model
- Annotation type: Existing gene model is a pseudogene
- Annotation type: Add a gene symbol
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- Result of: Merging of two or more gene models across scaffolds. Gene involved in merge:
- Result of: Merging of two or more gene models. Gene involved in merge:
- Result of: Splitting a gene model. Original gene model ID:
- Result of: Adding an exon to the gene model**
- Result of: Removing an exon from the gene model
- Result of:
- Data source for annotation:
- Note to curator:
- Selenocysteine insertion sequence at coordinates:
- CDS edit: Stop codon readthrough due to selenocysteine insertion
- CDS edit: sequencing error
- Added 5'UTR
- Added 3'UTR

Add Delete

Add Delete

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae



apollo

File View Tools Help

mmtorres

Annotation Info Editor

- User-created
- AROS_v0.5.2
- protein2genome

Add Delete

Pubmed IDs

12345678

Add Delete

Gene Ontology IDs

GO:0003677

Add Delete

Comments

I think this was an easy model.

Add Delete

Add Delete

Pubmed IDs

Add Delete

Gene Ontology IDs

Add Delete

Comments

Add Delete

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

900,000 1,000,000

1,031,880

ArosTmpM00

tr|N6TF59|N6TF59_9CUCU:Dendroc

tr|Q9GYV0|Q9GYV0_APIME:Apis_m

tr|E2AHC7|E2AHC7_CAMFO:Campor

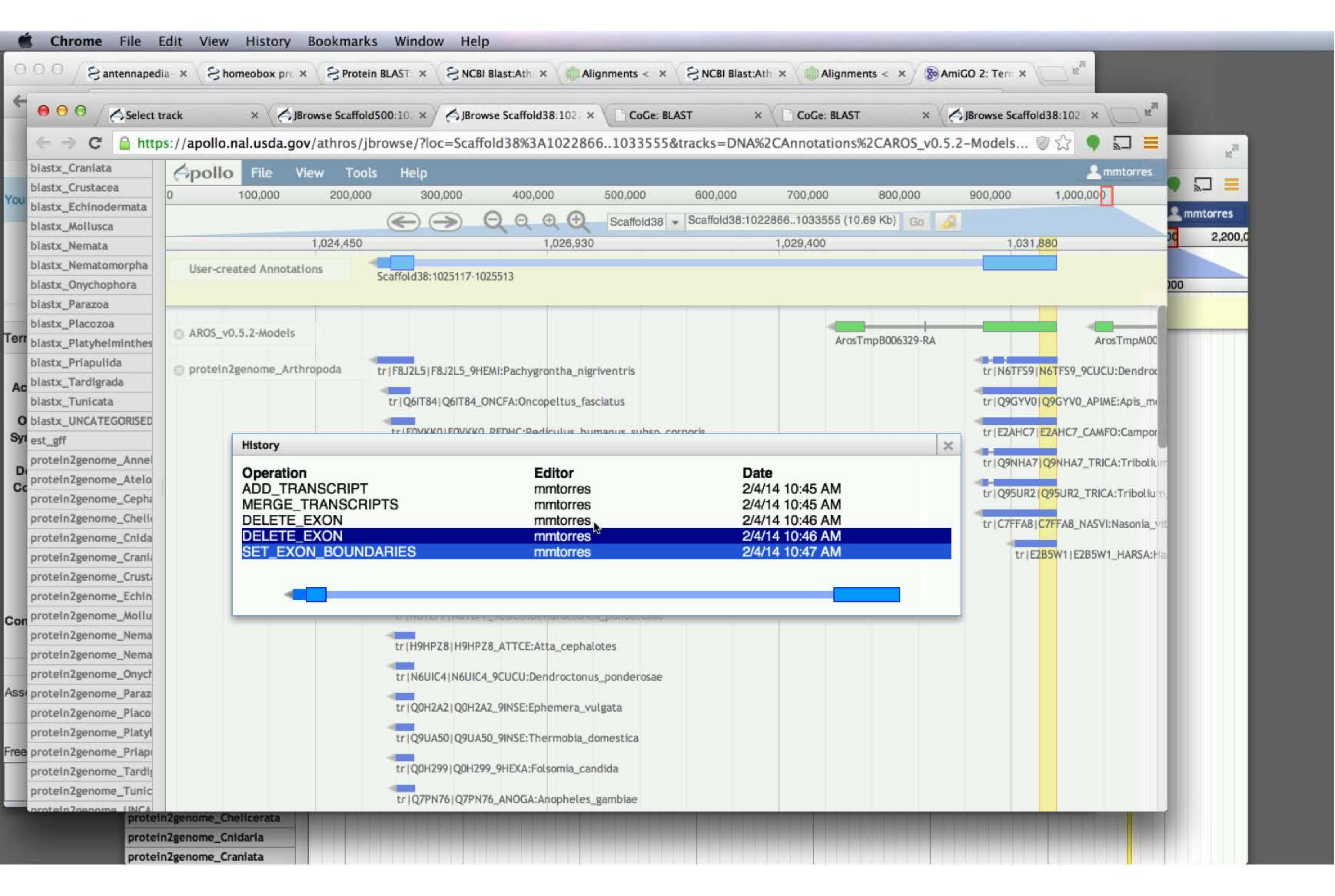
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tr|Q95UR2|Q95UR2_TRICA:Tribolium

