

Resource Summary Report

Generated by [NIF](#) on Aug 9, 2026

CSM-Toxin

RRID:SCR_025058

Type: Tool

Proper Citation

CSM-Toxin (RRID:SCR_025058)

Resource Information

URL: https://biosig.lab.uq.edu.au/csm_toxin/

Proper Citation: CSM-Toxin (RRID:SCR_025058)

Description: Web server for predicting protein toxicity. Protein toxicity classifier, which relies on protein primary sequence. Used for predicting toxicity of biologics.

Resource Type: software resource, data access protocol, web service

Defining Citation: [PMID:36839752](#)

Keywords: Protein toxicity classifier, predicting protein toxicity, protein primary sequence, predicting toxicity

Funding: University of Queensland ;
National Health and Medical Research Council of Australia ;
Victorian Governments Operational Infrastructure Support Program

Availability: Free, Freely available

Resource Name: CSM-Toxin

Resource ID: SCR_025058

Alternate URLs: https://biosig.lab.uq.edu.au/csm_toxin/predict

Record Creation Time: 20240305T200904+0000

Record Last Update: 20260808T190709+0000

Ratings and Alerts

No rating or validation information has been found for CSM-Toxin.

No alerts have been found for CSM-Toxin.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Naveed M, et al. (2026) Computational design of a multiepitope vaccine targeting VP1 and VP2 capsid proteins of simian virus 40 (SV40) for enhanced immune activation. Open medicine (Warsaw, Poland), 21(1), 20251284.

Santiago LR, et al. (2026) Animal Venoms as Peptide Libraries for the Discovery of Antiglioblastoma Agents. Biochemistry research international, 2026, 8307315.

Emadi SH, et al. (2026) Design and computational evaluation of a prophylactic and therapeutic multi-epitope vaccine candidate against cervical cancer. Virology journal, 23(1), 45.

Zhu L, et al. (2025) ToxDL 2.0: Protein toxicity prediction using a pretrained language model and graph neural networks. Computational and structural biotechnology journal, 27, 1538.

Bai C, et al. (2025) Machine Learning-Enabled Drug-Induced Toxicity Prediction. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(16), e2413405.

Naderian R, et al. (2025) Rational design of multi-epitope vaccine for Chandipura virus using an immunoinformatics approach. PloS one, 20(10), e0335147.

Arshad NF, et al. (2024) Engineering receptor-binding domain and heptad repeat domains towards the development of multi-epitopes oral vaccines against SARS-CoV-2 variants. PloS one, 19(8), e0306111.

Hashempour A, et al. (2024) Design of multivalent-epitope vaccine models directed toward the world's population against HIV-Gag polyprotein: Reverse vaccinology and immunoinformatics. PloS one, 19(9), e0306559.