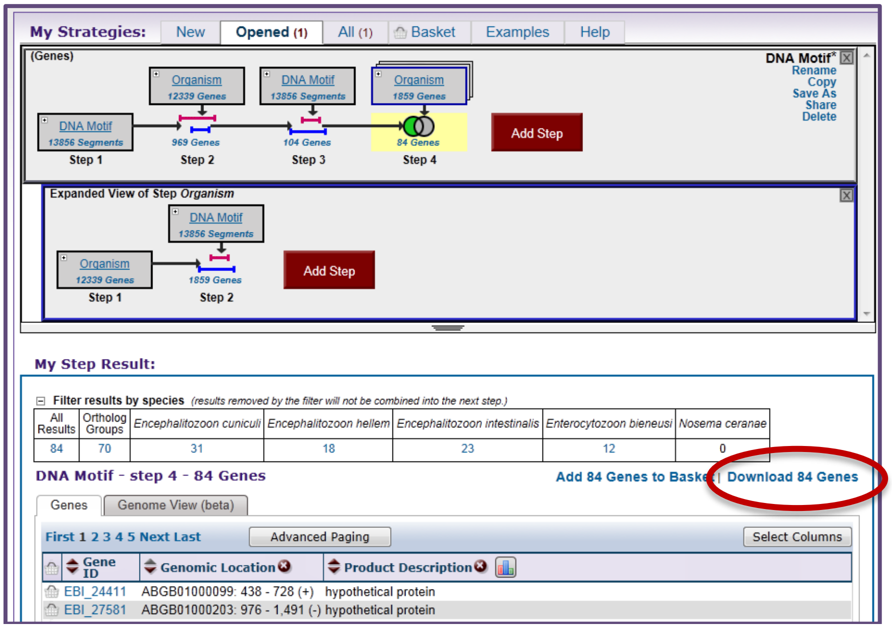
Data retrieval and download
Exercise 9

9.1 Downloading a set of results and associated data.

For this exercise you can start with any gene list of results. Start with any result list you generated this morning, such as the DNA Motif search.

Download this list of results with the following associated data: Genomic Location, Product Description, Transcript Length and Predicted GO Function.
Hint: click on the Download ## Genes link.



⊟ Filter results by species *(results removed by the filter will not be combined into the next step.)*

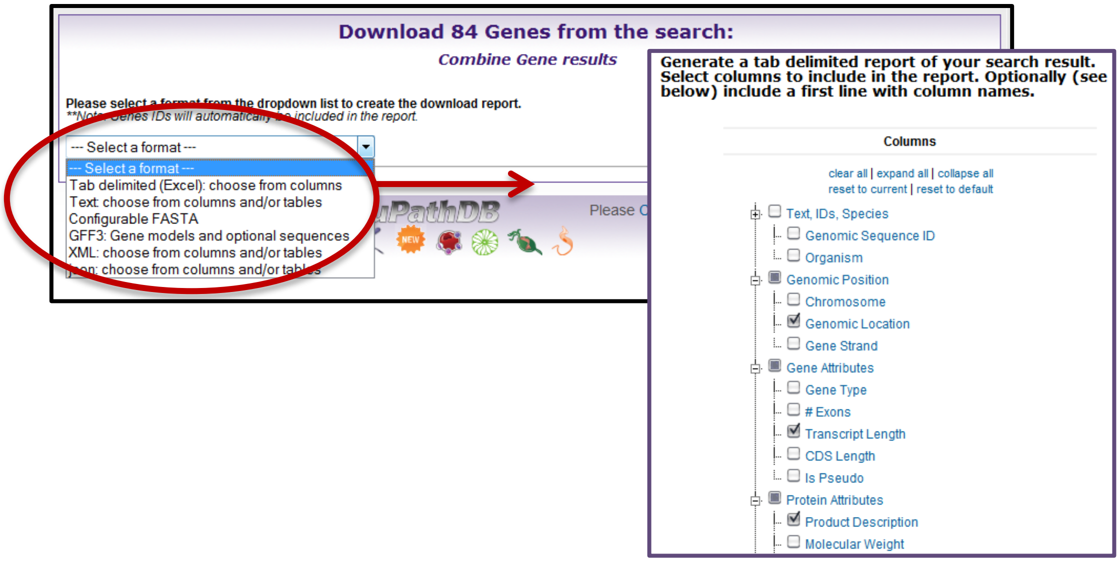
All Results	Ortholog Groups	*Encephalitozoon cuniculi*	*Encephalitozoon hellem*	*Encephalitozoon intestinalis*	*Enterocytozoon bieneusi*	*Nosema ceranae*
84	70	31	18	23	12	0

DNA Motif - step 4 - 84 Genes

Add 84 Genes to Basket | Download 84 Genes

Gene ID	Genomic Location	Product Description
EBI_24411	ABGB01000099: 438 - 728 (+)	hypothetical protein
EBI_27581	ABGB01000203: 976 - 1,491 (-)	hypothetical protein

Hint: select the type of report to download and then click on the boxes to customize your report. The gene ID is automatically downloaded and so is not an option in the popup.



