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 storage software, database, software resource, software application, data processing software

Defining Citation: PMID:10592239

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

Funding:

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: 20250521T060813+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 24 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zhu C, et al. (2024) Convergent Degenerated Regulatory Elements Associated with Limb Loss in Limbless Amphibians and Reptiles. Molecular biology and evolution, 41(11).

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.

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).

Xiong H, et al. (2022) Species Tree Estimation and the Impact of Gene Loss Following Whole-Genome Duplication. Systematic biology, 71(6), 1348.

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.

Shu JP, et al. (2022) Phylogenomic Analysis Reconstructed the Order Matoniales from

Paleopolyploidy Veil. Plants (Basel, Switzerland), 11(12).

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.

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).

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.

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.

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.

Zhang Z, et al. (2018) Contributions of substitutions and indels to the structural variations in ancient protein superfamilies. BMC genomics, 19(1), 771.

Schwentner M, et al. (2017) A Phylogenomic Solution to the Origin of Insects by Resolving Crustacean-Hexapod Relationships. Current biology : CB, 27(12), 1818.

Mirarab S, et al. (2014) ASTRAL: genome-scale coalescent-based species tree estimation. Bioinformatics (Oxford, England), 30(17), i541.

Hauser M, et al. (2013) kClust: fast and sensitive clustering of large protein sequence databases. BMC bioinformatics, 14, 248.

Mishra P, et al. (2011) A graph-based clustering method applied to protein sequences. Bioinformation, 6(10), 372.

Afek A, et al. (2011) Multi-scale sequence correlations increase proteome structural disorder and promiscuity. Journal of molecular biology, 409(3), 439.

Schad E, et al. (2011) The relationship between proteome size, structural disorder and organism complexity. Genome biology, 12(12), R120.

Yan RX, et al. (2011) Outer membrane proteins can be simply identified using secondary structure element alignment. BMC bioinformatics, 12, 76.