

# VEuPathDB: A bioinformatics resource for facilitating data exploration, analysis, and integration for vectors and eukaryotic pathogens

## Guided workshop International Babesiosis Meeting 2025 March 26, 2025, 10-11:40 AM

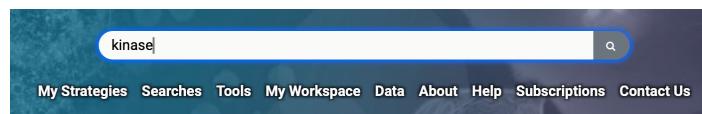
### Guided workshop objectives:

- Introduction to VEuPathDB resources focusing on PiroplasmaDB.org and VectorBase.org
- Use site search (hands-on exercise)
- Build a search strategy (hands-on exercise)
- Explore gene pages (hands-on exercise)
- Explore Single Cell data (Demo)

### Site Search

The site search is in the header of any VEuPathDB site and is available on every page. The site search queries the databases for your term or ID and returns a list of pages and documents that contain your query term.

1. **Search for a keyword.** Enter the word *kinase* in the site search window. Then click enter on your keyboard or click on the search icon.



**Site Search result format:** The site search returns a categorized list of pages and documents that contain your term. Site search results are summarized on the left with a details panel on the right. Changing the panel on the left will populate the details panel with that result. What is the total number of results with the word kinase? Are all the results genes?

All results matching **kinase**

1 - 20 of 8,016    Export as a Search Strategy ▶

Category	Count
Genome	7,247
Genes	5,564
Population biology	223
Metabolism	350
Compounds	193
Data access	3
Searches	1,683

**Filter results**  
Genome    **Genes** →  
Population biology  
Metabolism  
Compounds  
Data access  
Searches

**Filter fields**  
Select a result filter above

**Filter organisms**  
select all | clear all | expand all | collapse all  
Type a taxonomic name    Reference only  
Babesidae    Theileriidae

Gene - **BcabD6B2\_57170** mitogen-activated protein kinase kinase kinase 12  
Gene type: protein coding gene  
Organism: Babesia caballi USDA-D6B2  
Fields matched: Orthologs; Product description; Product descriptions (all)

Gene - **BcabD6B2\_33790** mitogen-activated protein kinase kinase kinase 13-B-like  
Gene type: protein coding gene  
Organism: Babesia caballi USDA-D6B2  
Fields matched: Orthologs; Product description; Product descriptions (all)

Gene - **BdWA1\_002139** bifunctional Phosphoglycerate kinase superfamily/Phosphoglycerate kinase/Phosphoglyc...  
Gene type: protein coding gene  
Organism: Babesia duncani strain WA1 2023  
Fields matched: EC descriptions and numbers; GO terms; InterPro domains; Orthologs; PDB chains; Product description; Product descriptions (all)

Gene - **BaOVIS\_016000** cyclin-dependent kinase-related kinase  
Gene type: protein coding gene  
Organism: Babesia ovis Seluk  
Fields matched: GO terms; InterPro domains; Orthologs; PDB chains; Product description; Product descriptions (all)

Gene - **BdWA1\_000014** bifunctional Diacylglycerol kinase/Diacylglycerol kinase

**Results are summarized by category.**

**Details panel with information about each item returned.**

**2. Filter the site search result by category:** How many genes included the word kinase in their product descriptions?

Filter the results so that you can only view gene results. Notice that a new section called “Filter Gene Fields” appears with additional filtering options. Select the *Product descriptions* field and choose *Apply*. Once a filter is applied, it can be removed by clicking on *Clear filter* (right panel below).

The figure consists of three side-by-side screenshots of a search interface. In the first screenshot, a red arrow points to the 'Filter Gene fields' section where the 'Product description' checkbox is selected. In the second screenshot, a red arrow points to the 'Apply' button, which is highlighted with a red box. In the third screenshot, a red box highlights the 'Clear filter' button, indicating that the filter has been applied and can be removed.

Filter Gene fields	Count
EC descriptions and numbers	1,942
GO terms	1,600
InterPro domains	1,981
Orthologs	6,056
PDB chains	1,258
Product description	1,232
Product descriptions (all)	1,232
User comments	76

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EC descriptions and numbers	1,942
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PDB chains	1,258
<b>Product description</b>	<b>1,232</b>
Product descriptions (all)	1,232
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<b>Product description</b>	<b>1,232</b>
Product descriptions (all)	1,232
User comments	76

**3. Filter the site search result by organism:** How many of the above genes are found in *Plasmodium falciparum* 3D7? Explore the *Filter organisms* section of the results filter and use the search filter to navigate the tree.

