

Strategies Tutorial

Note: This exercise uses PlasmoDB.org as an example, but the same functionality is available on a VEuPathDB resources.

Learning objectives:

- Build a multistep strategy
- Use the Text, GO Term, RNA-Seq, and SNP searches
- Combine search results using Boolean operators and the colocation tool
- Transform genes of one organism into their orthologs in another organism
- Infer expression timing from a well-studied organism onto another organism that lacks data.

In this tutorial you will find genes expressed in gametocytes that are likely proteases and have variation in their upstream regions, possibly affecting promoter regions and other gene features. The strategy you build will combine three different searches that query *P. falciparum* data, then transform the *P. falciparum* genes returned by those searches into their *P. vivax* orthologs and look for SNPs in the upstream regions of the *P. vivax* genes. The ortholog transform enables you make inferences about genes in *P. vivax*, an organism with limited functional data, based on existing data in the closely related and well-studied *P. falciparum*. The *P. vivax* genes returned by the search are likely to share two biological properties, proteolytic activity and expression in gametocytes, and show variation in their upstream regions, possibly affecting promoter regions or other gene features.

Strategies Overview:

The strategy system offers over 100 structured searches that can be combined to produce multi-step strategies. Each search queries a specific data set and **returns a list of IDs** that share the biological characteristic defined by the data.

Searches are accessible from the 'Search For...' menu on the home page and from the 'Searches' dropdown menu in the header of every page. Searches listed under Genes will return a list of gene IDs, while searches listed under 'SNPs' or 'Metabolic Pathways' will return record IDs representing SNPs, or metabolic pathways.

Search for... expand all | collapse all

Filter the searches below...

- Genes
 - Annotation, curation and identifiers
 - Epigenomics
 - Function prediction
 - EC Number
 - GO Term
 - Gene models
 - Genetic variation
 - Genomic Location
 - Immunology
 - Orthology and synteny
 - Pathways and interactions
 - Phenotype
 - Protein features and properties
 - Protein targeting and localization
 - Proteomics
 - Sequence analysis
 - Structure analysis
 - Taxonomy
 - Text
 - Text (product name, notes, etc.)
 - Transcriptomics
 - Microarray Evidence
 - RNA-Seq Evidence
- SNPs
 - Differences Between Two Groups of Isolates
 - Differences Within a Group of Isolates
 - Gene IDs
 - Genomic Location
 - SNP ID(s)

Site search, e.g. PF3D7_1133400 or *reductase or *binding protein

My Strategies Searches Tools My Workspace Data About

Expand all | Collapse all

Filter the searches below...

- Genes
- Organisms
- Popset Isolate Sequences
- Genomic Sequences
- Genomic Segments
- SNPs
- SNPs (from Array)
- ESTs
- Metabolic Pathways
- Compounds

Transform into related records

Orthologs
107 Genes






Step 4 Step 5

The 5 searches you will use in this tutorial are:

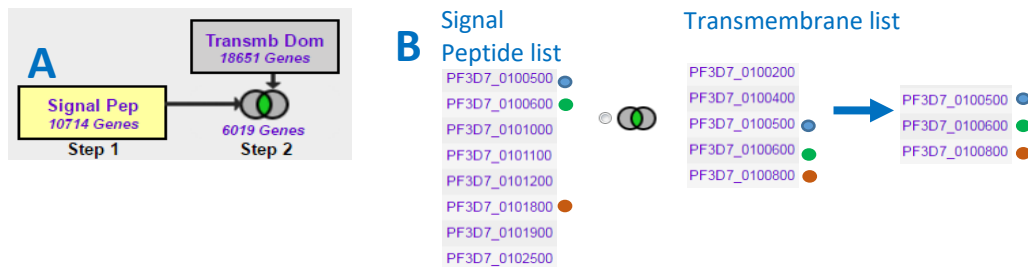
1. Identify Genes by Text (product name, notes, etc.) – The search compares your term against the text in the fields that you specify, returning the IDs of gene records that have a match.
2. Identify Genes by GO Term – Returns genes that have your specified Gene Ontology (GO) Term(s) or ID(s) assigned to them.
3. Identify Genes based on RNA Seq Evidence – PlasmoDB integrates raw RNA sequencing data from many different experiments and analyzes all data according to the same workflow to produce expression values. This search returns genes based on their transcript expression as measure by RNA sequencing.
4. Transform by Orthology – PlasmoDB integrates ortholog profiles from OrthoMCL. The OrthoMCL algorithm clusters proteins into ortholog groups based on BLAST similarity across at 150 genomes that span the tree of life. The transform we perform here will convert a list of genes in one organism to their orthologs in a different organism. In this case, we will transform a list of *P. falciparum* genes into their *P. vivax* orthologs.
5. Identify SNPs based on Differences within a Group of Isolates – PlasmoDB integrates whole genome resequencing of isolates and analyzes each isolate for single nucleotide polymorphisms compared to a reference genome. This search returns SNPs that are shared between all the *P. vivax* isolates that are integrated in PlasmoDB.