Download 84 Genes from the search:

Combine Gene results

Please select a format from the dropdown list to create the download report.
***Note: Genes IDs will automatically be included in the report.*

--- Select a format ---

- --- Select a format ---
- Tab delimited (Excel): choose from columns
- Text: choose from columns and/or tables
- Configurable FASTA
- GFF3: Gene models and optional sequences
- XML: choose from columns and/or tables
- json: choose from columns and/or tables

Generate a tab delimited report of your search result. Select columns to include in the report. Optionally (see below) include a first line with column names.

Columns

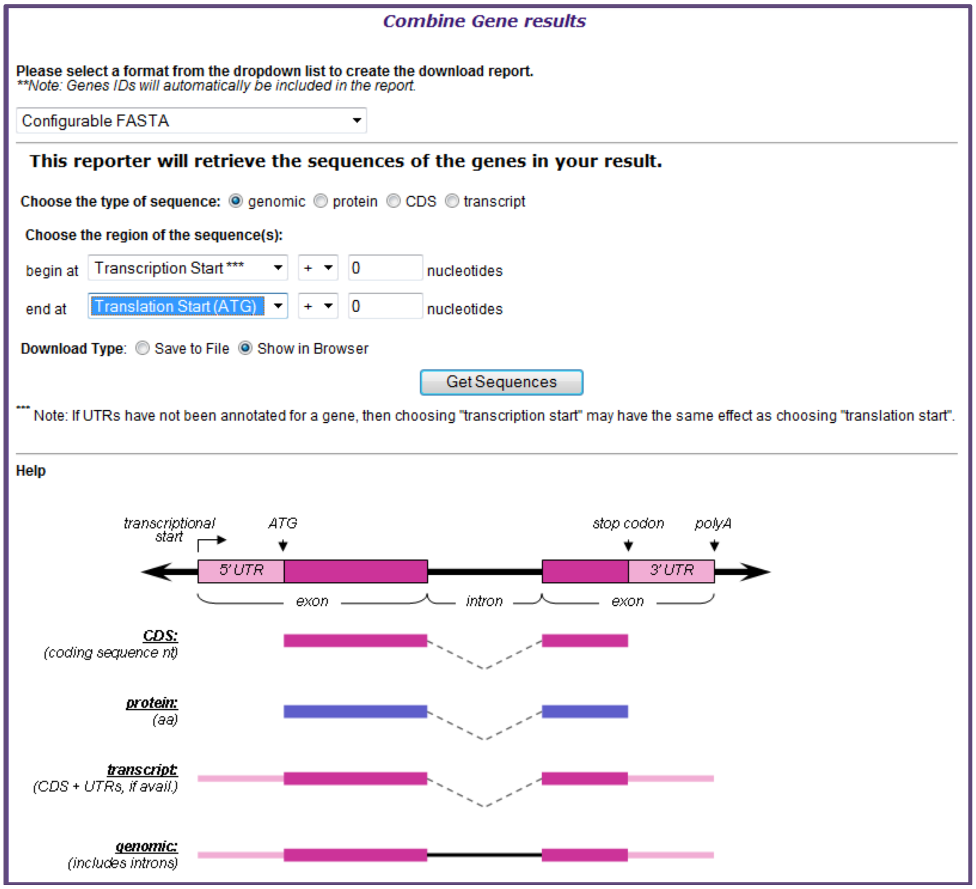
clear all | expand all | collapse all
reset to current | reset to default

- □ Text, IDs, Species
  - □ Genomic Sequence ID
  - □ Organism
- ▪ Genomic Position
  - □ Chromosome
  - ☑ Genomic Location
  - □ Gene Strand
- ▪ Gene Attributes
  - □ Gene Type
  - □ # Exons
  - ☑ Transcript Length
  - □ CDS Length
  - □ Is Pseudo
- ▪ Protein Attributes
  - ☑ Product Description
  - □ Molecular Weight

9.2 Download the sequences of genes in a list of results.

What if you are interested in examining the 5’ flanking sequences of these genes? How can you easily get this sequence for subsequent analysis?

