

# Resource Summary Report

Generated by [dkNET](#) on Aug 28, 2026

## Dali database

RRID:SCR\_006974

Type: Tool

### Proper Citation

Dali database (RRID:SCR\_006974)

### Resource Information

**URL:** <http://ekhidna.biocenter.helsinki.fi/dali/start>

**Proper Citation:** Dali database (RRID:SCR\_006974)

**Description:** Resource out of service. Documented on May, 5th, 2021. The Dali Database is based on all-against-all 3D structure comparison of protein structures in the Protein Data Bank (PDB). The structural neighborhoods and alignments are automatically maintained and regularly updated using the Dali search engine. The Dali Database contains structural alignments of PDB90 versus the full PDB using DaliLite. The data can be viewed interactively here, or downloaded in its entirety. Users may search by PDB identifier or keyword.

**Synonyms:** Dali Database

**Resource Type:** data or information resource, database

**Defining Citation:** [PMID:20457744](#)

**Keywords:** protein, protein 3d structure, protein structure

**Resource Name:** Dali database

**Resource ID:** SCR\_006974

**Alternate IDs:** nif-0000-02719

**Record Creation Time:** 20220129T080239+0000

**Record Last Update:** 20260821T193806+0000

### Ratings and Alerts

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

No alerts have been found for Dali database.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Konopka BM, et al. (2012) Quality assessment of protein model-structures based on structural and functional similarities. BMC bioinformatics, 13, 242.

Prusty D, et al. (2010) Single-stranded DNA binding protein from human malarial parasite Plasmodium falciparum is encoded in the nucleus and targeted to the apicoplast. Nucleic acids research, 38(20), 7037.

Manikandan K, et al. (2008) Functionally important segments in proteins dissected using Gene Ontology and geometric clustering of peptide fragments. Genome biology, 9(3), R52.

Mariño-Ramírez L, et al. (2006) Multiple independent evolutionary solutions to core histone gene regulation. Genome biology, 7(12), R122.