

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

TargetDB: Structural Genomics Target Search

RRID:SCR_007960

Type: Tool

Proper Citation

TargetDB: Structural Genomics Target Search (RRID:SCR_007960)

Resource Information

URL: <http://targetdb.pdb.org/>

Proper Citation: TargetDB: Structural Genomics Target Search (RRID:SCR_007960)

Description: TargetDB, a target registration database, provides information on the experimental progress and status of targets selected for structure determination. Search sequences from the PSI Structural Genomics Centers and other Structural Genomics projects. For more information about how these proteins were cloned, expressed, purified, or other experimental protocols please go to the Protein expression, purification, and crystallization DataBase.

Synonyms: TargetDB

Resource Type: database, data or information resource

Resource Name: TargetDB: Structural Genomics Target Search

Resource ID: SCR_007960

Alternate IDs: nif-0000-03535

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260808T190412+0000

Ratings and Alerts

No rating or validation information has been found for TargetDB: Structural Genomics Target Search.

No alerts have been found for TargetDB: Structural Genomics Target Search.

Data and Source Information

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Wang CY, et al. (2025) A systems-based approach to uterine fibroids identifies differential splicing associated with abnormal uterine bleeding. *Communications medicine*, 5(1), 318.

Tanner T, et al. (2024) In silico design and analysis of a multiepitope vaccine against Chlamydia. *Pathogens and disease*, 82.

Wang C, et al. (2023) Prediction of protein solubility based on sequence physicochemical patterns and distributed representation information with DeepSoluE. *BMC biology*, 21(1), 12.

Zhang Y, et al. (2020) In Situ Proteolysis Condition-Induced Crystallization of the XcpVWX Complex in Different Lattices. *International journal of molecular sciences*, 21(1).

De Cesco S, et al. (2020) TargetDB: A target information aggregation tool and tractability predictor. *PloS one*, 15(9), e0232644.

Shey RA, et al. (2019) In-silico design??of a multi-epitope vaccine candidate against onchocerciasis and related filarial diseases. *Scientific reports*, 9(1), 4409.

Yan S, et al. (2015) Predicting Crystallization Propensity of Proteins from Arabidopsis Thaliana. *Biological procedures online*, 17, 16.

Elslinger MA, et al. (2010) The JCSG high-throughput structural biology pipeline. *Acta crystallographica. Section F, Structural biology and crystallization communications*, 66(Pt 10), 1137.

Zhang L, et al. (2010) A towards-multidimensional screening approach to predict candidate genes of rheumatoid arthritis based on SNP, structural and functional annotations. *BMC medical genomics*, 3, 38.

Sampathkumar P, et al. (2010) Structures of PHR domains from *Mus musculus* Phr1 (Mycbp2) explain the loss-of-function mutation (Gly1092-->Glu) of the *C. elegans* ortholog RPM-1. *Journal of molecular biology*, 397(4), 883.

Coutard B, et al. (2010) The VIZIER project: overview; expectations; and achievements. *Antiviral research*, 87(2), 85.

Dessailly BH, et al. (2009) PSI-2: structural genomics to cover protein domain family space. *Structure (London, England : 1993)*, 17(6), 869.

Gao M, et al. (2008) DBD-Hunter: a knowledge-based method for the prediction of DNA-protein interactions. *Nucleic acids research*, 36(12), 3978.

Jaroszewski L, et al. (2008) Genome pool strategy for structural coverage of protein families. *Structure* (London, England : 1993), 16(11), 1659.

Galperin MY, et al. (2008) Telling bacteria: do not LytTR. *Structure* (London, England : 1993), 16(5), 657.

Janin J, et al. (2007) Structural genomics: winning the second half of the game. *Structure* (London, England : 1993), 15(11), 1347.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.

Blundell TL, et al. (2004) High-throughput X-ray crystallography for drug discovery. *Current opinion in pharmacology*, 4(5), 490.

Raymond S, et al. (2004) A data management system for structural genomics. *Proteome science*, 2(1), 4.