Resource Summary Report

Generated by RRID on Apr 28, 2025

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

Defining Citation: PMID:20457744

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

Funding:

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: 20250428T053752+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 120 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Navratna V, et al. (2024) Structure of the human heparan-?-glucosaminide N-acetyltransferase (HGSNAT). eLife, 13.

Licht JA, et al. (2024) They all rock: A systematic comparison of conformational movements in LeuT-fold transporters. Structure (London, England : 1993), 32(9), 1528.

Vergara-Cruces Á, et al. (2024) Structure of the plant plastid-encoded RNA polymerase. Cell, 187(5), 1145.

Mahana Y, et al. (2024) Structural evidence for protein-protein interaction between the non-canonical methyl-CpG-binding domain of SETDB proteins and C11orf46. Structure (London, England : 1993), 32(3), 304.

Li S, et al. (2023) The E301R protein of African swine fever virus functions as a sliding clamp involved in viral genome replication. mBio, 14(5), e0164523.

Motouchi S, et al. (2023) Identification of enzymatic functions of osmo-regulated periplasmic glucan biosynthesis proteins from Escherichia coli reveals a novel glycoside hydrolase

family. Communications biology, 6(1), 961.

Mesdaghi S, et al. (2023) Structural insights into pink-eyed dilution protein (Oca2). Bioscience reports, 43(7).

Holcomb DD, et al. (2022) Protocol to identify host-viral protein interactions between coagulation-related proteins and their genetic variants with SARS-CoV-2 proteins. STAR protocols, 3(3), 101648.

Glenn KC, et al. (2022) Biochemical and clinical studies of putative allergens to assess what distinguishes them from other non-allergenic proteins in the same family. Transgenic research, 31(4-5), 507.

Deák G, et al. (2022) Missense Variants Reveal Functional Insights Into the Human ARID Family of Gene Regulators. Journal of molecular biology, 434(9), 167529.

Fu J, et al. (2022) Legionella pneumophila temporally regulates the activity of ADP/ATP translocases by reversible ADP-ribosylation. mLife, 1(1), 51.

Xie T, et al. (2022) Rational exploration of fold atlas for human solute carrier proteins. Structure (London, England : 1993), 30(9), 1321.

Bragantini B, et al. (2021) The box C/D snoRNP assembly factor Bcd1 interacts with the histone chaperone Rtt106 and controls its transcription dependent activity. Nature communications, 12(1), 1859.

Zhou J, et al. (2021) Insights into the Neutralization and DNA Binding of Toxin-Antitoxin System ParESO-CopASO by Structure-Function Studies. Microorganisms, 9(12).

Crowe-McAuliffe C, et al. (2021) Structural Basis for Bacterial Ribosome-Associated Quality Control by RqcH and RqcP. Molecular cell, 81(1), 115.

Kolich LR, et al. (2020) Structure of MlaFB uncovers novel mechanisms of ABC transporter regulation. eLife, 9.

Orlandi C, et al. (2020) Antigen-Induced Allosteric Changes in a Human IgG1 Fc Increase Low-Affinity Fc? Receptor Binding. Structure (London, England : 1993), 28(5), 516.

Butt BG, et al. (2020) Insights into herpesvirus assembly from the structure of the pUL7:pUL51 complex. eLife, 9.

Ramsay EP, et al. (2020) Structure of human RNA polymerase III. Nature communications, 11(1), 6409.

Mesdaghi S, et al. (2020) In silico prediction of structure and function for a large family of transmembrane proteins that includes human Tmem41b. F1000Research, 9, 1395.