Hint: use same list of results as in 9.1. Go to the download section and select “Configurable FASTA”. Now, retrieve the 500 nucleotides upstream of the start site of your genes.



Combine Gene results

Please select a format from the dropdown list to create the download report.
***Note: Genes IDs will automatically be included in the report.*

Configurable FASTA ▾

This reporter will retrieve the sequences of the genes in your result.

Choose the type of sequence: ● genomic ○ protein ○ CDS ○ transcript

Choose the region of the sequence(s):

begin at Transcription Start*** ▾ + ▾ 0 nucleotides

end at Translation Start (ATG) ▾ + ▾ 0 nucleotides

Download Type: ○ Save to File ● Show in Browser

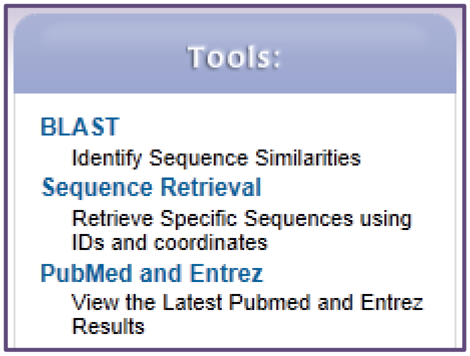
Get Sequences

*** Note: If UTRs have not been annotated for a gene, then choosing "transcription start" may have the same effect as choosing "translation start".

Help

Note, that you can access and download sequence with the sequence retrieval tool (SRT) accessed from the tools menu on the home page:

- Retrieve Sequences By Gene IDs.
- Retrieve Sequences By Genomic Sequence IDs.
- Retrieve Multiple Sequence Alignments by Contig / Genomic Sequence IDs.
- Retrieve Sequences By Open Reading Frame IDs.



Tools:

BLAST
Identify Sequence Similarities

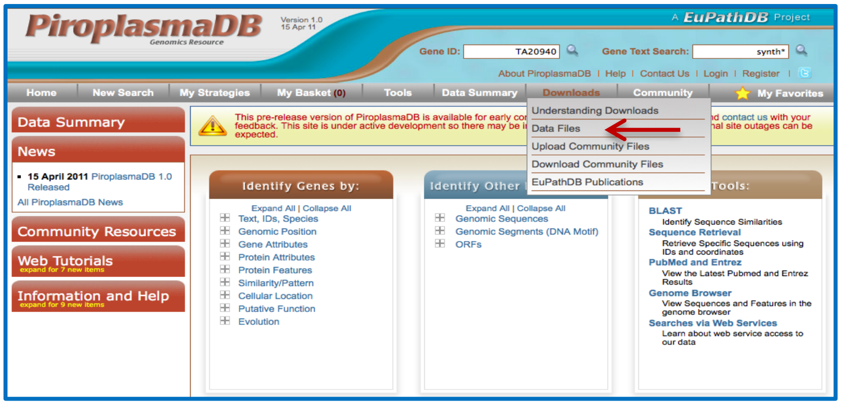
Sequence Retrieval
Retrieve Specific Sequences using IDs and coordinates

PubMed and Entrez
View the Latest Pubmed and Entrez Results

9.3 Downloading large data files such as all coding sequences or all protein sequences for an entire genome.

For this exercise use any EuPathDB site. The example below illustrates a use case in PiroplasmaDB: http://piroplasmadb.org

Download files are available in the file download section of all EuPathDB sites Hint: select “Data Files” under the “Download” menu in the grey tool bar.



This pre-release version of PiroplasmaDB is available for early co[...] feedback. This site is under active development so there may be i[...] expected. [...]d contact us with your [...]al site outages can be

