KFC2: A knowledgeâ€based hot spot prediction method density, and plasticity features

Proteins: Structure, Function and Bioinformatics

79, 2671-2683

DOI: 10.1002/prot.23094

Citation Report

#	Article	IF	Citations
1	Proteinâ€“protein binding affinity prediction on a diverse set of structures. Bioinformatics, 2011, 27, 3002-3009.	1.8	103
2	PocketQuery: protein-protein interaction inhibitor starting points from protein-protein interaction structure. Nucleic Acids Research, 2012, 40, W387-W392.	6.5	79
3	Prediction of hot spots in protein interfaces using a random forest model with hybrid features. Protein Engineering, Design and Selection, 2012, 25, 119-126.	1.0	60
4	HotRegion: a database of predicted hot spot clusters. Nucleic Acids Research, 2012, 40, D829-D833.	6.5	90
5	Modulating Protein-Protein Interactions: From Structural Determinants of Binding to Druggability Prediction to Application. Current Pharmaceutical Design, 2012, 18, 4630-4647.	0.9	54
6	A semi-supervised boosting SVM for predicting hot spots at protein-protein Interfaces. BMC Systems Biology, 2012, 6, S6.	3.0	13
7	Small-molecule inhibitor starting points learned from proteinâ€“protein interaction inhibitor structure. Bioinformatics, 2012, 28, 784-791.	1.8	59
8	Dataâ€driven models for protein interaction and design. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2221-2228.	1.5	5
9	Computational study and peptide inhibitors design for the CDK9 â€“ cyclin T1 complex. Journal of Molecular Modeling, 2013, 19, 1711-1725.	0.8	12
10	Boosting Prediction Performance of Proteinâ€“Protein Interaction Hot Spots by Using Structural Neighborhood Properties. Journal of Computational Biology, 2013, 20, 878-891.	0.8	38
11	Identification and characterization of a 43ÂkDa actin protein involved in the DENV-2 binding and infection of ECV304 cells. Microbes and Infection, 2013, 15, 310-318.	1.0	26
12	Nitric oxide synthase domain interfaces regulate electron transfer and calmodulin activation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3577-86.	3.3	84
13	Detection of peptideâ€binding sites on protein surfaces: The first step toward the modeling and targeting of peptideâ€mediated interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2096-2105.	1.5	95
14	Specialized Dynamical Properties of Promiscuous Residues Revealed by Simulated Conformational Ensembles. Journal of Chemical Theory and Computation, 2013, 9, 5127-5147.	2.3	39
15	Characterizing Changes in the Rate of Protein-Protein Dissociation upon Interface Mutation Using Hotspot Energy and Organization. PLoS Computational Biology, 2013, 9, e1003216.	1.5	29
16	BeAtMuSiC: prediction of changes in proteinâ€“protein binding affinity on mutations. Nucleic Acids Research, 2013, 41, W333-W339.	6.5	275
17	DBSI: DNA-binding site identifier. Nucleic Acids Research, 2013, 41, e160-e160.	6.5	27
18	Proteinâ€“protein interaction networks studies and importance of 3D structure knowledge. Expert Review of Proteomics, 2013, 10, 511-520.	1.3	17

