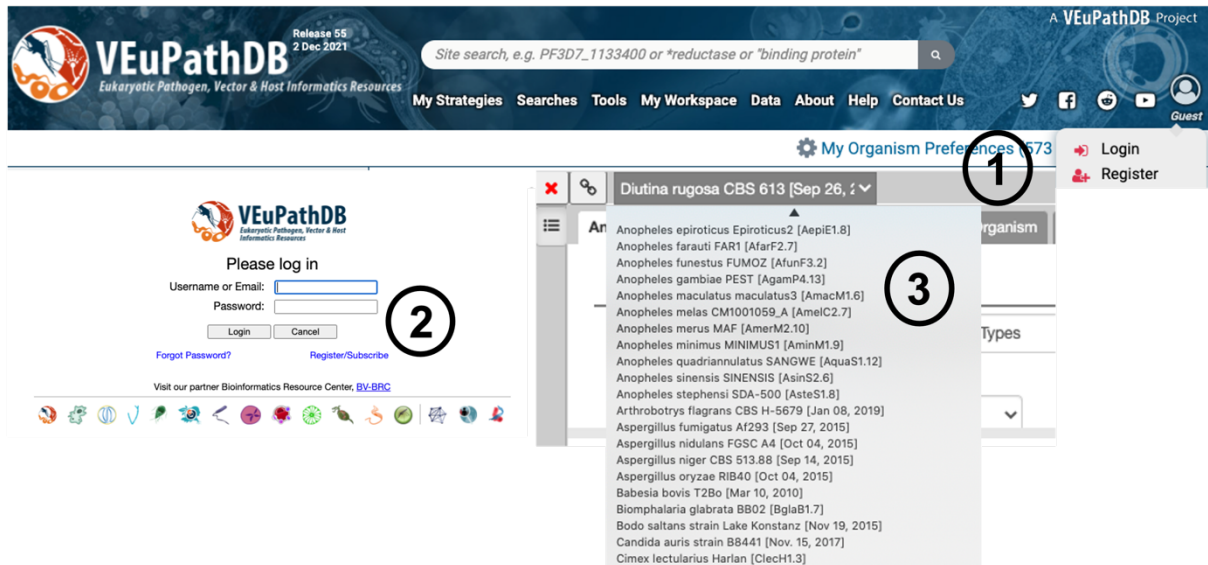


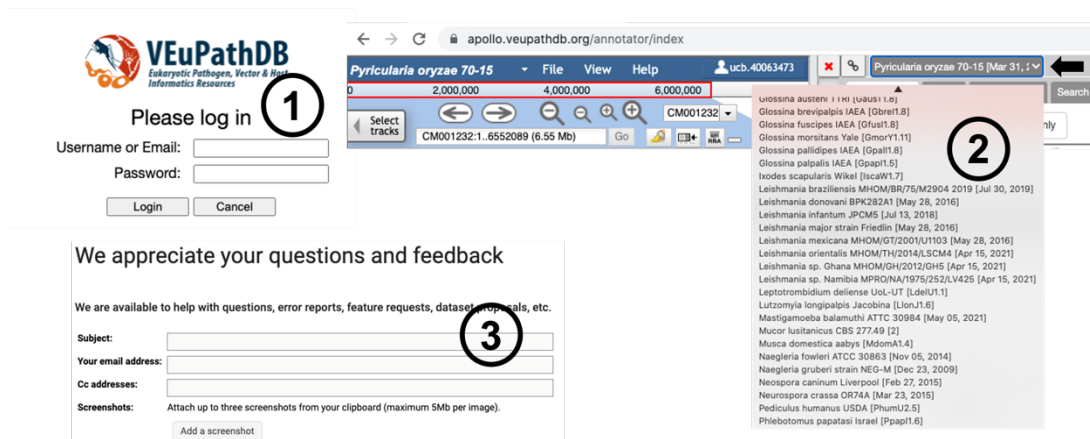
Do I need to register to use the VEuPathDB Apollo instance?

