

Functional annotation in Apollo

There are two options to add function annotation in VEuPathDB:

- 1) Adding a user comment on the gene record page
- 2) Using the community annotation tool Apollo

Functional annotation can involve:

- Adding or changing the description of a gene or product
- Assigning or changing a gene name/symbol
- Adding Gene Ontology (GO) terms
- Adding a publication
- Adding an EC number

In this manual we are showing you step by step how to add a gene name, product description and GO term to a gene in Apollo.

1) Accessing Apollo

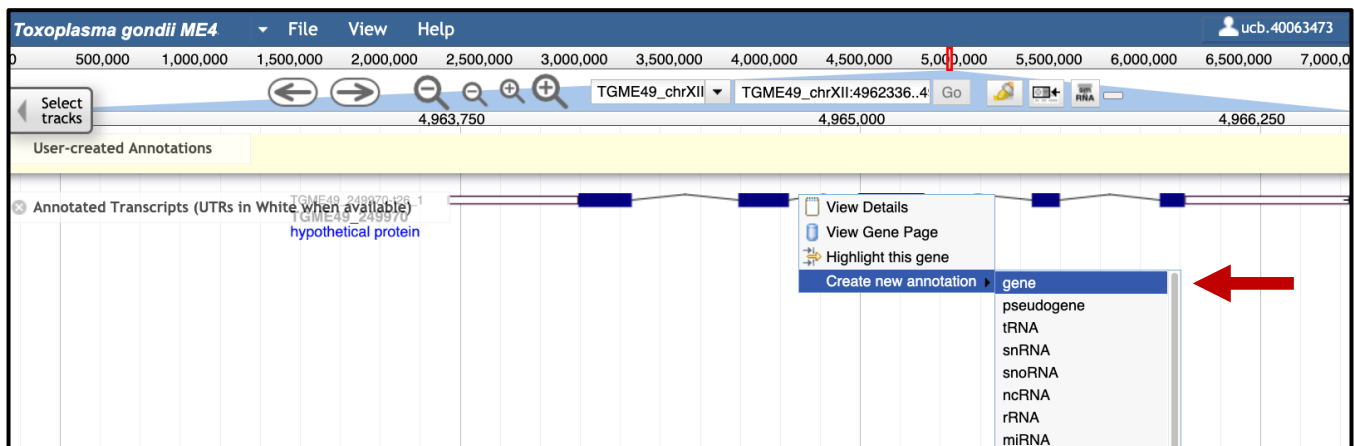
To access Apollo go to the gene record page of your gene of interest and click on the link **View and update community annotations in Apollo** (1). You can also access Apollo from the gene models section by clicking on the button **Annotate in Apollo** (2). Alternatively, go to the **Tools** menu and choose Apollo from the drop-down list (3).

The screenshot displays the ToxoDB website interface. At the top, the ToxoDB logo and navigation links are visible. The main content area shows the gene record for TGME49_249970, a hypothetical protein. A red circle highlights the link "View and update community annotations in Apollo" (1). Another red circle highlights the "Annotate in Apollo" button in the "Gene models" section (2). A third red circle highlights the "Tools" menu in the top navigation bar (3).

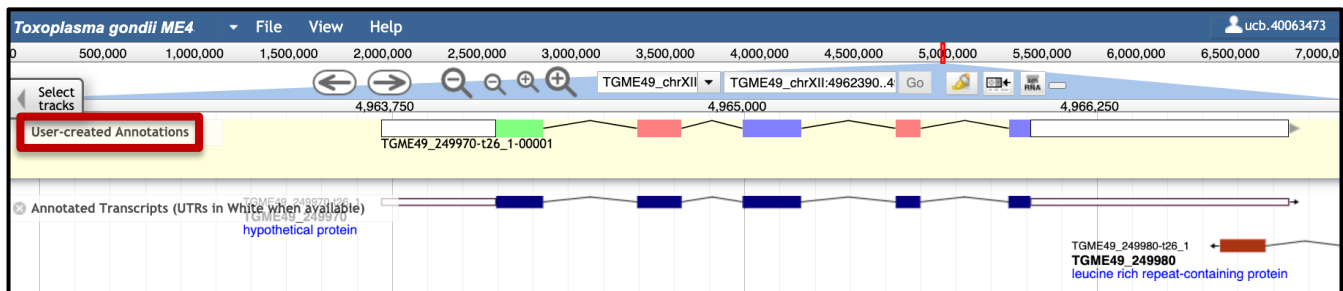
To use Apollo you need to be logged into VEuPathDB. If you have not done so yet log now into Apollo with your VEuPathDB user ID and password.

2) Dragging and dropping the annotation

Right click on the gene in the Annotated Transcripts track, select from the drop-down menu **Create new annotation > gene**.