#	Article	IF	Citations
19	From Protein-Protein Interactions to Rational Drug Design: Are Computational Methods Up to the Challenge?. Current Topics in Medicinal Chemistry, 2013, 13, 602-618.	1.0	23
20	IDENTIFYING MUTATION SPECIFIC CANCER PATHWAYS USING A STRUCTURALLY RESOLVED PROTEIN INTERACTION NETWORK. , 2014, , .		3
21	PredHS: a web server for predicting proteinâ€“protein interaction hot spots by using structural neighborhood properties. Nucleic Acids Research, 2014, 42, W290-W295.	6.5	59
22	Deciphering the Binding of Caveolin-1 to Client Protein Endothelial Nitric-oxide Synthase (eNOS). Journal of Biological Chemistry, 2014, 289, 13273-13283.	1.6	54
23	ECMIS: computational approach for the identification of hotspots at protein-protein interfaces. BMC Bioinformatics, 2014, 15, 303.	1.2	14
24	Prediction of hot spots in protein interfaces using extreme learning machines with the information of spatial neighbour residues. IET Systems Biology, 2014, 8, 184-190.	0.8	13
25	A Cell-penetrating Antibody Fragment against HIV-1 Rev Has High Antiviral Activity. Journal of Biological Chemistry, 2014, 289, 20222-20233.	1.6	20
26	Hot-spot analysis to dissect the functional protein-protein interface of a tRNA-modifying enzyme. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2713-2732.	1.5	17
27	Prediction of hot spots residues in proteinâ€“protein interface using network feature and microenvironment feature. Chemometrics and Intelligent Laboratory Systems, 2014, 131, 16-21.	1.8	17
28	Hot spot-based design of small-molecule inhibitors for proteinâ€“protein interactions. Bioorganic and Medicinal Chemistry Letters, 2014, 24, 2546-2554.	1.0	131
29	Structural insights from GRP78â€“NF-ÎºB binding interactions: A computational approach to understand a possible neuroprotective pathway in brain injuries. Journal of Theoretical Biology, 2014, 345, 43-51.	0.8	8
30	Evolutionarily conserved and conformationally constrained short peptides might serve as DNA recognition elements in intrinsically disordered regions. Molecular BioSystems, 2014, 10, 1469.	2.9	4
31	Are hot-spots occluded from water?. Journal of Biomolecular Structure and Dynamics, 2014, 32, 186-197.	2.0	11
32	Functional Evolution of Ribonuclease Inhibitor: Insights from Birds and Reptiles. Journal of Molecular Biology, 2014, 426, 3041-3056.	2.0	56
33	Protein painting reveals solvent-excluded drug targets hidden within native proteinâ€“protein interfaces. Nature Communications, 2014, 5, 4413.	5.8	45
34	Structural analysis and modeling reveals new mechanisms governing ESCRT-III spiral filament assembly. Journal of Cell Biology, 2014, 206, 763-777.	2.3	115
35	Hot spots in proteinâ€“protein interfaces: Towards drug discovery. Progress in Biophysics and Molecular Biology, 2014, 116, 165-173.	1.4	140
36	Integrating water exclusion theory into Î² contacts to predict binding free energy changes and binding hot spots. BMC Bioinformatics, 2014, 15, 57.	1.2	8