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vit

tr|E2B5W1|E2B5W1_HARSA:Ha

- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata



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Scaffold38 Scaffold38:1022866..1033555 (10.69 Kb) Go

1,024,450 1,026,930 1,029,400 1,031,880

User-created Annotations Scaffold38:1025117-1025513

AROS_v0.5.2-Models ArosTmpB006329-RA ArosTmpM00

protein2genome_Arthropoda tr|F8J2L5|F8J2L5_9HEMI:Pachygrontha_nigriventris

tr|Q6IT84|Q6IT84_ONCFA:Oncopeltus_fasciatus

tr|LEQVKK0|LEQVKK0_REDHC:Radiculus_humans_subsp_carpalis

tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae

tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera

tr|E2AHC7|E2AHC7_CAMFO:Camponotus_rugosus

tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_confusum

tr|Q95UR2|Q95UR2_TRICA:Tribolium_confusum

tr|C7FFA8|C7FFA8_NASVI:Nasonia_vitripennis

tr|E2B5W1|E2B5W1_HARSA:Harmonia_axyridis

tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes

tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

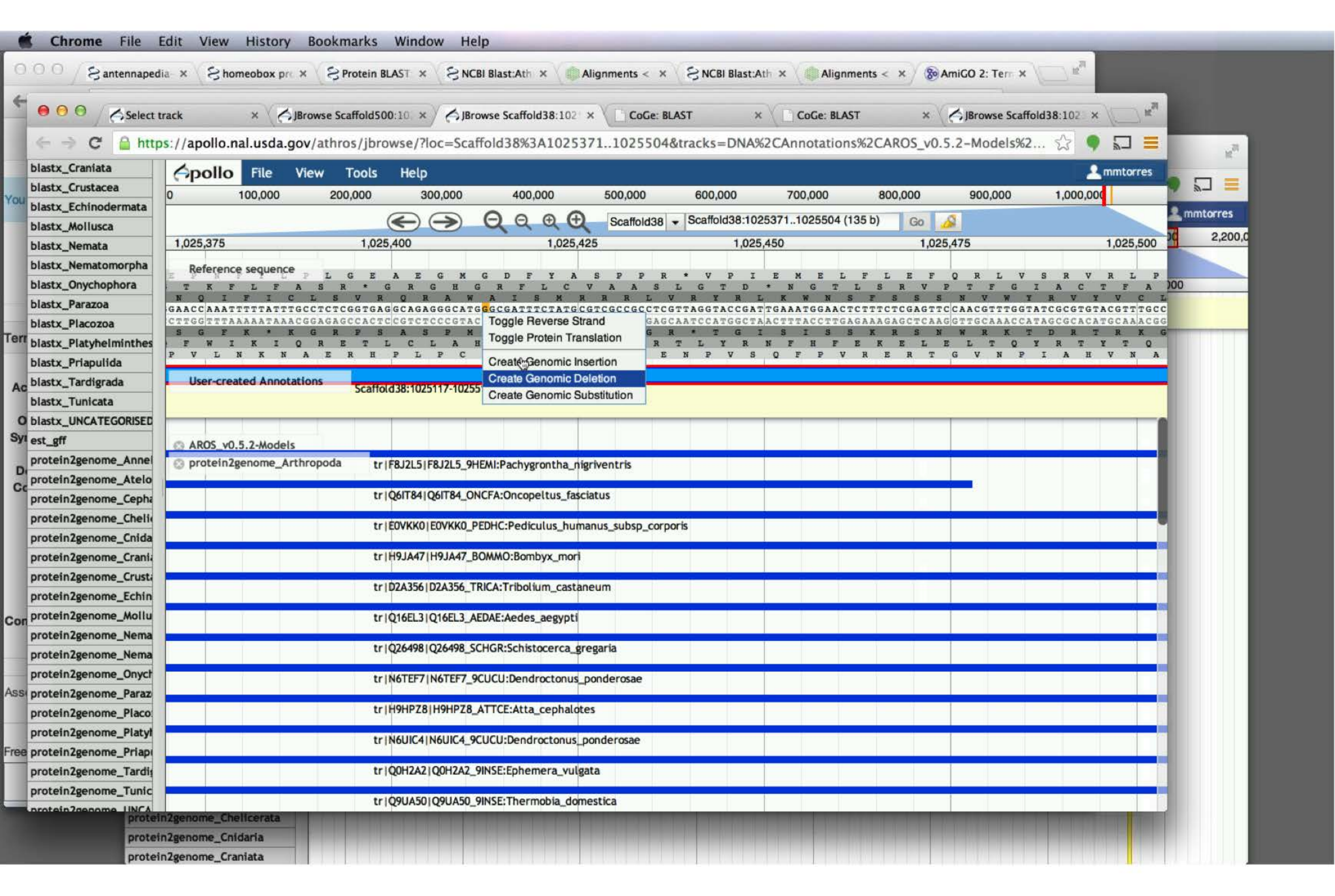
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tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica

tr|Q0H299|Q0H299_9HEXA:Folsomia_candida

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

Operation	Editor	Date
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DELETE_EXON	mmtorres	2/4/14 10:46 AM
DELETE_EXON	mmtorres	2/4/14 10:46 AM
SET_EXON_BOUNDARIES	mmtorres	2/4/14 10:47 AM



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Scaffold38 Scaffold38:1025371..1025504 (135 b) Go

