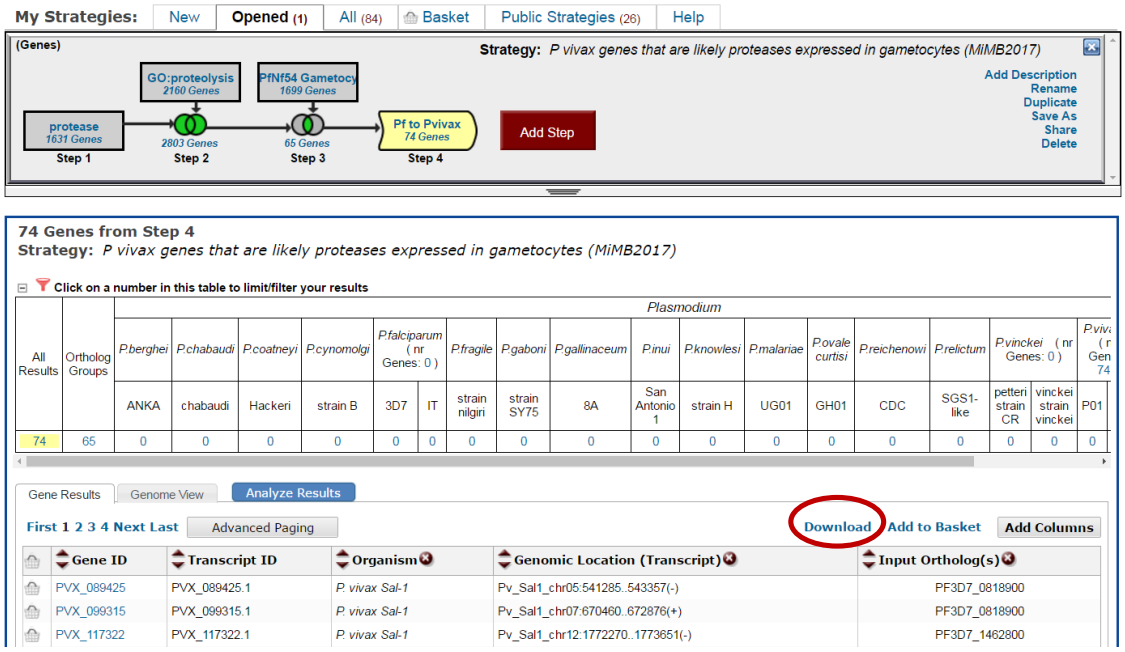
Data retrieval and download

1a Downloading a set of gene results and associated data from a search result

For this exercise, you can start with any result list you generated this morning, or use this shared strategy that returns a list of *P. vivax* genes that are likely proteases expressed in gametocytes.

http://plasmodb.org/plasmo/im.do?s=2db873c2b03b57bf

Use the Download tool to create a table with one row per gene and columns for the associated data: Genomic Location, Product Description, Transcript Length and all Curated GO Function. Which report type would you choose to create your table?



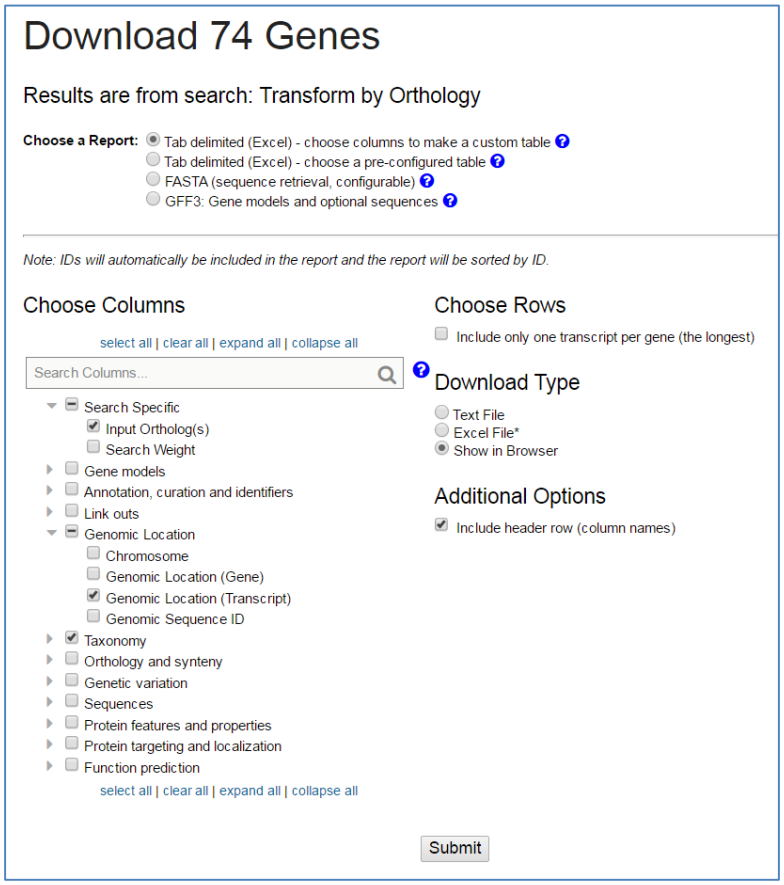
- **Tab delimited (Excel) - choose columns to make a custom table**– create a file with one row per gene and unlimited (almost) columns per gene. Any data that is available as a column on the result page can be downloaded with this option.
    - **Tab-delimited** text, also known as **tab-separated** values (TSV), is a format that can be created or viewed by most spreadsheet programs and text editors. The TSV format follows these rules: Each entry in the **file** takes up a single line. The first line in the **file** is the header line, which labels each field.

