

Resource Summary Report

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ASTRAL Compendium for Sequence and Structure Analysis

RRID:SCR_001886

Type: Tool

Proper Citation

ASTRAL Compendium for Sequence and Structure Analysis (RRID:SCR_001886)

Resource Information

URL: <http://astral.berkeley.edu/>

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Description: It provides databases and tools useful for analyzing protein structures and their sequences. It is partially derived from, and augments the SCOP: Structural Classification of Proteins database, a database created by manual inspection and abetted by a battery of automated methods, aims to provide a detailed and comprehensive description of the structural and evolutionary relationships between all proteins whose structure is known. Most of the resources provided here depend upon the coordinate files maintained and distributed by the Protein Data Bank. Sponsors: This work is supported by grants from the NIH (1-P50-GM62412, 1-K22-HG00056) and the Searle Scholars Program (01-L-116), and by the US Department of Energy under contract DE-AC03-76SF00098.

Abbreviations: ASTRAL

Synonyms: ASTRAL Compendium for Sequence and Structure Analysis, The ASTRAL Compendium for Sequence and Structure Analysis

Resource Type: data or information resource, data processing software, data storage software, database, software application, software resource

Defining Citation: [PMID:10592239](#)

Keywords: gene, amino acid, homology, protein sequence, protein structure

Availability: Free, Available for download, Freely available

Resource Name: ASTRAL Compendium for Sequence and Structure Analysis

Resource ID: SCR_001886

Alternate IDs: nif-0000-02580

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260903T234502+0000

Ratings and Alerts

No rating or validation information has been found for ASTRAL Compendium for Sequence and Structure Analysis.

No alerts have been found for ASTRAL Compendium for Sequence and Structure Analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Tao W, et al. (2026) Conflict in ant phylogeny results from complex interaction between multiple evolutionary signals and tree reconstruction artifacts. *Molecular biology and evolution*, 43(4).

Bi D, et al. (2026) Integrating ANI and phylogenies for re-evaluation of *Fusobacterium* taxonomy and disease associations. *Nature communications*, 17(1).

Liu G, et al. (2026) Extraordinary diversity of antiviral immune-related gene families across 38 bat species. *BMC biology*, 24(1).

Chang CY, et al. (2026) Phylotranscriptomics and genome-size evidence clarify the Taiwanese *Cirsium japonicum* complex and delimit *C. brevicaule* and allied East Asian thistles. *BMC plant biology*, 26(1).

Liu MD, et al. (2026) Revisiting the phylogeny of *Conioselinum* (Apiaceae) by integrating nrDNA, plastomes and morphology evidence. *BMC plant biology*, 26(1).

Qi Z, et al. (2025) Telomere-to-telomere genome assembly of *Electrophorus electricus* provides insights into the evolution of electric eels. *GigaScience*, 14.

Ren L, et al. (2025) Genomes reveal pervasive distant hybridization in nature among cyprinid fishes. *GigaScience*, 14.

Citu C, et al. (2025) Identification and catalog of viral transcriptional regulators in human diseases. *iScience*, 28(3), 112081.

- Zhu C, et al. (2024) Convergent Degenerated Regulatory Elements Associated with Limb Loss in Limbless Amphibians and Reptiles. *Molecular biology and evolution*, 41(11).
- Gagalova KK, et al. (2022) The genome of the forest insect pest *Pissodes strobi* reveals genome expansion and evidence of a *Wolbachia* endosymbiont. *G3 (Bethesda, Md.)*, 12(4).
- Virrueta Herrera S, et al. (2022) High levels of inbreeding with spatial and host-associated structure in lice of an endangered freshwater seal. *Molecular ecology*, 31(18), 4593.
- Xiong H, et al. (2022) Species Tree Estimation and the Impact of Gene Loss Following Whole-Genome Duplication. *Systematic biology*, 71(6), 1348.
- Shu JP, et al. (2022) Phylogenomic Analysis Reconstructed the Order Matoniales from Paleopolyploidy Veil. *Plants (Basel, Switzerland)*, 11(12).
- Ren T, et al. (2022) Molecular evolution and phylogenetic relationships of *Ligusticum* (Apiaceae) inferred from the whole plastome sequences. *BMC ecology and evolution*, 22(1), 55.
- Ufimov R, et al. (2021) Relative performance of customized and universal probe sets in target enrichment: A case study in subtribe Malinae. *Applications in plant sciences*, 9(7), e11442.
- Yang H, et al. (2021) Comparative transcriptomics highlights convergent evolution of energy metabolic pathways in group-living spiders. *Zoological research*, 42(2), 195.
- Berger CA, et al. (2021) Shifts in morphology, gene expression, and selection underlie web loss in Hawaiian Tetragnatha spiders. *BMC ecology and evolution*, 21(1), 48.
- Wang M, et al. (2021) High-quality genome assembly of an important biodiesel plant, *Euphorbia lathyris* L. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 28(6).
- van Kruistum H, et al. (2021) Parallel Genomic Changes Drive Repeated Evolution of Placentas in Live-Bearing Fish. *Molecular biology and evolution*, 38(6), 2627.
- Mu Y, et al. (2021) Whole genome sequencing of a snailfish from the Yap Trench (~7,000 m) clarifies the molecular mechanisms underlying adaptation to the deep sea. *PLoS genetics*, 17(5), e1009530.