1. To use Apollo you need a VEuPathDB account. If you don't have an account yet you can register on any of the VEuPathDB sites.
2. You can also register on the Apollo website: <https://apollo.veupathdb.org>. Once you've registered log in with your Username and Password.
3. Once you've logged in, choose your genome of interest from the genome drop-down menu and start annotating!



How can I request a genome to be added in Apollo?

1. Before requesting a genome check the list of genomes that are currently available in Apollo. Open Apollo with the following link: <https://apollo.veupathdb.org>. Please note to open it, you need to log into VEuPathDB.
2. Click on the genome drop-down menu and scroll down to see if your genome of interest is present in the VEuPathDB Apollo instance.
3. If you cannot find it, please get in touch with us: <https://veupathdb.org/veupathdb/app/contact-us>
We will recheck if it is possible to add your genome of interest and get back to you as soon as possible.



How do I update functional annotation in Apollo?

- Log into VEuPathDB
- From the gene record page select “View and update community annotations in Apollo”
- With a right click on the gene in the Annotated Transcript track open the drop-down menu and select “Create new annotation > gene”
- Right click on the gene in the User-created Annotations, select “Open Annotation”
- The annotation panel is on the right-hand side. You can now add functional annotation, i.e. Symbol.
- Select the tab Gene Product to add a product description with metadata. There are additional tabs to add Gene Ontology terms (the tab GO) and the tab DbXref to add publications.
- Once you’ve added the functional annotation select from the Status drop-down menu “Finished”.
- The new product is visible the following day on the gene record page in the section “Apollo product description”.

Step 1: ToxoDB Gene Record

Gene: TGME49_202220 hypothetical protein

Type: protein coding gene
Chromosome: VIIa
Location: TGME49_chrVIIa:3,509,010..3,514,137(-)
Species: *Toxoplasma gondii*
Strain: ME49
Status: Reference Strain

Step 2: Apollo Interface

Right-click on the gene in the Annotated Transcript track to open the context menu.

Step 3: Create new annotation

Select "Create new annotation > gene" from the context menu.

Step 4: Open Annotation

Right-click on the gene in the User-created Annotations track to open the context menu and select "Open Annotation (alt-click)".

Step 5: Gene Product Tab

Click on the "Gene Product" tab in the annotation panel.

Step 6: Add new Gene Product

Click on "Add new Gene Product to TGME49_202220-t26_1".

Step 7: Gene Product Details

Fill in the details for the new gene product:

- Product: IMC suture-associated protein IS/
- Symbol: ISAP1
- Status: Finished

Step 8: Apollo Product Description

The updated annotation is visible in the "Apollo product description" section of the gene record page.

How do I update structural annotation in Apollo?

1. Log into VEuPathDB
2. From the gene record page select “View and update community annotations in Apollo”
3. With a right click on the gene in the Annotated Transcript track open the drop-down menu and select “Create new annotation > gene”
4. Right click on the gene in the User-created Annotations, select “Open Annotation”
5. The annotation panel is on the right-hand side. Select the tab Tracks.
6. Select evidence tracks from Draggable Annotation
7. Drag and drop the evidence into the User-created Annotations area
8. With a right-click on the gene in the User-created Annotations area open the drop-down menu. There are options to merge exons, split and duplicate genes. Choose the modification as appropriate.
9. Once you’ve finished modifying the gene structure, choose the Annotations tab and select the status finished.

The screenshots illustrate the process of updating structural annotation in Apollo:

- Step 1:** ToxoDB gene page for TGME49_223950 (hypothetical protein).
- Step 2:** Clicking "View and update community annotations in Apollo" on the ToxoDB page.
- Step 3:** Right-clicking on a gene in the "Annotated Transcript" track and selecting "Create new annotation > gene".
- Step 4:** Right-clicking on a gene in the "User-created Annotations" track and selecting "Open Annotation".
- Step 5:** Selecting the "Tracks" tab in the annotation panel.
- Step 6:** Selecting evidence tracks from the "Draggable Annotation" section.
- Step 7:** Dragging evidence tracks into the "User-created Annotations" area.
- Step 8:** Right-clicking on a gene in the "User-created Annotations" area and selecting "Merge" from the context menu.
- Step 9:** Selecting "Finished" from the status dropdown in the annotation details panel.

