

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

DOMMINO - Database Of MacroMolecular InteractiOns

RRID:SCR_005958

Type: Tool

Proper Citation

DOMMINO - Database Of MacroMolecular InteractiOns (RRID:SCR_005958)

Resource Information

URL: <http://dommino.org>

Proper Citation: DOMMINO - Database Of MacroMolecular InteractiOns (RRID:SCR_005958)

Description: DOMMINO is a comprehensive structural database on macromolecular interactions. As of June, 2011, it contains more than 407,000 binary interactions. The distinctive features of DOMMINO are: # Automated updates: DOMMINO is fully automated and is designed to update itself on a weekly basis, one day after a PDB weekly update. Thus, the community will be able to study macromolecular interactions almost immediately after they are released by PDB. # Coverage of non-domain mediated interactions: In addition to domain-domain and domain-peptide interactions the database characterizes the interaction between domains and unstructured protein regions that are not parts of a domain, such as inter-domain linkers and N- and C-termini. The interactions that involve the latter unstructured parts of proteins have been included to the database for the first time providing additional ~186,000 interactions (~45% of the total number of interactions, as of June, 2011). # Coverage of new structural domains: DOMMINO employs one of the most accurate structural classifications of proteins, SCOP. In addition to the existing SCOP-annotated domains, we employ a state-of-the-art machine learning approach to classify newer protein structures into existing SCOP families. With the progress of structural genomics, we do not expect a significant growth of the number of structurally novel folds or protein families and therefore our method allows covering almost all new protein structures. In total, using this predictive approach has allowed us to add more than 261,000 new interactions, almost twice as many as existing SCOP-annotated interactions. # The web-interface is designed to give the user a possibility of a flexible search as well as the capability to study macromolecular interactions in a PDB structure at the interaction network level and at the individual interface level. The web interface of the DOMMINO database includes a comprehensive list of help topics linked to the specific actions. In addition, we have designed a step-by-step tutorial that covers all aspects of working with the data from DOMMINO using the web interface.

Abbreviations: DOMMINO

Synonyms: Database Of MacroMolecular INteractiOns

Resource Type: data or information resource, database

Defining Citation: [PMID:22135305](#)

Keywords: macromolecular interaction, macromolecule, structural domain, non-domain mediated interaction, protein, domain, peptide, interaction, protein-protein interaction, protein-peptide interaction, protein-dna interactions, protein-rna interactions, rna-rna interactions, rna-dna interactions, interface structure, bio.tools

Funding: NSF DBI-0845196

Resource Name: DOMMINO - Database Of MacroMolecular INteractiOns

Resource ID: SCR_005958

Alternate IDs: biotools:dommino, nlx_151316

Alternate URLs: <http://orion.rnet.missouri.edu/~nz953/DOMMINO/>,
<https://bio.tools/dommino>

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260905T133132+0000

Ratings and Alerts

No rating or validation information has been found for DOMMINO - Database Of MacroMolecular INteractiOns.

No alerts have been found for DOMMINO - Database Of MacroMolecular INteractiOns.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Kuang X, et al. (2016) DOMMINO 2.0: integrating structurally resolved protein-, RNA-, and DNA-mediated macromolecular interactions. Database : the journal of biological databases and curation, 2016.