

# Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

## WebApollo: A Web-Based Sequence Annotation Editor for Community Annotation

RRID:SCR\_005321

Type: Tool

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### Proper Citation

WebApollo: A Web-Based Sequence Annotation Editor for Community Annotation  
(RRID:SCR\_005321)

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### Resource Information

**URL:** <http://icebox.lbl.gov:8080/ApolloWebDemo/jbrowse/>

**Proper Citation:** WebApollo: A Web-Based Sequence Annotation Editor for Community Annotation (RRID:SCR\_005321)

**Description:** WebApollo is an extensible web-based sequence annotation editor for community annotation. No software download is required and the annotations are saved to a centralized database with real-time annotation updating. (The edit server mediates annotation changes made by multiple users.) The Web based client uses JBrowse, is fast and highly interactive. WebApollo accesses many types of genomic data including access to public data from UCSC, Ensembl, and GMOD Chado databases. Source code (BSD License) \* Client source code: <https://github.com/berkeleybop/jbrowse> \* Annotation editing engine: <http://code.google.com/p/apollo-web> \* Data model and I/O layer: <http://code.google.com/p/gbol> \* Trellis server code: <http://code.google.com/p/genomancer>

**Abbreviations:** WebApollo

**Synonyms:** WebApollo - A Web-Based Sequence Annotation Editor for Community Annotation

**Resource Type:** software resource, service resource, production service resource, source code

**Keywords:** sequence, annotation, genome

**Resource Name:** WebApollo: A Web-Based Sequence Annotation Editor for Community Annotation

**Resource ID:** SCR\_005321

**Alternate IDs:** nlx\_144381

**Record Creation Time:** 20220129T080229+0000

**Record Last Update:** 20260731T042708+0000

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## Ratings and Alerts

No rating or validation information has been found for WebApollo: A Web-Based Sequence Annotation Editor for Community Annotation.

No alerts have been found for WebApollo: A Web-Based Sequence Annotation Editor for Community Annotation.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 13 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Cicconardi F, et al. (2024) Novel Sex-Specific Genes and Diverse Interspecific Expression in the Antennal Transcriptomes of Ithomiine Butterflies. *Genome biology and evolution*, 16(10).

Jongepier E, et al. (2022) Convergent Loss of Chemoreceptors across Independent Origins of Slave-Making in Ants. *Molecular biology and evolution*, 39(1).

Reynolds M, et al. (2022) Annotation of putative circadian rhythm-associated genes in *Diaphorina citri* (Hemiptera: Liviidae). *GigaByte (Hong Kong, China)*, 2022, gigabyte48.

Grace R, et al. (2022) Genomic identification, annotation, and comparative analysis of Vacuolar-type ATP synthase subunits in *Diaphorina*??*citri*. *GigaByte (Hong Kong, China)*, 2022, gigabyte39.

Wang W, et al. (2021) Strain-specific genome evolution in *Trypanosoma cruzi*, the agent of Chagas disease. *PLoS pathogens*, 17(1), e1009254.

Haag KL, et al. (2020) Microsporidia with Vertical Transmission Were Likely Shaped by Nonadaptive Processes. *Genome biology and evolution*, 12(1), 3599.

Zhao H, et al. (2020) Mycoparasitism illuminated by genome and transcriptome sequencing of *Coniothyrium minitans*, an important biocontrol fungus of the plant pathogen *Sclerotinia sclerotiorum*. *Microbial genomics*, 6(3).

Wang G, et al. (2019) Mitochondrial genome in *Hypsizygus marmoreus* and its evolution in *Dikarya*. *BMC genomics*, 20(1), 765.

Saur IM, et al. (2019) Multiple pairs of allelic MLA immune receptor-powdery mildew AVRA effectors argue for a direct recognition mechanism. *eLife*, 8.

Gilbert MK, et al. (2018) Whole genome comparison of *Aspergillus flavus* L-morphotype strain NRRL 3357 (type) and S-morphotype strain AF70. *PloS one*, 13(7), e0199169.

Papanicolaou A, et al. (2016) The whole genome sequence of the Mediterranean fruit fly, *Ceratitidis capitata* (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. *Genome biology*, 17(1), 192.

Schuelke TA, et al. (2016) De novo genome assembly of *Geosmithia morbida*, the causal agent of thousand cankers disease. *PeerJ*, 4, e1952.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. *Database : the journal of biological databases and curation*, 2015.