How do I know if my new gene structure is correct in Apollo?

1. Check if your gene has a Start and Stop site. You can do this by zooming in. Alternatively, right click on the gene to open the menu and select Get sequence. With this option you can recheck if there is a correct Start. You only need to check for correct start and stop sites if your gene does not have annotated UTRs.
2. Check splice sites. In most Eukaryotes the majority of splice sites at the exon/intron boundaries appear as 5'-...exon]GT/AG[exon...-3'. An exclamation mark in Apollo shows non-canonical splice sites.
3. Check if you can annotate UTRs, for example using RNA-Seq data. A useful track that could help with this is the "Combined RNA-Seq plot". This track combines all RNA-Seq plots available for your genome of interest. You can find this track by searching for "combine".
4. Check sequence similarity by running blast. Right click on the gene in the User-created Annotations area, open the drop down menu and select Get sequence. Copy the sequence to the clipboard and run blast (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>).

Figure 1 shows a screenshot of the Genomic Workbench interface. The interface displays four numbered annotations:

- Annotation 1:** Shows the reference sequence and user-created annotations for the region around TGME49_chrX. The sequence is displayed in a multi-colored format, and the user-created annotations track shows a red box for TGME49_223920-t26_1-00001.
- Annotation 2:** Shows the user-created annotations track, highlighting the red box for TGME49_223920-t26_1-00001.
- Annotation 3:** Shows the annotations track with a 'combine' button, indicating that the annotations are being combined.
- Annotation 4:** Shows the sequence track, displaying the sequence of the selected region: >24a0283c-cf6e-4adc-b66f-4de6928f4e09 (Sequence:exon) 245 residues [TGME49_chrX:3440383-344216]. The sequence is shown in a multi-colored format, and the user-created annotations track shows a red box for TGME49_223920-t26_1-00001.

Which evidence code should be used when adding GO terms or gene products in Apollo?

1. IDA is used if the GO term/product has been experimentally verified
2. ISS: GO term/product is inferred from similarity. For GO annotations add GO_REF:0000024 as reference. GO references describe the methods and procedures used in creating such annotations.
3. ISM: GO term/product is inferred from InterPro/Pfam domain. Add GO_REF:000011 in the reference field for GO annotations.
4. IMP: GO term/product is inferred from mutant phenotype

Additional information on evidence codes can be found here:

<http://geneontology.org/docs/guide-go-evidence-codes>

A list of GO references can be found here:

<http://current.geneontology.org/metadata/gorefs/index.html>

The figure displays four screenshots of the Apollo GO Annotation Guidance interface, each illustrating a different evidence code and its associated reference field.

- Screenshot 1:** Shows the 'Aspect' dropdown set to 'CC' (cellular component) and the 'Go Term' field containing 'GO:0020011'. The 'Relationship between Gene Product and GO Term' is 'part of'. The 'Evidence' dropdown is set to 'IDA (ECO:0000314): direct assay evidence used in manual assertion'. The 'Reference' field is set to 'PMID' with the value '17449654'.
- Screenshot 2:** Shows the 'Aspect' dropdown set to 'BP' (biological process) and the 'Go Term' field containing 'GO:0016571'. The 'Relationship between Gene Product and GO Term' is 'involved in'. The 'Evidence' dropdown is set to 'ISS (ECO:0000250): sequence similarity evidence used in manual assertion'. The 'Reference' field is set to 'GO_REF' with the value '0000024'.
- Screenshot 3:** Shows the 'Aspect' dropdown set to 'MF' (molecular function) and the 'Go Term' field containing 'GO:0003676'. The 'Relationship between Gene Product and GO Term' is 'enables'. The 'Evidence' dropdown is set to 'ISM (ECO:0000255): inferred from sequence model'. The 'Reference' field is set to 'GO_REF' with the value '0000011'.
- Screenshot 4:** Shows the 'Aspect' dropdown set to 'BP' (biological process) and the 'Go Term' field containing 'GO:0042493'. The 'Relationship between Gene Product and GO Term' is 'involved in'. The 'Evidence' dropdown is set to 'IMP (ECO:0000315): mutant phenotype evidence used in manual assertion'. The 'Reference' field is set to 'PMID' with the value '24352242'.

