Current Project :

Anastrepha fraterculus Male Asm

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Welcome! [x]

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

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 proje

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.

Instructions

Project Summary

Edit Project

Reset Expiration   Close this Project   Delete this Project

Project Details

Project Name	Anastrepha fraterculus Male Asm
Project ID	t_65b8fb5ec8f89
Owner	rivabros2
Workflow Stage	Annotate
Description	*No description provided*
Create Date	2024-01-30 10:36:30
Days until expire	40
Project Type	Invertebrate
Project Prefix	Aa

Sequence Details

Sequence group name	ragtag.scafMaleCanuPurgPolishYahs.fasta	
Sequence version	v1.0	
Sequence type	scaffold	
Number of sequences	68	
FASTA file of sequences	ragtag.scafMaleCanuPurgPolishYahs.fasta	714.48 MB
GenSAS Sequence Map	ragtag.scafMaleCanuPurgPolishYahs.fasta.map	2.25 KB

Project Organism Details

Common Name	
Genus	Anastrepha
Species	anastrepha fraterculus
Infraspecific Name	
Cultivar	
Strain	sp1
NCBI Taxonomy ID	95504
Genetic Code	Standard Code

Job Queue Full Report

Job Name	Tool Name	Tool Type	Status	Submit Date	Complete Date	J
RepeatMaskerDfam	RepeatMasker	Repeat Masking	Completed	2024-01-30 13:33:47	2024-01-31 20:57:23	
RepeatModeler_denovo	RepeatModeler	Repeat Masking	Completed	2024-01-30 13:34:12	2024-02-26 02:27:14	
Masked Repeat Consensus	Mask Sequence Consensus	Repeat Masking	Completed	2024-02-01 11:25:57	2024-02-01 08:33:24	
DIAMOND Inv prot	DIAMOND proteins	Protein Alignment	Completed	2024-02-01 13:40:05	2024-02-02 14:30:07	
PASa rnaseq Afrater	PASA	Transcript Alignment	Completed	2024-02-01 13:41:11	2024-02-01 13:27:24	
HISAT2	HISAT2	Transcript Alignment	Completed	2024-02-05 09:26:57	2024-02-05 05:18:22	
HISAT2v2	HISAT2	Transcript Alignment	Completed	2024-02-05 09:27:21	2024-02-05 05:18:23	
HISAT2v3	HISAT2	Transcript Alignment	Completed	2024-02-05 09:27:47	2024-02-05 05:57:24	
GeneMarkES	GeneMarkES	Gene Prediction	Completed	2024-02-05 09:28:09	2024-02-05 12:42:33	
SNAPfly	SNAP	Gene Prediction	Completed	2024-02-05 09:31:09	2024-02-05 09:18:25	
Augustusv2male	Augustus	Gene Prediction	Completed	2024-02-05 09:33:43	2024-02-08 06:48:23	
RNAmmerv1	RNAmmer	Other Feature	Completed	2024-02-05 10:32:52	2024-02-05 12:42:34	
tRNAscan-SEv1	tRNAscan-SE	Other Feature	Completed	2024-02-05 10:33:19	2024-02-05 13:39:21	
FGENESHv1	FGENESH	Gene Prediction	No results	2024-02-05 11:01:18	2024-02-05 12:51:13	
HISAT2v3_2	HISAT2	Transcript Alignment	Completed	2024-02-05 11:23:49	2024-02-05 13:42:23	
BRAKERv1	BRAKER	Gene Prediction	Completed	2024-02-05 14:11:12	2024-02-06 09:45:22	
FGENESHv2	FGENESH	Gene Prediction	No results	2024-02-06 10:27:34	2024-02-06 05:36:18	
EMmarkEsSnapDiamonPASA	EvidenceModeler	Consensus Gene Prediction	Completed	2024-02-06 10:45:07	2024-02-08 11:52:23	
EMBrakv1PASAMarkSnPDiamon	EvidenceModeler	Consensus Gene Prediction	Completed	2024-02-07 09:35:40	2024-02-09 06:59:19	
diptera_odb10-76066	BUSCO Protein	Assessment Prot	Completed	2024-02-08 10:49:47	2024-02-08 12:18:24	
EMBrakerv1Augv2PASAmarkSnap	EvidenceModeler	Consensus Gene Prediction	Completed	2024-02-08 11:54:40	2024-02-10 17:40:18	
PASARefin_Brakerv1	PASA Refinement	Gene Refinement	Completed	2024-02-09 15:22:49	2024-02-09 19:03:23	
diptera_odb10-76057	BUSCO Protein	Assessment Prot	Completed	2024-02-09 15:28:24	2024-02-09 11:45:23	
diptera_odb10-76102	BUSCO Protein	Assessment Prot	Completed	2024-02-09 15:28:24	2024-02-09 12:03:23	
diptera_odb10-76083	BUSCO Protein	Assessment Prot	Completed	2024-02-09 15:28:24	2024-02-09 12:21:22	
diptera_odb10-76055	BUSCO Protein	Assessment Prot	Completed	2024-02-09 15:28:24	2024-02-09 11:09:23	
diptera_odb10-76056	BUSCO Protein	Assessment Prot	Completed	2024-02-09 15:28:24	2024-02-09 11:18:22	
BLASTpRefinBrakerv1	BLAST protein vs protein (blastp)	Functional Analysis	Completed	2024-02-10 09:37:39	2024-02-12 17:27:22	
DIamnRefinBrakerv1	DIAMOND Functional	Functional Analysis	Completed	2024-02-10 09:38:35	2024-02-10 06:33:22	
InterproRefinBrakerv1	InterProScan	Functional Analysis	Completed	2024-02-10 09:39:03	2024-02-12 00:21:07	
PfamRefinBrakerv1	Pfam	Functional Analysis	Completed	2024-02-10 09:39:29	2024-02-10 20:54:23	
SignalPRefinBtakerv1	SignalP	Functional Analysis	Completed	2024-02-10 09:39:59	2024-02-10 22:12:22	
diptera_odb10-76134	BUSCO Protein	Assessment Prot	Completed	2024-02-11 12:31:58	2024-02-11 07:57:27	
Annotations a1	Publishing	Publish	Completed	2024-02-14 09:56:29	2024-02-14 17:09:24	
SSR_Male	SSR Finder	Other Feature	Completed	2024-06-12 10:46:46	2024-06-12 07:15:11	

(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