

Australian Apollo Service



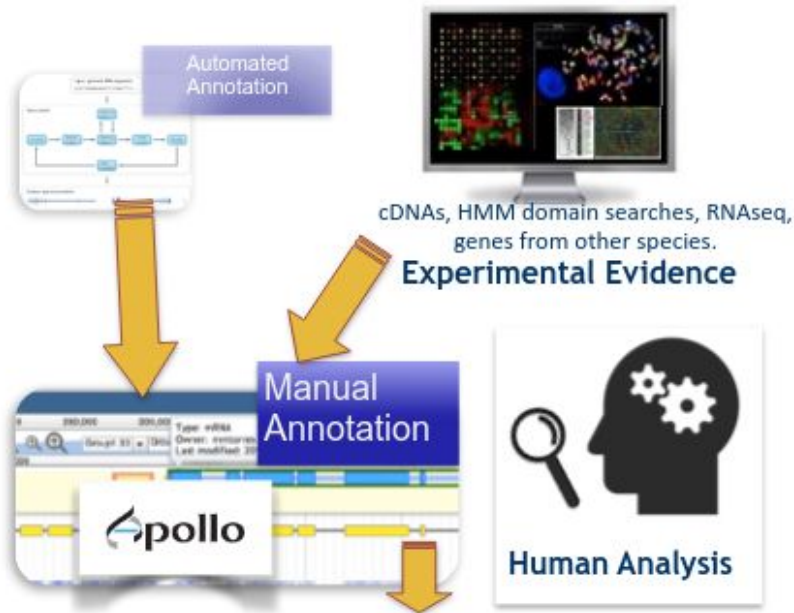
Apollo Portal

Apollo Portal is an Australian genome curation and editing portal

[Sign Up](#)



So what is Apollo?



Lewis S, Searle S, Harris N et al. (2002)
Apollo: a sequence annotation editor. Genome
Biology 3, research0082.1.
<https://doi.org/10.1186/gb-2002-3-12-research0082>

Dunn NA, Unni DR, Diesh C, Munoz-Torres M, Harris
NL, et al. (2019)
Apollo: Democratizing genome annotation. PLOS
Computational Biology 15(2): e1006790.
<https://doi.org/10.1371/journal.pcbi.1006790>

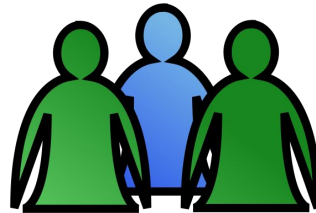
Image:
<https://training.galaxyproject.org/training-material/topics/genome-annotation/tutorials/apollo/slides-plain.html>

High priorities identified in community consultations

I need a genome browser-based system where I can upload and view supporting data alongside the annotations

I need a hosted system that I can use quickly after registering so that I won't waste time in setting it up myself

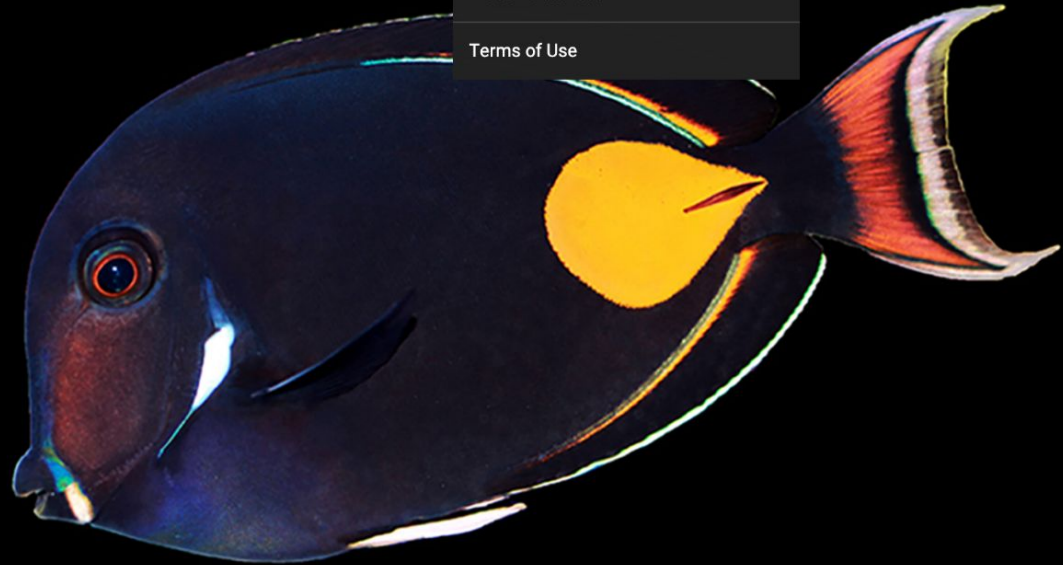
I need a web-based system to manually correct genome annotations that allows me to share and compare with colleagues



