

Resource Summary Report

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TM-align

RRID:SCR_024390

Type: Tool

Proper Citation

TM-align (RRID:SCR_024390)

Resource Information

URL: <https://zhanglab.ccmb.med.umich.edu/TM-align/>

Proper Citation: TM-align (RRID:SCR_024390)

Description: Software tool for protein structure alignment based on TM-score.Used to identify structural alignment between protein pairs that combines the TM-score rotation matrix and Dynamic Programming. Used for sequence independent protein structure comparisons.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:15849316](#)

Keywords: protein structure alignment, TM-score, identify structural alignment between protein pairs, sequence independent protein structure comparisons,

Availability: Free, Available for download, Freely available,

Resource Name: TM-align

Resource ID: SCR_024390

Alternate IDs: OMICS_03646

Alternate URLs: <https://sources.debian.org/src/tm-align/>

Record Creation Time: 20230830T050218+0000

Record Last Update: 20260821T194254+0000

Ratings and Alerts

No rating or validation information has been found for TM-align.

No alerts have been found for TM-align.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Ghasemi F, et al. (2026) Expansion, functional diversification, and gene fusion events in the Ato protein family. *iScience*, 29(7), 116467.

Budhathoki A, et al. (2025) Designing modular genetic sensors with TtgR/AcrR family transcriptional regulators by using a statistical and data-driven approach. *Nucleic acids research*, 53(22).

Jibon MDK, et al. (2025) In-silico analysis of deleterious non-synonymous SNPs in the human AVPR1a gene linked to autism. *BMC genomics*, 26(1), 492.

van Hooff JJE, et al. (2025) Repeated duplications and losses shaped SMC complex evolution from archaeal ancestors to modern eukaryotes. *Cell reports*, 44(7), 115855.

Waheed S, et al. (2024) Identification and In-Silico study of non-synonymous functional SNPs in the human SCN9A gene. *PloS one*, 19(2), e0297367.

Sarkar B, et al. (2024) Comprehensive characterization of high-risk coding and non-coding single nucleotide polymorphisms of human CXCR4 gene. *PloS one*, 19(12), e0312733.

Shobade SO, et al. (2024) Plant root associated chitinases: structures and functions. *Frontiers in plant science*, 15, 1344142.

Roy AS, et al. (2024) A computational approach for structural and functional analyses of disease-associated mutations in the human CYLD gene. *Genomics & informatics*, 22(1), 4.

Xiong EH, et al. (2024) Functional genomic analysis of genes important for *Candida albicans* fitness in diverse environmental conditions. *Cell reports*, 43(8), 114601.

Zhang R, et al. (2023) Discovering Deleterious Single Nucleotide Polymorphisms of Human AKT1 Oncogene: An In Silico Study. *Life (Basel, Switzerland)*, 13(7).

Li H, et al. (2023) Secreted LRPAP1 binds and triggers IFNAR1 degradation to facilitate virus evasion from cellular innate immunity. *Signal transduction and targeted therapy*, 8(1), 374.

Quijano-Barraza JM, et al. (2023) Evolution and functional role prediction of the CYP6DE and CYP6DJ subfamilies in *Dendroctonus* (Curculionidae: Scolytinae) bark beetles. *Frontiers in molecular biosciences*, 10, 1274838.

Rajput N, et al. (2021) Identification and in silico Characterization of Deleterious Single Nucleotide Variations in Human ZP2 Gene. *Frontiers in cell and developmental biology*, 9, 763166.

Akhtar M, et al. (2021) Characterization of Rheumatoid Arthritis Risk-Associated SNPs and Identification of Novel Therapeutic Sites Using an In-Silico Approach. *Biology*, 10(6).

Tan Q, et al. (2020) Is oseltamivir suitable for fighting against COVID-19: In silico assessment, in vitro and retrospective study. *Bioorganic chemistry*, 104, 104257.