

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>

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

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: 20260803T040751+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 124 mentions in open access literature.

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

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.

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.

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.

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.

Salaududdin 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.

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.

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.

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.

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.

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.

Ayyagari VS, et al. (2022) Design of a multi-epitope-based vaccine targeting M-protein of SARS-CoV2: an immunoinformatics approach. *Journal of biomolecular structure & dynamics*, 40(7), 2963.

Latif A, et al. (2022) Overexpression of the AGL42 gene in cotton delayed leaf senescence through downregulation of NAC transcription factors. *Scientific reports*, 12(1), 21093.

El-Sayed S, et al. (2022) Probing the effect of NEK7 and cofactor interactions on dynamics of NLRP3 monomer using molecular simulation. *Protein science : a publication of the Protein Society*, 31(10), e4420.

Antonelli ACB, et al. (2022) In silico construction of a multiepitope Zika virus vaccine using immunoinformatics tools. *Scientific reports*, 12(1), 53.

Kathwate GH, et al. (2022) In silico Design and Characterization of Multi-epitopes Vaccine for SARS-CoV2 from Its Spike Protein. *International journal of peptide research and therapeutics*, 28(1), 37.