[Getting Started](#)[User Documentation](#)[Training, Tutorials & Other Resources](#)[FAQs](#)[Video Resources](#)[Terms of Use](#)

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User Documentation

This document provides guidance and information about:

1. [How Do I Sign Up for an Apollo Instance?](#)
2. [What Data Files Are Required To Create Genome Tracks In Apollo?](#)
3. [How Do I Prepare My Data Prior to Upload?](#)
4. [How Do I Generate a Public-Key?](#)
5. [How Do I Upload Data and Create a Genome Track via the Command Line?](#)
6. [How Do I Upload Data and Create a Genome Track via the Apollo \(browser\) Interface?](#)
7. [How Do I Make My Genome Public?](#)
8. [How Do I Manually Annotate My Genome In Apollo?](#)

FAQs

^ What is the Apollo Service?

The Apollo software package is a web-based tool for visualising genomic contents and manually improving gene predictions against a reference genome collaboratively. The Apollo Service provides Australian-based researchers with customised, localised Apollo instances for their genome projects.

∨ How can I get an Apollo Instance?

∨ Can I trial Apollo before signing up?

∨ I am a non-Australian-based researcher, can I access the Apollo Service?

∨ Can Apollo automatically annotate my genome?

∨ How can I get training to use Apollo?



Sign Up

Eligibility Criteria

Please note that the Principal Investigator must be affiliated with a recognised Australian academic or research institute. All form elements marked with a * must be filled out. If you have any queries about this form or the questions therein, please contact support at apollo-support@genome.edu.au.

I confirm the Principal Investigator belongs to a **recognised Australian institute**. *

Research Group/Lab or Consortium name (NB: the names of all Research Labs/Consortia using this service are listed on [this page](#)) *

Website link to Research Group/Lab or Consortium

Suggested Apollo Host Name *

Genome Annotation

Genome Annotation Process

- **Genome preparation** (repeat identification and masking),
- **Structural annotation** (identifying the location and structure of genes and other genomic features),
- **Functional annotation** (predicting function of the genomic features),
- **Manual correction** (i.e. curation of automatically-produced genomic features), and
- **Visualisation** (typically using a genome browser displaying multiple data tracks).

