

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: 20260829T182519+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 [dkNET](#) .

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).

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).

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.

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.