

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. The new product is visible the following day on the gene record page in the section “Apollo product description”.

ToxoDB
Toxoplasma Informatics Resources
Release 54
8 Sept 2021

Add to basket Add to favorites Download 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

View 1 user comment, or add a comment
View and update community annotations in Apollo

Annotations Tracks Ref Sequence Search Organism Users Groups Admin

Show All Show Visible Only

40d3cd6b-4cf9-452f-93e-c ID All Types GO: GP: Prov Reference Sequence All Users All Status

Rows 25 1-1 of 1

Name	Type	Length	Updated
TGME49_202220-t26_1	gene	5,128	Oct 13, 2021
TGME49_202220-t26_1-00001	mRNA	5,128	Oct 13, 2021

gene: TGME49_202220-t26_1 Link to annotation Close()

Details GO Gene Product Provenance DbXref Comment Attributes

Go ID Sync name with transcript Obsolete Annotations

Type gene Status No status select

Name TGME49_202220-t26_1

Symbol ISAP1

Aliases (1 separated)

Description

Location 3509010 - 3514137 strand(-) Partial: 3' 5'

Ref Sequence TGME49_chrVIIa

Owner ucb.40063473

Created Oct 13, 2021 10:43 AM

Updated Oct 13, 2021 10:43 AM

2 Annotation, curation and identifiers

Search section names

- 1 Gene models
- 2 Annotation, curation and identifiers
- 3 Link outs
- 4 Genomic Location
- 5 Literature

Apollo Product Description Data sets

The product description as annotated by a user in Apollo. To view or edit the annotations, press the 'Annotate in Apollo' button above on this page.

Apollo Product Description	Apollo Transcript ID
IMC suture-associated protein ISAP1	TGME49_202220-t26_1

Toxoplasma gondii ME49 File View Help

Select tracks 3,508,750 3,510,000 3,511,250 3,512,500 3,513,750 4,000,000

User-created Annotations

Annotated Transcripts (UTRs in White when available)

sgtone deacetylase HDAC5
Toxoplasma gondii ME49
TGME49_202220
hypothetical protein

View Details
View Gene Page
Highlight this gene
Create new annotation: gene
pseudogene
iRNA
snRNA

Toxoplasma gondii ME49 File View Help

Select tracks 3,508,750 3,510,000 3,511,250 3,512,500 3,513,750 4,000,000

User-created Annotations

TGME49_202220-t26_1-00001

Annotated Transcripts (UTRs in White when available)

sgtone deacetylase HDAC5
Toxoplasma gondii ME49
TGME49_202220
hypothetical protein

Get Sequence (meta-click)
Get GFF3 (alt-meta-click)
Zoom to Base Level
Open Annotation (alt-click)
Close editor

Toxoplasma gondii ME49 ucb.40063473 Add new Gene Product to TGME49_202220-t26_1

GO Annotation Guidance

Product IMC suture-associated protein ISAP1 Alternate Evidence ECO:0000314 IDA (ECO:0000314): direct assay evidence used in manual assertion Evidence Code Info

With Prefix ID + Add

Reference PMID 34634933 + Add

Save Cancel

Details GO Gene Product Provenance DbXref Comment Attributes

Go ID Sync name with transcript Obsolete Annotations

Type gene Status No status selected Not Finished Finished Requires Curator Rejected

TGME49_202220 expand all collapse all

Search section names

- 1 Gene models
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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 following steps:

- Screenshot 1:** Shows the ToxoDB gene page for *TGME49_223950* (hypothetical protein). It includes the gene's location (Chromosome X: 3,431,664-3,437,897) and species (*Toxoplasma gondii*).
- Screenshot 2:** Shows the Apollo interface with the "User-created Annotations" track. A right-click on the gene opens a context menu with options like "View Details", "View Gene Page", "Highlight this gene", and "Create new annotation > gene".
- Screenshot 3:** Shows the Apollo interface with the "User-created Annotations" track. A right-click on the gene opens a context menu with options like "Get Sequence (meta-click)", "Get GFF3 (alt-meta-click)", "Zoom to Base Level", "Open Annotation (alt-click)", and "Close editor".
- Screenshot 4:** Shows the Apollo interface with the "User-created Annotations" track. A right-click on the gene opens a context menu with options like "Get Sequence (meta-click)", "Get GFF3 (alt-meta-click)", "Zoom to Base Level", "Open Annotation (alt-click)", and "Close editor".
- Screenshot 5:** Shows the Apollo interface with the "User-created Annotations" track. A right-click on the gene opens a context menu with options like "Get Sequence (meta-click)", "Get GFF3 (alt-meta-click)", "Zoom to Base Level", "Open Annotation (alt-click)", and "Close editor".
- Screenshot 6:** Shows the Apollo interface with the "User-created Annotations" track. A right-click on the gene opens a context menu with options like "Get Sequence (meta-click)", "Get GFF3 (alt-meta-click)", "Zoom to Base Level", "Open Annotation (alt-click)", and "Close editor".
- Screenshot 7:** Shows the Apollo interface with the "User-created Annotations" track. A right-click on the gene opens a context menu with options like "Get Sequence (meta-click)", "Get GFF3 (alt-meta-click)", "Zoom to Base Level", "Open Annotation (alt-click)", and "Close editor".
- Screenshot 8:** Shows the Apollo interface with the "User-created Annotations" track. A right-click on the gene opens a context menu with options like "Get Sequence (meta-click)", "Get GFF3 (alt-meta-click)", "Zoom to Base Level", "Open Annotation (alt-click)", and "Close editor".
- Screenshot 9:** Shows the Apollo interface with the "User-created Annotations" track. A right-click on the gene opens a context menu with options like "Get Sequence (meta-click)", "Get GFF3 (alt-meta-click)", "Zoom to Base Level", "Open Annotation (alt-click)", and "Close editor".