Before we get started... a few words about combining search results:

Each search returns a list of IDs. When two searches are combined, the two result sets (list of IDs) are merged. The table shows the 5 options for combining search results.

Operator	:	Combined Result will contain:
 1 INTERSECT 2	:	IDs in common between the two lists
 1 UNION 2	:	IDs from list 1 and list 2
 1 MINUS 2	:	IDs unique to 1
 2 MINUS 1	:	IDs unique to 2
 1 Relative to 2	:	IDs whose features are near each other (collocated) in the genome

If the searches return the same type of genomic feature they can be combined using any of the 5 operators (i.e. search 1 returns genes, search 2 returns genes as in screenshot group A below).




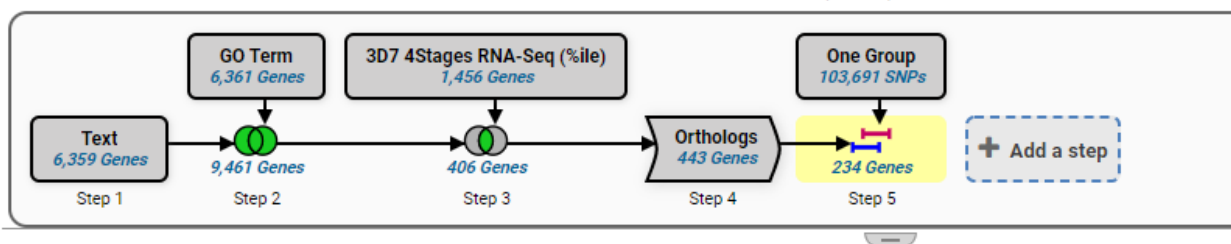
However, searches that return different genomic features will yield no results when combined with intersect, union or minus operators. This is illustrated in screenshot groupings C and D below. Because genes and SNPs are different genomic features, there are no IDs in the list of genes (Step 1) that are present in the list of SNPs (Step 2). To combine a search that returns genes with a search that returns SNPs, you must use the collocation option (1 relative to 2). We know the genomic location of each gene and each SNP and the collocation option is designed to return features based on their relative genomic location, i.e. SNPs that are near or within genes.



Build the Strategy:

Find *P. vivax* genes that are possible proteases, likely expressed during the gametocyte stages and contain SNPs in their upstream regions. This search strategy employs 4 searches, an ortholog transform and the colocation tool to integrate SNP information. Steps 1 and 2 return *P. falciparum* proteases using two different lines of evidence – a text search in step 1 and a Gene Ontology (GO) term search in step 2. These searches are combined with a union to obtain a more comprehensive list of possible proteases. Step 3 returns genes with evidence for expression during the gametocyte stages based on RNA sequencing data collected in *P. falciparum*. Steps 2 and 3 are combined using the intersect operator to produce a list of genes that have BOTH biological properties: these genes are likely proteases with evidence for expression during gametocyte stages. In the next step, the *P. falciparum* genes returned in the step 3 result are transformed into their *P. vivax* orthologs. This results in a set of 125 *P. vivax* genes with suspected protease activity and expression in gametocytes based on annotation and experimental evidence from *P. falciparum*, an organism for which more complete annotation and functional genomics data is available. In Step 5 we look for single nucleotide polymorphisms (SNPs) among isolates of *P. vivax* and collocate these SNPs to the upstream regions of the *P. vivax* genes. The final result is a set of 32 *P. vivax* genes that are likely proteases expressed in the gametocyte stage and that have SNPs in their upstream regions. Your strategy should look like this when you are done:

PvP01 proteases expressed in gametocytes and with upstream SNPs (2022) 



Step by Step Instructions

1. Run a text search using protease as the text term.

Identify Genes by Text (product name, notes, etc.): Using the Text Search, find genes whose records contain the term 'protease'. To reach the text search, click on the link in the home page 'Search For...' menu. The page opens showing a list of parameters that are needed to query the data. Every search is loaded with default parameters so that you can click Get Answer and run the search. Change the Text term to 'protease' and click Get Answer to initiate the search. The search results are displayed in the My Strategies section which consists of a strategy panel followed by a filter table and a result table.

Navigation: >PlasmoDB >Search for Genes >Text >Text (product name, notes, etc.)

Identify Genes based on Text (product na

57 selected, out of 57

select all | clear all | expand all | collapse all

Filter list below...

