Resource Summary Report

Generated by NIF on Apr 26, 2025

Skylign

RRID:SCR_001176
Type: Tool

Proper Citation

Skylign (RRID:SCR_001176)

Resource Information

URL: http://skylign.org/

Proper Citation: Skylign (RRID:SCR_001176)

Description: A tool for creating logos representing both sequence alignments and profile hidden Markov models. The interactive logos enable scrolling, zooming, and inspection of underlying values. Skylign can avoid sampling bias in sequence alignments by down-weighting redundant sequences and by combining observed counts with informed priors. It also simplifies the representation of gap parameters, and can optionally scale letter heights based on alternate calculations of the conservation of a position.

Abbreviations: Skylign

Synonyms: Skylign - Interactive logos for alignments and profile HMMs

Resource Type: service resource, data analysis service, software resource, production service resource, analysis service resource

Defining Citation: PMID:24410852

Keywords: sequence alignment, profile, logo, bio.tools

Funding:

Availability: Creative Commons Attribution License, v3 Unported

Resource Name: Skylign

Resource ID: SCR_001176

Alternate IDs: biotools:skylign, OMICS_02182

Alternate URLs: https://bio.tools/skylign

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250426T055435+0000

Ratings and Alerts

No rating or validation information has been found for Skylign.

No alerts have been found for Skylign.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Tromer EC, et al. (2021) Repurposing of synaptonemal complex proteins for kinetochores in Kinetoplastida. Open biology, 11(5), 210049.

Danso D, et al. (2018) New Insights into the Function and Global Distribution of Polyethylene Terephthalate (PET)-Degrading Bacteria and Enzymes in Marine and Terrestrial Metagenomes. Applied and environmental microbiology, 84(8).

Liu MM, et al. (2018) Investigating the Campylobacter jejuni Transcriptional Response to Host Intestinal Extracts Reveals the Involvement of a Widely Conserved Iron Uptake System. mBio, 9(4).

Fang X, et al. (2018) F-CphI represents a new homing endonuclease family using the Endo VII catalytic motif. Mobile DNA, 9, 27.

Parra M, et al. (2017) Phylogenetic Diversity in Core Region of Hepatitis C Virus Genotype 1a as a Factor Associated with Fibrosis Severity in HIV-1-Coinfected Patients. BioMed research international, 2017, 1728456.

Vercellino I, et al. (2017) Role of the nucleotidyl cyclase helical domain in catalytically active dimer formation. Proceedings of the National Academy of Sciences of the United States of America, 114(46), E9821.

Koedijk DGAM, et al. (2017) Differential epitope recognition in the immunodominant staphylococcal antigen A of Staphylococcus aureus by mouse versus human IgG antibodies. Scientific reports, 7(1), 8141.

Hobbs M, et al. (2017) Long-read genome sequence assembly provides insight into ongoing retroviral invasion of the koala germline. Scientific reports, 7(1), 15838.

Vakkasoglu AS, et al. (2017) D-helix influences dimerization of the ATP-binding cassette (ABC) transporter associated with antigen processing 1 (TAP1) nucleotide-binding domain. PloS one, 12(5), e0178238.

Santamaría ME, et al. (2017) MATI, a Novel Protein Involved in the Regulation of Herbivore-Associated Signaling Pathways. Frontiers in plant science, 8, 975.

Maimanakos J, et al. (2016) Sequence-Based Screening for Rare Enzymes: New Insights into the World of AMDases Reveal a Conserved Motif and 58 Novel Enzymes Clustering in Eight Distinct Families. Frontiers in microbiology, 7, 1332.

Haack FS, et al. (2016) Molecular Keys to the Janthinobacterium and Duganella spp. Interaction with the Plant Pathogen Fusarium graminearum. Frontiers in microbiology, 7, 1668.

Carmell MA, et al. (2016) A widely employed germ cell marker is an ancient disordered protein with reproductive functions in diverse eukaryotes. eLife, 5.