# **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

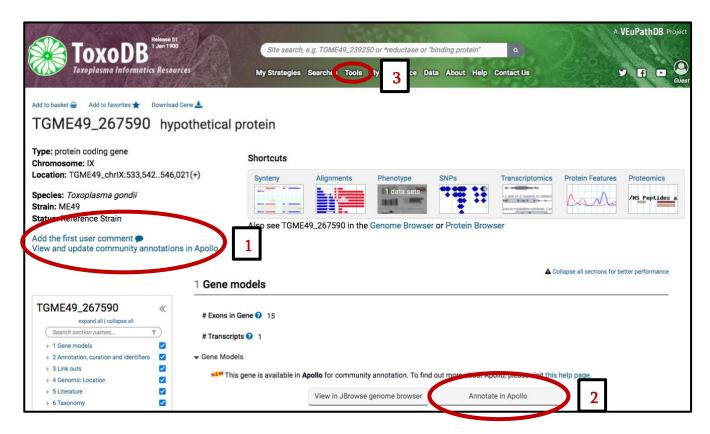
#### **Functional annotation can involve:**

- 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

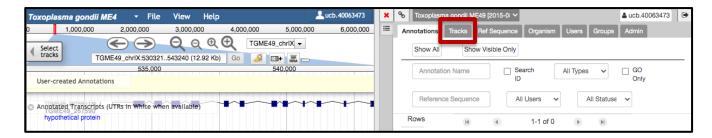
To access Apollo go to the gene record page of your gene of interest and click on the link **View and update community annotations in Apollo (1)**. You can also access Apollo from the gene models section by clicking on the button **Annotate in Apollo (2)**. Alternatively, go to the **Tools** menu and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



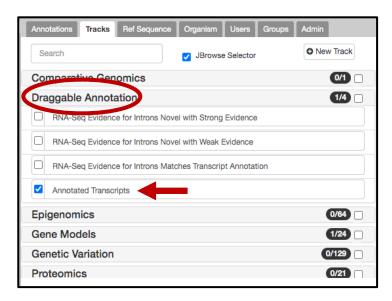
To use Apollo you need to be logged into VEuPathDB. If you have not done so yet log now into Apollo with your VEuPathDB user ID and password.

# 2) Dragging and dropping the annotation

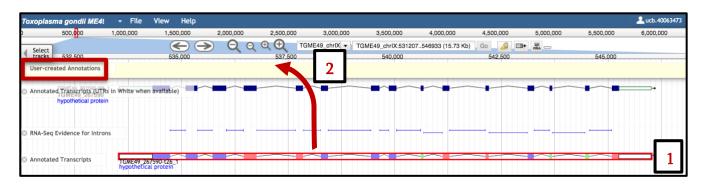
Select on the menu on the right-hand side the tab Tracks.



Click on the menu item **Draggable Annotation** and select **Annotated Transcripts**.

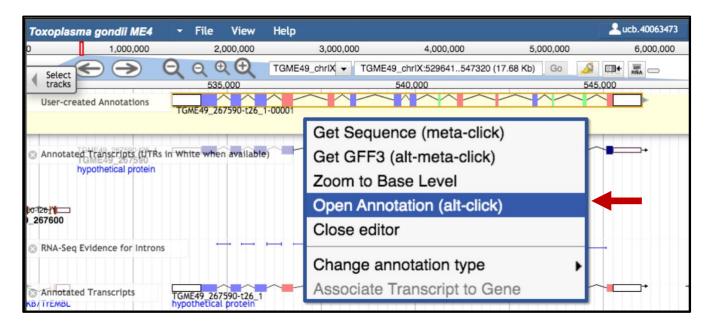


You can now see your gene of interest in the Annotated Transcript track. Select the gene model by clicking on one of the introns or by double clicking on the gene model (1). The gene model will show up with red boundaries. Drag and drop the gene into the User-created Annotations area (2).

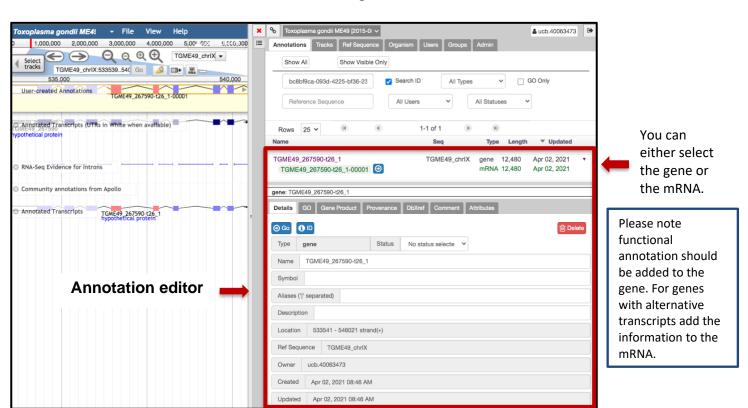


### 3) Opening of the Annotation editor window

Select the gene in the User-created Annotation 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.