The figure consists of two side-by-side screenshots of a search interface. In the left screenshot, a red arrow points to the 'Filter organisms' search bar containing 'duncani'. Another red arrow points to the 'Babesia duncani strain WA1 2023 [Ref]' entry in the list, which is highlighted with a red box. In the right screenshot, a red box highlights the 'Apply' button, indicating that the filter has been applied.

Filter Gene fields	Count
EC descriptions and numbers	1,942
GO terms	1,600
InterPro domains	1,981
Orthologs	6,056
PDB chains	1,258
<b>Product description</b>	<b>1,232</b>
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Product descriptions (all)	1,232
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4. **Export the results to a search strategy.** Use the blue *Export as a search strategy* button at the top right-hand side of the results. Once exported, you can take advantage of over 100 specialized searches using the Add Step button. We will learn more about this in a future exercise.

Genes matching kinase (filtered by fields and organisms)

1 - 20 of 105

**Filter results**  Hide zero counts  
Genome Genes  Clear filter 105

Gene - BdWA1\_002139 bifunctional Phosphoglycerate kinase superfamily/Phosphoglycerate kinase/Phosphoglycerate kinase  
Gene type: protein coding gene  
Organism: Babesia duncani strain WA1 2023  
> Fields matched: EC descriptions and numbers; GO terms; InterPro domains; Orthologs; PDB chains; Product description; Product description (all)

My Search Strategies

Opened (1) All (133) Public (4) Help

Unnamed Search Strategy \*

Text 105 Genes  Add a step

Step 1

105 Genes (87 ortholog groups) Revise this search

5. **Identify all the orthologs of the *B. duncani* genes in all organisms in PiroplasmaDB.** 1. Click on the “Add a step” button to reveal a popup. 2. Select the “Transform in related Records” option. 3. then click the “Orthologs” button. 4. In the next popup, select all organisms and click on the “Run Step” button.

PiroplasmaDB Piroplasma Informatics Resources Release 68 7 May 2024

Site search, e.g. TA14985 or \*reductase or "binding protein"

My Strategies Searches Tools My Workspace Data About Help Subscriptions Contact Us

Add a step to your search strategy

Combine with other Genes

Transform 105 Genes into...

Orthologs  
Metabolic Pathways  
Compounds

Add a step to your search strategy

Your Genes from Step 1 will be converted into Orthologs

Configure Search Learn More View Data Sets Used

Reset values to default

Organism

16 selected, out of 16

Babesia bovis strain BOND [Ref]  
Babesia bovis 72b [Ref]  
Babesia caballi USA-0482 [Ref]  
Babesia divergens strain 1802A [Ref]  
Babesia duncani strain WA1 2023 [Ref]  
Babesia microti strain RI [Ref]

Reference only

Syntetic Orthologs Only?

Run Step

- Notice you now have a second step with the results of all orthologs in PiroplasmaDB.
- The step that is highlighted in yellow indicates what results you are viewing.
- You can expand the organisms on the left to see the distribution of orthologs across organisms.
- The central portion includes a list of all the gene results.

Unnamed Search Strategy \*

Step 1: Text  
105 Genes

Step 2: Orthologs  
1,406 Genes

+ Add a step

1,406 Genes (87 ortholog groups) Revise this search

Gene Results | Genome View | Analyze Results

Genes: 1,406 Transcripts: 1,407 Show Only One Transcript Per Gene Show only the Genes in my basket.

Organism Filter

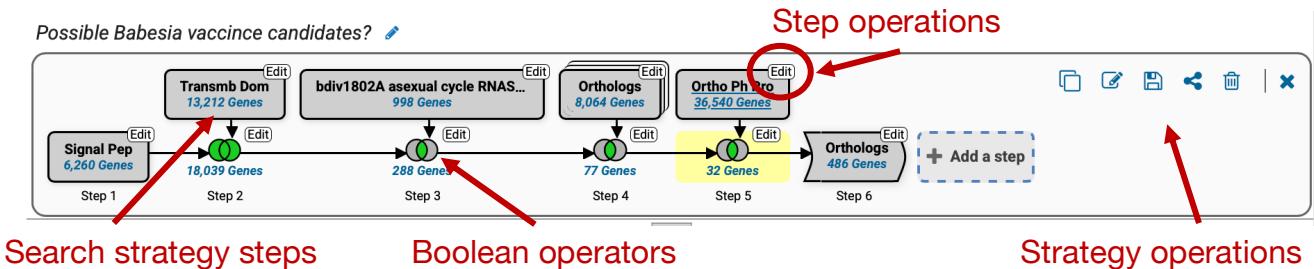
select all | clear all | expand all | collapse all  
Hide zero counts | Reference only

Search organisms... ?

