

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 resource, software application, 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: 20260808T190033+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 3874 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Xiao W, et al. (2026) Metabolite-gated vascular contractility switch: OXGR1 activation mechanism enables agonist therapy for rosacea erythema. *Cell*, 189(7), 1990.

Ma M, et al. (2026) The heterozygous c.2241G>C variation in FGFR2 may cause autosomal dominant Kirner's deformity in a Chinese Han pedigree. *BMC medical genomics*, 19(1), 36.

Åstrand A, et al. (2026) Structure-activity relationship of prevalent synthetic cannabinoid metabolites on hCB1 in vitro and in silico dynamics. *Acta pharmacologica Sinica*, 47(3), 776.

Dey P, et al. (2026) Hotspot mutations in HER2 interfaces destabilize structure, causing breast cancer treatment failure. *Oncogene*, 45(3), 414.

Rahimi-Farsi N, et al. (2026) Immunoinformatic-driven design of a multi-epitope vaccine against *Helicobacter pylori*. *Biochemistry and biophysics reports*, 45, 102498.

Mahdeen AA, et al. (2026) A novel mRNA-based multiepitope vaccine candidate against *Cryptosporidium hominis* and *Cryptosporidium parvum* employing reverse-vaccinology and immunoinformatics approaches. *PloS one*, 21(2), e0343643.

Juez-Castillo G, et al. (2026) Heme limitation induces LHR2, an essential gene for *Leishmania* pathogenesis. *PLoS pathogens*, 22(2), e1013993.

Siddiquee NH, et al. (2026) Design of a global population-covering multi-epitope mRNA vaccine against Lassa virus using immunoinformatics. *Scientific reports*, 16(1).

Lachowicz JI, et al. (2026) Zinc Coordination by Thymosin β 4: Structural Determinants and Functional Implications. *International journal of molecular sciences*, 27(4).

Abebe MA, et al. (2026) In silico Design and Analysis of Engineered Proteins Containing Multi-Epitope and Immunodominant Domains Derived From *Rickettsia prowazekii* Antigens. *Bioinformatics and biology insights*, 20, 11779322261461934.

Ishwar D, et al. (2026) In silico design of a multi-epitope vaccine targeting DENV-1 and DENV-3. *Scientific reports*, 16(1), 5308.

Caetano-Anollés G, et al. (2026) Revisiting Eck and Dayhoff's Building Block Model of Ferredoxin Evolution on Dayhoff's 100th Birthday. *Journal of molecular evolution*, 94(1), 52.

Liu Y, et al. (2026) A short antimicrobial peptides family demonstrates efficacy to infection via a multimodal mechanism of action. *Antimicrobial agents and chemotherapy*, 70(2), e0134325.

Martín-Blecua I, et al. (2026) The unique role of nucS-mediated noncanonical mismatch repair in *Mycobacterium tuberculosis* resistance evolution. *mBio*, 17(2), e0331025.

Bermudes-Contreras JD, et al. (2026) Molecular dynamics simulation of thermal activation of human TRPV1. *Molecular biology research communications*, 15(1), 39.

Zheng W, et al. (2026) Deep-learning-based single-domain and multidomain protein structure prediction with D-I-TASSER. *Nature biotechnology*, 44(4), 641.

Pugh HL, et al. (2026) The Resistance-Nodulation-Division efflux pump EefABC is highly conserved within lineages of *E. coli* commonly associated with infection. *Microbial genomics*, 12(1).

Sharma M, et al. (2026) The ASC-c isoform as a modulator of inflammasome activation: Insights into molecular mechanisms and therapeutic applications. *The Journal of biological chemistry*, 302(5), 111353.

He Y, et al. (2026) Identification of two novel MVD mutations and one novel FDPS mutation in Chinese patients with porokeratosis. *Frontiers in medicine*, 13, 1760287.

Zhou Y, et al. (2026) Genome-wide identification and gene expression analysis of AhNHXs in peanut. *BMC plant biology*, 26(1).