#	Article	IF	Citations
37	Solventâ€accessible surface area: How well can be applied to hotâ€spot detection?. Proteins: Structure, Function and Bioinformatics, 2014, 82, 479-490.	1.5	22
38	Interolog interfaces in proteinâ€“protein docking. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1940-1946.	1.5	6
39	PPCheck: A Webserver for the Quantitative Analysis of Protein-Protein Interfaces and Prediction of Residue Hotspots. Bioinformatics and Biology Insights, 2015, 9, BBI.S25928.	1.0	61
40	A Web Resource for Standardized Benchmark Datasets, Metrics, and Rosetta Protocols for Macromolecular Modeling and Design. PLoS ONE, 2015, 10, e0130433.	1.1	85
41	Surfing the Protein-Protein Interaction Surface Using Docking Methods: Application to the Design of PPI Inhibitors. Molecules, 2015, 20, 11569-11603.	1.7	61
42	The D0 Ig-like Domain Plays a Central Role in the Stronger Binding of KIR3DL2 to B27 Free H Chain Dimers. Journal of Immunology, 2015, 194, 1591-1601.	0.4	8
43	Medicinal value of asiaticoside for Alzheimerâ€™s disease as assessed using single-molecule-detection fluorescence correlation spectroscopy, laser-scanning microscopy, transmission electron microscopy, and in silico docking. BMC Complementary and Alternative Medicine, 2015, 15, 118.	3.7	26
44	The FTMap family of web servers for determining and characterizing ligand-binding hot spots of proteins. Nature Protocols, 2015, 10, 733-755.	5.5	496
45	Solvent Accessible Surface Area-Based Hot-Spot Detection Methods for Proteinâ€“Protein and Proteinâ€“Nucleic Acid Interfaces. Journal of Chemical Information and Modeling, 2015, 55, 1077-1086.	2.5	33
46	Burial Level Change Defines a High Energetic Relevance for Protein Binding Interfaces. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 410-421.	1.9	1
47	A new scoring function for proteinâ€“protein docking that identifies native structures with unprecedented accuracy. Physical Chemistry Chemical Physics, 2015, 17, 2378-2387.	1.3	14
48	CCharPPI web server: computational characterization of proteinâ€“protein interactions from structure. Bioinformatics, 2015, 31, 123-125.	1.8	61
49	A Machine Learning Approach for Hot-Spot Detection at Protein-Protein Interfaces. International Journal of Molecular Sciences, 2016, 17, 1215.	1.8	46
50	Deciphering Dimerization Modes of PAS Domains: Computational and Experimental Analyses of the AhR:ARNT Complex Reveal New Insights Into the Mechanisms of AhR Transformation. PLoS Computational Biology, 2016, 12, e1004981.	1.5	28
51	Predicting Proteinâ€“Protein Interactions from the Molecular to the Proteome Level. Chemical Reviews, 2016, 116, 4884-4909.	23.0	289
52	Transthyretin variants with improved inhibition of Î²-amyloid aggregation. Protein Engineering, Design and Selection, 2016, 29, 209-218.	1.0	22
53	Structure-based design and confirmation of peptide ligands for neuronal polo-like kinase to promote neuroregeneration. Computational Biology and Chemistry, 2016, 61, 238-244.	1.1	2
54	Accurate Prediction of Protein Hot Spots Residues Based on Gentle AdaBoost Algorithm. Lecture Notes in Computer Science, 2016, , 742-749.	1.0	1

#	Article	IF	Citations
55	Molecular modeling of structural and functional variance in the SAGA deubiquitinating module caused by Sgf73 Y57A mutation. RSC Advances, 2016, 6, 74991-75001.	1.7	1
56	CryptoSite: Expanding the Druggable Proteome by Characterization and Prediction of Cryptic Binding Sites. Journal of Molecular Biology, 2016, 428, 709-719.	2.0	190
57	Computational modeling of protein assemblies. Current Opinion in Structural Biology, 2017, 44, 179-189.	2.6	47
58	PRMT7 Interacts with ASS1 and Citrullinemia Mutations Disrupt the Interaction. Journal of Molecular Biology, 2017, 429, 2278-2289.	2.0	9
59	Network analysis and in silico prediction of proteinâ€“protein interactions with applications in drug discovery. Current Opinion in Structural Biology, 2017, 44, 134-142.	2.6	76
60	Combining ancestral sequence reconstruction with protein design to identify an interface hotspot in a key metabolic enzyme complex. Proteins: Structure, Function and Bioinformatics, 2017, 85, 312-321.	1.5	14
61	In silico methods for design of biological therapeutics. Methods, 2017, 131, 33-65.	1.9	49
62	Inhibition of TRAF6-Ubc13 interaction in NFkB inflammatory pathway by analyzing the hotspot amino acid residues and proteinâ€“protein interactions using molecular docking simulations. Computational Biology and Chemistry, 2017, 70, 116-124.	1.1	10
63	SpotOn: High Accuracy Identification of Protein-Protein Interface Hot-Spots. Scientific Reports, 2017, 7, 8007.	1.6	77
64	Protein binding hot spots prediction from sequence only by a new ensemble learning method. Amino Acids, 2017, 49, 1773-1785.	1.2	35
65	Method for predicting hot spot residues at protein-protein interface based on the extreme learning machine. , 2017, , .		1
66	Understanding Insulin Endocrinology in Decapod Crustacea: Molecular Modelling Characterization of an Insulin-Binding Protein and Insulin-Like Peptides in the Eastern Spiny Lobster, Sagmariasus verreauxi. International Journal of Molecular Sciences, 2017, 18, 1832.	1.8	37
67	Modeling of RAS complexes supports roles in cancer for less studied partners. BMC Biophysics, 2017, 10, 5.	4.4	10
68	Flex ddG: Rosetta Ensemble-Based Estimation of Changes in Proteinâ€“Protein Binding Affinity upon Mutation. Journal of Physical Chemistry B, 2018, 122, 5389-5399.	1.2	192
69	Identification of Strategic Residues at the Interface of Antigenâ€“Antibody Interactions by In Silico Mutagenesis. Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 438-448.	2.2	6
70	Complementarity of stability patches at the interfaces of protein complexes: Implication for the structural organization of energetic hot spots. Proteins: Structure, Function and Bioinformatics, 2018, 86, 229-236.	1.5	4
71	Probing the cooperative mechanism of the Î¼â€“Î´ opioid receptor heterodimer by multiscale simulation. Physical Chemistry Chemical Physics, 2018, 20, 29969-29982.	1.3	24
72	PredT4SE-Stack: Prediction of Bacterial Type IV Secreted Effectors From Protein Sequences Using a Stacked Ensemble Method. Frontiers in Microbiology, 2018, 9, 2571.	1.5	107