	Gene ID	Transcript ID	Organism	Genomic Location (Gene)	Product Description
	BBBOND_0309020	BBBOND_0309020-t26..t1	Babesia bigemina strain BOND	LK391709:2,250,813..2,252,821(-)	protein kinase domain containing protein
	BBOV_III005470	BBOV_III005470..t1	Babesia bovis T2Bo	CM031754:1,169,200..1,171,522(+)	Protein kinase domain family protein
	BEWA_021430	BEWA_021430-t26..t1	Theileria equi strain WA	CP001669:732,251..734,744(-)	protein kinase domain containing protein
	BOVATA_005630	BOVATA_005630-t37..t1	Babesia ovata strain Miyake	BDSAO1000001:1,376,907..1,378,974(-)	calcium-dependent kinase CDPK5
	BaOViS_005760	BaOViS_005760..t1	Babesia ovis Selcuk	BLVY01000004:101,170..103,158(+)	calcium-dependent kinase CDPK5
	BcabD6B2_01970	BcabD6B2_01970..t1	Babesia caballi USDA-D6B2	BPLF01000001:474,609..476,947(-)	calcium-dependent protein kinase
	BdWA1_001904	BdWA1_001904..t1	Babesia duncani strain WA 2023	CM053816:840,637..842,940(-)	bifunctional EF-hand domain/Protein kinase
	Bdiv_035940c	Bdiv_035940c-t42..t1	Babesia divergens strain 1802A	JAHBMH010000073:1,000,829..1,002,904(-)	protein kinase domain containing protein
	Bmr1_04g07905	Bmr1_04g07905-t32..t1	Babesia microti strain Rl	LN871599:1,132,283..1,134,306(+)	calcium-dependent protein kinase
	CF000624	CF000624..mRNA	Cytauxzoon felis strain Winnie	JAIQCW010000046:48,975..52,404(+)	calmodulin-domain protein kinase, puta
	CF001488	CF001488..mRNA	Cytauxzoon felis strain Winnie	JAIQCW010000094:9,740..12,184(-)	calcium-dependent protein kinase, puta
	MACJ_000788	MACJ_000788..t1	Theileria orientalis Fish Creek	CP056065:2,235,721..2,237,738(-)	unspecified product

## Search Strategies

Search strategies in VEuPathDB resources allow you to combine results from different datatype searches using Boolean operators (e.g. Intersect, union, minus). Search strategies enable you to develop *in silico* experiments based on data from the species of interest or from other species (or strains) by leveraging orthology.



## Getting started with your first search strategy

There are a few things to consider before developing a search strategy:

1. What is your question? Or what are you trying to find out? (overall strategy)
2. Can you break down your question into smaller components? (strategy steps)
3. What data or analyses can be used to answer the various components of your main question?
4. How will you combine the different components of your question? Ie. Which Boolean operators.

### Example question

**Big question:** I would like to identify possible *Babesia* vaccine candidates.

### Let's break it down:

1. What are the characteristics of a *Babesia* protein that might be a good vaccine candidate?
  - a. Secreted protein (proteins with a predicted secretory signal peptide).
  - b. Membrane proteins (proteins with transmembrane domains).
  - c. Expressed at a specific developmental stage (transcriptomics and/or proteomics).
  - d. What about homology with host proteins? (proteins with specific phyletic patterns).

## Running your first search

1. Explore the types of searches available in PiroplasmaDB. What searches can identify genes that are secreted or membrane-bound? Expand the menu on the left-hand side of the home page and look at the available searches. Hint: try filtering the searches with a keyword like “signal peptide,” “secreted,” or “transmembrane.”