☒ Haemoproteidae
☒ Plasmodiidae

select all | clear all | expand all | collapse all

Choose all organisms

Text term (use * as wildcard)

protease

Enter protease

Fields

☒ Alternate product descriptions
☒ Apollo Annotations
☒ EC descriptions and numbers
☒ Epitopes from IEDB
☒ External links
☒ Gene ID
☒ Gene name or symbol
☒ Gene type
☒ Genomic sequence ID
☒ GO terms
☒ InterPro domains
☒ Metabolic pathways
☒ Names, IDs, and aliases
☒ Notes from annotators
☒ Organism
☒ Ortholog group
☒ Orthologs
☒ PDB chains
☒ Product descriptions
☒ PubMed
☒ Rodent malaria phenotype
☒ Transcripts
☒ User comments

select all | clear all

Leave all fields checked. We will use the default setting here.

Click Get Answer to initiate the search

Get Answer

Parameters:

Organism	:	Default - all
Text term (use * as wildcard)	:	protease
Fields	:	Default - all

Results and strategy: You created a one-step strategy by running the text search. The strategy returns 6539 genes that are annotated with the word 'protease'. This annotation could appear in any field that you searched. You can analyze this result by exploring the hits. Look at the data in the columns of the result table. You can add more data with the Add Columns button. Clicking a gene ID in the

first column will take you to that gene's record page. Please explore your results to see if they make sense. For example, gene product names might contain the word 'protease'. Functional data assigned to the genes (GO terms and EC numbers) may indicate protease activity.

Strategy Box showing your one-step strategy

Filter table showing the distribution of hits across the

Result List showing all hits from the search

Gene ID	Transcript ID	Organism	Genomic Location (Gene)	Product Description
HtarL_000017900	HtarL_000017900...	Haemoproteus tartakovskyi strain SISKIN1	LSRZ01000007:31,041..31,490(+)	hypothetical protein
HtarL_000021300	HtarL_000021300...	Haemoproteus tartakovskyi strain SISKIN1	LSRZ01000009:63,972..65,153(+)	26S protease regulatory subunit
HtarL_000033100	HtarL_000033100...	Haemoproteus tartakovskyi strain SISKIN1	LSRZ01000018:51,994..53,506(+)	rhomboid protease ROM1
HtarL_000035200	HtarL_000035200...	Haemoproteus tartakovskyi strain SISKIN1	LSRZ01000020:43,196..46,273(+)	ATP-dependent protease, pu
HtarL_000035500	HtarL_000035500...	Haemoproteus tartakovskyi strain SISKIN1	LSRZ01000020:50,926..54,873(+)	ubiquitin carboxyl-terminal h
HtarL_000050500	HtarL_000050500...	Haemoproteus tartakovskyi strain SISKIN1	LSRZ01000034:11,611..13,812(-)	ubiquitin carboxyl-terminal h
HtarL_000094500	HtarL_000094500...	Haemoproteus tartakovskyi strain SISKIN1	LSRZ01000034:11,611..13,812(-)	26S protease regulatory sub
HtarL_000095900	HtarL_000095900...	Haemoproteus tartakovskyi strain SISKIN1	LSRZ01000034:11,611..13,812(-)	cysteine proteinase falcipar
HtarL_000097100	HtarL_000097100...	Haemoproteus tartakovskyi strain SISKIN1	LSRZ01000034:11,611..13,812(-)	plasmepsin X

Add a step choosing to run a search for genes annotated with the biological process gene ontology term – GO:0006508: proteolysis. Gene Ontology annotations offer a second line of evidence for finding proteases. The ontologies are a controlled vocabulary for describing the molecular function, biological process and subcellular location of a gene product. GO annotations in PlasmidDB were either provided by the sequencing and annotation centers or inferred based on a gene's similarity to protein domains from the [InterPro](#) databases. The GO Term search returns a gene if it is annotated with the GO term that you are looking for. Let's use that search to look for genes annotated with GO:0006508: proteolysis. We will union the text search results with our GO term results when we combine the results of the two searches.

Navigation: Add Step >Combine with other Genes >1 union 2 > A new search >GO Term

protease

6,359 Genes

+

Add a step

Step 1

Combine with other Genes

Step 1

Step 2

Transform into related records

Step 1

Step 2

Use Genomic Colocation to combine with other features

Step 1

Step 2

Add a step to your search strategy

1 Choose how to combine with other Genes

1 INTERSECT 2

1 UNION 2

1 MINUS 2

2 MINUS 1

2 Choose which Genes to combine. From...

A new search

An existing strategy

My basket

GO

Function prediction

GO Term

Text

Text (product name, notes, etc.)

Search for and choose the GO Term search.

Which organism is chosen by default for this search? Click 'select all' to run the search on all organisms

Begin typing Proteolysis and then choose the correct GO term from the list

Click Run Step to initiate the search

Add Step

Add Step 2 : GO Term

Organism

Filter list below...