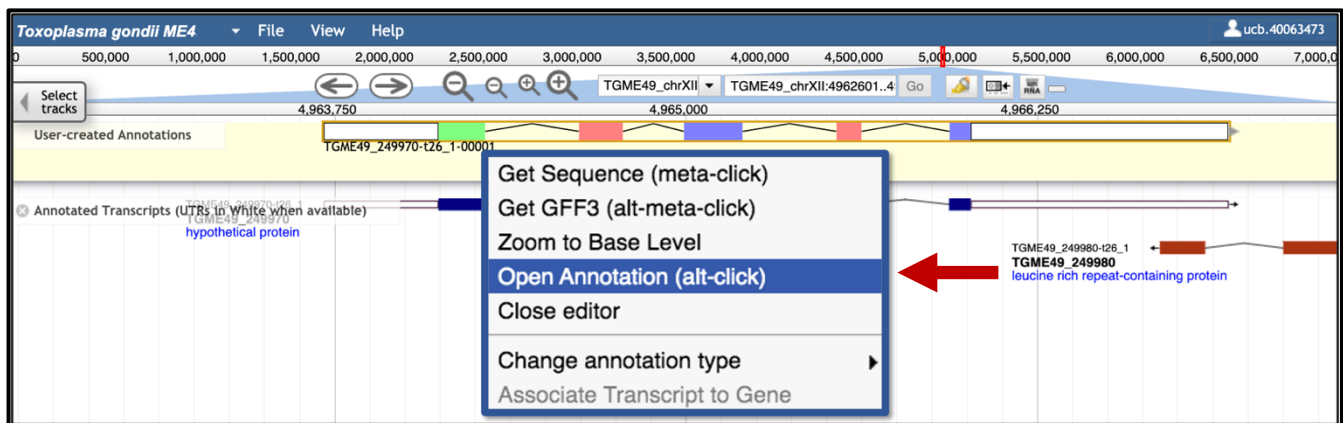


You can now see your gene of interest in the User-created Annotations track.



3) Opening of the Annotation editor window

Select the gene in the User-created Annotations track and with a right-click open the drop-down menu and choose **Open Annotation**. Alternatively, you can use the short-cut **alt-click**.



The annotation editor window is now shown on the right-hand side.

Annotation editor →

You can either select the gene or the mRNA.

Please note functional annotation should be added to the gene. For genes with alternative transcripts add the information to the mRNA.

4) Adding Functional annotation

In this example we are showing you how to improve the functional annotation of TGME49_249970. This gene is currently annotated as hypothetical protein. It has been experimentally characterised in the following publication:

<https://pubmed.ncbi.nlm.nih.gov/26962945/>

Gene name/symbol: APH

Gene product: Acylated pleckstrin-homology domain-containing protein

GO term: microneme

PMID: 26962945

Adding a gene name/symbol

Once the annotations panel (1) is open click on the details tab (2) and add the gene name in the field Symbol (3). In our example the new gene name/symbol is APH.

Search: *Toxoplasma gondii* ME49 [Mar 22, ▾] ucb.40063473

Annotations 1 Ref Sequence Organism Users Groups Admin

Show All Show Visible Only

0cecc08e-205b-405f-8199- ID All Types GO GP Prov

Reference Sequence All Users All Statuses

Rows 25 ▾ 1-1 of 1

| Name | Seq | Type | Length | Updated |
|---------------------------|---------------|------|--------|--------------|
| TGME49_249970-t26_1 | TGME49_chrXII | gene | 3,220 | May 27, 2021 |
| TGME49_249970-t26_1-00001 | | mRNA | 3,220 | May 27, 2021 |

gene: TGME49_249970-t26_1 [Link to annotation](#) [Close\(x\)](#)

Details 2 Gene Product Provenance DbXref Comment Attributes

Go ID Sync name with transcript ☐ Obsolete Delete

Type gene Status No status selecte ▾

Name TGME49_249970-t26_1

Symbol APH 3

Aliases ('|' separated)

Description

Location 4963712 - 4966931 strand(+) Partial: ☐ 3' ☐ 5'

Ref Sequence TGME49_chrXII

Owner ucb.40063473

Created May 27, 2021 03:13 PM

Updated May 27, 2021 03:13 PM

Adding a product description

To add a product description choose the tab Gene Product (1) and click on **New** at the bottom of the editor window (2).

Gene Product editor window for TGME49_249970-t26_1. The 'Gene Product' tab is selected. The 'New' button is highlighted at the bottom left.

Fill in the fields product, evidence and PMID. Click on Save. More information about evidence codes can be found here: <http://geneontology.org/docs/guide-go-evidence-codes>

Add new Gene Product to TGME49_249970-t26_1

GO Annotation Guidance

Product: Acylated pleckstrin-homology dor

Evidence: ECO:0000314

With: Prefix : ID + Add

Reference: PMID : 26962945

Note: + Add

Save Cancel

Adding GO terms

Choose the tab GO in the editor window, fill in the required fields and click on Save.