The screenshot shows the PiroplasmaDB homepage. On the left, there is a search bar with the placeholder "Site search, e.g. TA14985 or \*reductase or binding protein". Below it is a "Search for..." dropdown menu with the word "signal" typed in. A red box highlights this search term, and a red arrow points to it from the left. To the right of the search bar is a "My Organism Preferences (24 of 24) enabled" button. The main content area features a "Search for..." section with a tree view of categories like Genes, Proteins, and Metabolites. A red box highlights the "Genes" category, and a red arrow points to the "Predicted Signal Peptide" option under it. To the right is an "Overview of Resources and Tools" section with various links and icons for Take a Tour, Subscription, User Survey Results, Funding, Getting Started, Search Strategies, Genome Browser, Transcriptomic Resources, and Downloads. Below this is a "Subscription" section with information about the new subscription model and a "Subscribe Now" button. At the bottom is a "Tutorials and Exercises" section.

2. Start by searching for all genes in PiroplasmaDB with a predicted secretory signal peptide (all organisms).

### Identify Genes based on Predicted Signal Peptide

The screenshot shows the PiroplasmaDB search strategy builder. At the top, there are buttons for "Configure Search", "Learn More", and "View Data Sets Used". Below is a "Reset values to default" button. The main area is titled "Unnamed Search Strategy \*". It shows a step labeled "Step 1" with a box containing "Signal Pep 6,260 Genes" and a "+ Add a step" button. A red circle highlights the "Get Answer" button at the bottom. On the left, there is a "Organism" section with "16 selected, out of 16" and checkboxes for Babesidae and Theileridae. There is also a "Reference only" checkbox. A red arrow points from the "Get Answer" button down to the "Get Answer" button.

3. Expand your strategy by adding a step of all genes with at least one transmembrane domain. Think about how you will combine the results of the transmembrane domain search and your previous signal peptide results.

The screenshot shows the PiroplasmaDB search interface. A red arrow points from the "Add a step to your search strategy" dialog at the top to the "Transform into related records" section below it. Another red arrow points from the "Transform into related records" section to the main search results window. The main window displays a search strategy named "Unnamed Search Strategy \*". Step 1 is "Signal Pep 6,260 Genes". Step 2 is "Transmb Dom 13,212 Genes". Step 3 is "18,039 Genes". The "Transform into related records" section shows a flow from "Transmb Dom 13,212 Genes" to "18,039 Genes". A third red arrow points from the "Transform into related records" section to the "Add a step to your search strategy" dialog at the bottom, which is titled "Add a step to your search strategy" and shows a search term "rnase".

4. Add another step and search for the RNAseq data.

This screenshot shows the continuation of the search strategy setup. The "Add a step to your search strategy" dialog at the top has "2 UNION 3" selected. The "Choose which Genes to combine. From..." section is set to "A new search". The search term "rnase" is entered in the search bar. The main search results window shows the updated strategy: Step 1 is "Signal Pep 6,260 Genes", Step 2 is "Transmb Dom 13,212 Genes", and Step 3 is "rnase". The "Transform into related records" section also includes "rnase" in its flow diagram.

**Notice that there are different data sets and different types of searches for each dataset:**

**FC:** Fold change search allows you to find genes with expression profiles by comparing experimental samples.

**DE:** Differential expression is available for experiments with biological replicates, enabling comparisons with statistical power.

**P:** Percentile search allows you to identify genes expressed at the desired expression level compared to all other genes in the genome.

**SA:** Sense anti-sense searches are available for strand-specific data, enabling exploration of antisense expression compared to sense expression.

For this step, select the percentile search for the *B. divergens* experiment: “Synchronous intraerythrocytic stage time course transcriptome.”

Configure this search to find all genes highly expressed at the early and late merogony stages (0, 10, and 12 hrs).

Add a step to your search strategy
X

### Search for Genes by RNA-Seq Evidence

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

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

Filter Data Sets: 7 rows

Organism	Data Set	Choose a Search
<i>Babesia bigemina</i> strain BOND	ⓘ Calf blood stage vs tick kinete stage transcriptome of <i>B. bigemina</i> (Capelli-Peixoto et al. 2022)	
<i>Babesia bovis</i> T2Bo	ⓘ Transcriptome during development (Ueti et al.)	
<i>Babesia divergens</i> strain 1802A	ⓘ Synchronous intraerythrocytic stage time course transcriptome (Elsworth et al.)	
<i>Babesia duncani</i> strain WA1 2023	ⓘ Babesia duncani strain WA1 2023 transcriptome (Singh et al 2023)	
<i>Babesia</i> sp. Xinjiang Xinjiang	ⓘ Merozoite transcriptome (Guan et al.)	
<i>Theileria annulata</i> strain Ankara	ⓘ Transcriptome from infected B cells (Cheeseman, Jannet, Lourenço and Villares et al.)	
<i>Theileria parva</i> strain Muguga	ⓘ Schizont transcriptome for <i>Theileria parva</i> (JC Silva)	