Plasmodium

select all | clear all | expand all | collapse all

Evidence

Curated

Computed

Limit to GO Slim terms

Yes

No

GO Term or GO ID

Begin typing to see suggestions...

Begin typing to see suggestions to choose from (CTRL or CMD click to select multiple)

GO Term or GO ID wildcard search

N/A

Run Step

Give this search a name (optional)

Give this search a weight (optional)

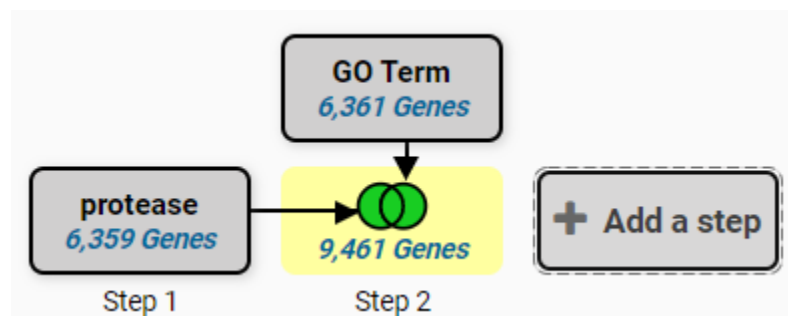
Parameters:

Organism	:	Choose All
Evidence	:	Default
Limit to GO Slim Terms?	:	Default
GO Term or GO ID	:	GO:0006508 : proteolysis
Free Text (use '*' for wildcard)	:	N/A

Combine:



Strategy Result: The GO term search returned 6,361 genes annotated with the proteolysis GO term. The union of the text and GO search returns 9,461 genes that are suspected to have proteolytic activity.



2. **Add a step choosing to run a search for genes based on Transcript Expression using RNA-Seq Evidence.** Since PlasmoDB has integrated several RNA sequencing data sets you must first choose what data set (experiment) to search before you are taken to the search form to choose parameters. Use the Filter Data set tool to choose the Percentile search (P) for '**Strand specific Transcriptomes of 4 life cycle stages (Lopez-Barragan et al)**'. This data set contains the RNA sequencing analysis of two gametocyte samples. Running the percentile search using the default parameters will return the genes whose expression levels are in the top 20% for those samples.

Navigation: Add Step >Combine with other Genes >2 intersect 3 >A new search >RNA Seq Evidence

Step 1: protease 6,359 Genes

Step 2: GO Term 6,361 Genes

9,461 Genes

+ Add a step

Add a step to your search strategy

1 Choose *how to combine* with other Genes

☒ 2 INTERSECT 3
 ☐ 2 UNION 3
 ☐ 2 MINUS 3
 ☐ 3 MINUS 2

2 Choose *which Genes to combine*. From...

☒ A new search
 ☐ An existing strategy
 ☐ My basket

RNA

Gene models
 Q Gene Model Characteristics
 Transcriptomics
 Q Microarray Evidence
 Q RNA-Seq Evidence

Search for and choose the RNA-Seq evidence.

Add a step to your search strategy

Search for Genes by RNA-Seq Evidence

The results will be ☐ intersected with ☐ the results of Step 2.

Filter Data Set: strand

Legend: DE Differential Expression FC Fold Change P Percentile SA SenseAntisense

Organism	Data Set	FC	P	SA
Plasmodium falciparum 3D7	Strand specific transcriptomes of 4 life cycle stages (Lopez-Barragan et al.)	FC	P	SA
Plasmodium falciparum 3D7	Intraerythrocytic development cycle transcriptome (2018) (Toenhake et al.)	FC	P	SA
Plasmodium falciparum 3D7	Strand specific transcriptome of the intraerythrocytic developmental cycle (Siegel et al.)	FC	P	SA

Add a step to your search strategy

Experiment

Strand specific transcriptomes of 4 life cycle stages - Sense

Samples

☐ Late Trophozoite
☐ Schizont
☒ Gametocyte II
☒ Gametocyte V
 select all | clear all

Minimum expression percentile

80

Maximum expression percentile

100

Matches Any or All Selected Samples?

any

Protein Coding Only:

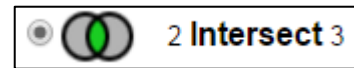
protein coding

Run Step

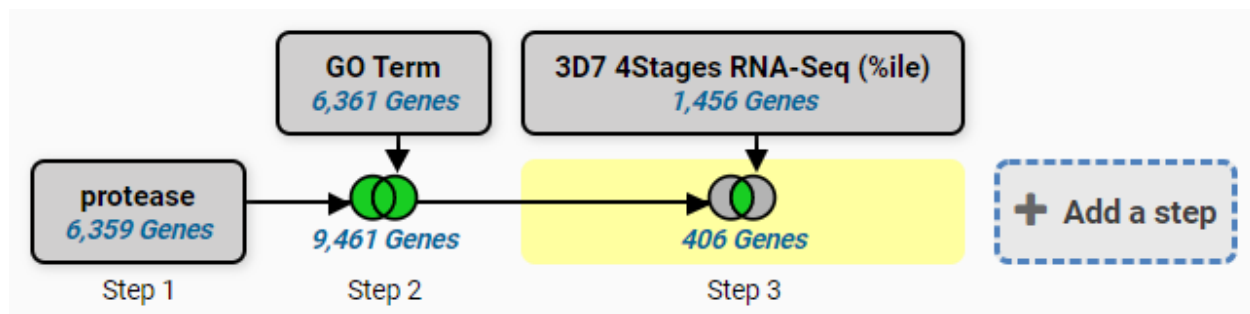
Parameters:

Experiment	:	Strand specific transcriptomes of 4 life cycle stages sense strand
Samples	:	Gametocyte II, Gametocyte V
Minimum expression percentile	:	default
Maximum expression percentile	:	default
Matches Any or All Selected Samples?	:	default
Protein Coding Only:	:	default

Combine: Intersecting this search with the previous result will produce a list of genes that are common to both result lists.



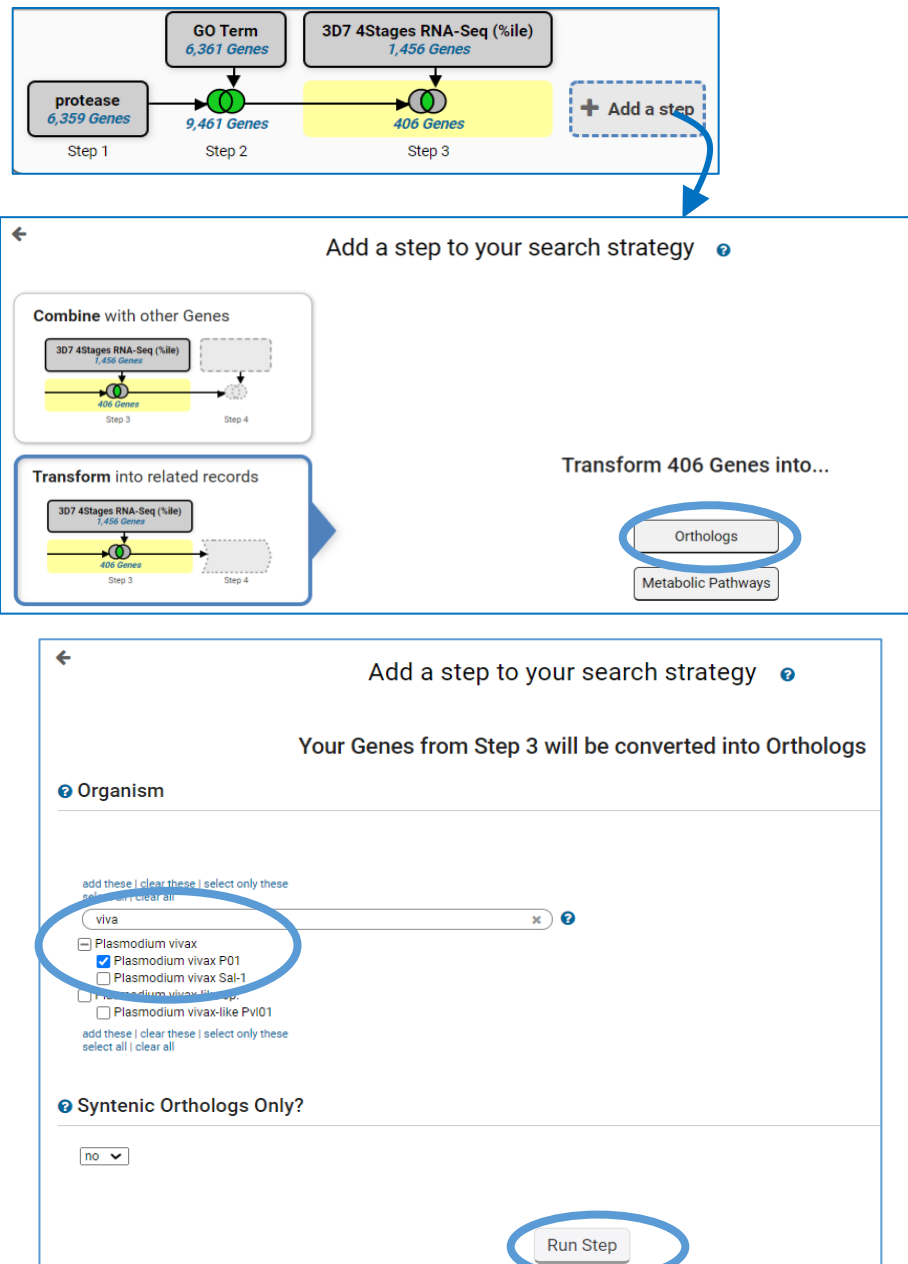
Strategy result: We have a three-step strategy that returns 406 *P. falciparum* genes that are suspected proteases with evidence for expression in gametocytes based on RNA Sequencing data. Explore your gene list!!



