Resource Summary Report

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InterDom

RRID:SCR_007742
Type: Tool

Proper Citation

InterDom (RRID:SCR_007742)

Resource Information

URL: http://interdom.i2r.a-star.edu.sg/

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Description: InterDom is a database of putative interacting protein domains derived from multiple sources, ranging from domain fusions (Rosetta Stone), protein interactions (DIP and BIND), protein complexes (PDB), to scientific literature (MEDLINE). Interdom focuses on providing supporting evidence for validating and annotating detected protein interactions and complexes based on putative protein domain interactions. InterDom enhances the quality of in silico derivations by adopting an integrative strategy, assigning higher confidence to domain interactions that are independently derived from different data sources and methods.

Synonyms: InterDom

Resource Type: data or information resource, database

Keywords: software

Funding:

Resource Name: InterDom

Resource ID: SCR_007742

Alternate IDs: nif-0000-03031

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250525T032310+0000

Ratings and Alerts

No rating or validation information has been found for InterDom.

No alerts have been found for InterDom.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Bao Y, et al. (2019) Toward more accurate prediction of caspase cleavage sites: a comprehensive review of current methods, tools and features. Briefings in bioinformatics, 20(5), 1669.

Li X, et al. (2019) Prediction of Protein-Protein Interactions Based on Domain. Computational and mathematical methods in medicine, 2019, 5238406.

Xu B, et al. (2018) Reconstruction of the Protein-Protein Interaction Network for Protein Complexes Identification by Walking on the Protein Pair Fingerprints Similarity Network. Frontiers in genetics, 9, 272.

Li X, et al. (2016) Biomolecular Network-Based Synergistic Drug Combination Discovery. BioMed research international, 2016, 8518945.

Zhang W, et al. (2016) Inference of domain-disease associations from domain-protein, protein-disease and disease-disease relationships. BMC systems biology, 10 Suppl 1(Suppl 1), 4.

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.

Ozawa Y, et al. (2010) Protein complex prediction via verifying and reconstructing the topology of domain-domain interactions. BMC bioinformatics, 11, 350.

Coulibaly I, et al. (2008) Bioinformatic tools for inferring functional information from plant microarray data II: Analysis beyond single gene. International journal of plant genomics, 2008, 893941.

Guimarães KS, et al. (2006) Predicting domain-domain interactions using a parsimony approach. Genome biology, 7(11), R104.