Differential Expression   Fold Change   **Percentile**

Configure Search   Learn More   View Data Sets Used

**Experiment**

Synchronous intraerythrocytic stage time course transcriptome unstranded

**Samples**

0hr  
 2hr  
 4hr  
 6hr  
 8hr  
 10 hr  
 12 hr  
 asynchronous  
[select all](#) | [clear all](#)

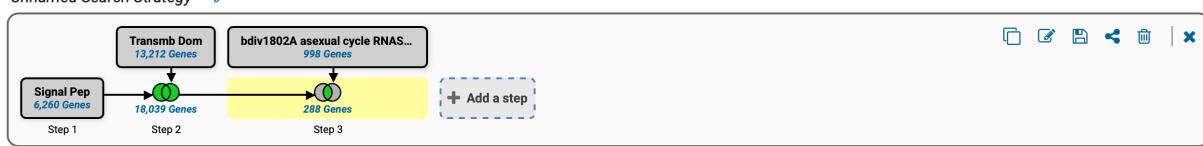
**Minimum expression percentile**

**Maximum expression percentile**

**Matches Any or All Selected Samples?**

**Protein Coding Only:**

Unnamed Search Strategy \*



5. How many of your genes do not have orthologs in mammals? To find out, add a step, then run the “Orthology Phylogenetic Profile” search. Configure this search to find all genes in PiroplasmaDB that do not have orthologs in mammals.

**Find genes in these organisms**

16 selected, out of 16  
 select all |  clear all |  expand all |  collapse all  
 Reference only

Filter list below...  
 Babesidae  
 Theileriidae

**Select orthology profile**

Click on to determine which organisms to include or exclude in the orthology profile.  
( = no constraints | = must be in group | = must not be in group | = mixture of constraints)

mam

All Organisms  
 Eukaryota (EUKA)  
 Metazoa (META)  
 Chordata (CHOR)  
 Mammalia (MAMM)  
 Bos taurus breed Hereford (btau)  
 Canis lupus familiaris isolate SID07034 (clup)  
 Cavia porcellus 2N (cpor)  
 Equus caballus (Horse) (ecab)  
 Gorilla gorilla gorilla (Western lowland gorilla) (ggor)  
 Homo sapiens REF (hsap)  
 Loxodonta africana (African elephant) (lafr)  
 Monodelphis domestica (Gray short-tailed opossum) (mdom)  
 Macaca fascicularis REF (mfas)  
 Myotis lucifugus (Little brown bat) (mluc)  
 Macaca mulatta isolate AG07107 (mmua)  
 Macaca mulatta isolate 17573 (mmu)  
 Mus musculus C57BL/6J (mmus)  
 Myotis myotis mMyoMyo1 (mmyo)  
 Ornithorhynchus anatinus (Duckbill platypus) (oana)  
 Physeter macrocephalus (Sperm whale) (Physeter catodon) (phma)  
 Pan troglodytes (Chimpanzee) (ptr)  
 Rattus norvegicus BN/NhsdMcwi (rnor)

**Run Step**

**My Search Strategies**

Opened (1) All (135) Public (4) Help

Possible Babesia vaccine candidates?

Transmb Dom 13,212 Genes   
Step 1  
Signal Pop 8,260 Genes   
Step 2  
bdv1802A asexual cycle RNAs... 998 Genes   
Step 3  
Ortho Ph Pro 36,540 Genes   
Step 4  
+ Add a step

186 Genes (148 ortholog groups)

Analyze Results

Gene Results | Genome View | Gene Ontology Enrichment | **Analyze Results**

Organism Filter  
 Babesidae  
 Theileriidae  
Show only the Genes in my basket.

Rows per page: 500

Gene ID Transcript ID Geomeric Location (Gene) Product Description Interpro Description  
Bdv\_000160c Bdv\_000160c-42,1 JAHBMH0100000031..64% hypothetical protein, conserved N/A  
Bdv\_000180c Bdv\_000180c-42,1 JAHBMH0100000032,264..3035() hypothetical protein, conserved N/A  
Bdv\_000200c Bdv\_000200c-42,1 JAHBMH0100000035,017..5,760() secreted antigen 1 N/A  
Bdv\_0002110c Bdv\_0002110c-42,1 JAHBMH010000003423,054..423,908() secreted antigen 1 N/A

Gene Results | Genome View | Gene Ontology Enrichment | New Analysis

Analyze your Gene results with a tool below.

