

# Resource Summary Report

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## ModBase

RRID:SCR\_004642

Type: Tool

### Proper Citation

ModBase (RRID:SCR\_004642)

### Resource Information

**URL:** <http://salilab.org/modbase>

**Proper Citation:** ModBase (RRID:SCR\_004642)

**Description:** A database of three-dimensional protein models calculated by comparative modeling. ModBase is organized into datasets, which are either available to the public, to the academic community, or to specific users. 20 unique amidohydrolase and 41 unique enolase structures have been determined have been included in the database.

**Synonyms:** ModBase

**Resource Type:** data or information resource, database

**Defining Citation:** [PMID:18948282](#), [PMID:21097780](#)

**Keywords:** FASEB list

**Resource Name:** ModBase

**Resource ID:** SCR\_004642

**Alternate IDs:** nif-0000-03153

**Record Creation Time:** 20220129T080225+0000

**Record Last Update:** 20260804T043242+0000

### Ratings and Alerts

No rating or validation information has been found for ModBase.

No alerts have been found for ModBase.

### Data and Source Information

## Usage and Citation Metrics

We found 85 mentions in open access literature.

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

Heimer G, et al. (2025) Biallelic PIGM Coding Variant Causes Intractable Epilepsy and Intellectual Disability Without Thrombotic Events. *Clinical genetics*, 107(2), 179.

Arachchige NDS, et al. (2025) Comprehensive bioinformatics analysis of selected germline variants of uncertain significance identified in a cohort of Sri Lankan hereditary breast cancer patients. *Human genomics*, 19(1), 12.

Kiouri DP, et al. (2025) Structure-Based Approaches for Protein-Protein Interaction Prediction Using Machine Learning and Deep Learning. *Biomolecules*, 15(1).

Vemula D, et al. (2025) Proteome-wide identification of druggable targets and inhibitors for multidrug-resistant *Pseudomonas aeruginosa* using an integrative subtractive proteomics and virtual screening approach. *Heliyon*, 11(4), e42584.

Dhyani KM, et al. (2025) The ATPase activity of yeast chromosome axis protein Hop1 affects the frequency of meiotic crossovers. *Nucleic acids research*, 53(3).

Tsokas P, et al. (2024) KIBRA anchoring the action of PKM $\gamma$  maintains the persistence of memory. *Science advances*, 10(26), eadl0030.

Takeuchi F, et al. (2024) Potential Contribution of Cell Adhesion Molecule 1 to the Binding of SARS-CoV-2 Spike Protein to Mouse Nasal Mucosa. *Cells, tissues, organs*, 213(4), 326.

Wu Y, et al. (2023) Fn-Dps, a novel virulence factor of *Fusobacterium nucleatum*, disrupts erythrocytes and promotes metastasis in colorectal cancer. *PLoS pathogens*, 19(1), e1011096.

Xiong D, et al. (2023) 3D structural human interactome reveals proteome-wide perturbations by disease mutations. *bioRxiv : the preprint server for biology*.

Reyes-González J, et al. (2023) Brain radiotoxicity-related 15CAcBRT gene expression signature predicts survival prognosis of glioblastoma patients. *Neuro-oncology*, 25(2), 303.

Tasleem M, et al. (2023) *Pseudomonas putida* Metallothionein: Structural Analysis and Implications of Sustainable Heavy Metal Detoxification in Madinah. *Toxics*, 11(10).

Kashif M, et al. (2023) Recombinant expression and preliminary characterization of Peptidyl-prolyl cis/trans-isomerase Rrd1 from *Saccharomyces cerevisiae*. *PLoS one*, 18(6), e0282749.

Kosoglu K, et al. (2023) Structural coverage of the human interactome. *Briefings in bioinformatics*, 25(1).

Briata P, et al. (2022) LncRNA EPR-induced METTL7A1 modulates target gene translation. *Nucleic acids research*, 50(13), 7608.

Peng J, et al. (2022) Intermolecular Interactions Drive Protein Adaptive and Coadaptive Evolution at Both Species and Population Levels. *Molecular biology and evolution*, 39(1).

Paniagua G, et al. (2022) KSR induces RAS-independent MAPK pathway activation and modulates the efficacy of KRAS inhibitors. *Molecular oncology*, 16(17), 3066.

Kashif M, et al. (2022) Recombinant expression and biophysical characterization of Mrt4 protein that involved in mRNA turnover and ribosome assembly from *Saccharomyces cerevisiae*. *Bioengineered*, 13(4), 9103.

Ben Khemis I, et al. (2021) Steric and energetic characterizations of mouse and human musk receptors activated by nitro musk smelling compounds at molecular level: Statistical physics treatment and molecular docking analysis. *International journal of biological macromolecules*, 188, 333.

Hyland EM, et al. (2021) Adaptive Evolution in TRIF Leads to Discordance between Human and Mouse Innate Immune Signaling. *Genome biology and evolution*, 13(12).

Bommana S, et al. (2021) Tryptophan Operon Diversity Reveals Evolutionary Trends among Geographically Disparate *Chlamydia trachomatis* Ocular and Urogenital Strains Affecting Tryptophan Repressor and Synthase Function. *mBio*, 12(3).