

Resource Summary Report

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trRosetta

RRID:SCR_021181

Type: Tool

Proper Citation

trRosetta (RRID:SCR_021181)

Resource Information

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

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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: simulation software, software resource, software application, service resource

Defining Citation: [PMID:31896580](#)

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

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NIGMS R01 GM092802;
NIH Office of the Director DP5 OD026389

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: 20260731T043042+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 67 mentions in open access literature.

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

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).

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

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.

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.

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

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

Salaududdin M, et al. (2024) Development of membrane protein-based vaccine against lumpy skin disease virus (LSDV) using immunoinformatic tools. *Veterinary medicine and science*, 10(3), e1438.

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.

Rani NA, et al. (2024) Development of multi epitope subunit vaccines against emerging carp viruses Cyprinid herpesvirus 1 and 3 using immunoinformatics approach. *Scientific reports*, 14(1), 11783.

Chen Y, et al. (2024) Epitope screening and self-assembled nanovaccine molecule design of PDCoV-S protein based on immunoinformatics. *Frontiers in microbiology*, 15, 1402963.

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.

Zia K, et al. (2024) Comparative genomics and bioinformatics approaches revealed the role of CC-NBS-LRR genes under multiple stresses in passion fruit. *Frontiers in genetics*, 15, 1358134.

Liu D, et al. (2024) Epitope screening and vaccine molecule design of PRRSV GP3 and GP5 protein based on immunoinformatics. *Journal of cellular and molecular medicine*, 28(3), e18103.

Chen Y, et al. (2024) The microprotein HDSP promotes gastric cancer progression through activating the MECOM-SPINK1-EGFR signaling axis. *Nature communications*, 15(1), 8381.