Gene Ontology Enrichment   
Metabolic Pathway Enrichment  
Word Enrichment  
kinase phosphatase exported membrane

Explore these results – do these make sense? Are any functions enriched in these results? You can find this out by running a GO enrichment analysis:

- Click on the Analyze Results tab.
- Click on the GO enrichment option.
- Select a GO category to enrich for (e.g., Biological process, cellular component, or molecular function).

The screenshot shows the 'Gene Ontology Enrichment' analysis page. At the top, there are tabs for 'Gene Results', 'Genome View', 'Gene Ontology Enrichment', 'Gene Ontology Enrichment\*', and 'Analyze Results'. The 'Analyze Results' tab is selected. Below the tabs, the title 'Gene Ontology Enrichment' is displayed with a subtitle 'Find Gene Ontology terms that are enriched in your gene result. [Read More](#)'. A 'Parameters' section contains dropdown menus for 'Organism' (set to 'Babesia divergens strain 1802A'), 'Ontology' (set to 'Biological Process'), and 'Evidence' (set to 'Computed'). There are also checkboxes for 'Curated' and 'select all | clear all'. Under 'Limit to GO Slim terms', there are 'No' and 'Yes' options, with 'No' selected. A 'P-Value cutoff' input field is set to '0.05' with a range from '(0 - 1)'. A 'Submit' button is at the bottom of the parameters section. Below this, the 'Analysis Results' section displays a table with 22 rows of data. The columns are: GO ID, GO Term, Genes in the build with this term, Genes in your result with this term, Percent of build genes in your result, Fold enrichment, Odds ratio,  $\text{log}_2 \text{P-value}$ , Benjamini, and Bonferroni. The first few rows of data are as follows:

GO ID	GO Term	Genes in the build with this term	Genes in your result with this term	Percent of build genes in your result	Fold enrichment	Odds ratio	$\text{log}_2 \text{P-value}$	Benjamini	Bonferroni
GO.0022857	transmembrane transporter activity	70	7	10.0	6.29	8.66	7.39e-5	4.13e-3	6.13e-3
GO.0046873	metal ion transmembrane transporter activity	7	3	42.9	26.94	51.44	1.22e-4	4.13e-3	1.01e-2
GO.0005215	transporter activity	78	7	9.0	5.64	7.65	1.49e-4	4.13e-3	1.24e-2
GO.0022890	inorganic cation transmembrane transporter activity	34	4	11.8	7.40	9.36	1.73e-3	2.83e-2	1.44e-1
GO.0008324	cation transmembrane transporter activity	34	4	11.8	7.40	9.36	1.73e-3	2.83e-2	1.44e-1

Buttons for 'Open in ReVigo', 'Show Word Cloud', and 'Download' are located at the top right of the results table.

The strategy developed in this exercise may be accessed using this link:

<https://piroplasmadb.org/piro/app/workspace/strategies/import/675977aaf00d34a0>

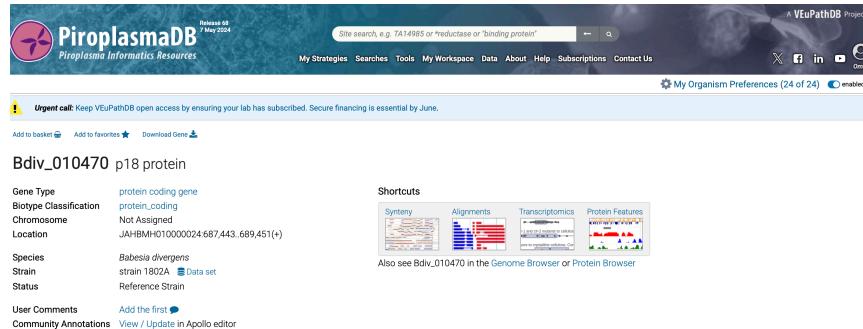
A variation of the above strategy that leverages proteomics data from *B. microti* may be accessed using this link:

<https://piroplasmadb.org/piro/app/workspace/strategies/import/9278e3760f15e57d>

## Gene Pages

Gene pages provide an encyclopedic view of all the information available in the database on a gene-by-gene basis.

1. Visit the gene page for Bdiv\_010470:  
[https://piroplasmadb.org/piro/app/record/gene/Bdiv\\_010470](https://piroplasmadb.org/piro/app/record/gene/Bdiv_010470)
2. What is this gene called?



