

Resource Summary Report

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

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: 20260912T195902+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 34 mentions in open access literature.

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

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.

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

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.

Mesquita FP, et al. (2023) In silico analysis of ACE2 from different animal species provides new insights into SARS-CoV-2 species spillover. *Future virology*.

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.

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.

Tian W, et al. (2022) Engineering mesophilic GH11 xylanase from *Cellulomonas flavigena* by rational design of N-terminus substitution. *Frontiers in bioengineering and*

biotechnology, 10, 1044291.

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.

Jana ID, et al. (2022) Targeting an evolutionarily conserved "E-L-L" motif in spike protein to identify a small molecule fusion inhibitor against SARS-CoV-2. PNAS nexus, 1(5), pgac198.

Chakraborty S, et al. (2022) Decoding the effects of spike receptor binding domain mutations on antibody escape abilities of omicron variants. Biochemical and biophysical research communications, 627, 168.

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.

Tang L, et al. (2022) Effects of Module Truncation of a New Alginate Lyase VxAly7C from Marine *Vibrio xiamenensis* QY104 on Biochemical Characteristics and Product Distribution. International journal of molecular sciences, 23(9).

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.

Narsimulu B, et al. (2022) Biophysical and Structural Characterization of Ribulose-5-phosphate Epimerase from *Leishmania donovani*. ACS omega, 7(1), 548.

Hsueh SS, et al. (2022) Insights to Human γ D-Crystallin Unfolding by NMR Spectroscopy and Molecular Dynamics Simulations. International journal of molecular sciences, 23(3).

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

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 α suppresses angiogenesis and potentiates gemcitabine therapy in pancreatic cancer in vivo. Cancer biology & medicine, 18(3), 772.