

Resource Summary Report

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I-TASSER

RRID:SCR_014627

Type: Tool

Proper Citation

I-TASSER (RRID:SCR_014627)

Resource Information

URL: <http://zhanglab.ccmb.med.umich.edu/I-TASSER/>

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Description: Web server as integrated platform for automated protein structure and function prediction. Used for protein 3D structure prediction. Resource for automated protein structure prediction and structure-based function annotation.

Synonyms: Iterative Threading Assembly Refinement, Iterative Threading ASSEmbly Refinement

Resource Type: software application, software resource, data analysis software, data processing software

Defining Citation: [DOI:10.1186/1471-2105-9-40](#), [DOI:10.1093/nar/gkv342](#), [PMID:20360767](#), [PMID:18215316](#)

Keywords: Automated prediction, protein structure prediction, protein function prediction, protein 3D structure, amino acid sequence, alignment, simulation, 3D atomic model, protein, bio.tools

Funding: NIGMS GM083107;
NIGMS GM084222

Availability: Free, Available for download, Freely available

Resource Name: I-TASSER

Resource ID: SCR_014627

Alternate IDs: biotools:i-tasser, SCR_018803

Alternate URLs: <https://bio.tools/i-tasser>

License: GPL

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260729T044354+0000

Ratings and Alerts

No rating or validation information has been found for I-TASSER.

No alerts have been found for I-TASSER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3702 mentions in open access literature.

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

Nobari MB, et al. (2025) The Lpp-OmpA-BtaE fusion protein causes a protective immune response against *Brucella melitensis* in mice. *Scientific reports*, 15(1), 27210.

Lloyd AR, et al. (2025) In silico drug repurposing at the cytoplasmic surface of human aquaporin 1. *PloS one*, 20(1), e0314151.

Pillay P, et al. (2025) Identification and purification of a novel bacteriophage T7 endonuclease from the Kogelberg Biosphere Reserve (KBR) biodiversity hotspot. *Biotechnology reports (Amsterdam, Netherlands)*, 45, e00877.

Dong Q, et al. (2025) Nuclear farnesoid X receptor protects against bone loss by driving osteoblast differentiation through stabilizing RUNX2. *Bone research*, 13(1), 20.

Li YX, et al. (2025) Succinylation enables IDE to act as a hub of larval tissue destruction and adult tissue reconstruction during insect metamorphosis. *Science advances*, 11(6), eads0643.

Khan T, et al. (2025) The Omicron variant BA.2.86.1 of SARS- CoV-2 demonstrates an altered interaction network and dynamic features to enhance the interaction with the hACE2. *Scientific reports*, 15(1), 6482.

Kandelis-Shalev S, et al. (2025) SUN-domain proteins of the malaria parasite *Plasmodium falciparum* are essential for proper nuclear division and DNA repair. *mBio*, 16(4), e0021625.

Costa VAF, et al. (2025) Structure-Based Identification of Non-covalent Prolyl Oligopeptidase 80 Inhibitors Targeting *Trypanosoma cruzi* Cell Entry. *Journal of chemical information and modeling*, 65(5), 2636.

Tawfeeq C, et al. (2025) G Protein Selectivity in Dopamine Receptors is Determined before GDP Release. *Biochemistry*, 64(11), 2439.

Lu D, et al. (2025) Multimeric protein interaction and complex prediction: Structure, dynamics and function. *Computational and structural biotechnology journal*, 27, 1975.

Zhang J, et al. (2025) Fusaric acid-mediated S-glutathionylation of MaAKT1 channel confers the virulence of Foc TR4 to banana. *PLoS pathogens*, 21(4), e1013066.

Kong AS, et al. (2025) In-silico analysis of nsSNPs in BCL-2 family proteins: Implications for colorectal cancer pathogenesis and therapeutics. *Biochemistry and biophysics reports*, 42, 101957.

Yu S, et al. (2025) Immunogenicity Evaluation of Epitope-Based Vaccine on Target of RNAIII-Activating Protein (TRAP) of *Staphylococcus Aureus*. *Biology*, 14(6).

Achappa S, et al. (2025) Exploration of effective pharmacological inhibitors for NS5 protein through computational approach: A strategy to combat the neglected Kyasanur forest disease virus. *PloS one*, 20(7), e0325613.

Colombini M, et al. (2025) Phenotypic dichotomy in *Crotalus durissus ruruima* venom and potential consequences for clinical management of snakebite envenomations. *PLoS neglected tropical diseases*, 19(8), e0013296.

Yuan H, et al. (2025) DDX39B K63-linked ubiquitination mediated by TRIM28 promotes NSCLC metastasis by enhancing ECAD lysosomal degradation. *Signal transduction and targeted therapy*, 10(1), 221.

Petro JL, et al. (2025) Myonectin and metabolic health: a systematic review. *Frontiers in endocrinology*, 16, 1557142.

Qu M, et al. (2025) Structural bioinformatics approaches for predicting novel drug targets in hepatitis C virus proteins: a comprehensive analysis. *Scientific reports*, 15(1), 27011.

Maghraby A, et al. (2025) Genome-wide identification, characterization, and functional analysis of the CHX, SOS, and RLK genes in *Solanum lycopersicum* under salt stress. *Scientific reports*, 15(1), 1142.

Zeng Q, et al. (2025) HDAC6 deacetylates TRIM56 to negatively regulate cGAS-STING-mediated type I interferon responses. *EMBO reports*, 26(3), 720.