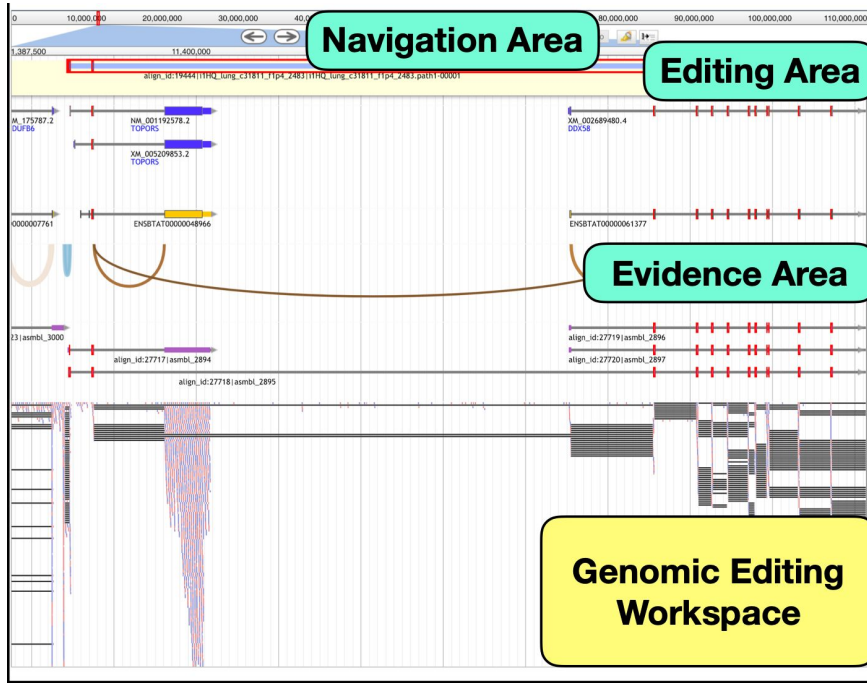
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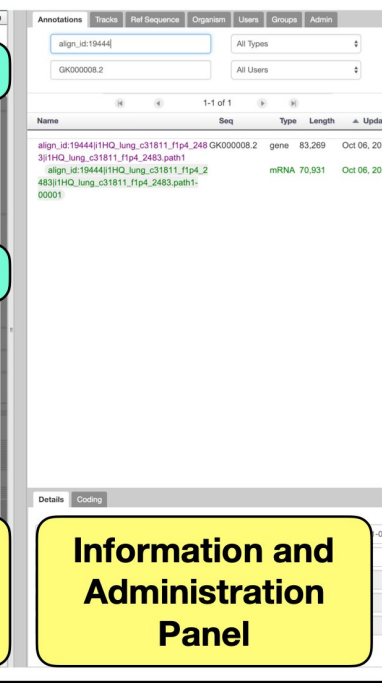
Getting Started in Apollo

The Apollo Software

A



B



The Apollo Software has two main panels: A genome Editing Workspace (A) and a configurable Administration Panel (B).

Ref: <https://doi.org/10.1371/journal.pcbi.1006790>

File Types

Table 1. Required Data Files for Genome Track Creation.

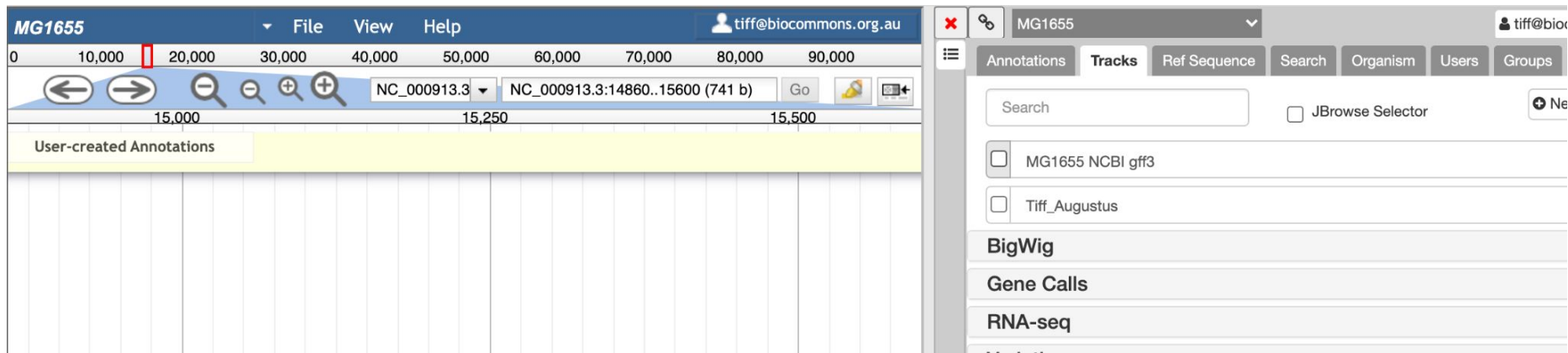
| File Format | Description | Requirement |
|-------------|---|-------------|
| Fasta | Genome Reference File | Mandatory |
| Fai | Genome Reference Index File | Mandatory |
| Gff3 | Genome Annotation File | Mandatory |
| Gff3.gz | Genome Annotation Compressed File | Mandatory |
| 2bit | Genomic Sequence in Binary File | Optional |
| Bam | Alignment File | Optional |
| Bai | Alignment Index File | Optional |
| Vcf | Variant Calling File | Optional |
| Vcf.gz | Variant Calling Index File | Optional |
| bw | A compressed, indexed, binary format of genome-wide signal data | Optional |

