

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on May 19, 2025

3DID: 3D Interacting Domains

RRID:SCR_007425

Type: Tool

Proper Citation

3DID: 3D Interacting Domains (RRID:SCR_007425)

Resource Information

URL: <http://3did.irbbarcelona.org>

Proper Citation: 3DID: 3D Interacting Domains (RRID:SCR_007425)

Description: A database of domain-domain and peptide-mediated interactions of known 3D structures. The database of 3D Interaction Domains (3did) is a collection of domain-domain and domain-peptide interactions for which high-resolution three-dimensional structures are known. 3did exploits structural information to provide critical molecular details necessary for understanding how these interactions occur. It also offers an overview of how similar in structure are interactions between different members of the same protein family. The database also contains GO-based functional annotations and interactions between yeast proteins from large-scale interaction discovery studies. Sponsors: This resource is partially supported by the Spanish Ministerio de Educacin y Ciencia (PSE-010000-2007-1 and BIO2007-62426) and the 3D-Repertoire from the European Commission under FP6 contract LSHG-CT-2005-512028. Keywords: Database, Domain, Peptide, Protein, 3D structure, Interaction, Dimensional, Structure, Molecular, Functional, Annotation, Interaction, Yeast, Study, Research,

Synonyms: 3DID

Resource Type: database, data or information resource

Funding:

Resource Name: 3DID: 3D Interacting Domains

Resource ID: SCR_007425

Alternate IDs: nif-0000-00555

Record Creation Time: 20220129T080241+0000

Record Last Update: 20250519T204721+0000

Ratings and Alerts

No rating or validation information has been found for 3DID: 3D Interacting Domains.

No alerts have been found for 3DID: 3D Interacting Domains.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Zingg D, et al. (2022) Truncated FGFR2 is a clinically actionable oncogene in multiple cancers. Nature, 608(7923), 609.

Akbar R, et al. (2021) A compact vocabulary of paratope-epitope interactions enables predictability of antibody-antigen binding. Cell reports, 34(11), 108856.

Louadi Z, et al. (2021) DIGGER: exploring the functional role of alternative splicing in protein interactions. Nucleic acids research, 49(D1), D309.

Ghedira K, et al. (2020) An Integrative Computational Approach for the Prediction of Human-Plasmodium Protein-Protein Interactions. BioMed research international, 2020, 2082540.

Tang L, et al. (2019) Transcriptomic Insights into Innate Immunity Responding to Red Rot Disease in Red Alga Pyropia yezoensis. International journal of molecular sciences, 20(23).

Taylor WR, et al. (2017) Algorithms for matching partially labelled sequence graphs. Algorithms for molecular biology : AMB, 12, 24.

Mahajan G, et al. (2017) Using structural knowledge in the protein data bank to inform the search for potential host-microbe protein interactions in sequence space: application to Mycobacterium tuberculosis. BMC bioinformatics, 18(1), 201.

Teyra J, et al. (2017) Comprehensive Analysis of the Human SH3 Domain Family Reveals a Wide Variety of Non-canonical Specificities. Structure (London, England : 1993), 25(10), 1598.

Ding D, et al. (2016) K-shell Analysis Reveals Distinct Functional Parts in an Electron Transfer Network and Its Implications for Extracellular Electron Transfer. *Frontiers in microbiology*, 7, 530.

Jubb H, et al. (2015) Flexibility and small pockets at protein-protein interfaces: New insights into druggability. *Progress in biophysics and molecular biology*, 119(1), 2.

Sable R, et al. (2015) Surfing the Protein-Protein Interaction Surface Using Docking Methods: Application to the Design of PPI Inhibitors. *Molecules (Basel, Switzerland)*, 20(6), 11569.

Mosca R, et al. (2014) 3did: a catalog of domain-based interactions of known three-dimensional structure. *Nucleic acids research*, 42(Database issue), D374.

Li BQ, et al. (2012) Prediction of protein-protein interaction sites by random forest algorithm with mRMR and IFS. *PloS one*, 7(8), e43927.

Stein A, et al. (2011) 3did: identification and classification of domain-based interactions of known three-dimensional structure. *Nucleic acids research*, 39(Database issue), D718.

Kiel C, et al. (2011) Structural and functional protein network analyses predict novel signaling functions for rhodopsin. *Molecular systems biology*, 7, 551.