

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 30, 2026

trRosetta

RRID:SCR_021181

Type: Tool

Proper Citation

trRosetta (RRID:SCR_021181)

Resource Information

URL: <https://yanglab.nankai.edu.cn/trRosetta/>

Proper Citation: trRosetta (RRID:SCR_021181)

Description: Software tool for fast and accurate protein structure prediction. Builds protein structure based on direct energy minimizations with restrained Rosetta. Restraints include inter-residue distance and orientation distributions, predicted by deep residual neural network. Homologous templates are included in network prediction to improve accuracy for easy targets.

Synonyms: transformed restrained Rosetta

Resource Type: service resource, simulation software, software application, software resource

Defining Citation: [PMID:31896580](#)

Keywords: protein structure, restraint-guided structure generation, protein structure prediction

Funding: China Scholarship Council ;
Fok Ying-Tong Education Foundation ;
Key Laboratory for Medical Data Analysis and Statistical Research of Tianjin ;
National Natural Science Foundation of China ;
NIGMS R01 GM092802;
NIH Office of the Director DP5 OD026389;
Thousand Youth Talents Plan of China

Availability: Free, Freely available

Resource Name: trRosetta

Resource ID: SCR_021181

Alternate URLs: <https://github.com/gjoni/trRosetta>

License: MIT License

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260829T182713+0000

Ratings and Alerts

No rating or validation information has been found for trRosetta.

No alerts have been found for trRosetta.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 100 mentions in open access literature.

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

Akter S, et al. (2026) Immunoinformatics approach to engineer a multi-epitope vaccine against SdrG in skin commensal Staphylococcus epidermidis. PloS one, 21(3), e0327534.

Usmani SF, et al. (2026) Genome-wide identification of ADK gene family associated with heat stress tolerance in chili (Capsicum annuum L.). BMC genomic data, 27(1).

Vaghefinezhad N, et al. (2026) In vitro and In silico Analysis of SCIN rs376349889 as a Potential Biomarker for Gastric and Colorectal Cancers. Avicenna journal of medical biotechnology, 18(1), 79.

Afshan G, et al. (2025) Immunoinformatics-Based development of a Multi-Epitope vaccine candidate targeting coinfection by Klebsiella pneumoniae and Acinetobacter baumannii. BMC infectious diseases, 25(1), 894.

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. Heliyon, 11(1), e41714.

Tombari W, et al. (2025) A novel mRNA-based multi-epitope vaccine for rabies virus computationally designed via reverse vaccinology and immunoinformatics. Scientific reports, 15(1), 30355.

Han IH, et al. (2025) Conformation-sensitive targeting of CD18 depletes M2-like tumor-associated macrophages resulting in inhibition of solid tumor progression. Journal for immunotherapy of cancer, 13(4).

Sritharan S, et al. (2025) Consensus structure prediction of *A. thaliana*'s MCTP4 structure using prediction tools and coarse grained simulations of transmembrane domain dynamics. *PloS one*, 20(7), e0326993.

Li S, et al. (2025) Immunoinformatics method to design universal multi-epitope nanoparticle vaccine for TGEV S protein. *Scientific reports*, 15(1), 10931.

Naz H, et al. (2025) Utilizing the subtractive proteomics approach to design ensemble vaccine against *Candida lusitanae* for immune response stimulation; a bioinformatics study. *PloS one*, 20(2), e0316264.

Ysrafil Y, et al. (2025) Mosaic vaccine design targeting mutational spike protein of SAR-CoV-2: An immunoinformatics approach. *BioImpacts : BI*, 15, 26443.

Meng Y, et al. (2025) Protein structure prediction via deep learning: an in-depth review. *Frontiers in pharmacology*, 16, 1498662.

Chakraborty A, et al. (2025) In silico evidence of monkeypox F14 as a ligand for the human TLR1/2 dimer. *Frontiers in immunology*, 16, 1544443.

Albocher-Kedem N, et al. (2025) Uncovering the mechanism for polar sequestration of the major bacterial sugar regulator by high-throughput screens and 3D interaction modeling. *Cell reports*, 44(3), 115436.

Li S, et al. (2024) Epitopes screening and vaccine molecular design of PEDV S protein based on immunoinformatics. *Scientific reports*, 14(1), 19537.

Moin AT, et al. (2024) Computational design and evaluation of a polyvalent vaccine for viral nervous necrosis (VNN) in fish to combat Betanodavirus infection. *Scientific reports*, 14(1), 27020.

Abid A, et al. (2024) Reverse Vaccinology Approach to Identify Novel and Immunogenic Targets against *Streptococcus gordonii*. *Biology*, 13(7).

Naveed M, et al. (2024) Development and immunological evaluation of an mRNA-based vaccine targeting *Naegleria fowleri* for the treatment of primary amoebic meningoencephalitis. *Scientific reports*, 14(1), 767.

Xiao D, et al. (2024) Using metabolic abnormalities of carriers in the neonatal period to evaluate the pathogenicity of variants of uncertain significance in methylmalonic acidemia. *Frontiers in genetics*, 15, 1403913.

Moin AT, et al. (2024) In-silico formulation of a next-generation polyvalent vaccine against multiple strains of monkeypox virus and other related poxviruses. *PloS one*, 19(5), e0300778.