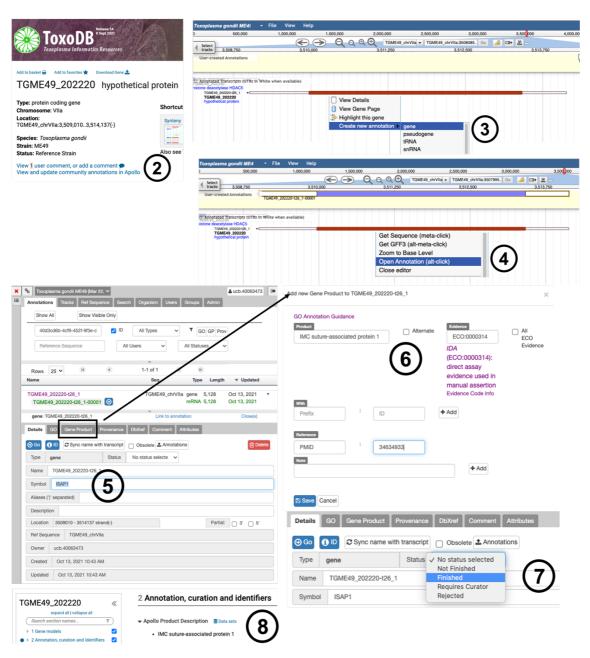
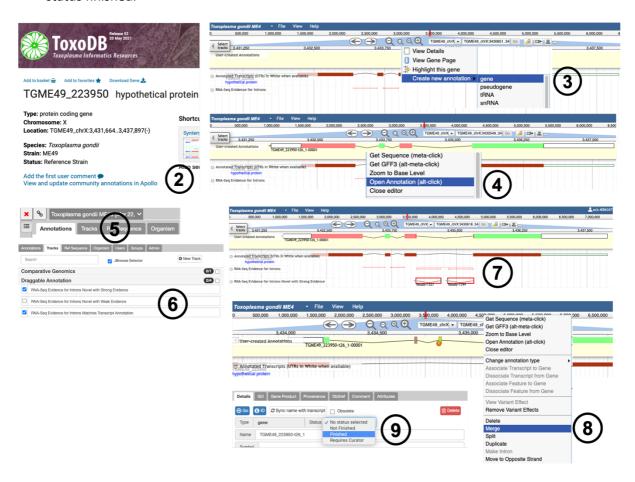
How do I update functional annotation in Apollo?

- 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. You can now add functional annotation, i.e. Symbol.
- 6. 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.
- 7. Once you've added the functional annotation select from the Status drop-down menu "Finished".
- 8. If you used the tab gene product to add a product description with metadata, the new product is visible the following day on the gene record page in the section "Apollo product description".



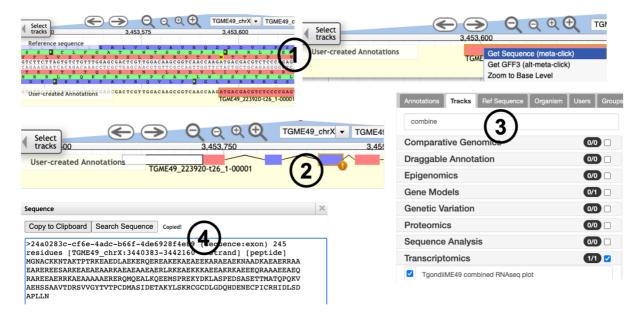
How do I update structural annotation in Apollo?

- 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.



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).



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

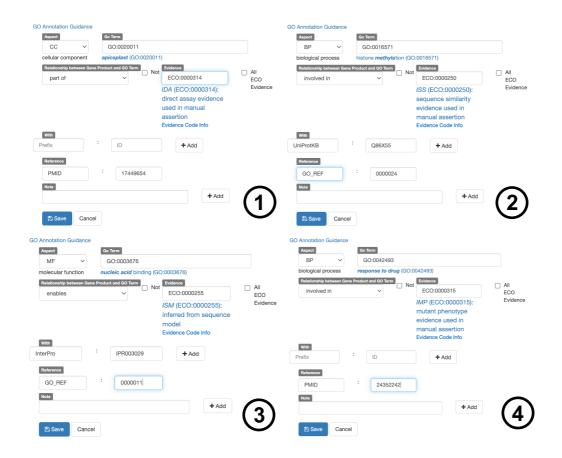
- 1. IDA is used if the GO term/product has been experimentally verified
- ISS: GO term/product is inferred from similarity. For GO annotations add GO_REF:0000024 as
 reference. GO references describe the methods and procedures used in creating such
 annotations.
- 3. ISM: GO term/product is inferred 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



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 nucleotide" or "Blat protein" 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.