#	Article	IF	Citations
73	Enhanced Prediction of Hot Spots at Protein-Protein Interfaces Using Extreme Gradient Boosting. Scientific Reports, 2018, 8, 14285.	1.6	68
74	Machine Learning Approaches for Proteinâ€“Protein Interaction Hot Spot Prediction: Progress and Comparative Assessment. Molecules, 2018, 23, 2535.	1.7	67
75	Analysis of single amino acid variations in singlet hot spots of proteinâ€“protein interfaces. Bioinformatics, 2018, 34, i795-i801.	1.8	22
76	PseUI: Pseudouridine sites identification based on RNA sequence information. BMC Bioinformatics, 2018, 19, 306.	1.2	105
77	Hot Spot-Based Design of Small-Molecule Inhibitors for Protein-Protein Interactions. , 2018, , 53-71.		1
78	Structural Prediction of Proteinâ€“Protein Interactions by Docking: Application to Biomedical Problems. Advances in Protein Chemistry and Structural Biology, 2018, 110, 203-249.	1.0	13
79	Protein-protein interface hot spots prediction based on a hybrid feature selection strategy. BMC Bioinformatics, 2018, 19, 14.	1.2	86
80	EPO does not promote interaction between the erythropoietin and beta-common receptors. Scientific Reports, 2018, 8, 12457.	1.6	21
81	Node-Weighted Amino Acid Network Strategy for Characterization and Identification of Protein Functional Residues. Journal of Chemical Information and Modeling, 2018, 58, 2024-2032.	2.5	20
82	Evolution of In Silico Strategies for Protein-Protein Interaction Drug Discovery. Molecules, 2018, 23, 1963.	1.7	87
83	Structural insights into pharmacophore-assisted in silico identification of proteinâ€“protein interaction inhibitors for inhibition of human toll-like receptor 4 â€“ myeloid differentiation factor-2 (hTLR4â^'MD-2) complex. Journal of Biomolecular Structure and Dynamics, 2019, 37, 1968-1991.	2.0	12
85	Proteomics and Non-proteomics Approaches to Study Stable and Transient Protein-Protein Interactions. Advances in Experimental Medicine and Biology, 2019, 1140, 121-142.	0.8	3
86	Elevated neoantigen levels in tumors with somatic mutations in the HLA-A, HLA-B, HLA-C and B2M genes. BMC Medical Genomics, 2019, 12, 107.	0.7	68
87	Specific inter-domain interactions stabilize a compact HIV-1 Gag conformation. PLoS ONE, 2019, 14, e0221256.	1.1	2
88	Interactome of Glyceraldehyde-3-Phosphate Dehydrogenase Points to the Existence of Metabolons in Paracoccidioides lutzii. Frontiers in Microbiology, 2019, 10, 1537.	1.5	26
89	Computational analysis of hot spots and binding mechanism in the PD-1/PD-L1 interaction. RSC Advances, 2019, 9, 14944-14956.	1.7	23
90	Presence of actin binding motif in VgrG-1 toxin of Vibrio cholerae reveals the molecular mechanism of actin cross-linking. International Journal of Biological Macromolecules, 2019, 133, 775-785.	3.6	12
91	Feature Design for Protein Interface Hotspots Using KFC2 and Rosetta. Association for Women in Mathematics Series, 2019, , 177-197.	0.1	0

