

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

MAKER Web Annotation Service

RRID:SCR_005318

Type: Tool

Proper Citation

MAKER Web Annotation Service (RRID:SCR_005318)

Resource Information

URL: <http://www.yandell-lab.org/software/mwas.html>

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Description: The MAKER Web Annotation Service (MWAS) is an easily configurable web-accessible genome annotation pipeline. It's purpose is to allow research groups with small to intermediate amounts of eukaryotic and prokaryotic genome sequence (i.e. BAC clones, small whole genomes, preliminary sequencing data, etc.) to independently annotate and analyze their data and produce output that can be loaded into a genome database. MWAS is build on the stand alone genome annotation pipeline MAKER, and users who wish to annotate larger datasets and whole genomes are free to download MAKER for use on their own systems. MWAS identifies repeats, aligns ESTs and proteins to a genome, produces ab-initio gene predictions and automatically synthesizes these data into gene annotations having evidence-based quality values. MWAS can also automatically train popular gene prediction algorithms for use on new genomes for which pre-existing information is limited. MAKER is a member of the Generic Model Organism Database (GMOD) project and output produced by this site can be directly used with other GMOD tools. Annotations can be directly viewed online by the user via GBrowse, JBrowse, and Apollo, or they can be downloaded for local analysis and integration into a genome database. MWAS also supplies summary statistics on sequence features via the Sequence Ontology tool SOBA. MWAS should prove especially useful for emerging model organism genome projects with minimal bioinformatics expertise and computer resources, since a user can produce final genome annotations without having to install and configure any software locally.

Abbreviations: MWAS

Resource Type: data access protocol, production service resource, service resource, software resource, web service

Keywords: data management, human genome map, genome annotation, annotation, curation, genome, sequence

Resource Name: MAKER Web Annotation Service

Resource ID: SCR_005318

Alternate IDs: nlx_144374

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260903T234749+0000

Ratings and Alerts

No rating or validation information has been found for MAKER Web Annotation Service.

No alerts have been found for MAKER Web Annotation Service.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

He K, et al. (2023) MHC architecture in amphibians - ancestral reconstruction, gene rearrangements and duplication patterns. *Genome biology and evolution*, 15(5).

He K, et al. (2021) Long-Read Genome Assemblies Reveal Extraordinary Variation in the Number and Structure of MHC Loci in Birds. *Genome biology and evolution*, 13(2).

Jin S, et al. (2021) A chromosome-level genome assembly of the oriental river prawn, *Macrobrachium nipponense*. *GigaScience*, 10(1).

Xu G, et al. (2020) Genome and population sequencing of a chromosome-level genome assembly of the Chinese tapertail anchovy (*Coilia nasus*) provides novel insights into migratory adaptation. *GigaScience*, 9(1).

Cinar HN, et al. (2016) Comparative sequence analysis of *Cyclospora cayetanensis* apicoplast genomes originating from diverse geographical regions. *Parasites & vectors*, 9(1), 611.

Miller HC, et al. (2015) Major Histocompatibility Complex Genes Map to Two Chromosomes in an Evolutionarily Ancient Reptile, the Tuatara *Sphenodon punctatus*. *G3 (Bethesda, Md.)*, 5(7), 1439.

Straub SC, et al. (2011) Building a model: developing genomic resources for common milkweed (*Asclepias syriaca*) with low coverage genome sequencing. *BMC genomics*, 12, 211.