- **Tab delimited (Excel) - choose a pre-configured table** – This option allows you to download data that has multiple associations per gene, such as multiple GO terms assigned to one gene. The file structure is NOT one row per gene. Only one table can be downloaded at a time.

- **FASTA (sequence retrieval, configurable)** – create a multi-fasta file of your sequences. Each sequence begins with a single-line description, which contains greater-than (“>”) symbol, followed by lines of sequence data. You have the option to configure the start and end points of the sequence

- **GFF3: Gene models and optional sequences** –a simple **tab delimited** format for describing genomic features in a 9-column text file. GFF stands for *Generic Feature Format*. GFF3 allows multi-level grouping and multi-level descriptive attributes.

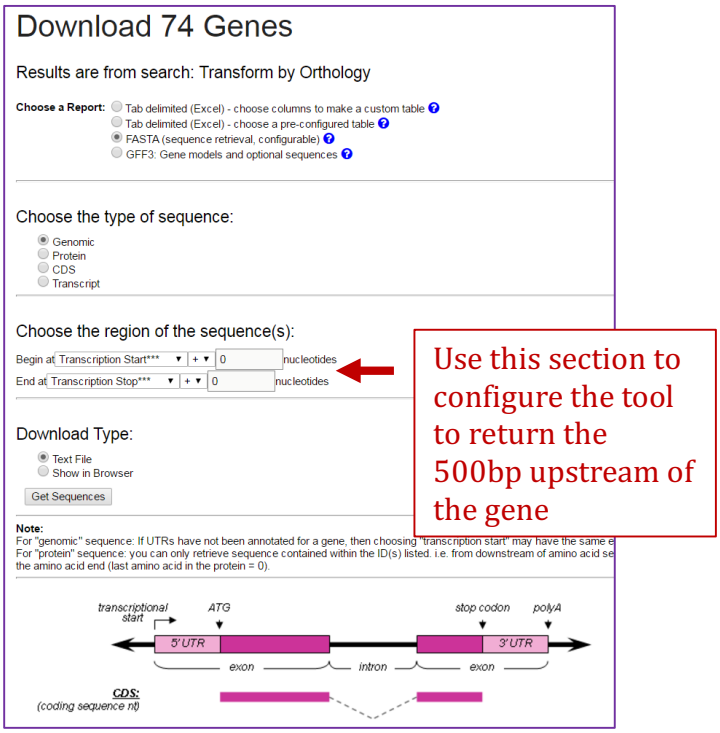
  Hint: choose the option for a ‘Tab delimited (Excel) - choose columns to make a custom table’ to open the tool. Under Choose Columns you can either expand every category and browse to find the data you want, or you can use the search function.



1b **Download the genomic sequences of genes in a list of results.** This is a good way to get sequences for further analysis.

Use same list of results as in 1a. Choose Download again but this time choose **FASTA (sequence retrieval, configurable).** Explore the tool. What kind of sequences can you retrieve? Protein? Genomic? Coding?

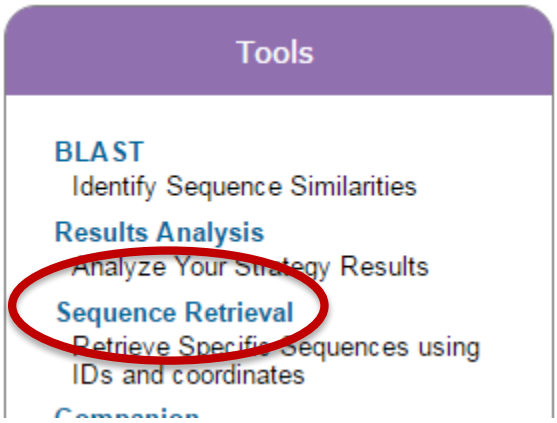
Download your gene sequences in fasta format and include the 500bp upstream of the start sites.



Now retrieve 5' UTR sequences for the list of genes. Begin with setting a transcription start parameter at 0 and end at a translation start (ATG) and parameter (-1). Setting a translation start (ATG) site parameter to (-1) eliminates incorporating "A" of the start codon into the 5' UTR sequence.

1c **Use the Sequence Retrieval Tool to download the genomic sequence for your genes**.

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



The tool contains several options for downloading sequences.