#	Article	IF	Citations
92	An Overview of Computational Methods, Tools, Servers, and Databases for Drug Repurposing. , 2019, , 743-780.		16
93	Rational Design of Antiangiogenic Helical Oligopeptides Targeting the Vascular Endothelial Growth Factor Receptors. Frontiers in Chemistry, 2019, 7, 170.	1.8	10
94	Deamidation disrupts native and transient contacts to weaken the interaction between UBC13 and RING-finger E3 ligases. ELife, 2019, 8, .	2.8	11
95	Association of functional variants and protein-to-protein physical interactions of human MutY homolog linked with familial adenomatous polyposis and colorectal cancer syndrome. Non-coding RNA Research, 2019, 4, 155-173.	2.4	1
96	Identifying Driver Interfaces Enriched for Somatic Missense Mutations in Tumors. Methods in Molecular Biology, 2019, 1907, 51-72.	0.4	4
97	In silico structure-based design of enhanced peptide inhibitors targeting RNA polymerase PAN-PB1C interaction. Computational Biology and Chemistry, 2019, 78, 273-281.	1.1	3
98	Calculation of hot spots for proteinâ€“protein interaction in p53/PMIâ€MDM2/MDMX complexes. Journal of Computational Chemistry, 2019, 40, 1045-1056.	1.5	22
99	Methods for Discovering and Targeting Druggable Protein-Protein Interfaces and Their Application to Repurposing. Methods in Molecular Biology, 2019, 1903, 1-21.	0.4	29
100	A feature-based approach to predict hot spots in proteinâ€“DNA binding interfaces. Briefings in Bioinformatics, 2020, 21, 1038-1046.	3.2	31
101	Prediction and targeting of GPCR oligomer interfaces. Progress in Molecular Biology and Translational Science, 2020, 169, 105-149.	0.9	13
102	Identification of a Cry1Fa binding site of cadherin in Plutella xylostella through fragment exchanging and molecular docking methods. International Journal of Biological Macromolecules, 2020, 146, 62-69.	3.6	3
103	Interaction of Isocitrate Lyase with Proteins Involved in the Energetic Metabolism in Paracoccidioides lutzii. Journal of Fungi (Basel, Switzerland), 2020, 6, 309.	1.5	2
104	Computational design of antagonist peptides based on the structure of secreted frizzled-related protein-1 (SFRP1) aiming to inhibit Wnt signaling pathway. Journal of Biomolecular Structure and Dynamics, 2022, 40, 2169-2188.	2.0	11
105	SPOTONE: Hot Spots on Protein Complexes with Extremely Randomized Trees via Sequence-Only Features. International Journal of Molecular Sciences, 2020, 21, 7281.	1.8	12
106	Supercomputer-Based Ensemble Docking Drug Discovery Pipeline with Application to Covid-19. Journal of Chemical Information and Modeling, 2020, 60, 5832-5852.	2.5	134
107	iPNHOT: a knowledge-based approach for identifying protein-nucleic acid interaction hot spots. BMC Bioinformatics, 2020, 21, 289.	1.2	11
109	Expression of quasi-equivalence and capsid dimorphism in the Hepadnaviridae. PLoS Computational Biology, 2020, 16, e1007782.	1.5	10
110	Effects of SARSâ€CoVâ€2 mutations on protein structures and intraviral proteinâ€“protein interactions. Journal of Medical Virology, 2021, 93, 2132-2140.	2.5	85

