Resource Summary Report

Generated by dkNET on Apr 22, 2025

BLASTClust

RRID:SCR_016641
Type: Tool

Proper Citation

BLASTClust (RRID:SCR_016641)

Resource Information

URL: https://www.ncbi.nlm.nih.gov/Web/Newsltr/Spring04/blastlab.html

Proper Citation: BLASTClust (RRID:SCR_016641)

Description: Software tool as a program within the standalone BLAST package used to cluster either protein or nucleotide sequences. Used to make non redundant sequence sets.

Resource Type: software resource, sequence analysis software, data analysis software, data processing software, software application

Keywords: cluster, protein, nucleotide, sequence, pairwise, match, sequence

Funding:

Availability: Free, Freely available

Resource Name: BLASTClust

Resource ID: SCR_016641

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250422T055942+0000

Ratings and Alerts

No rating or validation information has been found for BLASTClust.

No alerts have been found for BLASTClust.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 80 mentions in open access literature.

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

Mozaffari S, et al. (2024) STRPsearch: fast detection of structured tandem repeat proteins. Bioinformatics (Oxford, England), 40(12).

Xie TT, et al. (2024) Blue Vane and Pan Traps Are More Effective for Profiling Multiple Facets of Bee Diversity in Subtropical Forests. Insects, 15(11).

Gutierrez-Diaz A, et al. (2024) Systematic computational hunting for small RNAs derived from ncRNAs during dengue virus infection in endothelial HMEC-1 cells. Frontiers in bioinformatics, 4, 1293412.

Shenoy A, et al. (2024) M-Ionic: prediction of metal-ion-binding sites from sequence using residue embeddings. Bioinformatics (Oxford, England), 40(1).

Ding K, et al. (2024) Leveraging conformal prediction to annotate enzyme function space with limited false positives. PLoS computational biology, 20(5), e1012135.

Karnachuk OV, et al. (2024) Novel thermophilic genera Geochorda gen. nov. and Carboxydochorda gen. nov. from the deep terrestrial subsurface reveal the ecophysiological diversity in the class Limnochordia. Frontiers in microbiology, 15, 1441865.

Rakesh S, et al. (2024) Reappraisal of the DNA phosphorothioate modification machinery: uncovering neglected functional modalities and identification of new counter-invader defense systems. Nucleic acids research, 52(3), 1005.

Zhang F, et al. (2023) HybridRNAbind: prediction of RNA interacting residues across structure-annotated and disorder-annotated proteins. Nucleic acids research, 51(5), e25.

Martínez-Rendón J, et al. (2023) Ouabain Induces Transcript Changes and Activation of RhoA/ROCK Signaling in Cultured Epithelial Cells (MDCK). Current issues in molecular biology, 45(9), 7538.

Yan K, et al. (2023) PreTP-2L: identification of therapeutic peptides and their types using two-layer ensemble learning framework. Bioinformatics (Oxford, England), 39(4).

Komaki-Yasuda K, et al. (2023) The RNA-binding KH-domain in the unique transcription factor of the malaria parasite is responsible for its transcriptional regulatory activity. PloS one, 18(12), e0296165.

Cong H, et al. (2023) Protein-protein interaction site prediction by model ensembling with hybrid feature and self-attention. BMC bioinformatics, 24(1), 456.

Zimmermann B, et al. (2023) Topological structures and syntenic conservation in sea anemone genomes. Nature communications, 14(1), 8270.

Burroughs AM, et al. (2023) New biochemistry in the Rhodanese-phosphatase superfamily: emerging roles in diverse metabolic processes, nucleic acid modifications, and biological conflicts. NAR genomics and bioinformatics, 5(1), lqad029.

Kibby EM, et al. (2023) Bacterial NLR-related proteins protect against phage. Cell, 186(11), 2410.

Holland J, et al. (2022) Structure-conditioned amino-acid couplings: How contact geometry affects pairwise sequence preferences. Protein science : a publication of the Protein Society, 31(4), 900.

Khramushin A, et al. (2022) Matching protein surface structural patches for high-resolution blind peptide docking. Proceedings of the National Academy of Sciences of the United States of America, 119(18), e2121153119.

Stringer B, et al. (2022) PIPENN: protein interface prediction from sequence with an ensemble of neural nets. Bioinformatics (Oxford, England), 38(8), 2111.

Newton MAH, et al. (2022) Secondary structure specific simpler prediction models for protein backbone angles. BMC bioinformatics, 23(1), 6.

Jiang Z, et al. (2022) Dissecting and predicting different types of binding sites in nucleic acids based on structural information. Briefings in bioinformatics, 23(1).