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Reference sequence
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S G F K * K G R P S A S P M G R * T G I S I S S K R S N W R K T D R T R X G
F W I K I Q R E T L C L A H R T L Y R N F H F E K E L E L T Q Y R T Y T Q
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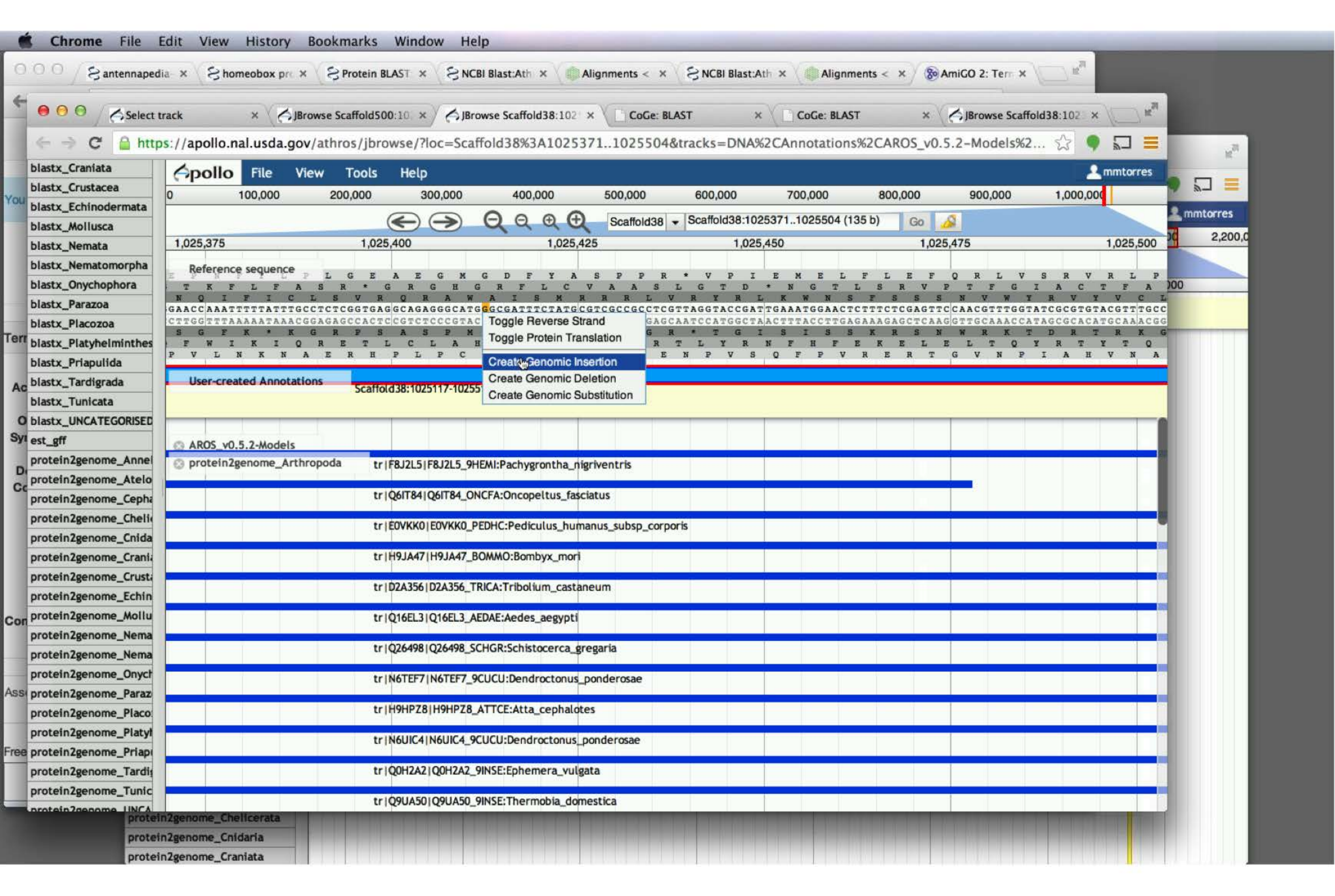
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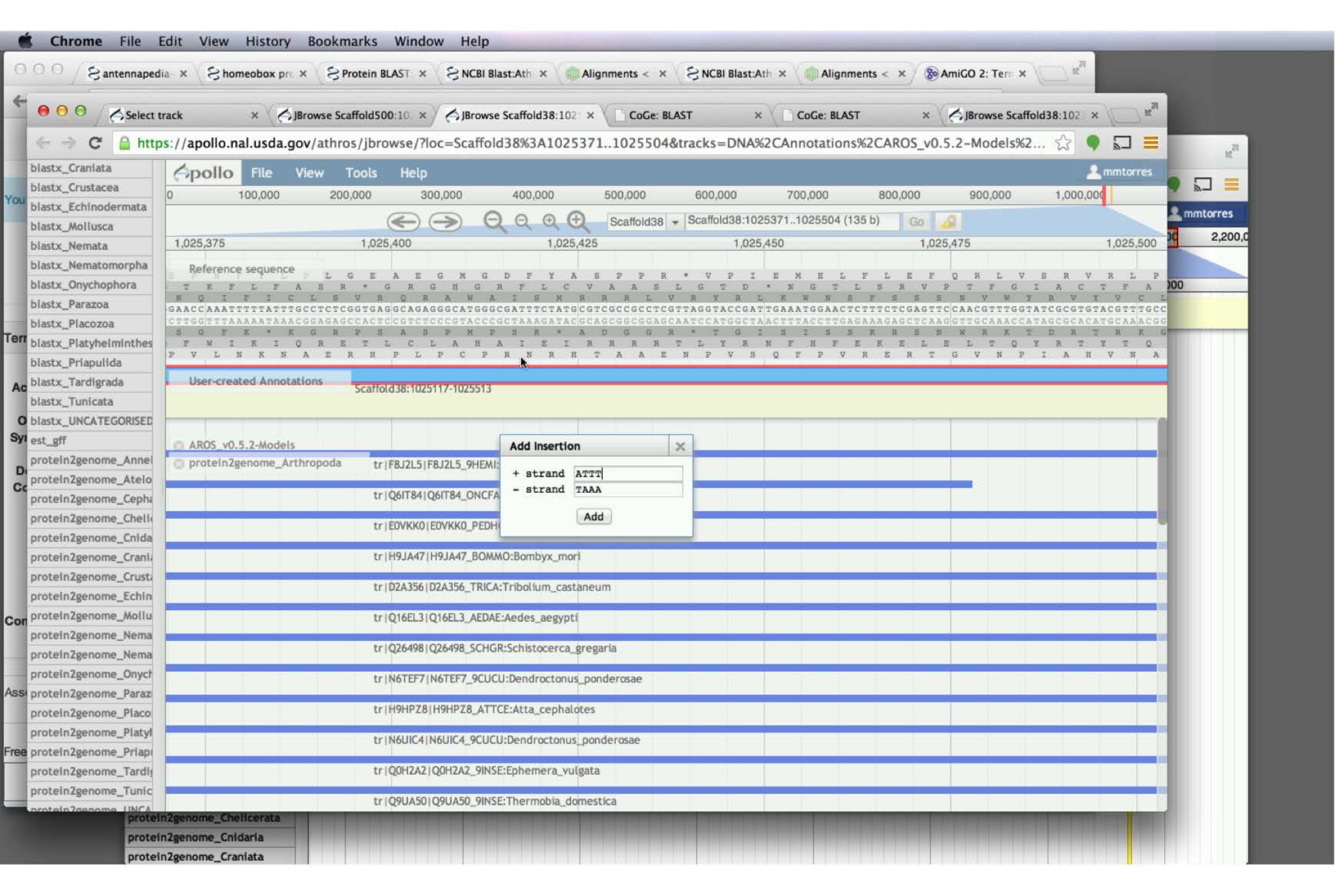
User-created Annotations Scaffold38:1025117-10255

