

Resource Summary Report

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Dali Server

RRID:SCR_013433

Type: Tool

Proper Citation

Dali Server (RRID:SCR_013433)

Resource Information

URL: http://ekhidna.biocenter.helsinki.fi/dali_server

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Description: Network service for comparing protein structures in 3D. You submit the coordinates of a query protein structure and Dali compares them against those in the Protein Data Bank (PDB). You receive an email notification when the search has finished. In favourable cases, comparing 3D structures may reveal biologically interesting similarities that are not detectable by comparing sequences. Requests can also be submitted by e-mail to dali-server at helsinki dot fi. The body of the e-mail message must contain atomic coordinates in PDB format. If you want to know the structural neighbours of a protein already in the Protein Data Bank (PDB), you can find them in the Dali Database. If you want to superimpose two particular structures, you can do it in the pairwise DaliLite server. Academic users may download the DaliLite program for local use.

Synonyms: Dali

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

Defining Citation: [PMID:20457744](#)

Keywords: Protein structure comparison server, protein structure, comparison server, bio.tools, FASEB list

Availability: Free, Freely available

Resource Name: Dali Server

Resource ID: SCR_013433

Alternate IDs: biotools:dali

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

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260819T044401+0000

Ratings and Alerts

No rating or validation information has been found for Dali Server.

No alerts have been found for Dali Server.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 534 mentions in open access literature.

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

Wang X, et al. (2026) Structural and mechanistic insights into azetidine-associated ?KG-NHFe enzyme OkaE with multifunctional catalysis. *Nature communications*, 17(1).

De'Ath C, et al. (2026) YdbL directly modulates YdbH-YnbE bridge formation to maintain *Escherichia coli* outer membrane homeostasis. *bioRxiv : the preprint server for biology*.

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).

Timinskas K, et al. (2026) Diversity and distribution of bacterial DNA polymerases. *Nucleic acids research*, 54(4).

Morvay A, et al. (2026) Synergistic role of CSPBP and SGS1 in sporozoite entry into *Aedes aegypti* salivary glands. *Scientific reports*, 16(1).

Roberts CS, et al. (2026) The type II secretion system utilizes GspN for transport of lipoproteins to the *Acinetobacter baumannii* cell surface. *mBio*, 17(1), e0344925.

Merchant AT, et al. (2026) Semantic design of functional de novo genes from a genomic language model. *Nature*, 649(8097), 749.

Chen R, et al. (2026) Phosphorylation of PfiA modulates Pf4 phage production through PfiA/PfiT stoichiometric reconfiguration in *Pseudomonas aeruginosa*. *Science advances*, 12(14), eaeb5480.

Pan YX, et al. (2026) Integration of transcriptomics and gut microbiomics reveals walnut septum polyphenols alleviate HFD-induced lipid disorders. *NPJ science of food*, 10(1).

Martín-Hurtado A, et al. (2026) The oncogenic CCDC6-RET fusion protein is a dual ATP- and ADP-dependent kinase. *Nature communications*, 17(1).

White K, et al. (2026) Diversity and prevalence of dairy streptococcal phages in two European dairy fermentation facilities over a one-year period. *Microbial genomics*, 12(5).

Yu H, et al. (2026) Clemizole inhibits CrtN-driven staphyloxanthin biosynthesis in *Staphylococcus aureus* to enhance host immune clearance. *Communications biology*, 9(1).

Dai Q, et al. (2026) *Yersinia pseudotuberculosis* secretes an Fe (II)-binding effector to evade calprotectin-mediated nutritional immunity. *Stress biology*, 6(1).

Bose P, et al. (2026) Structural basis of secreted acid phosphatase polymerization in the *Leishmania* parasite. *Protein science : a publication of the Protein Society*, 35(5), e70591.

Saito Y, et al. (2026) Heterologous expression and structural characterization of polyamide 4-degrading enzyme from a soil bacterium. *Frontiers in microbiology*, 17, 1811100.

Yang K, et al. (2026) Structural mechanism of Borna disease virus 1 RNA polymerase autoinhibition and suramin-mediated inhibition. *Cell reports*, 45(6), 117462.

Black JJ, et al. (2026) The *Legionella pneumophila* effector SidL is an adenylyltransferase that modifies the glycolytic intermediate 3-phosphoglycerate. *Molecular cell*.

Niu B, et al. (2026) Oligomerization-Dependent Regulation of LrhA Controls Bacterial Flagellar Biosynthesis. *Journal of molecular biology*, 438(7), 169682.

Selvaraj MK, et al. (2026) Evaluating the evolutionary relationship of TATA binding protein (TBP) with various folding patterns of protein domains using support vector machine (SVM). *Scientific reports*, 16(1).

Dabiri M, et al. (2026) Computational optimization of DEK1 calpain domain solubility through integrated structural modelling and data-driven targeted mutagenesis. *Scientific reports*, 16(1).