

Resource Summary Report

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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>

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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, Dimentional, Structure, Molecular, Functional, Annotation, Interaction, Yeast, Study, Research,

Synonyms: 3DID

Resource Type: data or information resource, database

Resource Name: 3DID: 3D Interacting Domains

Resource ID: SCR_007425

Alternate IDs: nif-0000-00555

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260912T200147+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 30 mentions in open access literature.

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

Huang G, et al. (2025) Large-scale protein interactome reveals lineage-specific genes driving plant-parasitic nematode adaptive innovations. *Science advances*, 11(33), eadt5107.

Cao X, et al. (2025) Enhancing cross-domain protein and peptide interaction with retrained deep learning models. *Briefings in bioinformatics*, 26(5).

Yue Y, et al. (2024) Integration of molecular coarse-grained model into geometric representation learning framework for protein-protein complex property prediction. *Nature communications*, 15(1), 9629.

Banik M, et al. (2024) Prediction of virus-host interactions and identification of hot spot residues of DENV-2 and SH3 domain interactions. *Archives of microbiology*, 206(4), 162.

Vitting-Seerup K, et al. (2023) Most protein domains exist as variants with distinct functions across cells, tissues and diseases. *NAR genomics and bioinformatics*, 5(3), lqad084.

Gong Y, et al. (2022) HypDB: A functionally annotated web-based database of the proline hydroxylation proteome. *PLoS biology*, 20(8), e3001757.

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.

Ma JX, et al. (2021) Computationally Reconstructed Interactome of *Bradyrhizobium diazoefficiens* USDA110 Reveals Novel Functional Modules and Protein Hubs for Symbiotic Nitrogen Fixation. *International journal of molecular sciences*, 22(21).

Poot Velez AH, et al. (2020) Protein-Protein Interactions Efficiently Modeled by Residue Cluster Classes. *International journal of molecular sciences*, 21(13).

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

Kumar S, et al. (2019) Inferring pathogen-host interactions between *Leptospira interrogans* and *Homo sapiens* using network theory. *Scientific reports*, 9(1), 1434.

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).

García-Pérez CA, et al. (2018) Proteome-wide analysis of human motif-domain interactions mapped on influenza A virus. *BMC bioinformatics*, 19(1), 238.

Budowski-Tal I, et al. (2018) A Novel Geometry-Based Approach to Infer Protein Interface Similarity. *Scientific reports*, 8(1), 8192.

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.

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

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.