

Resource Summary Report

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ToxinPred

RRID:SCR_018542

Type: Tool

Proper Citation

ToxinPred (RRID:SCR_018542)

Resource Information

URL: <http://crdd.osdd.net/raghava/toxinpred/>

Proper Citation: ToxinPred (RRID:SCR_018542)

Description: Software package for peptides designing and prediction. In silico approach for predicting toxicity of peptides and proteins. Used for predicting peptide toxicity or non toxicity, minimum mutations in peptides for increasing or decreasing their toxicity, toxic regions in proteins.

Resource Type: software toolkit, service resource, analysis service resource, software resource, production service resource

Defining Citation: [PMID:29300301](#)

Keywords: Toxin, toxicity, toxicity prediction, peptide toxicity prediction, peptide design, protein, peptide mutation, toxic region, protein toxic region

Funding: Department of Biotechnology Govt. of India ;
Council of Scientific and Industrial Research Govt. of India

Availability: Free, Freely available

Resource Name: ToxinPred

Resource ID: SCR_018542

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260817T040617+0000

Ratings and Alerts

No rating or validation information has been found for ToxinPred.

No alerts have been found for ToxinPred.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 244 mentions in open access literature.

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

Sankar S, et al. (2026) Computational prediction of cyclotides from *Viola odorata* as potential inhibitors against the neuraminidase of *Streptococcus pneumoniae*. *Molecular diversity*, 30(1), 991.

Mongkolnkrajang U, et al. (2026) Bee pollen-derived peptide with dual DPP-IV Inhibition and glucose transport modulation. *Scientific reports*, 16(1).

Wang G, et al. (2026) Characterization and screening of a novel octapeptide from protein hydrolysates of *Crassostrea gigas* and its immunomodulatory effects on RAW264.7 cells. *Food chemistry: X*, 34, 103684.

Shen W, et al. (2026) Identification of Novel Anti-Inflammatory Peptides from Jellyfish *Nemopilema nomurai* Enzymatic Hydrolysate: An Integrated In Silico Analysis and Cellular Evaluation. *Marine drugs*, 24(6).

Wang Y, et al. (2026) Identification of Conserved Cross-Reactive B-Cell Epitopes in CPV1 and CPV2 L1 Proteins with Vaccine Potential. *Vaccines*, 14(6).

Srivastava R, et al. (2026) Immunoinformatic insights for design and clinical prospects of pan-RAS cancer vaccine. *Frontiers in medicine*, 13, 1727976.

Shuvo MN, et al. (2026) Computational and immunoinformatics approaches for designing phytocompound-based drugs and a multi-epitope vaccine targeting FemA, a cell wall protein of *Staphylococcus aureus*. *PloS one*, 21(4), e0346271.

Pasha AVK, et al. (2026) Immunoinformatics-Based Multi-Epitope Vaccine Targeting *Helicobacter Pylori*. *Cancer reports (Hoboken, N.J.)*, 9(1), e70441.

Yang H, et al. (2026) From Waste to Bioactive Ingredient: Integrated Extraction, Identification, and Validation of Novel Antioxidant Peptides from Xuefeng Black-Bone Chicken Bones. *Foods (Basel, Switzerland)*, 15(5).

Doostmohammadi A, et al. (2026) Phylogeny-guided multi-epitope vaccine design targeting conserved and divergent regions of *Brucella* OMP2, OMP25, and OMP31: an immunoinformatics study. *BMC immunology*, 27(1).

Ramirez-Cando LJ, et al. (2026) Computational Design and Immunoinformatic Analysis of a Broad-Spectrum Edible Multi-Epitope Vaccine Against *Salmonella* for Poultry. *Veterinary sciences*, 13(2).

Zheng N, et al. (2026) In silico design of a novel multi-epitope mRNA vaccine candidate for BtHKU5-CoV-2 using immunoinformatics. PLoS neglected tropical diseases, 20(4), e0013517.

Rahimi-Farsi N, et al. (2026) Immunoinformatic-driven design of a multi-epitope vaccine against *Helicobacter pylori*. Biochemistry and biophysics reports, 45, 102498.

Li X, et al. (2026) Serine protease HtrA promotes *Campylobacter jejuni* intestinal colonization through degrading antimicrobial peptide LL-37. Science advances, 12(21), eade1996.

Lv H, et al. (2026) Marine Peptides from *Solenocera crassicornis* Are Associated with Improved Metabolic, Hepatic, and Intestinal Markers During Diet Normalization in HFD-Induced Obese Mice. Nutrients, 18(12).

Batool N, et al. (2026) In Silico Design and Subsequent Expression of Human Papillomavirus-16 and -18 L1 Vaccine Antigens in Broccoli. Vaccines, 14(3).

Ali A, et al. (2026) TZ1391: a computationally designed circular mRNA multi-epitope vaccine candidate against *Mycobacterium tuberculosis* via TLR3 immunomodulation. BMC immunology, 27(1).

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

Munieswaran G, et al. (2026) Immunoinformatic-guided design of a polo-like kinase 1 (PLK1)-targeted multi-epitope vaccine with preliminary in vitro validation. Frontiers in bioinformatics, 6, 1843200.

Mei Y, et al. (2026) Unveiling novel antioxidant peptides from silver carp (*Hypophthalmichthys molitrix*) bone collagen and underlying multi-dimensional mechanism by integrating in silico, in vitro, and in cellulo approaches. Food chemistry: X, 37, 104070.