

Resource Summary Report

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RAMPAGE

RRID:SCR_017590

Type: Tool

Proper Citation

RAMPAGE (RRID:SCR_017590)

Resource Information

URL: <http://mordred.bioc.cam.ac.uk/~rapper/rampage.php>

Proper Citation: RAMPAGE (RRID:SCR_017590)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 23, 2021. Web based structural analysis tool for any uploaded PDB file, producing Ramachandran plots, computing dihedral angles and extracting sequence from PDB. Used to visualize dihedral angles ? against ? of amino acid residues in protein structure.

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

Keywords: Ramachandran, plot, analysis, upload, PDB, file, computing, dihedral, angle, extracting, sequence, protein, amino acid, residue, structure

Availability: THIS RESOURCE IS NO LONGER IN SERVICE.

Resource Name: RAMPAGE

Resource ID: SCR_017590

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260810T040718+0000

Ratings and Alerts

No rating or validation information has been found for RAMPAGE.

No alerts have been found for RAMPAGE.

Data and Source Information

Usage and Citation Metrics

We found 136 mentions in open access literature.

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

Paulo DGS, et al. (2026) Peptides Derived From Reactive Center Loops Inhibit Digestive Trypsin-Like Enzymes in Lepidopteran Pests. Archives of insect biochemistry and physiology, 121(1), e70123.

Wang Z, et al. (2025) Pan-cancer analysis reveals the potential role of DHCR24 in bladder cancer via interactions with HRAS to facilitate cholesterol synthesis. Oncology letters, 30(2), 385.

Ponnusamy P, et al. (2025) Design of a Multi-Epitope Vaccine Candidate Against Infectious Laryngotracheitis Virus Affecting Poultry by Computational Approaches. Biology, 14(7).

Vasistha P, et al. (2025) Effector proteins of Funneliformis mosseae BR221: unravelling plant-fungal interactions through reference-based transcriptome analysis, in vitro validation, and protein-protein docking studies. BMC genomics, 26(1), 42.

Nobari MB, et al. (2025) The Lpp-OmpA-BtaE fusion protein causes a protective immune response against Brucella melitensis in mice. Scientific reports, 15(1), 27210.

Tapajóz RCS, et al. (2024) Chimeric lipoproteins for leptospirosis vaccine: immunogenicity and protective potential. Applied microbiology and biotechnology, 108(1), 424.

Abid A, et al. (2024) Humoral and cellular immunity in response to an in silico-designed multi-epitope recombinant protein of Theileria annulata. Frontiers in immunology, 15, 1400308.

Yun JS, et al. (2024) In silico analysis for the development of multi-epitope vaccines against Mycobacterium tuberculosis. Frontiers in immunology, 15, 1474346.

Salaududin M, et al. (2024) Development of membrane protein-based vaccine against lumpy skin disease virus (LSDV) using immunoinformatic tools. Veterinary medicine and science, 10(3), e1438.

Nebangwa DN, et al. (2024) Predictive immunoinformatics reveal promising safety and anti-onchocerciasis protective immune response profiles to vaccine candidates (Ov-RAL-2 and Ov-103) in anticipation of phase I clinical trials. PloS one, 19(10), e0312315.

Ngernsombat C, et al. (2024) Repurposing FDA-approved drugs targeting FZD10 in nasopharyngeal carcinoma: insights from molecular dynamics simulations and experimental validation. Scientific reports, 14(1), 31461.

Thapa S, et al. (2023) Exploring the microbial diversity and characterization of cellulase and hemicellulase genes in goat rumen: a metagenomic approach. BMC biotechnology,

23(1), 51.

Rahimnahal S, et al. (2023) Biochemical and molecular characterization of novel keratinolytic protease from *Bacillus licheniformis* (KRLr1). *Frontiers in microbiology*, 14, 1132760.

Chehelgerdi M, et al. (2023) Immunoinformatic prediction of potential immunodominant epitopes from *cagW* in order to investigate protection against *Helicobacter pylori* infection based on experimental consequences. *Functional & integrative genomics*, 23(2), 107.

Mao Y, et al. (2023) Designing a multi-epitope vaccine against *Peptostreptococcus anaerobius* based on an immunoinformatics approach. *Synthetic and systems biotechnology*, 8(4), 757.

Mashhadi Abolghasem Shirazi M, et al. (2023) Alum and a TLR7 agonist combined with built-in TLR4 and 5 agonists synergistically enhance immune responses against HPV RG1 epitope. *Scientific reports*, 13(1), 16801.

Srivastava S, et al. (2023) Exploring the structural basis to develop efficient multi-epitope vaccines displaying interaction with HLA and TAP and TLR3 molecules to prevent NIPAH infection, a global threat to human health. *PloS one*, 18(3), e0282580.

Ilyas M, et al. (2023) Molecular Characterization of Germin-like Protein Genes in *Zea mays* (ZmGLPs) Using Various In Silico Approaches. *ACS omega*, 8(18), 16327.

AlGhamdi NA, et al. (2022) Emerging of composition variations of SARS-CoV-2 spike protein and human ACE2 contribute to the level of infection: in silico approaches. *Journal of biomolecular structure & dynamics*, 40(6), 2635.

Fiorilli V, et al. (2022) A structural homologue of the plant receptor D14 mediates responses to strigolactones in the fungal phytopathogen *Cryphonectria parasitica*. *The New phytologist*, 234(3), 1003.