Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 9, 2025

Protein Interactions Calculator

RRID:SCR_018574
Type: Tool

Proper Citation

Protein Interactions Calculator (RRID:SCR_018574)

Resource Information

URL: http://pic.mbu.iisc.ernet.in

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Description: Web server for inter residue interaction calculations in single site. Determines accessible surface area and residue depth, which is distance of residue from surface of protein. Recognizes specific kind of interactions, such as apolar–apolar residue interactions or ionic interactions, that are formed between buried or exposed residues or near surface or deep inside. Recognizes interactions including disulphide bonds, hydrophobic interactions, ionic interactions, hydrogen bonds, aromatic- aromatic interactions, aromatic-sulphur interactions and cation interactions within protein or between proteins in complex.

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

Defining Citation: PMID:17584791

Keywords: Protein interaction, interaction calculation, single site, accessible surface are, residue depth, protein surface, residue distance, residue interaction, protein complex, bio.tools

Funding: Department of Biotechnology Government of India

Availability: Free, Freely available

Resource Name: Protein Interactions Calculator

Resource ID: SCR_018574

Alternate IDs: biotools:pic

Alternate URLs: https://bio.tools/pic

Old URLs: http://crick.mbu.iisc.ernet.in/~PIC

Record Creation Time: 20220129T080340+0000

Record Last Update: 20250407T220513+0000

Ratings and Alerts

No rating or validation information has been found for Protein Interactions Calculator.

No alerts have been found for Protein Interactions Calculator.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 27 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Giotas E, et al. (2024) The Multifunctional Preprotein Binding Domain of SecA. Chembiochem : a European journal of chemical biology, 25(23), e202400621.

Sakoh T, et al. (2024) Aromatic residues in N-terminal domain of archaeal trehalase affect the folding and activity of catalytic domain. Applied microbiology and biotechnology, 108(1), 441.

Boonkua S, et al. (2024) Development of chimeric MrNV virus-like particles capable of binding to SARS-CoV-2-susceptible cells and reducing infection by pseudovirus variants. Scientific reports, 14(1), 31431.

Xi X, et al. (2023) Improvement of the stability and catalytic efficiency of heparan sulfate N-sulfotransferase for preparing N-sulfated heparosan. Journal of industrial microbiology & biotechnology, 50(1).

Verma DK, et al. (2023) Hydrophobic interaction between the TM1 and H8 is essential for rhodopsin trafficking to vertebrate photoreceptor outer segments. The Journal of biological chemistry, 299(12), 105412.

Jana ID, et al. (2022) Targeting an evolutionarily conserved "E-L-L" motif in the spike protein

to develop a small molecule fusion inhibitor against SARS-CoV-2. bioRxiv : the preprint server for biology.

Antil M, et al. (2022) Rv1915 and Rv1916 from Mycobacterium tuberculosis H37Rv form in vitro protein-protein complex. Biochimica et biophysica acta. General subjects, 1866(6), 130130.

Souza PFN, et al. (2022) ACE2-derived peptides interact with the RBD domain of SARS-CoV-2 spike glycoprotein, disrupting the interaction with the human ACE2 receptor. Journal of biomolecular structure & dynamics, 40(12), 5493.

Sharma U, et al. (2022) Dynamics of the secreted frizzled related protein Sizzled and potential implications for binding to bone morphogenetic protein-1 (BMP-1). Scientific reports, 12(1), 14850.

Amaral JL, et al. (2022) Quantum biochemistry, molecular docking, and dynamics simulation revealed synthetic peptides induced conformational changes affecting the topology of the catalytic site of SARS-CoV-2 main protease. Journal of biomolecular structure & dynamics, 40(19), 8925.

Jiao L, et al. (2022) Thermostability Improvement of L-Asparaginase from Acinetobacter soli via Consensus-Designed Cysteine Residue Substitution. Molecules (Basel, Switzerland), 27(19).

Kumar J, et al. (2021) Designing of Nucleocapsid Protein Based Novel Multi-epitope Vaccine Against SARS-COV-2 Using Immunoinformatics Approach. International journal of peptide research and therapeutics, 27(2), 941.

Roy M, et al. (2021) Probing the Peculiarity of EhRabX10, a pseudoRab GTPase, from the Enteric Parasite Entamoeba histolytica through In Silico Modeling and Docking Studies. BioMed research international, 2021, 9913625.

Kang G, et al. (2021) VHH212 nanobody targeting the hypoxia-inducible factor 1? suppresses angiogenesis and potentiates gemcitabine therapy in pancreatic cancer in vivo. Cancer biology & medicine, 18(3), 772.

Krishnamurthy S, et al. (2021) A nexus of intrinsic dynamics underlies translocase priming. Structure (London, England : 1993), 29(8), 846.

Schmitz T, et al. (2021) NMR-Based Structural Characterization of a Two-Disulfide-Bonded Analogue of the FXIIIa Inhibitor Tridegin: New Insights into Structure-Activity Relationships. International journal of molecular sciences, 22(2).

Resende PC, et al. (2021) The ongoing evolution of variants of concern and interest of SARS-CoV-2 in Brazil revealed by convergent indels in the amino (N)-terminal domain of the spike protein. Virus evolution, 7(2), veab069.

Xu QY, et al. (2020) [Phenotypic and genetic analysis of a pedigree with inherited antithrombin deficiency]. Zhonghua xue ye xue za zhi = Zhonghua xueyexue zazhi, 41(7),

589.

Khorvash M, et al. (2020) Molecular interactions between monoclonal oligomer-specific antibody 5E3 and its amyloid beta cognates. PloS one, 15(5), e0232266.

Stutz C, et al. (2020) A single mutation increases heavy-chain heterodimer assembly of bispecific antibodies by inducing structural disorder in one homodimer species. The Journal of biological chemistry, 295(28), 9392.