- 15 April 2011 PiroplasmaDB 1.0 Released

All PiroplasmaDB News

Identify Sequence Similarities

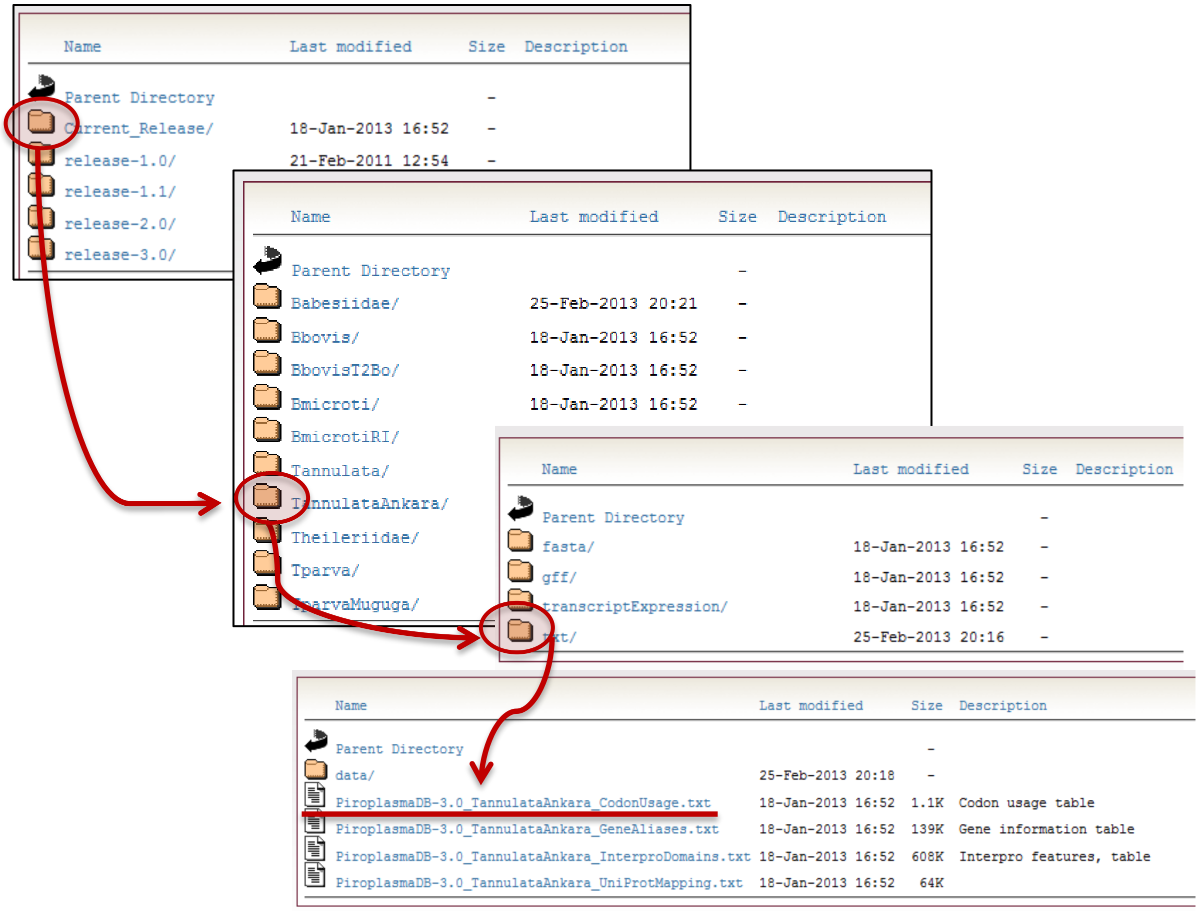
Retrieve Specific Sequences using IDs and coordinates

View the Latest Pubmed and Entrez Results

View Sequences and Features in the genome browser

Learn about web service access to our data

Hint: navigate through the subfolders and find the files containing codon usage information for *T. annulata* Ankara. Folders without a strain designation contain species level data.



```
Name                 Last modified      Size  Description

Parent Directory                          -
Current_Release/     18-Jan-2013 16:52    -
release-1.0/         21-Feb-2011 12:54    -
release-1.1/
release-2.0/
release-3.0/
```

```
Name                 Last modified      Size  Description

Parent Directory                          -
Babesiidae/          25-Feb-2013 20:21    -
Bbovis/              18-Jan-2013 16:52    -
BbovisT2Bo/          18-Jan-2013 16:52    -
Bmicroti/            18-Jan-2013 16:52    -
BmicrotiRI/
Tannulata/
TannulataAnkara/
Theileriidae/
Tparva/
TparvaMuguga/
```

```
Name                       Last modified      Size  Description

Parent Directory                                -
fasta/                     18-Jan-2013 16:52    -
gff/                       18-Jan-2013 16:52    -
transcriptExpression/      18-Jan-2013 16:52    -
txt/                       25-Feb-2013 20:16    -
```

```
Name                                                 Last modified      Size  Description

Parent Directory                                                          -
data/                                                25-Feb-2013 20:18    -
PiroplasmaDB-3.0_TannulataAnkara_CodonUsage.txt      18-Jan-2013 16:52  1.1K  Codon usage table
PiroplasmaDB-3.0_TannulataAnkara_GeneAliases.txt     18-Jan-2013 16:52  139K  Gene information table
PiroplasmaDB-3.0_TannulataAnkara_InterproDomains.txt 18-Jan-2013 16:52  608K  Interpro features, table
PiroplasmaDB-3.0_TannulataAnkara_UniProtMapping.txt  18-Jan-2013 16:52   64K
```