

Resource Summary Report

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Vector Alignment Search Tool

RRID:SCR_010655

Type: Tool

Proper Citation

Vector Alignment Search Tool (RRID:SCR_010655)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/Structure/VAST/vast.shtml>

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Description: VAST is a computer algorithm developed at NCBI and used to identify similar protein 3-dimensional structures by purely geometric criteria, and to identify distant homologs that cannot be recognized by sequence comparison. Related structures for every structure in MMDB are pre-computed using VAST and accessible via links on the MMDB Structure Summary pages. The VAST Search page also allows you to compare the coordinates of a newly resolved structure in PDB format against all structures in MMDB to find its neighbors. Protein structure neighbors in Entrez are determined by direct comparison of 3-dimensional protein structures with the VAST algorithm. Each of the more than 87,804 domains in MMDB is compared to every other one. From the MMDB Structure summary pages, retrieved via Entrez, structure neighbors are available for protein chains and individual structural domains. If you already know a PDB/MMDB-Id you can try this at once, using the input form in the right column. VAST Search is a service that allows searching for structural neighbors starting with a set of 3D-coordinates specified by the user. This service is meant to be used with newly determined protein structures that are not yet part of MMDB. Structure neighbors for proteins already in MMDB have been pre-computed and can simply be looked up from MMDB's Structure summary pages!

Abbreviations: VAST

Synonyms: Vector Alignment Search Tool (VAST)

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

Defining Citation: [PMID:8804824](#), [PMID:8710828](#)

Keywords: gold standard, bio.tools

Resource Name: Vector Alignment Search Tool

Resource ID: SCR_010655

Alternate IDs: nlx_68740, biotools:vast

Alternate URLs: <https://bio.tools/vast>

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260905T133159+0000

Ratings and Alerts

No rating or validation information has been found for Vector Alignment Search Tool.

No alerts have been found for Vector Alignment Search Tool.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Raffaelli T, et al. (2024) Structural analysis of a U-superfamily conotoxin containing a mini-granulin fold: Insights into key features that distinguish between the ICK and granulin folds. The Journal of biological chemistry, 300(4), 107203.

Bhandari V, et al. (2023) The RavA-ViaA chaperone complex modulates bacterial persistence through its association with the fumarate reductase enzyme. The Journal of biological chemistry, 299(10), 105199.

Cheng X, et al. (2022) The genome wide analysis of Tryptophan Aminotransferase Related gene family, and their relationship with related agronomic traits in Brassica napus. Frontiers in plant science, 13, 1098820.

Rangel-Garcia CI, et al. (2021) Identification of a unique endoplasmic retention motif in the Xenopus GIRK5 channel and its contribution to oocyte maturation. FEBS open bio, 11(4), 1093.

Early JJ, et al. (2018) An automated high-resolution in vivo screen in zebrafish to identify chemical regulators of myelination. eLife, 7.

Gaona-López C, et al. (2016) Diversity and Evolutionary Analysis of Iron-Containing (Type-III) Alcohol Dehydrogenases in Eukaryotes. PloS one, 11(11), e0166851.

Geraghty JP, et al. (2013) Automatic segmentation of male pelvic anatomy on computed tomography images: a comparison with multiple observers in the context of a multicentre

clinical trial. Radiation oncology (London, England), 8, 106.

Crepin T, et al. (2011) A hybrid structural model of the complete *Brugia malayi* cytoplasmic asparaginyl-tRNA synthetase. Journal of molecular biology, 405(4), 1056.

Gangaiah D, et al. (2010) Polyphosphate kinase 2: a novel determinant of stress responses and pathogenesis in *Campylobacter jejuni*. PloS one, 5(8), e12142.

Heidema AG, et al. (2010) Sex-specific effects of CNTF, IL6 and UCP2 polymorphisms on weight gain. Physiology & behavior, 99(1), 1.

Rosas-Murrieta NH, et al. (2010) Interaction of mumps virus V protein variants with STAT1-STAT2 heterodimer: experimental and theoretical studies. Virology journal, 7, 263.

Zou J, et al. (2009) Origin and evolution of the RIG-I like RNA helicase gene family. BMC evolutionary biology, 9, 85.

Wójtowicz H, et al. (2009) Unique structure and stability of HmuY, a novel heme-binding protein of *Porphyromonas gingivalis*. PLoS pathogens, 5(5), e1000419.

Mazumder R, et al. (2008) Structure-guided comparative analysis of proteins: principles, tools, and applications for predicting function. PLoS computational biology, 4(9), e1000151.

Wei L, et al. (2008) Muscle-specific GSTM2-2 on the luminal side of the sarcoplasmic reticulum modifies RyR ion channel activity. The international journal of biochemistry & cell biology, 40(8), 1616.

Kann MG, et al. (2007) The identification of complete domains within protein sequences using accurate E-values for semi-global alignment. Nucleic acids research, 35(14), 4678.

Sun PD, et al. (2004) Overview of protein structural and functional folds. Current protocols in protein science, Chapter 17(1), 1711.