# 4) Adding Functional annotation

In this example we are showing you how to improve the functional annotation of TGME49\_267590. This gene is currently annotated as hypothetical protein. It has been experimentally characterised in the following publication:

https://pubmed.ncbi.nlm.nih.gov/27594426

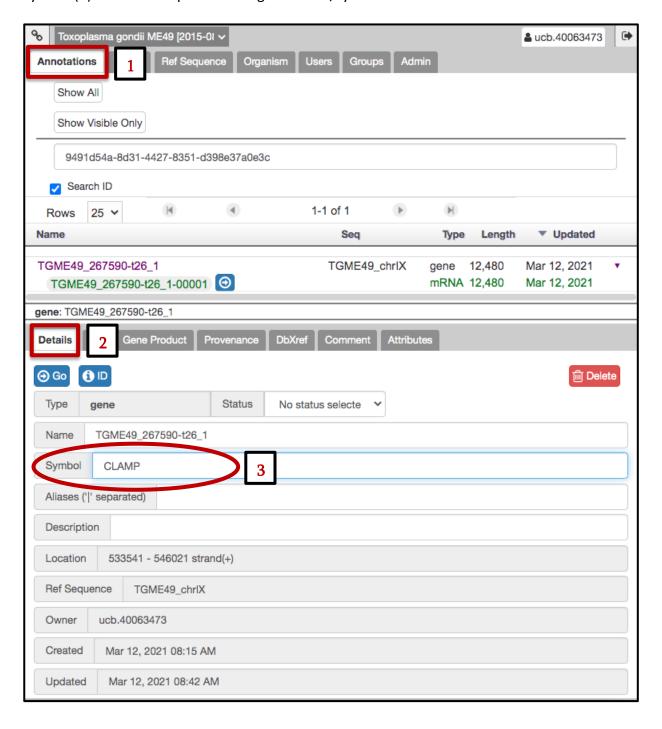
Gene name/symbol: CLAMP

Gene product: Claudin-like apicomplexan microneme protein

GO term: microneme PMID: 27594426

# 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 CLAMP.



# 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).

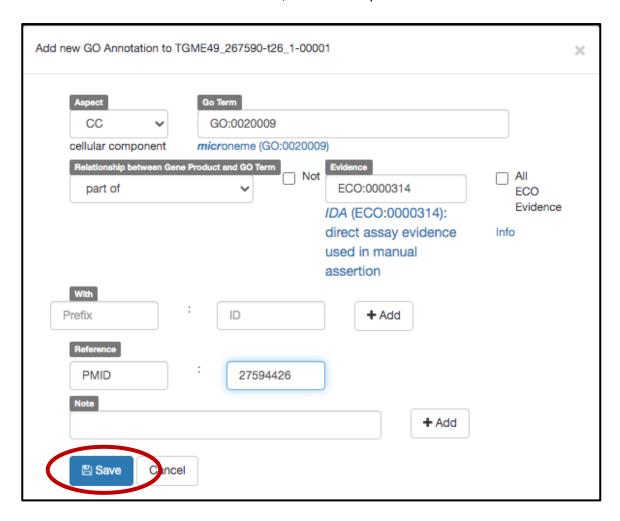


Fill in the fields product, evidence and PMID. Click on Save. More information about evidence codes can be found here: <a href="http://geneontology.org/docs/guide-go-evidence-codes">http://geneontology.org/docs/guide-go-evidence-codes</a>



# **Adding GO terms**

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

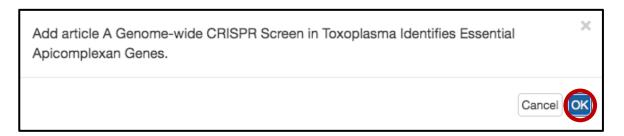


# Adding a PubMed ID

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



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

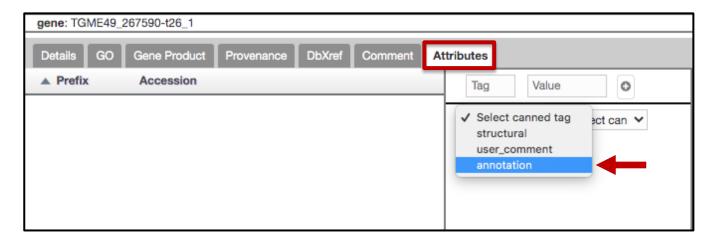


You can also add additional database identifiers (DbXref), i.e. EC numbers.

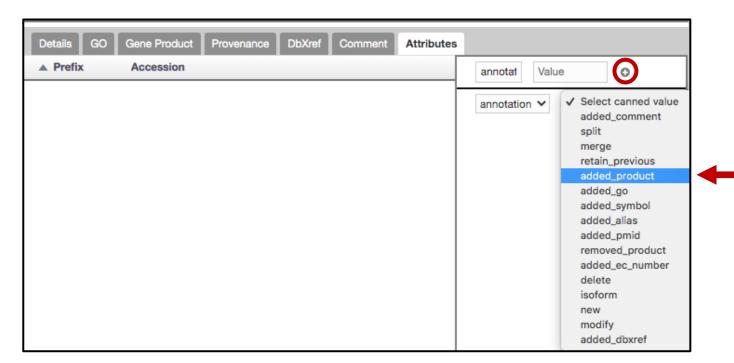


# 5) Finalising the functional annotation

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

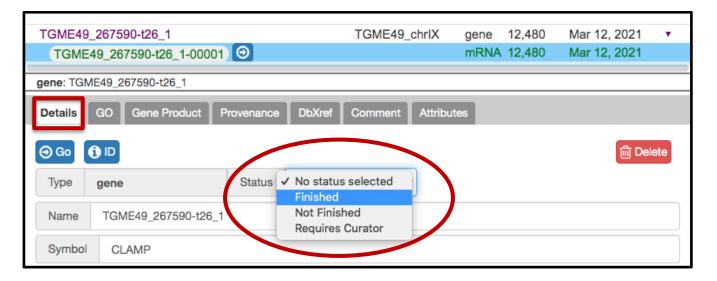


From the "Select canned value" drop-down menu choose **added\_product**. Repeat this and choose **added\_symbol**, **added\_go** and **added\_pmid**. Finally click on the **+** sign.





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



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