How do I add a new gene model in Apollo based on a blast match?

1. Log into VEuPathDB
2. Select on the right-hand side the tab "Search", choose "Blat protein" or "Blat nucleotide" from the drop-down menu and paste in the sequence. Select the tick box "All genome sequences" if you want to search all chromosomes/contigs of your genome of interest. Click on Search.
3. You can now select the search results. They are shown in yellow.
4. If you want to create a gene model based on the search result, click on Action and select Create annotation.

Panel 2: Search Interface

Annotations Tracks Ref Sequence **Search** Organism Users Groups Admin

Blat protein ☒ All genome sequences Search Clear

MEEGKKEKSLGGQNDQGVQSRSLRVSAVCVSNLASERRKSSGGNSLRVSLPQTRSASLRFLSLVFCCLF
AAVASVCGKALDFHSDAPLSRLSLVLVDWLSPLPGSSSPSCFASSEEDGGAQSRDPDRGEEQSRDPER
EEERPSEGSPRTEKTDACRGQRGEASPSVARLPSSLLSHAIWNTNCLGSCHAETRASLAGDRNAST
LLPSSPLSSSSASEVFSRRSNLSVSRPPLCEGVLLPCSLLLGLLRVAPLLMALSNALLHCQFRA

Panel 3: Search Results

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ID	Start	End	Strand	Score	Significance	Identity	Action
TGME49_2,613,817	2,614,875	1	685	0	99.43	--	
TGME49_482,522	482,608	-1	26	42	62.07	--	
TGME49_1,812,902	1,812,964	1	22	620	66.67	--	

Panel 4: Create Annotation

Annotations Tracks Ref Sequence **Search** Organism Users Groups Admin

Blat protein ☒ All genome sequences Search Clear

MEEGKKEKSLGGQNDQGVQSRSLRVSAVCVSNLASERRKSSGGNSLRVSLPQTRSASLRFLSLVFCCLF
AAVASVCGKALDFHSDAPLSRLSLVLVDWLSPLPGSSSPSCFASSEEDGGAQSRDPDRGEEQSRDPER
EEERPSEGSPRTEKTDACRGQRGEASPSVARLPSSLLSHAIWNTNCLGSCHAETRASLAGDRNAST
LLPSSPLSSSSASEVFSRRSNLSVSRPPLCEGVLLPCSLLLGLLRVAPLLMALSNALLHCQFRA

1-50 of 190

ID	Start	End	Strand	Score	Significance	Identity	Action
TGME49_2,613,817	2,614,875	1	685	0	99.43	--	

Save sequence
Create annotation

What happens to my annotations in Apollo?

1. Once you are happy with your annotation select the status “Finished” in the Annotation panel.
2. Within 24 hours the product descriptions that have been added to the tab gene product in Apollo will be shown on the gene record page in the Annotation, curation and identifiers section.
3. The gene model will appear on the live site on the gene record page in the community annotations track in JBrowse.
4. The annotations will remain in Apollo indefinitely or until they are incorporated into the main gene record.

The screenshot displays the Apollo genome annotation interface. On the left, the 'Details' panel for gene **TGME49_202620-126_1** shows its status as **Finished** (marked with a circled 1). The 'Annotation, curation and identifiers' panel on the right shows the 'Apollo Product Description' as **Dense granule protein GRA64** (marked with a circled 2). Below these panels, the 'View in JBrowse genome browser' button is visible. The main JBrowse track at the bottom shows the gene model for **TGME49_202620** (marked with a circled 3), including transcripts and protein models like **TGME49_202620-126_1** and **TGME49_202620** (ATP-dependent metalloproteinase HFB subfamily protein).