

Resource Summary Report

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MODELLER

RRID:SCR_008395

Type: Tool

Proper Citation

MODELLER (RRID:SCR_008395)

Resource Information

URL: <http://salilab.org/modeller/modeller.html>

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Description: Software tool as Program for Comparative Protein Structure Modelling by Satisfaction of Spatial Restraints. Used for homology or comparative modeling of protein three dimensional structures. User provides alignment of sequence to be modeled with known related structures and MODELLER automatically calculates model containing all non hydrogen atoms.

Resource Type: data or information resource, portal, simulation software, software application, software resource, topical portal

Keywords: comparative, protein, structure, modelling, satisfaction, spatial, restrain, homology, 3D, alignment, sequence, hydrogen, atom, cluster

Funding: IBM ;
Intel ;
NIGMS P01 GM71790;
NIGMS R01 GM54762;
NIGMS U54 GM62529;
NIH P01 A135707;
Sandler Family Supporting Foundation

Availability: Restricted

Resource Name: MODELLER

Resource ID: SCR_008395

Alternate IDs: nif-0000-30054

License URLs: https://salilab.org/modeller/download_installation.html

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260912T195703+0000

Ratings and Alerts

No rating or validation information has been found for MODELLER.

No alerts have been found for MODELLER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5873 mentions in open access literature.

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

Chirasani VR, et al. (2026) Characterization of cardiac disease-associated mutations in RyR2 Ca²⁺- and caffeine-binding sites. American journal of physiology. Cell physiology, 330(4), C807.

Shi R, et al. (2026) Tumor-intrinsic FDFT1 determines coordinated macrophage anti-tumor immunity. Developmental cell, 61(6), 1238.

Pinto CS, et al. (2026) Actin arginylation alters myosin engagement and F-actin patterning despite structural conservation. The Journal of cell biology, 225(1).

Rathore U, et al. (2026) Systematic discovery of pro- and anti-HIV host factors in primary human CD4⁺ T cells. Cell, 189(12), 3651.

Noguchi Y, et al. (2026) Association of HLA-DRB1 pocket structures with susceptibility and prognosis of Graves' and Hashimoto's disease. Endocrine journal, 73(3), 383.

Lackner M, et al. (2026) The molecular basis of intrinsic resistance to azoles in Rhizopus arrhizus. Antimicrobial agents and chemotherapy, 70(1), e0133725.

Pan Q, et al. (2026) Systematic evaluation of computational tools to predict the effects of mutations on protein-ligand binding affinity in the absence of experimental structures. Briefings in bioinformatics, 27(1).

Méndez-Ruette M, et al. (2026) A pathogenic mutation in ?-SNAP impairs membrane lipid binding by concealing a critical hydrophobic loop. Communications biology, 9(1).

Acharya N, et al. (2026) STI1 domain engages transient helices to mediate Dsk2 phase separation and proteasome condensation. The EMBO journal, 45(8), 2712.

Rodríguez-Santos G, et al. (2026) Molecular Dynamics Simulations Provide Further Insights into the Allosteric Regulation of the Kinesin-5 Motor Domain by Loop 5. *Journal of chemical information and modeling*, 66(7), 4101.

Zhu X, et al. (2026) Preparation and application of Taq DNA polymerase monoclonal antibody guided by structural domain analysis. *PloS one*, 21(3), e0345402.

Hefetz A, et al. (2026) Ternary complexes in protein-DNA interactions: Kinetics and mechanisms. *The Journal of biological chemistry*, 302(1), 111024.

Zhang N, et al. (2026) Time-resolved multiomics profiling reveals chromatin O-GlcNAc modification promotes senescence-associated transcriptional program. *Nature communications*, 17(1), 1406.

Chao KW, et al. (2026) Human class B1 GPCR modulation by plasma membrane lipids. *Communications biology*, 9(1).

Song R, et al. (2026) Cytoskeletal remodeling promotes tunneling nanotube formation and drives cardiac resident cell mitochondrial transfer in sepsis. *Science advances*, 12(11), ead3266.

Wagenknecht JB, et al. (2026) Multi-State Structural Genomics Enables Large-Scale, Mechanistic, and Context-Specific Classification of ABCC6 Genetic Variants Implicated in Calcification Diseases. *International journal of molecular sciences*, 27(4).

Ferdous S, et al. (2026) Investigation of potential hinge region for Mycobacterium tuberculosis topoisomerase I conformational change during catalysis. *bioRxiv : the preprint server for biology*.

Chen Z, et al. (2026) Dynamic-GLEP: a dynamics-informed deep learning framework for ligand efficacy prediction in representative Class A GPCRs. *Briefings in bioinformatics*, 27(1).

Garay E, et al. (2026) A High-Coverage Epitope-Based Vaccine Design for EIAV Envelope Polyprotein Using an Immunoinformatic Approach. *Veterinary sciences*, 13(3).

Khavani M, et al. (2026) A Systematic Benchmark Study of Free Energy Methods for Quantifying Light-Responsive Binding Affinities of Photoswitchable Antagonists of Beta-Adrenergic Receptors. *Journal of medicinal chemistry*, 69(8), 9265.