AROS_v0.5.2-Models

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protein2genome_Cephalopoda	tr Q6IT84 Q6IT84_ONCFA:Oncopeltus_fasciatus
protein2genome_Chelicerata	tr E0VKK0 E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis
protein2genome_Cnidaria	tr H9JA47 H9JA47_BOMMO:Bombyx_mori
protein2genome_Crustacea	tr D2A356 D2A356_TRICA:Tribolium_castaneum
protein2genome_Echinodermata	tr Q16EL3 Q16EL3_AEDAE:Aedes_aegypti
protein2genome_Mollusca	tr Q26498 Q26498_SCHGR:Schistocerca_gregaria
protein2genome_Nematoda	tr N6TEF7 N6TEF7_9CUCU:Dendroctonus_ponderosae
protein2genome_Nematoda	tr H9HPZ8 H9HPZ8_ATTCE:Atta_cephalotes
protein2genome_Onychophora	tr N6UIC4 N6UIC4_9CUCU:Dendroctonus_ponderosae
protein2genome_Parazoa	tr Q0H2A2 Q0H2A2_9INSE:Ephemera_vulgata
protein2genome_Placozoa	tr Q9UA50 Q9UA50_9INSE:Thermobia_domestica
protein2genome_Platyhelminthes	
protein2genome_Priapulida	
protein2genome_Tardigrada	
protein2genome_Tunicata	

protein2genome_Chelicerata
protein2genome_Cnidaria
protein2genome_Craniata





- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
- protein2genome_Ateleta
- protein2genome_Cephalopoda
- protein2genome_Chelicerata
- protein2genome_Cnidaria
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- protein2genome_Onychophora
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- protein2genome_Platyhelminthes
- protein2genome_Priapulida
- protein2genome_Tardigrada
- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

apollo File View Tools Help

mmortres

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Scaffold38 Scaffold38:1025371..1025504 (135 b) Go