E. coli Test Data

- *Escherichia coli*, MG1655, K-12 wild-type strain
- Publicly available data
- Subset of complete genome (100KB)

Logging into the Apollo Training Instance

<https://training.genome.edu.au/apollo/>



The screenshot displays the Apollo genome browser interface. The main window shows a sequence view for the MG1655 genome. The top bar includes a menu (File, View, Help) and a user profile (tiff@biocommons.org.au). The sequence view shows a scale from 0 to 90,000 with a red vertical bar at approximately 15,000. Below the scale is a search bar containing 'NC_000913.3' and a 'Go' button. The main area shows a yellow 'User-created Annotations' track. On the right, a tracks panel is visible with tabs for 'Annotations', 'Tracks', 'Ref Sequence', 'Search', 'Organism', 'Users', and 'Groups'. The 'Tracks' tab is active, showing a search bar and a list of tracks: 'MG1655 NCBI gff3' and 'Tiff_Augustus'. Below the tracks panel, there are sections for 'BigWig', 'Gene Calls', and 'RNA-seq'.

Getting Data Into Apollo

tinyurl.com/2021ApolloData

Getting Data Into Apollo.

File 1: Augustus.gff3

tinyurl.com/2021ApolloData

- Under 'Tracks' tab
- Select '+New Track'
- Select 'GFF3'
- 'Enter Track Name' - Augustus
- 'Choose File' - augustus.gff3
- Select 'Upload'

Getting Data Into Apollo

File 2: Blastp_vs_swissprot.gff3

tinyurl.com/2021ApolloData

- Under 'Tracks' tab
- Select '+New Track'
- Select 'GFF3'
- 'Enter Track Name' - Blastp_vs_swissprot
- Under 'Top Type' - protein_match
- Under 'Category' - 'MyCategory'

Getting Data Into Apollo

File 2: Blastp_vs_swissprot.gff3

tinyurl.com/2021ApolloData

- Under 'Tracks' tab / Select '+New Track' / Select 'GFF3'
- 'Enter Track Name' - Blastp_vs_swissprot
- Under 'Top Type' - protein_match
- Under 'Category' - 'MyCategory'
- Under 'Track Configuration JSON'
- Under "type"
- Replace "JBrowse/View/Track/HTMLFeatures" to -
"WebApollo/View/Track/DraggableNeatHTMLFeatures"


Getting Data Into Apollo

File 2: Blastp_vs_swissprot.gff3

tinyurl.com/2021ApolloData

Add Track

GFF3 ▾

Track Name
Blast_vs_swissprot 

Top Type (remove for single-level features)
protein_match

Category
MyCategory

Track Configuration JSON

```
{ "storeClass": "JBrowse/Store/SeqFeature/GFF3",  
  "urlTemplate": "raw/Blast_vs_swissprot.gff",  
  "label": "Blast_vs_swissprot",  
  "type": "WebApollo/View/Track/DruggableN  
eathTMLFeatures", "style":  
  { "className": "feature",  
    "key": "Blast_vs_swissprot",  
    "topLevelFeatures": "protein_match",  
  }  
}
```

*.gff *.gff3 *.gff.gz *.gff3.gz

No file chosen

Getting Data Into Apollo

File 2: Blastp_vs_swissprot.gff3

tinyurl.com/2021ApolloData

- Under 'Tracks' tab / Select '+New Track' / Select 'GFF3'
- 'Enter Track Name' - Blastp_vs_swissprot / Under 'Top Type' - protein_match / Under 'Category' - 'MyCategory'
- Under 'Track Configuration JSON' / Under "type"
- Replace "JBrowse/View/Track/HTMLFeatures" to -
"WebApollo/View/Track/DraggableNeatHTMLFeatures"
- 'Choose File' - Blastp_vs_swissprot.gff3
- Select 'Upload'