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>).

The screenshot displays the Apollo genome browser interface with several key components:

- Top Panel:** Shows the reference sequence and user-created annotations for the gene *TGME49*. A right-click context menu is open over a gene model, showing options: "Get Sequence (meta-click)", "Get GFF3 (alt-meta-click)", and "Zoom to Base Level".
- Gene Model:** A track showing the gene structure with exons as boxes and introns as lines. A zoomed-in view of a splice site is shown below, with a circled '2' highlighting the splice site. The sequence is *TGME49_223920-t26_1-00001*.
- Sequence Window:** A window titled "Sequence" is open, showing the nucleotide sequence of the gene. A circled '4' highlights the "Copy to Clipboard" button. The sequence is:


```
>24a0283c-cf6e-4adc-b66f-4de6928f4e89 (sequence:exon) 245
residues [TGME49_chrX:3440383-3442160 (-strand)] [peptide]
MGNACKKNTAKTPTRKEADLAERQEREAEKAEAEKAEAEKNAADKAEAEERRAA
EAREERESARKEAEAEAEAEAEAEAEERLRKEAEKKKAEAEKRAEEQRAAEAEQ
RAREEAERRKAEAEAEAEAEAEAEAEERQEQEALQEQEEMSPREKYDKLASPEDSASETTMATQPKV
AEHSSAAVTDRTSVVGYTVTPCDMASIDETAKYLSKRCGCDLGDQHDENECPICRHIDLS
APLLN
```
- Tracks Panel:** A panel on the right side of the interface shows various tracks. A circled '3' highlights the "combine" track, which is selected. The tracks listed are:

Annotations	Tracks	Ref Sequence	Organism	Users	Groups
combine					
Comparative Genomics	0/0				
Draggable Annotation	0/0				
Epigenomics	0/0				
Gene Models	0/1				
Genetic Variation	0/0				
Proteomics	0/0				
Sequence Analysis	0/0				
Transcriptomics	1/1				

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' (apicoplast). The 'Relationship between Gene Product and GO Term' is set to 'part of'. The 'Evidence' dropdown is set to 'IDA (ECO:0000314): direct assay evidence used in manual assertion'. The 'Reference' field is empty.
- Screenshot 2:** Shows the 'Aspect' dropdown set to 'BP' (biological process) and the 'Go Term' field containing 'GO:0016571' (histone methylation). The 'Relationship between Gene Product and GO Term' is set to '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:0000024'.
- Screenshot 3:** Shows the 'Aspect' dropdown set to 'MF' (molecular function) and the 'Go Term' field containing 'GO:0003676' (nucleic acid binding). The 'Relationship between Gene Product and GO Term' is set to 'enables'. The 'Evidence' dropdown is set to 'ISM (ECO:0000255): inferred from sequence model'. The 'Reference' field is set to 'GO_REF:000011'.
- Screenshot 4:** Shows the 'Aspect' dropdown set to 'BP' (biological process) and the 'Go Term' field containing 'GO:0042493' (response to drug). The 'Relationship between Gene Product and GO Term' is set to 'involved in'. The 'Evidence' dropdown is set to 'IMP (ECO:0000315): mutant phenotype evidence used in manual assertion'. The 'Reference' field is set to 'PMD: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

MEEGKKEKSLSGQSDQGVQSRSLRSVACVSNLASERRKSSGGNSLRVSLPQTRSASLRFLSVFCCGLF
AAVASVCGKLALDFHSQAPLSRLSLVLVDWLSPLPGSSSPCFASEEDGGAQSRDPDRGEEQSRDPER
EERPSSEGSPTREKTGDACRGQRGEASPSVARLPSSLLSLHAIWNTNCFLGSCHAETRASLAGDRNAST
LLPSSPLSSSASEVFSRRNSLSVRPPLSCGVLLPCSLLLGLLRVAPLLMALSNALLHCQFRA

Panel 3: Search Results

1-50 of 190

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: Action Menu

Save sequence
Create annotation

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.