1,025,375 1,025,400 1,025,425 1,025,450 1,025,475 1,025,500

Reference sequence

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User-created Annotations Scaffold38:1025117-1025513

AROS_v0.5.2-Models

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tr|H9JA47|H9JA47_BOMMO:Bombyx_mori

tr|D2A356|D2A356_TRICA:Tribolium_castaneum

tr|Q16EL3|Q16EL3_AEDAE:Aedes_aegypti

tr|Q26498|Q26498_SCHGR:Schistocerca_gregaria

tr|N6TEF7|N6TEF7_9CUCU:Dendroctonus_ponderosae

tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes

tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata

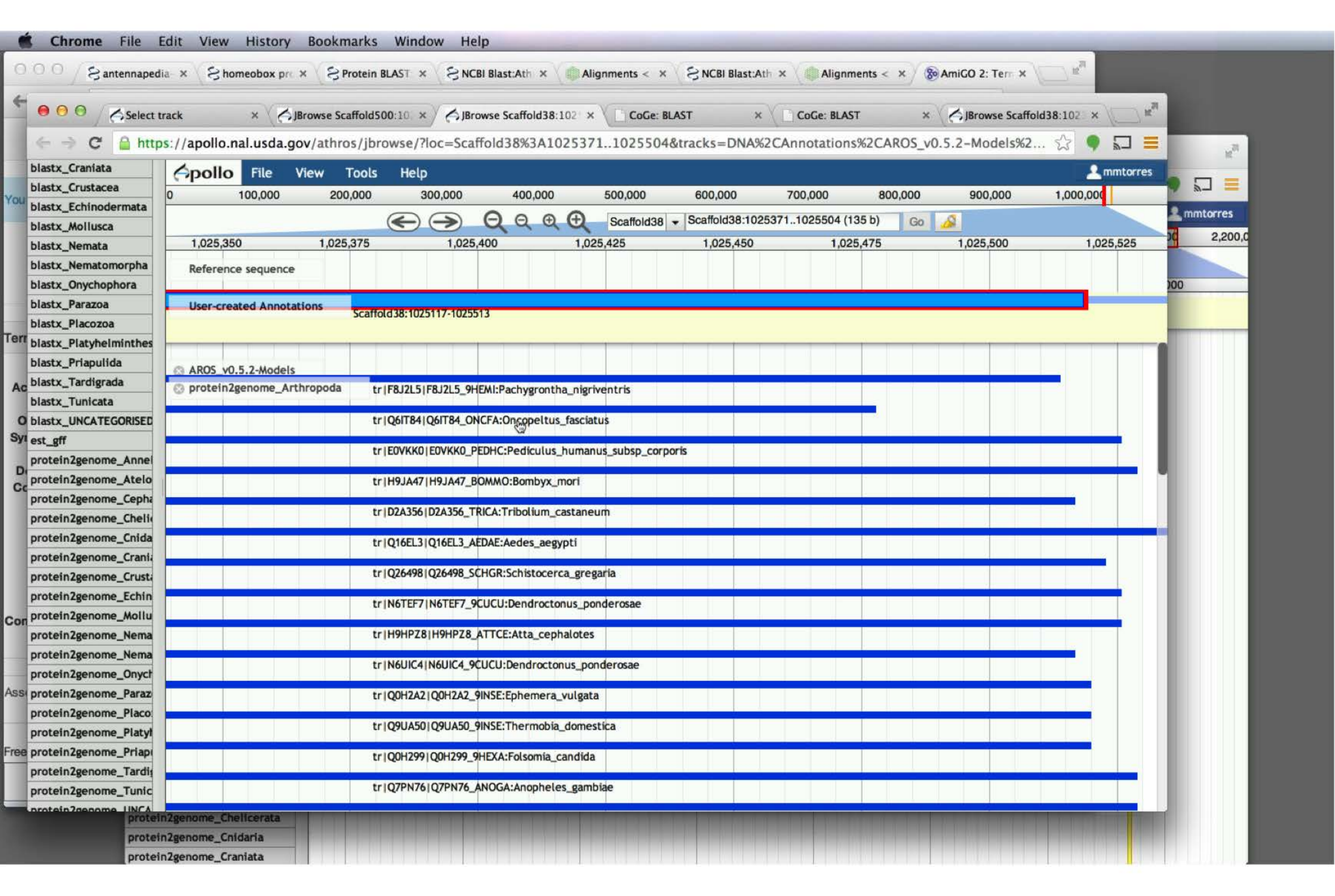
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Add Insertion

