

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Automatic Generated Test-Sets Database for Protein-Protein Docking

RRID:SCR_002281

Type: Tool

Proper Citation

Automatic Generated Test-Sets Database for Protein-Protein Docking
(RRID:SCR_002281)

Resource Information

URL: <http://bibiserv.techfak.uni-bielefeld.de/agt-sdp/>

Proper Citation: Automatic Generated Test-Sets Database for Protein-Protein Docking
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Description: Database providing automatic test cases for protein-protein docking. A consensus-type approach is proposed processing the whole PDB and classifying protein structures into complexes and unbound proteins by combining information from three different approaches. Out of this classification test cases are generated automatically. All calculations were run on the database. The information stored is available via a web interface. The user can choose several criteria for generating his own subset out of the test cases, e.g. for testing docking algorithms. In unbound protein-protein docking, the complex of two proteins is predicted using the unbound conformations of the proteins (Halperin et al.,2002). For testing of docking algorithms, two unbound proteins which form a known complex have to be identified, so that the result of the docking algorithm can be compared to the known complex. For the identification of test cases, the structures taken from the PDB have to be classified as unbound proteins or complexes and unbound proteins with a 100% sequence identity to one complex part have to be searched. By now, most groups use handpicked test sets. The largest collection of test cases used so far is described by Chen et al. (Chen et al.,2003) and contains 31 test cases for unbound docking. Because of the exponential growth of available protein structures in the PDB, automatic generation of test cases will become more and more important in the future.

Abbreviations: AGT-SDP

Resource Type: data or information resource, database

Defining Citation: [PMID:15479711](#)

Keywords: algorithm, alignment, classification, comparison, complex, conformation, design, docking, genome, primer, protein, rna, structure, unbound, protein domain, protein classification, protein-protein docking

Funding: DFG

Availability: Acknowledgement requested, The community can contribute to this resource

Resource Name: Automatic Generated Test-Sets Database for Protein-Protein Docking

Resource ID: SCR_002281

Alternate IDs: nif-0000-21012

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260905T133117+0000

Ratings and Alerts

No rating or validation information has been found for Automatic Generated Test-Sets Database for Protein-Protein Docking.

No alerts have been found for Automatic Generated Test-Sets Database for Protein-Protein Docking.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.