

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## 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 processing software, data analysis 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:** 20260801T190826+0000

### Ratings and Alerts

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

No alerts have been found for TM-align.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 9 mentions in open access literature.

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

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.

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.