| Sequences | Project | GFF3 | Evidence | Repeats | Masking | Align | Structural | Consensus | OGS | Refine | Functional | Annotate | Publish |

Welcome! [x]

Project

Job Queue [x]

Click the buttons above to move through the annotation workflow. As you complete a stage the next button becomes available. Click the **Sequence** button to begin.

Click the **Job Queue** to view the analysis jobs for the project. Click the **Browser** tab to view the predicted features aligned to the genomic sequence. Click the **Sharing** tab to share the project with other Ger

Tabs will appear here to provide the content needed for each stage. Some tabs can be closed and re-opened later but others will always remain. The tabs will provide instructions for each workflow stage.

Project

GenSAS

Project Summary

Edit Project

Welcome to Genome Sequence A

Reset Expiration | Close this Project | Delete this Project

Project Details

Project Name	AfratercFemale
Project ID	t_65c8f29b20b43
Owner	rivabros2
Workflow Stage	Annotate
Description	*No description provided*
Create Date	2024-02-11 13:15:23
Days until expire	40
Project Type	Invertebrate
Project Prefix	Af

Sequence Details

Sequence group name	ragtagScafFemaleCanuPurgPolish.fasta	
Sequence version	v1.0	
Sequence type	scaffold	
Number of sequences	58	
FASTA file of sequences	ragtagScafFemaleCanuPurgPolish.fasta	725.51 MB
GenSAS Sequence Map	ragtagScafFemaleCanuPurgPolish.fasta.map	1.73 KB

Project Organism Details

Common Name	anstrephafrat
Genus	Anastrepha
Species	fraterculus
Infraspecific Name	
Cultivar	
Strain	
NCBI Taxonomy ID	95504
Genetic Code	Standard Code

Job Queue Full Report

Job Name	Tool Name	Tool Type	Status	Submit Date	Complete Date	Job Queue*
RepeatMaskerFemaledfam	RepeatMasker	Repeat Masking	Completed	2024-02-11 13:16:53	2024-02-11 18:09:23	
Masked Repeat Consensus	Mask Sequence Consensus	Repeat Masking	Completed	2024-02-12 00:00:21	2024-02-11 21:06:07	
HISAT1_female	HISAT2	Transcript Alignment	Completed	2024-02-12 10:00:05	2024-02-12 05:54:25	
DiamProtv1	DIAMOND proteins	Protein Alignment	Completed	2024-02-12 10:00:47	2024-02-12 05:51:07	
HISAT_53	HISAT2	Transcript Alignment	Completed	2024-02-12 10:02:57	2024-02-12 06:48:26	

Job Name	Tool Name	Tool Type	Status	Submit Date	Complete Date	Job Queue*
HISAT_51	HISAT2	Transcript Alignment	Completed	2024-02-12 10:03:34	2024-02-12 06:48:27	
HISAT_sp2	HISAT2	Transcript Alignment	Completed	2024-02-12 10:04:30	2024-02-12 07:39:25	
DiamProtInvert	DIAMOND proteins	Protein Alignment	Completed	2024-02-12 10:14:18	2024-02-13 09:33:25	
BRAKERv1Female	BRAKER	Gene Prediction	Completed	2024-02-12 12:40:34	2024-02-13 09:36:08	
BLATv1	BLAT	Transcript Alignment	Completed	2024-02-12 12:45:09	2024-02-12 18:03:25	
Augustusv1female	Augustus	Gene Prediction	Completed	2024-02-12 12:47:39	2024-02-22 09:45:06	
EmvBrakerv1	EvidenceModeler	Consensus Gene Prediction	Completed	2024-02-13 15:19:51	2024-02-14 10:58:03	
diptera_odb10-76187	BUSCO Protein	Assessment Prot	Completed	2024-02-13 15:21:24	2024-02-13 10:51:08	
PASA RefinBrakerv1	PASA Refinement	Gene Refinement	Completed	2024-02-13 15:23:14	2024-02-13 19:27:07	
BLASTpRefin	BLAST protein vs protein (blastp)	Functional Analysis	Completed	2024-02-14 09:32:00	2024-02-17 16:21:06	
DImndRefin	DIAMOND Functional	Functional Analysis	Completed	2024-02-14 09:32:22	2024-02-14 06:54:22	
InterProScanRefin	InterProScan	Functional Analysis	Completed	2024-02-14 09:32:33	2024-02-16 07:42:22	
PfamRefin	Pfam	Functional Analysis	Completed	2024-02-14 09:32:48	2024-02-14 14:36:07	
SignalP	SignalP	Functional Analysis	Completed	2024-02-14 09:32:58	2024-02-14 15:45:23	
Annotations a1	Publishing	Publish	Completed	2024-02-17 21:51:31	2024-02-17 18:15:06	
SSR_Female	SSR Finder	Other Feature	Completed	2024-06-12 10:49:01	2024-06-12 07:15:12	
tRNAscan-SE_female	tRNAscan-SE	Other Feature	Completed	2024-06-12 10:49:26	2024-06-12 07:42:10	
RNAmmer_Female	RNAmmer	Other Feature	Completed	2024-06-12 10:50:16	2024-06-12 08:48:11	

(N / T) where N is the position (Nth) of the job in Job Queue and T is the total number of jobs in Queue.

Jobs used in the following process cannot be deleted.

construction of masking sequences

construction of consensus gene predictions

protein analysis