

Resource Summary Report

Generated by [NIF](#) on Sep 19, 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: 20260919T195449+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 [NIF](#) .

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).

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.

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.

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.

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.

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.

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).

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.

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

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

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

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.

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.

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.

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

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.

Pratiwi SE, et al. (2024) A novel therapeutic multiepitope vaccine based on oncoprotein E6 and E7 of HPV 16 and 18: An in silico approach. *BiolImpacts : BI*, 14(5), 27846.

Feng Y, et al. (2024) Cortical microinfarcts potentiate recurrent ischemic injury through NLRP3-dependent trained immunity. *Cell death & disease*, 15(1), 36.