

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

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

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

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: 20260805T044207+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 5736 mentions in open access literature.

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

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

Kim RK, et al. (2026) A novel TM4SF4-targeting therapeutic antibody candidate with antitumor activity by blocking IGF1R and CD44 signaling and downregulating PD-L1 and B7-H4. Theranostics, 16(4), 1762.

Ali-Ahmad A, et al. (2026) Structure and dynamics of 2x(CENP-A/H4)2 octasome reveal a possible intermediate in centromeric chromatin. Life science alliance, 9(3).

Nath VR, et al. (2025) Ca²⁺ binding to Esyt modulates membrane contact site density in Drosophila photoreceptors. The Journal of cell biology, 224(5).

Yan X, et al. (2025) Intra-condensate demixing of TDP-43 inside stress granules generates pathological aggregates. Cell, 188(15), 4123.

Lucaciu SA, et al. (2025) Skin disease-associated GJB4 variants differentially influence connexin stability, cell viability and channel function. The Journal of physiology, 603(15), 4383.

Ojha S, et al. (2025) Efflux pump modulation by Montelukast and its roles in restoring antibiotic susceptibility in multidrug-resistant Staphylococcus aureus. EBioMedicine, 114, 105658.

Zhang T, et al. (2025) ENKD1 modulates innate immune responses through enhanced geranylgeranyl pyrophosphate synthase activity. Cell reports, 44(3), 115397.

Fernández-Yagüe MA, et al. (2025) Mechanochemical waves in focal adhesions during cell migration. Science advances, 11(40), eadw6425.

- Basrai A, et al. (2025) Computational analyses of drug resistance mutations in katG and emb complexes in Mycobacterium tuberculosis. *Proteins*, 93(1), 359.
- Saadabadi A, et al. (2025) Insights into Molecular Interactions and Biological Effect of Natural Stilbenoids at the TRPA1 Ion Channel. *ChemMedChem*, 20(3), e202400501.
- Drabek M, et al. (2025) Investigation of Muscarinic Acetylcholine Receptor M3 Activation in Atomistic Detail: A Chemist's Viewpoint. *ChemMedChem*, 20(3), e202400633.
- Ranjbar KJ, et al. (2025) Bioinformatics analysis of the in silico engineered protein vaccine with and without Escherichia coli heat labile enterotoxin adjuvant on the model of Klebsiella pneumoniae. *Scientific reports*, 15(1), 7321.
- Toyonaga T, et al. (2025) Dimeric assembly of F1-like ATPase for the gliding motility of Mycoplasma. *Science advances*, 11(9), eadr9319.
- Zheng B, et al. (2025) Discovery of a heparan sulfate binding domain in monkeypox virus H3 as an anti-poxviral drug target combining AI and MD simulations. *eLife*, 13.
- Samuel Russell PP, et al. (2025) Enzymes in a human cytoplasm model organize into submetabolon complexes. *Proceedings of the National Academy of Sciences of the United States of America*, 122(5), e2414206122.
- Krapež G, et al. (2025) In Vitro Functional Validation of an Anti-FREM2 Nanobody for Glioblastoma Cell Targeting. *Antibodies (Basel, Switzerland)*, 14(1).
- Sadler CJ, et al. (2025) Adding a Twist to Lateral Flow Immunoassays: A Direct Replacement of Antibodies with Helical Affibodies, from Selection to Application. *Journal of the American Chemical Society*, 147(14), 11925.
- Wang R, et al. (2025) Development of a recombinant Ang1 variant with enhanced Tie2 binding and its application to attenuate sepsis in mice. *Science advances*, 11(3), eads1796.
- Alrouji M, et al. (2025) Virtual screening and molecular dynamics simulations identify repurposed drugs as potent inhibitors of Histone deacetylase 1: Implication in cancer therapeutics. *PloS one*, 20(1), e0316343.