Resource Summary Report

Generated by T1D on Sep 5, 2026

Mustang

RRID:SCR_024126
Type: Tool

Proper Citation

Mustang (RRID:SCR_024126)

Resource Information

URL: https://lcb.infotech.monash.edu/mustang/

Proper Citation: Mustang (RRID:SCR_024126)

Description: Software tool for structural alignment of multiple protein structures. Used to produce sequence alignment. Reports multiple sequence alignment and corresponding superposition of structures.

Synonyms: mustang, MUltiple (protein) STructural AligNment alGorithm, MUSTANG

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

Defining Citation: PMID:16736488

Keywords: structural alignment, multiple protein structures, produce sequence alignment,

Availability: Free, Available for download, Freely available,

Resource Name: Mustang

Resource ID: SCR_024126

Alternate IDs: OMICS_03642

Alternate URLs: https://sources.debian.org/src/mustang/

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260903T235933+0000

Ratings and Alerts

No rating or validation information has been found for Mustang.

No alerts have been found for Mustang.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Haas-Neill L, et al. (2025) The structural influence of the oncogenic driver mutation N642H in the STAT5B SH2 domain. Protein science : a publication of the Protein Society, 34(1), e70022.

Demoliner M, et al. (2021) Predominance of SARS-CoV-2 P.1 (Gamma) lineage inducing the recent COVID-19 wave in southern Brazil and the finding of an additional S: D614A mutation. Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases, 96, 105134.

do Carmo AL, et al. (2020) Competition Between Phenothiazines and BH3 Peptide for the Binding Site of the Antiapoptotic BCL-2 Protein. Frontiers in chemistry, 8, 235.

Gill K, et al. (2014) The rational design of specific peptide inhibitor against p38?? MAPK at allosteric-site: a therapeutic modality for HNSCC. PloS one, 9(7), e101525.