Resource Summary Report

Generated by dkNET on Apr 23, 2025

AUTO-MUTE

RRID:SCR_013033
Type: Tool

Proper Citation

AUTO-MUTE (RRID:SCR_013033)

Resource Information

URL: http://proteins.gmu.edu/automute/

Proper Citation: AUTO-MUTE (RRID:SCR_013033)

Description: AUTOmated server for predicting functional consequences of amino acid MUTations in protEins.

Abbreviations: AUTO-MUTE

Resource Type: production service resource, analysis service resource, service resource, data analysis service

Funding:

Resource Name: AUTO-MUTE

Resource ID: SCR_013033

Alternate IDs: OMICS_00126

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250423T060705+0000

Ratings and Alerts

No rating or validation information has been found for AUTO-MUTE.

No alerts have been found for AUTO-MUTE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

McCarty TC, et al. (2024) Respiratory Syncytial Virus Vaccine Design Using Structure-Based Machine-Learning Models. Viruses, 16(6).

Masso M, et al. (2015) Modeling functional changes to Escherichia coli thymidylate synthase upon single residue replacements: a structure-based approach. PeerJ, 3, e721.

Panigrahi P, et al. (2015) Engineering Proteins for Thermostability with iRDP Web Server. PloS one, 10(10), e0139486.

Masso M, et al. (2014) AUTO-MUTE 2.0: A Portable Framework with Enhanced Capabilities for Predicting Protein Functional Consequences upon Mutation. Advances in bioinformatics, 2014, 278385.

Doss CG, et al. (2014) Integrating in silico prediction methods, molecular docking, and molecular dynamics simulation to predict the impact of ALK missense mutations in structural perspective. BioMed research international, 2014, 895831.

Chen CW, et al. (2013) iStable: off-the-shelf predictor integration for predicting protein stability changes. BMC bioinformatics, 14 Suppl 2(Suppl 2), S5.

Verma R, et al. (2012) Computer-Aided Protein Directed Evolution: a Review of Web Servers, Databases and other Computational Tools for Protein Engineering. Computational and structural biotechnology journal, 2, e201209008.

Masso M, et al. (2010) Accurate and efficient gp120 V3 loop structure based models for the determination of HIV-1 co-receptor usage. BMC bioinformatics, 11, 494.

Lonquety M, et al. (2009) SPROUTS: a database for the evaluation of protein stability upon point mutation. Nucleic acids research, 37(Database issue), D374.