+ strand ATTC

- strand TAAAG

Add



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Scaffold38 Scaffold38:1025371..1025504 (135 b) Go

1,025,350 1,025,375 1,025,400 1,025,425 1,025,450 1,025,475 1,025,500 1,025,525

Reference sequence

User-created Annotations Scaffold38:1025117-1025513

AROS v0.5.2-Models

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tr|D2A356|D2A356_TRICA:Tribolium_castaneum

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tr|Q26498|Q26498_SCHGR:Schistocerca_gregaria

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tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata

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tr|Q0H299|Q0H299_9HEXA:Folsomia_candida

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

protein2genome_Chelicerata

protein2genome_Cnidaria

protein2genome_Craniata

protein2genome_Crustacea

protein2genome_Echinodermata

protein2genome_Mollusca

protein2genome_Nemata

protein2genome_Nematomorpha

protein2genome_Onychophora

protein2genome_Parazoa

protein2genome_Placozoa

protein2genome_Platyhelminthes

protein2genome_Priapulida

protein2genome_Tardigrada

protein2genome_Tunicata

protein2genome_UNCATEGORISED

est_gff

protein2genome_Annelida

protein2genome_Ateleta

protein2genome_Cephalopoda

protein2genome_Chelicerata

protein2genome_Cnidaria

protein2genome_Craniata

protein2genome_Crustacea

protein2genome_Echinodermata

protein2genome_Mollusca

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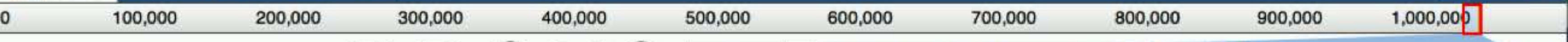
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protein2genome_Tardigrada

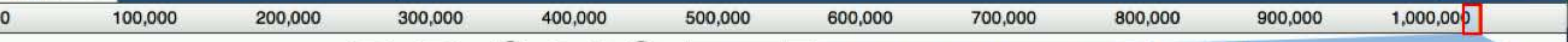
protein2genome_Tunicata

protein2genome_UNCATEGORISED

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- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata



- blastx_Craniata
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- protein2genome_Tardigrada
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- protein2genome_Chelicerata
- protein2genome_Cnidaria
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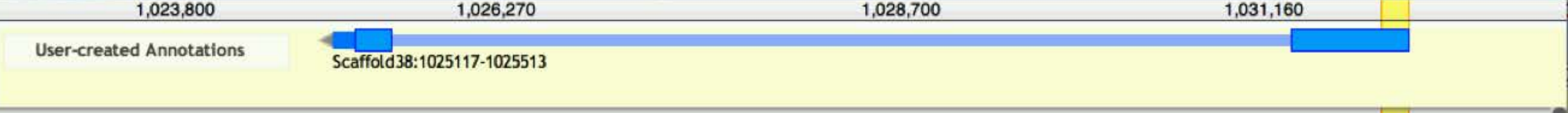
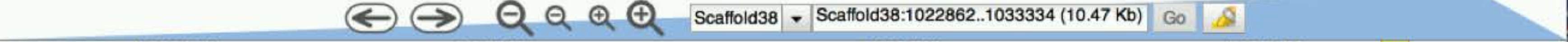
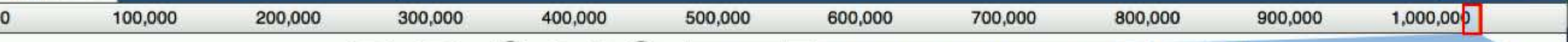
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- Edit config
- Save track data (selected)
- Show labels