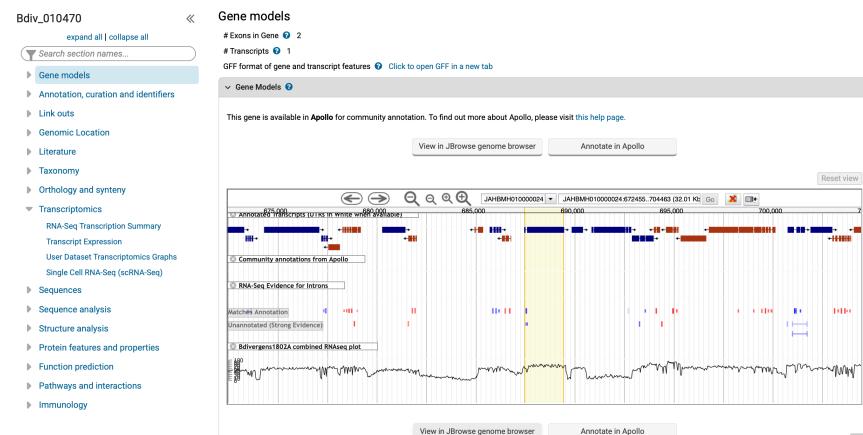
Bdiv\_010470 p18 protein

Gene Type: protein coding gene  
Biotype Classification: protein\_coding  
Chromosome: Not Assigned  
Location: JAHBMH010000024:687-443, 689,451(+)  
Species: Babesia divergens  
Strain: strain 1802A (data set)  
Status: Reference Strain  
User Comments: Add the first...  
Community Annotations: View / Update in Apollo editor

Shortcuts: Synteny, Alignments, Transcriptomics, Protein Features

Also see Bdiv\_010470 in the Genome Browser or Protein Browser

3. How many exons does this gene have? To find out, explore the gene model section.



Bdiv\_010470

expand all | collapse all

Search section names...

Gene models

# Exons in Gene 1  
# Transcripts 1  
GFF format of gene and transcript features Click to open GFF in a new tab

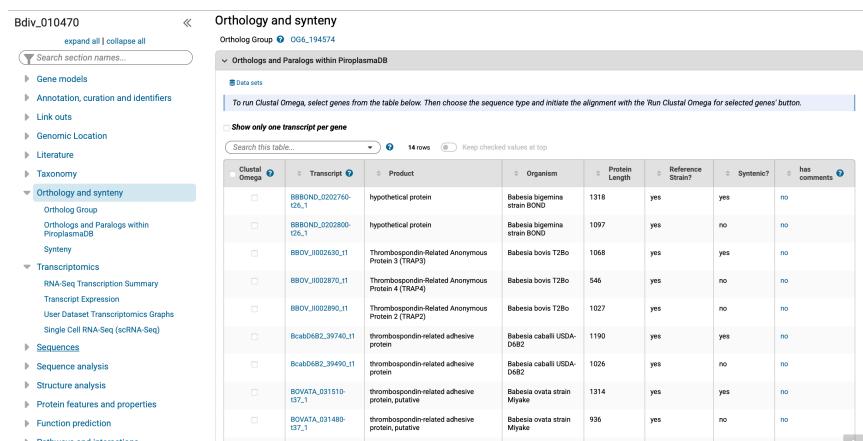
Gene Models

This gene is available in Apollo for community annotation. To find out more about Apollo, please visit this help page.

View in JBrowse genome browser Annotate in Apollo

Reset view

4. Does this gene have orthologs across organisms in PiroplasmaDB? What is it called in other organisms? To find out, explore the orthology section of the gene page.



Bdiv\_010470

expand all | collapse all

Search section names...

Gene models

Annotation, curation and identifiers

Link outs

Genomic Location

Literature

Taxonomy

Orthology and synteny

Transcriptomics

RNA-Seq Transcription Summary

Transcript Expression

User Dataset Transcriptomics Graphs

Single Cell RNA-Seq (scRNA-Seq)

