

Resource Summary Report

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iTasser

RRID:SCR_018803

Type: Tool

Proper Citation

iTasser (RRID:SCR_018803)

Resource Information

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

Proper Citation: iTasser (RRID:SCR_018803)

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

Resource Type: production service resource, data access protocol, analysis service resource, web service, software resource, standalone software, service resource, software application

Defining Citation: [DOI:10.1093/nar/gkv342](https://doi.org/10.1093/nar/gkv342), [PMID:20360767](https://pubmed.ncbi.nlm.nih.gov/20360767/), [PMID:18215316](https://pubmed.ncbi.nlm.nih.gov/18215316/)

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

Funding: NIGMS GM083107;
NIGMS GM084222

Availability: Free, Available for download, Freely available

Resource Name: iTasser

Resource ID: SCR_018803

License: GPL

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260903T235520+0000

Ratings and Alerts

No rating or validation information has been found for iTasser.

No alerts have been found for iTasser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 414 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Wu H, et al. (2026) Treatment with Minicircle DNA Expressing a FGF23 Fragment in a Clinically relevant Mouse Model of X-Linked Hypophosphatemic Rickets. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(4), e08870.

Lei XY, et al. (2025) Identification of MACF1 as a causative gene of generalised epilepsy. Journal of medical genetics, 62(7), 484.

Tian T, et al. (2025) ARGOS homolog evolution in brassicaceae and the role of BnaC6.ARGOS in conferring drought tolerance via expression-responsive localization and reduced seed porosity in rapeseed. BMC plant biology, 25(1), 1254.

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.

Moyeh MN, et al. (2025) In silico design and validation of a Plasmodium falciparum multi-epitope diagnostic antigen (PfMEDA1) for the diagnosis of falciparum malaria. BMC infectious diseases, 26(1), 12.

Zheng Y, et al. (2025) Study on the astringent mechanism of Chebulae fructus. Food chemistry: X, 29, 102825.

Zubair A, et al. (2025) Targeting HIV-1 conserved regions: An immunoinformatic pathway to vaccine innovation for the Asia. PloS one, 20(3), e0317382.

Yang G, et al. (2025) Preparation, expression, and anti-cancer effects of the novel fusion protein rONC-T7-pHLIP. Applied microbiology and biotechnology, 109(1), 207.

Chang C, et al. (2025) Biological activity analysis of baicalin nanodrugs: Nanosizing enhances antiviral and anti-inflammatory effects in the treatment of viral pneumonia. Journal of pharmaceutical analysis, 15(7), 101201.

Song J, et al. (2025) Optimizing therapeutic efficacy of antifungal peptides via strategic terminal amino acid modification. Journal of advanced research, 74, 555.

Mirzaie S, et al. (2025) Design of a novel multiepitope vaccine against glioblastoma by in silico approaches. *Scientific reports*, 15(1), 24046.

Zhang W, et al. (2025) CSMD1 as a causative gene of developmental and epileptic encephalopathy and generalized epilepsies. *Genes & diseases*, 12(4), 101473.

Lang X, et al. (2024) Case report: A novel PTCH1 frameshift mutation leading to nevoid basal cell carcinoma syndrome. *Frontiers in medicine*, 11, 1327505.

Hashempour A, et al. (2024) Design of multivalent-epitope vaccine models directed toward the world's population against HIV-Gag polyprotein: Reverse vaccinology and immunoinformatics. *PloS one*, 19(9), e0306559.

Mondrag??n-Rosas F, et al. (2024) Characterization of Tau95 led to the identification of a four-subunit TFIIIC complex in trypanosomatid parasites. *Applied microbiology and biotechnology*, 108(1), 109.

Yun JS, et al. (2024) In silico analysis for the development of multi-epitope vaccines against *Mycobacterium tuberculosis*. *Frontiers in immunology*, 15, 1474346.

Nellikka A, et al. (2024) *Bifidobacterium adolescentis* is resistant to pyrazinamide, isoniazid, and streptomycin. *Scientific reports*, 14(1), 29562.

Liu HK, et al. (2024) A CysteinyI-tRNA Synthetase Mutation Causes Novel Autosomal-Dominant Inheritance of a Parkinsonism/Spinocerebellar-Ataxia Complex. *Neuroscience bulletin*, 40(10), 1489.

Yang Y, et al. (2024) Interferon-induced transmembrane protein-1 competitively blocks Ephrin receptor A2-mediated Epstein-Barr virus entry into epithelial cells. *Nature microbiology*, 9(5), 1256.

Hsu SH, et al. (2024) RNF43 Inactivation Enhances the B-RAF/MEK Signaling and Creates a Combinatory Therapeutic Target in Cancer Cells. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 11(12), e2304820.