

Resource Summary Report

Generated by [dkNET](#) on Aug 6, 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: data access protocol, software resource, 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: 20260805T044543+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 5 mentions in open access literature.

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

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.

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.

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.