

Resource Summary Report

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

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

Availability: Free, Freely available

Resource Name: BLASTClust

Resource ID: SCR_016641

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260903T235350+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 94 mentions in open access literature.

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

Pang XY, et al. (2026) Adaptive Evolution of Odorant-Binding and Chemosensory Protein Gene Families in Genus *Drosophila* Fall??n, 1823 (Diptera, Drosophilidae). *Biomolecules*, 16(2).

Rakesh S, et al. (2026) Expanding the landscape of BREX diversity: uncovering multi-layered functional frameworks and identification of novel BREX-related defense systems. *Nucleic acids research*, 54(3).

Wang MQ, et al. (2026) Asynchrony and functional diversity couple herbivore community dynamics to host plant diversity. *Nature communications*, 17(1), 762.

Ben Salem I, et al. (2026) Genetic Diversity and Excretion Kinetics of Enteroviruses Excreted by Patients with Primary Immunodeficiency in Tunisia over a Five-Year Period (2020-2024). *Microorganisms*, 14(2).

Mou M, et al. (2026) Accurate Identification of Protein Binding Sites for All Drug Modalities Using ALLSites. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(10), e16530.

Chen JT, et al. (2025) Bottom-up and top-down effects combine to drive predator-prey interactions in a forest biodiversity experiment. *The Journal of animal ecology*, 94(10), 2035.

Wang X, et al. (2025) GTE-PPIS: a protein-protein interaction site predictor based on graph transformer and equivariant graph neural network. *Briefings in bioinformatics*, 26(3).

Rakesh S, et al. (2025) Unveiling the structural and functional implications of uncharacterized NSPs and variations in the molecular toolkit across arteriviruses. *NAR genomics and bioinformatics*, 7(2), lqaf035.

Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. *Molecular biology and evolution*, 42(3).

Li Y, et al. (2025) HSSPPI: hierarchical and spatial-sequential modeling for PPIs prediction. *Briefings in bioinformatics*, 26(2).

Wang P, et al. (2025) Deciphering gene redundancy in prokaryotic genomes provides evolutionary insights for pathogenicity and its roles in clinical infections. *Nature communications*, 16(1), 10797.

Shang P, et al. (2025) An intra-family conserved high-order RNA structure within the M ORF is important for arterivirus subgenomic RNA accumulation and infectious virus production. *Journal of virology*, 99(5), e0216724.

Sun G, et al. (2025) EGCPPIS: learning hierarchical equivariant graph representations with contrastive integration for protein-protein interaction site identification. *BMC*

bioinformatics, 26(1), 303.

Shimizu I, et al. (2025) DARUMA: a gateway to fast and easy prediction of intrinsically disordered regions. PeerJ. Computer science, 11, e3343.

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).

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

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.

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

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

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.