3. Add a step to the strategy that transforms the 406 *P. falciparum* genes into *P. vivax* genes.

P. falciparum is a well-studied organism with active curatorial efforts and large amounts of functional data. For example, PlasmoDB has 25 RNA sequencing and 12 microarray data sets integrated for *P. falciparum*, but only 5 RNA-Seq and 2 microarray for *P. vivax*. A researcher interested in *P. vivax* can take advantage of the *P. falciparum* data by creating a strategy based on *P. falciparum* data to retrieve genes with the biological properties they are interested in, and then transforming the results to their *P. vivax* orthologs.

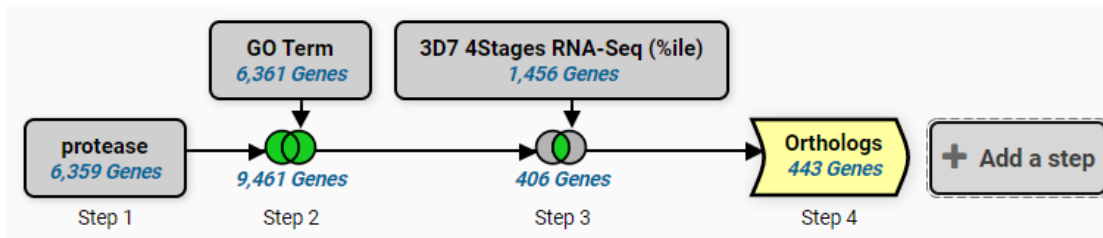
Navigation: >Add Step >Transform into related records >Orthologs



Parameters: Choose only *P. vivax* P01 in the Organism parameter of the Add Step Popup.

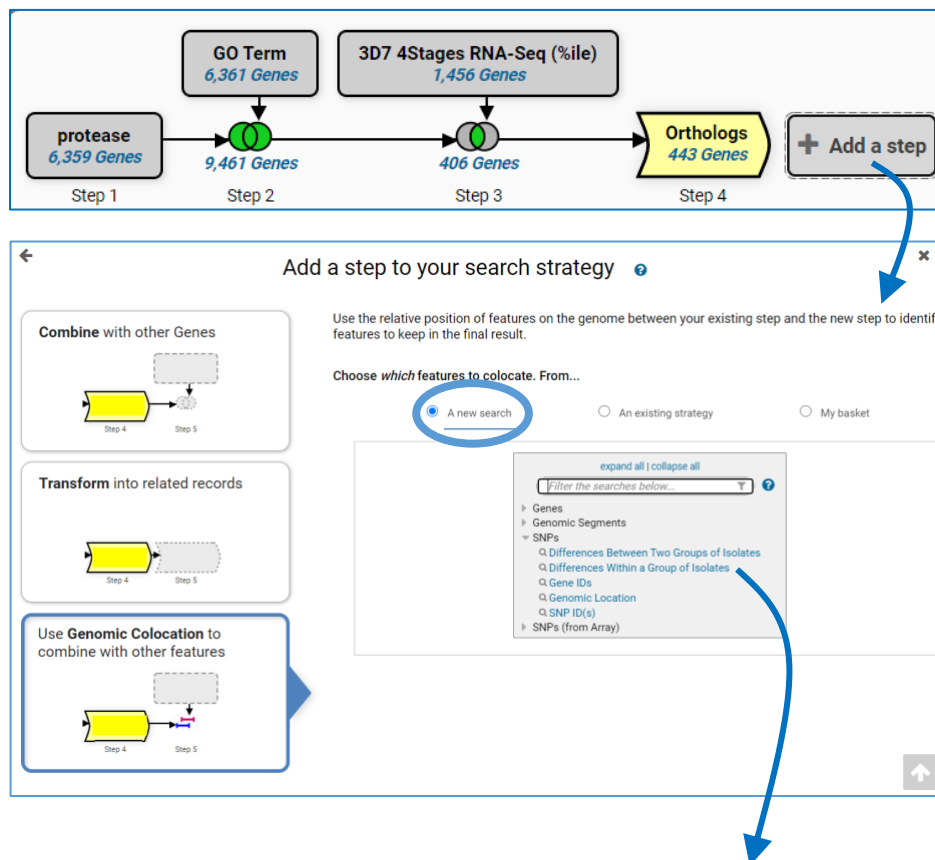
Combine: The ortholog transform function does not combine lists, but instead transforms the results into orthologs from a different species.