Sequences

Sequence analysis

Structure analysis

Protein features and properties

Function prediction

Pathways and interactions

Immunology

Orthology Group OOG\_194574

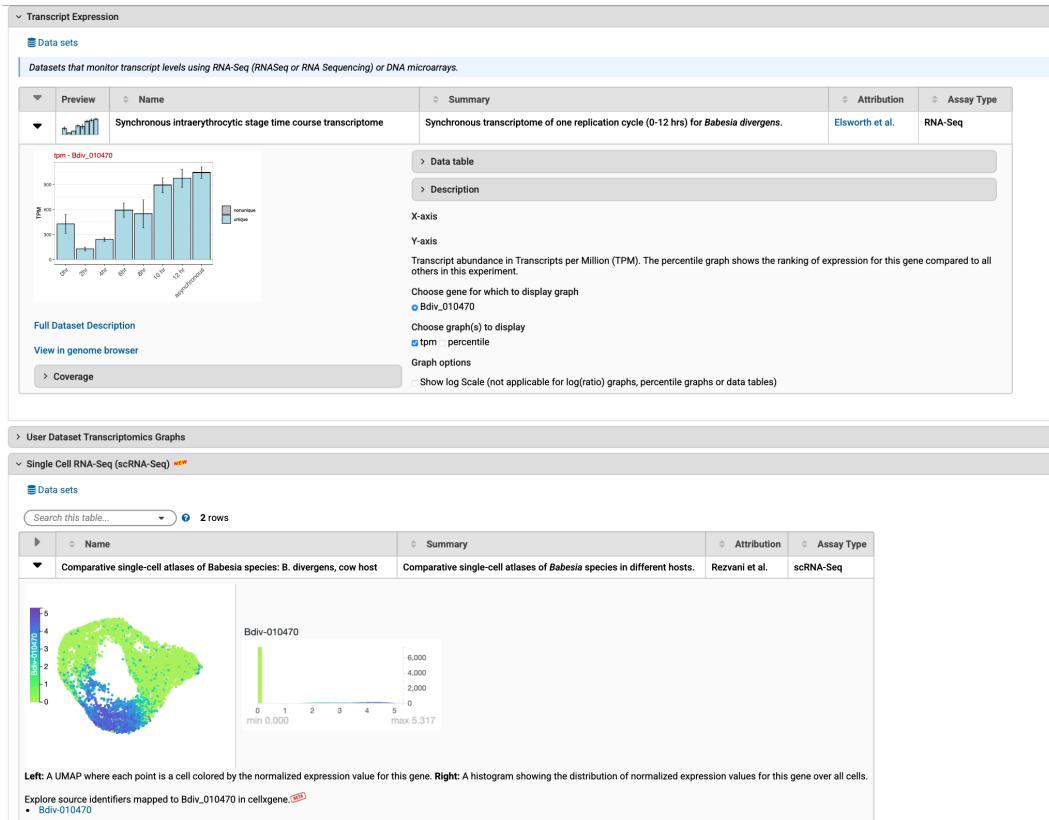
Orthologs and Paralogs within PiroplasmaDB

Show only one transcript per gene

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Clustal Omega	Transcript	Product	Organism	Protein Length	Reference Strain?	Syntomic?	has comments
BBBOND_00202760_1		hypothetical protein	Babesia bovinis strain BOND	1318	yes	yes	no
BBBOND_00202800_1		hypothetical protein	Babesia bovinis strain BOND	1097	yes	no	no
BBDV_JI020260_1		Thrombospondin-related anonymous Protein 3 (TRAP3)	Babesia bovis T2Bo	1068	yes	yes	no
BBDV_JI020287_1		Thrombospondin-related anonymous Protein 4 (TRAP4)	Babesia bovis T2Bo	546	yes	no	no
BBDV_JI020289_1		Thrombospondin-related anonymous Protein 2 (TRAP2)	Babesia bovis T2Bo	1027	yes	no	no
BcabD0682_39740_1		thrombospondin-related adhesive protein	Babesia caballi USDA-D982	1190	yes	yes	no
BcabD0682_39490_1		thrombospondin-related adhesive protein	Babesia caballi USDA-D982	1026	yes	no	no
BOVATA_031480_537_1		thrombospondin-related adhesive protein, putative	Babesia ovata strain Miyake	1314	yes	yes	no
BOVATA_031480_537_1		thrombospondin-related adhesive protein, putative	Babesia ovata strain Miyake	936	yes	no	no
BarbVis_016779_1		thrombospondin-related adhesive	Rhodnius suzukii	941	yes	yes	no

5. Explore the transcriptomics section of the gene page. Notice there are two types of transcriptomic data sets available: bulk and single-cell RNAseq. How do these data compare to each other?



6. Explore the protein features and properties section of the gene page. Does this gene have any InterPro domains?

