

Resource Summary Report

Generated by [kravitz2](#) on Sep 17, 2026

ADDA - Automatic Domain Decomposition Algorithm

RRID:SCR_007546

Type: Tool

Proper Citation

ADDA - Automatic Domain Decomposition Algorithm (RRID:SCR_007546)

Resource Information

URL: <http://ekhidna.biocenter.helsinki.fi/sqgraph/pairsdb>

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Description: This is a web interface for ADDA, an automatic algorithm for domain decomposition and clustering of all protein domain families. We use alignments derived from an all-on-all sequence comparison to define domains within protein sequences based on a global maximum likelihood model. ADDA is downloadable. There are three ways in which you can retrieve a protein sequence and its domains from ADDA. Sequences can be located using sequence identifiers and/or accession numbers, using a identical fragment lookup, or by running BLAST against all sequences in ADDA. ADDA is a protein sequence clustering algorithm. It takes a set of sequences and returns domain families. ADDA has two steps corresponding to the two aspects of the protein sequence clustering domain. First, ADDA splits protein sequences into domains. The idea behind ADDA is in principle the application of Occam's razor; the goal is to describe the diversity of protein sequences with a minimal set of protein domains. The algorithm behind ADDA approximates this minimal set. In practice ADDA works by looking at where BLAST alignments are located on the sequence and splits the sequences, so that as few as possible alignments are cut by domain boundaries and that as many alignments as possible stretch over complete domains. Secondly, ADDA takes all the domains and then arranges them in a minimum spanning tree, where the similarity between two domains is determined by their relative overlap given a BLAST alignment. Each link in the tree is then checked by a pairwise profile-profile comparison and links below a threshold are removed. The remaining connected components are then taken to represent protein domain families.

Abbreviations: ADDA

Synonyms: Automatic Domain Decomposition Algorithm

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Defining Citation: [PMID:12706730](#)

Resource Name: ADDA - Automatic Domain Decomposition Algorithm

Resource ID: SCR_007546

Alternate IDs: nif-0000-02535

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260912T195656+0000

Ratings and Alerts

No rating or validation information has been found for ADDA - Automatic Domain Decomposition Algorithm.

No alerts have been found for ADDA - Automatic Domain Decomposition Algorithm.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Staniszewska T, et al. (2021) Computational Optimization of the Size of Gold Nanorods for Single-Molecule Plasmonic Biosensors Operating in Scattering and Absorption Modes. The journal of physical chemistry. C, Nanomaterials and interfaces, 125(27), 14765.

Akter S, et al. (2017) Rapid and Highly Sensitive Non-Competitive Immunoassay for Specific Detection of Nodularin. Microorganisms, 5(3).

Tanhuanpää P, et al. (2016) Assessment of genetic diversity in Nordic timothy (Phleum pratense L.). Hereditas, 153, 5.

Leinonen J, et al. (2015) Radar signatures of snowflake riming: A modeling study. Earth and space science (Hoboken, N.J.), 2(8), 346.

Brzobohatý O, et al. (2015) Three-dimensional optical trapping of a plasmonic nanoparticle using low numerical aperture optical tweezers. Scientific reports, 5, 8106.

Sotton B, et al. (2012) Impact of toxic cyanobacterial blooms on Eurasian perch (Perca fluviatilis): experimental study and in situ observations in a peri-alpine lake. PloS one, 7(12), e52243.

Flynn M, et al. (2011) Molecular evolution of the LNX gene family. BMC evolutionary biology, 11, 235.

Alinsug MV, et al. (2009) Phylogenetic analysis, subcellular localization, and expression patterns of RPD3/HDA1 family histone deacetylases in plants. BMC plant biology, 9, 37.

Kelly L, et al. (2009) A survey of integral alpha-helical membrane proteins. Journal of structural and functional genomics, 10(4), 269.

Portugaly E, et al. (2006) EVEREST: automatic identification and classification of protein domains in all protein sequences. BMC bioinformatics, 7, 277.