Strategy Result: We have a four-step strategy that returns 443 *P. vivax* genes that are suspected proteases expressed in gametocytes based on *P. falciparum* RNA Sequencing data.



4. Add a step to the strategy that returns *P. vivax* SNPs and collocate those SNPs to the upstream 1000bp of the *P. vivax* genes in step 4. We can look for variation (SNPs) associated with the genes from Step 4. PlasmoDB integrates whole genome resequencing data from many isolates, and PlasmoDB contains 220 data sets from whole-genome sequencing of *P. vivax* isolates. PlasmoDB analyzes the whole genome sequencing reads by aligning them to the reference genome and then examines the genome one base at a time to find bases in the isolate that do not match the reference sequence. The SNPs are loaded in the database along with other information such as how many sequencing reads supported the SNP call and the genomic location of the SNP. The search we will use analyzes whole genome resequencing data from all *P. vivax* isolates to find SNPs shared between all isolates. You will notice that initiating the search does not immediately bring up the result, but instead leads you to the collocation tool.

Navigation: >Add Step >Use Genomic Colocation >A new search >Differences Within a Group of Isolates



← Add a step to your search strategy ⓘ

Organism
The organism you choose will determine the genome to which the SNPs have been mapped. That will also restrict the set of samples to those whose SNPs are aligned to the genome of those isolates to this genome.
 Plasmodium vivax P01

Samples
 220 Samples Total
 expand all | collapse all
 Find a variable
 [x] Proportion mapped reads
 [x] Average mapping coverage
 [x] Data Set
 [x] Parasite organism

Proportion mapped reads
 Min: 0 Mean: 0.64 Median: 0.85 Max: 0.98
 Select Proportion mapped reads from 0.0014 to 0.98 219 (>99%) of 220 Samples have data for this variable

Read frequency threshold
 80%

Minor allele frequency >=
 0

Percent isolates with a base call >=
 70

Run Step

Choose *Plasmodium vivax* P01

Use all 220 isolates (Do not filter)

Percent isolates with base call = 70

Parameters:

Organism	:	<i>P. vivax</i> P01
Isolates	:	Default = All Isolates (195)
Read frequency threshold	:	Default - 80%
Minor allele frequency >=	:	Default - 0
Percent isolates with a base call >=	:	Default - 70

Colocation: Because this search returns SNPs and not genes, the only option for combining the two result lists is by relative genomic location. Arrange the statement in the Colocation popup to read: **Return each Gene from step 4 whose upstream 1000bp region overlaps the exact region of a SNP in Step 5 and is on either strand.** Remember to indicate that you want to locate the SNPs in the upstream region of the gene.

← Add a step to your search strategy ⓘ

"Return each whose the of a SNP from the new step and is on

Region

Gene

☒ Upstream: bp

☐ Downstream: bp

☐ Custom:

begin at: bp

end at: bp

Region

SNP

☒ Exact

☐ Upstream: bp

☐ Downstream: bp

☐ Custom:

begin at: bp

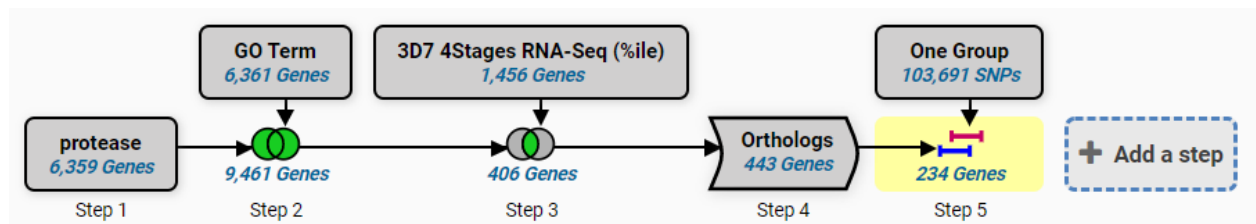
end at: bp

Run Step

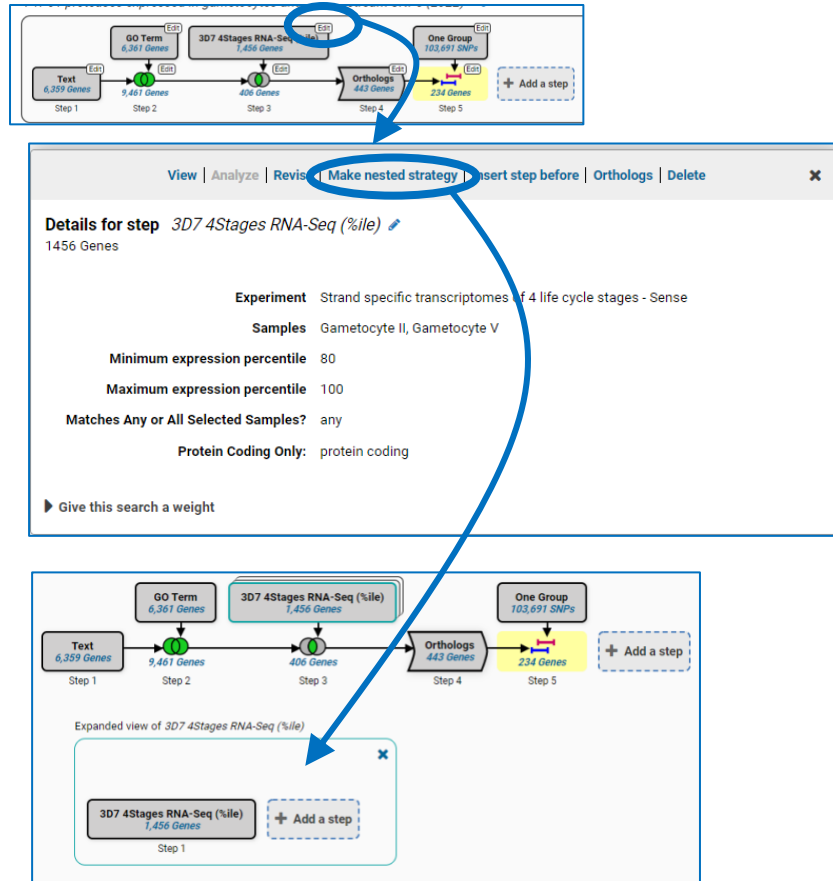
Strategy: Congratulations! You have completed the strategy and have a list of 234 *P. vivax* genes that are possible proteases, are likely expressed in gametocytes and have upstream SNPs.

This link will retrieve the completed strategy:

<https://plasmodb.org/plasmo/app/workspace/strategies/import/17290f4f96b5a94e>




5. **Revise your strategy to include more RNA Seq evidence.** The strategy takes advantage of a small portion of the data in PlasmoDB. For example, there are other RNA seq data sets in PlasmoDB that have information about gametocyte expression. The Nested tool will allow you to revise a step by adding addition searches before the step results are calculated.



Choose an operation for combining your new search with the previous gametocyte expression search. Choosing to intersect the two search results means that genes need to be in both gametocyte data sets. This will likely reduce the number of 'gametocyte genes' and result in stricter parameters. On the other hand, choosing to union the searches will likely increase the number of 'gametocyte genes', serving to broaden the search results. The example below requires that a 'gametocyte gene' be returned by both RNA seq searches. TRY IT!! (Click Add Step in the nested strategy to begin.)

← Add a step to your search strategy ⓘ

Search for Genes by RNA-Seq Evidence

The results will be  intersected with ▾ the results of Step 1.

Legend: S Similarity DE Differential Expression FC Fold Change P Percentile SA SenseAntisense

Filter Data Sets: gameto 1 result

Organism ⓘ	Data Set	Choose a Search
Plasmodium falciparum 3D7	Gametocyte Transcriptomes (Lasonder et al.)	S P SA

↓ Show All Data Sets ↓

Fold Change Percentile SenseAntisense

Experiment

- ☒ Gametocyte Transcriptomes - Sense
- ☐ Gametocyte Transcriptomes - Antisense

Samples

- ☒ male gametocyte
- ☒ female gametocyte
- [select all](#) | [clear all](#)

Minimum expression percentile

80

Maximum expression percentile

100

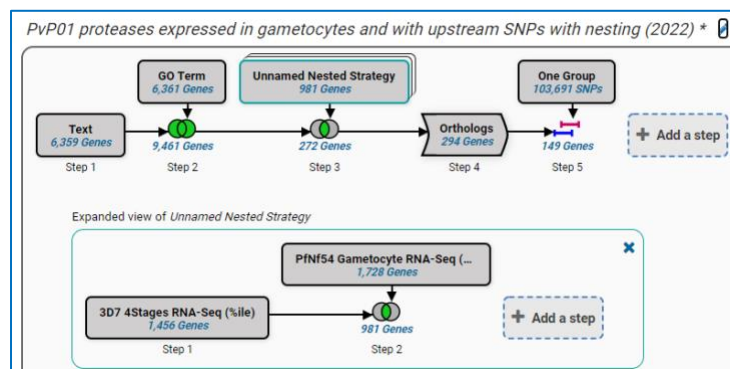
Matches Any or All Selected Samples?

any ▾

Protein Coding Only:

protein coding ▾

Run Step



Strategy with nesting:

<https://plasmodb.org/plasmo/app/workspace/strategies/import/660c27ef21e9bdc2>