Add new GO Annotation to TGME49_249970-t26_1

GO Annotation Guidance

Aspect
CC
cellular component

Go Term
GO:0020009
microneme (GO:0020009)

Relationship between Gene Product and GO Term
part of

☐ Not

Evidence
ECO:0000314
*IDA (ECO:0000314):
direct assay evidence
used in manual assertion*
Evidence Code Info

☐ All ECO Evidence

With
Prefix : ID + Add

Reference
PMID : 26962945

Note
+ Add

Save Cancel

Adding a PubMed ID

Choose the Tab DbXref in the annotation editor window, add the PMID as shown in the screenshot. Click on the + sign.

gene: TGME49_249970-t26_1 [Link to annotation](#) [Close\(x\)](#)

Details GO Gene Product Provenance **DbXref** Comment Attributes

| Prefix | Accession | PMID | Accession | |
|--------|-----------|----------|-----------|----------|
| | | 26962945 | | + |

A small window will come up showing the title of the Pubmed Article. Click OK.

Add article Phosphatidic Acid-Mediated Signaling Regulates Microneme Secretion in Toxoplasma.

Cancel **OK**

You can also add additional database identifiers (DbXref), i.e. EC numbers.

| | | | | | | | | | | | | | | | |
|----------|--|-----------|--|------|--|--------------|--|------------|--|--------|--|---------|--|------------|--|
| Details | | Coding | | GO | | Gene Product | | Provenance | | DbXref | | Comment | | Attributes | |
| ▲ Prefix | | Accession | | EC | | 2.7.1.1 | | | | | | | | | |
| | | | | PMID | | | | | | | | | | | |

5) Finalising the functional annotation

Go to the **Attributes** tab in the gene section, choose from the “Select canned tag” drop-down menu **annotation**.

| | | | | | | | | | | | | | |
|---------------------------|--|--------------------|--|---------------------|--|------------|--|--------------|--|------------|--|------------|--|
| gene: TGME49_249970-t26_1 | | Link to annotation | | Close(x) | | | | | | | | | |
| Details | | GO | | Gene Product | | Provenance | | DbXref | | Comment | | Attributes | |
| ▲ Prefix | | Accession | | Tag | | Value | | | | | | | |
| | | | | ✓ Select canned tag | | structural | | user_comment | | annotation | | | |

From the “Select canned value” drop-down menu choose **added_product**. Repeat this and choose **added_symbol**, **added_go** and **added_pmid**. Finally click on the + sign.

| | | | | | | | | | | | | | |
|----------|--|-----------|--|--------------|--|-----------------------|--|-----------------|--|-----------------|--|------------|--|
| Details | | GO | | Gene Product | | Provenance | | DbXref | | Comment | | Attributes | |
| ▲ Prefix | | Accession | | annotat | | Value | | | | | | | |
| | | | | annotation | | ✓ Select canned value | | added_comment | | split | | merge | |
| | | | | | | | | retain_previous | | added_product | | added_go | |
| | | | | | | | | added_symbol | | added_alias | | added_pmid | |
| | | | | | | | | removed_product | | added_ec_number | | delete | |
| | | | | | | | | isoform | | new | | modify | |
| | | | | | | | | added_dbxref | | | | | |

gene: TGME49_249970-t26_1 [Link to annotation](#) [Close\(x\)](#)

| Details | GO | Gene Product | Provenance | DbXref | Comment | Attributes |
|---|----|--------------|------------|--------|---------|---|
| <div> <div>▲ Prefix</div> <div>Accession</div> </div> | | | | | | <div>Tag</div> <div>Value</div> <div>+</div> |
| <div> <div>annotation</div> <div>added_symbol</div> </div> | | | | | | <div>Select can ▼</div> <div>Select can ▼</div> |
| <div> <div>annotation</div> <div>added_go</div> </div> | | | | | | |
| <div> <div>annotation</div> <div>added_product</div> </div> | | | | | | |
| <div> <div>annotation</div> <div>added_pmid</div> </div> | | | | | | |

In the last step, go back to the Details tab and add to the gene and mRNA the status **Finished**.

gene: TGME49_249970-t26_1 [Link to annotation](#) [Close\(x\)](#)

| Details | GO | Gene Product | Provenance | DbXref | Comment | Attributes |
|---|---------------------|--------------|------------|--|---------|------------|
| <div> <div>Go</div> <div>ID</div> <div>Sync name with transcript</div> <div>Obsolete</div> <div>Delete</div> </div> | | | | | | |
| Type | gene | | Status | <div> <div>✓ No status selected</div> <div>Not Finished</div> <div>Finished</div> <div>Requires Curator</div> </div> | | |
| Name | TGME49_249970-t26_1 | | | | | |
| Symbol | APH | | | | | |

Done! For additional questions, please get in touch with the VEuPathDB help desk.