

# Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

## 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:** analysis service resource, service resource, data analysis service, production service resource

**Resource Name:** AUTO-MUTE

**Resource ID:** SCR\_013033

**Alternate IDs:** OMICS\_00126

**Record Creation Time:** 20220129T080313+0000

**Record Last Update:** 20260728T043419+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 [kravitz2](#) .

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.