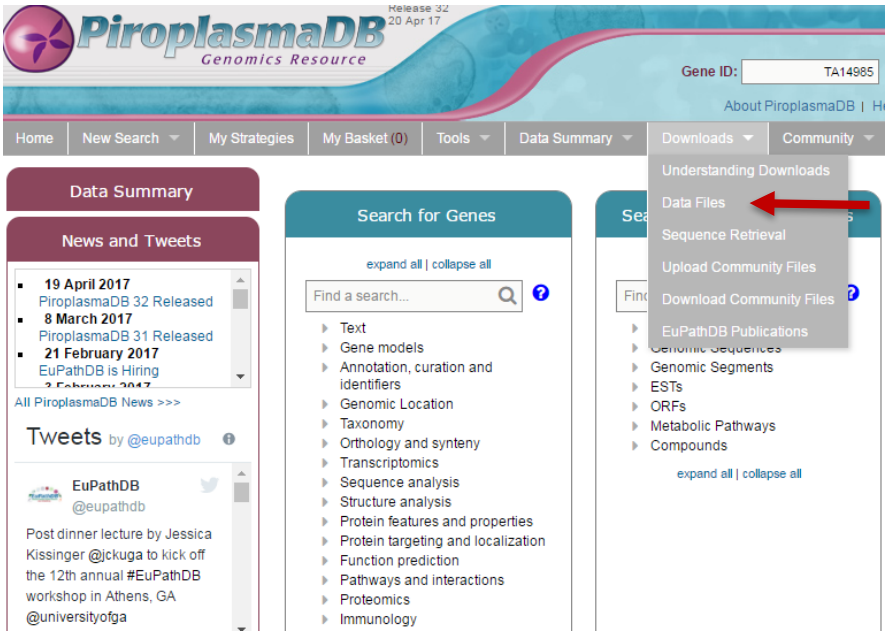
- Retrieve Sequences By Gene IDs.
- Retrieve Sequences By Genomic Sequence IDs.
- Retrieve Multiple Sequence Alignments by Contig / Genomic Sequence IDs.
- Retrieve Sequences By Open Reading Frame IDs.

Hint: copy the list of IDs from your gene result into the Retrieve Sequences by Gene ID option of the Sequence Retrieval Tool. How will you retrieve just the gene IDs for your genes? Maybe you can use the download tool described in 1a to retrieve only the IDs.

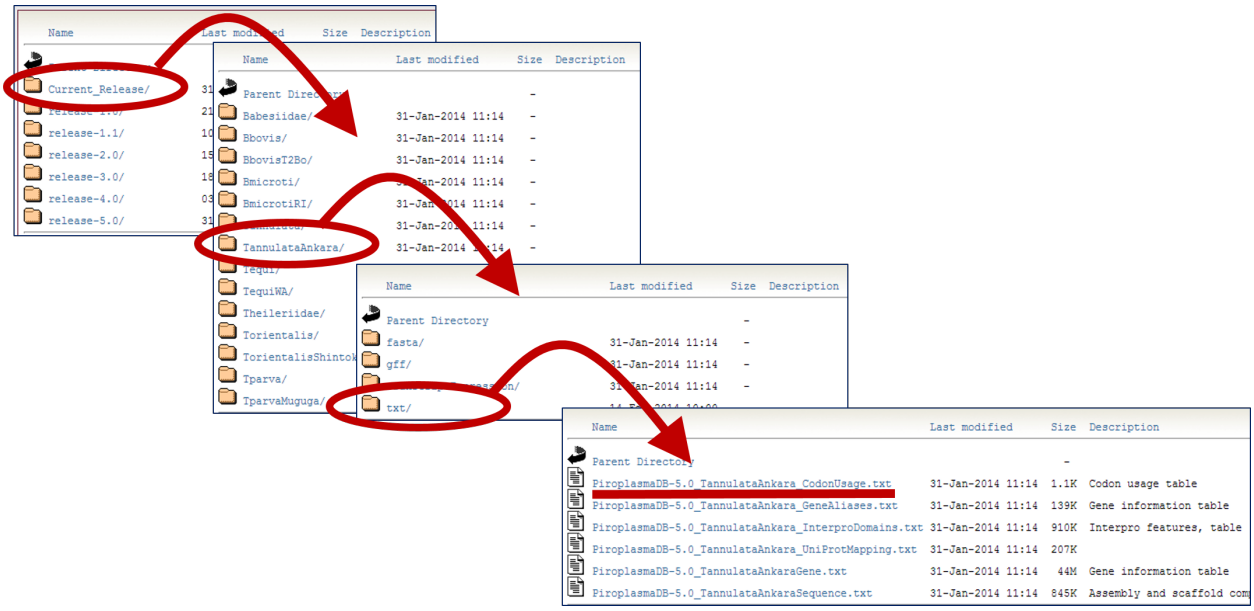
1d Downloading large data files such as all coding sequences or all protein sequences for an entire genome.

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

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



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



What other data are available for download? Do the directories make sense … fasta, gff , txt? How would you download the complete genome sequence and annotation for *T annulata* Ankara?