Getting Data Out Of Apollo

The screenshot displays the Apollo genome browser interface. On the left, a sequence viewer shows genomic coordinates from 0 to 414600.1. An export dialog box is open, titled "Export all sequence(s) from MG1655 as GFF3", with options for "GFF3" and "GFF3 with FASTA", and "Export" and "Cancel" buttons. On the right, the "Ref Sequence" panel for MG1655 is visible, showing search and export options. The "Export" section has "GFF3" selected, and "Selected sequences" is set to "All". Below this, a table lists the sequence details:

| Name | Length | Annotations |
|-------------|---------|-------------|
| NC_000913.3 | 100,000 | 1 |

At the bottom left, a terminal window shows the GFF3 output for the sequence:

```
##gff-version 3
##sequence-region NC_000913.3 1 100000
NC_000913.3 . gene 60358 63264 . - owner=ops@qfab.org;ID=310e31cf-404d-4898-a96
NC_000913.3 . mRNA 60358 63264 . - owner=ops@qfab.org;Parent=310e31cf-404d-4898
NC_000913.3 . CDS 60358 63264 . 0 Parent=16d163f2-571f-45cf-8563-9289cca6365e;
NC_000913.3 . exon 60358 63264 . - Parent=16d163f2-571f-45cf-8563-9289cca6365e;
###
##FASTA
>NC_000913.3
AGCTTTTCTGACTGCAACGGGCAATATGTCCTGTGTGGATTAAAAAGAGTGTC
TGATAGCCAGCTTCTGAACTGTTACCTGCCGTGAGTAAATAAAAATTTATTGACTTAGG
TCACATAACTCTTAAACCAATATAGGCATAGCCGACAGACAGATAAAAAATACAGAGTAC
ACAACATCCATGAAACGCATTAGCACCCACCAATACCACCCCATCACCATTACCACAGGT
AACGGTCCGGGCTGACCCGTACAGGAAACACAGAAAAACCCGACCTGACAGTCCGGG
CTTTTTTTCCGCAAGGTAAAGGTAAAGCAACCAATCCGAGTGTGAAGTTGGCGGT
ACATCAAGTGGCAAAATGCAAGAGGTTTTCTGCGTGTTCGCGATATTTCTGGAAAGCAATGCC
AGCCAGGGGACAGGTGGCCACCGTCTCTCTGCCCCCAGCAAAATCACCACACCTGGTG
GCGATGATTGAAAAACCAATTAGCCGGCCAGGATGCTTTACCCAATATCAGCGATGCCSAA
CGATTTTTTCCGCAACTTTTACCGGACTCCGCCGCCAGCCGGGTTCCCGCTGGCC
CAATGAAAAACTTTGTCGATCAGGAATTTGCCCAATAAAAACATGCTCGATGGCATT
AGTTGTTGGGCGAGTCCCGGATAGCATCAACGCTGCGCTGATTTGCCGTGGCGAGAAA
ATGTCGATCGCCATTATGGCCGGCTATTAGAAGCGCGGGTCAACAACGTTACTGTTATC
GATCCGTCGAAAAACTGCTGGCAGTGGGGCATTACCTCGAATCTACCCTCGATATTGCT
GAGTCCACCCCGGATTTGGCGCAAGCCGCAATCCGCGTATCATGATGGTGTGATGGCA
GGTTTACCAGCCGATTAAGAAAAAGCGCAACTGGTGTCTTGGACGCAACGGTCCGAC
```

Annotating together

Details Organisms Users Group Admin

1-25 of 26

| Name | Admin | Write | Export | Read |
|---------------|--------------------------|--------------------------|--------------------------|--------------------------|
| MG1655 | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> | <input type="checkbox"/> |
| MG1655_aperr | <input type="checkbox"/> | <input type="checkbox"/> | | |
| MG1655_awilli | <input type="checkbox"/> | <input type="checkbox"/> | | |

+ Add Group

Details Organisms Users Group Admin

Membership [Update Membership](#)

Next steps...

- Australian Apollo Service, visit:
<https://apollo-portal.genome.edu.au/>
- Apollo demo site:
<http://demo.genomearchitect.io/Apollo2/annotator/index>
Username: *demo@demo.com*
Password: *demo*
- Apollo Official Google Group:
<https://groups.google.com/a/lbl.gov/g/apollo>



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