protein2genome_Arthropoda

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- tr|Q6IT84|Q6IT84_ONCFA:Oncopeltus_fasciatus
- tr|E0VKK0|E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis
- tr|H9JA47|H9JA47_BOMMO:Bombyx_mori
- tr|D2A356|D2A356_TRICA:Tribolium_castaneum
- tr|Q6IT83|Q6IT83_ONCFA:Oncopeltus_fasciatus
- tr|Q16EL3|Q16EL3_AEDAE:Aedes_aegypti
- tr|Q26498|Q26498_SCHGR:Schistocerca_gregaria
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- tr|Q0H299|Q0H299_9HEXA:Folsomia_candida
- tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
- blastx_Placozoa
- blastx_Platyhelminthes
- blastx_Priapulida
- blastx_Tardigrada
- blastx_Tunicata
- blastx_UNCATEGORISED
- est_gff
- protein2genome_Annelida
- protein2genome_Atelocerata
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- protein2genome_Cnidaria
- protein2genome_Craniata
- protein2genome_Crustacea
- protein2genome_Echinodermata
- protein2genome_Mollusca
- protein2genome_Nematomorpha
- protein2genome_Nemata
- protein2genome_Onychophora
- protein2genome_Parazoa
- protein2genome_Placozoa
- protein2genome_Platyhelminthes
- protein2genome_Priapulida
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- protein2genome_Tunicata
- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata



- blastx_Craniata
- blastx_Crustacea
- blastx_Echinodermata
- blastx_Mollusca
- blastx_Nemata
- blastx_Nematomorpha
- blastx_Onychophora
- blastx_Parazoa
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- blastx_Platyhelminthes
- blastx_Priapulida
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- protein2genome_UNCATEGORISED
- protein2genome_Chelicerata
- protein2genome_Cnidaria
- protein2genome_Craniata

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Add combination track

Add sequence search track

Scaffold38 Scaffold38:1022862..1033334 (10.47 Kb) Go

1,026,270 1,028,700 1,031,160

User-created Scaffold38:1025117-1025513

AROS_v0.5.2-Models

protein2genome_Arthropoda

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tr|Q6IT84|Q6IT84_ONCFA:Oncopeltus_fasciatus

tr|E0VKK0|E0VKK0_PEDHC:Pediculus_humanus_subsp_corporis

tr|H9JA47|H9JA47_BOMMO:Bombyx_mori

tr|D2A356|D2A356_TRICA:Tribolium_castaneum

tr|Q6IT83|Q6IT83_ONCFA:Oncopeltus_fasciatus

tr|Q16EL3|Q16EL3_AEDAE:Aedes_aegypti

tr|Q26498|Q26498_SCHGR:Schistocerca_gregaria

tr|N6TEF7|N6TEF7_9CUCU:Dendroctonus_ponderosae

tr|H9HPZ8|H9HPZ8_ATTCE:Atta_cephalotes

tr|N6UIC4|N6UIC4_9CUCU:Dendroctonus_ponderosae

tr|Q0H2A2|Q0H2A2_9INSE:Ephemera_vulgata

tr|Q9UA50|Q9UA50_9INSE:Thermobia_domestica

tr|Q0H299|Q0H299_9HEXA:Folsomia_candida

tr|Q7PN76|Q7PN76_ANOGA:Anopheles_gambiae

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tr|N6TFS9|N6TFS9_9CUCU:Dendroctonus_ponderosae

tr|Q9GYV0|Q9GYV0_APIME:Apis_mellifera

tr|E2AHC7|E2AHC7_CAMFO:Camponotus_rufus

tr|Q9NHA7|Q9NHA7_TRICA:Tribolium_castaneum

tr|Q95UR2|Q95UR2_TRICA:Tribolium_castaneum

tr|C7FFA8|C7FFA8_NASVI:Nasonia_muscardina

tr|E2B5W1|E2B5W1_HARSA:Harmonia_axyridis

