Resource Summary Report

Generated by nidm-terms on Jul 29, 2026

DaliLite Pairwise comparison of protein structures

RRID:SCR_003047
Type: Tool

Proper Citation

DaliLite Pairwise comparison of protein structures (RRID:SCR_003047)

Resource Information

URL: http://www.ebi.ac.uk/Tools/dalilite/indexhtml

Proper Citation: DaliLite Pairwise comparison of protein structures (RRID:SCR_003047)

Description: Tool that computes optimal and suboptimal structural alignments between two protein structures. It will compare all chains in the first structure against all chains in the second (unless specific chain IDs are given). The resulting superimposed coordinate files can be downloaded or viewed interactively in Jmol. The Dali method optimizes a weighted sum of similarities of intramolecular distances. Suboptimal alignments do not overlap the optimal alignment or each other. Suboptimal alignments detected by the program are reported if the Z-score is above 2; they may be of interest if there are internal repeats in either structure. SOAP Web services are also available.

Abbreviations: DaliLite

Synonyms: DaliLite - Pairwise alignment of protein structures

Resource Type: service resource, data analysis service, data access protocol, software resource, production service resource, web service, analysis service resource

Defining Citation: PMID:10980157

Keywords: pairwise alignment, protein structure, alignment, protein, structure

Availability: Free, Freely available

Resource Name: DaliLite Pairwise comparison of protein structures

Resource ID: SCR_003047

Alternate IDs: nif-0000-30431

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260729T044035+0000

Ratings and Alerts

No rating or validation information has been found for DaliLite Pairwise comparison of protein structures.

No alerts have been found for DaliLite Pairwise comparison of protein structures.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 58 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Pei J, et al. (2025) Case Studies of Orphan Domain Reclassification in ECOD by Expert Curation. Proteins, 93(10), 1780.

Liu H, et al. (2025) 3-D substructure search by transitive closure in AlphaFold database. Protein science : a publication of the Protein Society, 34(6), e70169.

Pei J, et al. (2025) Using evolutionary context to classify difficult protein folds. PLoS computational biology, 21(12), e1013773.

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.

Rakesh S, et al. (2024) Reappraisal of the DNA phosphorothioate modification machinery: uncovering neglected functional modalities and identification of new counter-invader defense systems. Nucleic acids research, 52(3), 1005.

Burroughs AM, et al. (2023) New biochemistry in the Rhodanese-phosphatase superfamily: emerging roles in diverse metabolic processes, nucleic acid modifications, and biological conflicts. NAR genomics and bioinformatics, 5(1), lqad029.

M Iyer L, et al. (2021) Jumbo Phages: A Comparative Genomic Overview of Core Functions and Adaptions for Biological Conflicts. Viruses, 13(1).

Kaur G, et al. (2021) Bacterial death and TRADD-N domains help define novel apoptosis and immunity mechanisms shared by prokaryotes and metazoans. eLife, 10.

Kaur G, et al. (2020) Highly regulated, diversifying NTP-dependent biological conflict systems with implications for the emergence of multicellularity. eLife, 9.

Sun H, et al. (2020) Resensitizing carbapenem- and colistin-resistant bacteria to antibiotics using auranofin. Nature communications, 11(1), 5263.

Burroughs AM, et al. (2020) Identification of Uncharacterized Components of Prokaryotic Immune Systems and Their Diverse Eukaryotic Reformulations. Journal of bacteriology, 202(24).

Schaeffer RD, et al. (2019) ECOD: identification of distant homology among multidomain and transmembrane domain proteins. BMC molecular and cell biology, 20(1), 18.

Shang F, et al. (2019) Crystal structure of the Siderophore-interacting protein SIP from Aeromonas hydrophila. Biochemical and biophysical research communications, 519(1), 23.

Yang Y, et al. (2019) Plant glutathione biosynthesis revisited: redox-mediated activation of glutamylcysteine ligase does not require homo-dimerization. The Biochemical journal, 476(7), 1191.

Lykins JD, et al. (2018) CSGID Solves Structures and Identifies Phenotypes for Five Enzymes in Toxoplasma gondii. Frontiers in cellular and infection microbiology, 8, 352.

Deb D, et al. (2018) Application of alignment-free bioinformatics methods to identify an oomycete protein with structural and functional similarity to the bacterial AvrE effector protein. PloS one, 13(4), e0195559.

Srouji JR, et al. (2017) The evolution of function within the Nudix homology clan. Proteins, 85(5), 775.

Matelska D, et al. (2017) Comprehensive classification of the PIN domain-like superfamily. Nucleic acids research, 45(12), 6995.

Fuchs ACD, et al. (2017) The Architecture of the Anbu Complex Reflects an Evolutionary Intermediate at the Origin of the Proteasome System. Structure (London, England : 1993), 25(6), 834.

Ulrich V, et al. (2016) Biochemical and structural characterisation of the second oxidative crosslinking step during the biosynthesis of the glycopeptide antibiotic A47934. Beilstein journal of organic chemistry, 12, 2849.