#	Article	IF	Citations
111	Computational Hotâ€Spot Analysis of the SARSâ€CoVâ€2 Receptor Binding Domain/ACE2 Complex**. ChemBioChem, 2021, 22, 1196-1200.	1.3	5
112	Molecular dynamics analysis of the binding of human interleukinâ€6 with interleukinâ€6 <scp>Î±â€receptor</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 163-173.	1.5	4
113	Interacting with Hemoglobin: Paracoccidioides spp. Recruits hsp30 on Its Cell Surface for Enhanced Ability to Use This Iron Source. Journal of Fungi (Basel, Switzerland), 2021, 7, 21.	1.5	5
114	Prediction, Analysis, Visualization, and Storage of Proteinâ€"Protein Interactions Using Computational Approaches. , 2021, , 265-346.		1
115	Design of novel peptide inhibitors against the conserved bacterial transcription terminator, Rho. Journal of Biological Chemistry, 2021, 296, 100653.	1.6	4
116	Robust principal component analysisâ€based prediction of <scp>proteinâ€protein</scp> interaction hot spots. Proteins: Structure, Function and Bioinformatics, 2021, 89, 639-647.	1.5	11
118	In silico Approaches for the Design and Optimization of Interfering Peptides Against Proteinâ€"Protein Interactions. Frontiers in Molecular Biosciences, 2021, 8, 669431.	1.6	38
119	An improved DNA-binding hot spot residues prediction method by exploring interfacial neighbor properties. BMC Bioinformatics, 2021, 22, 253.	1.2	4
120	Hotspot Coevolution Is a Key Identifier of Near-Native Protein Complexes. Journal of Physical Chemistry B, 2021, 125, 6058-6067.	1.2	1
121	The dual role of SrbA from Paracoccidioides lutzii: a hypoxic regulator. Brazilian Journal of Microbiology, 2021, 52, 1135-1149.	0.8	0
122	Dockingâ€based generation of antibodies mimicking <scp>Cry1A</scp>/<scp>1B</scp> protein binding sites as potential insecticidal agents against diamondback moth (Plutella xylostella). Pest Management Science, 2021, 77, 4593-4606.	1.7	6
124	The ribosomal protein eL21 interacts with the protein lysine methyltransferase SMYD2 and regulates its steady state levels. Biochimica Et Biophysica Acta - Molecular Cell Research, 2021, 1868, 119079.	1.9	1
125	Predicting functional consequences of mutations using molecular interaction network features. Human Genetics, 2022, 141, 1195-1210.	1.8	9
126	Designing an epitope vaccine against Dermatophagoides pteronyssinus: An in silico study. Acta Tropica, 2021, 222, 106028.	0.9	11
127	Rational design of a potent macrocyclic peptide inhibitor targeting the PD-1/PD-L1 proteinâ€"protein interaction. RSC Advances, 2021, 11, 23270-23279.	1.7	6
128	Boosting Prediction Performance of Protein-Protein Interaction Hot Spots by Using Structural Neighborhood Properties. Lecture Notes in Computer Science, 2013, , 333-344.	1.0	3
129	Rosetta custom score functions accurately predict Î”Î”G of mutations at proteinâ€"protein interfaces using machine learning. Chemical Communications, 2020, 56, 6774-6777.	2.2	10
131	Rapid prediction of crucial hotspot interactions for icosahedral viral capsid self-assembly by energy landscape atlasing validated by mutagenesis. PLoS Computational Biology, 2020, 16, e1008357.	1.5	2

#	Article	IF	Citations
132	Tracking Molecular Recognition at the Atomic Level with a New Protein Scaffold Based on the OB-Fold. PLoS ONE, 2014, 9, e86050.	1.1	20
133	Lactoferrin binding protein B â€“ a bi-functional bacterial receptor protein. PLoS Pathogens, 2017, 13, e1006244.	2.1	27
134	Discovery of peptide inhibitors targeting human programmed death 1 (PD-1) receptor. Oncotarget, 2016, 7, 64967-64976.	0.8	42
135	Predicting hot spots in protein interfaces based on protrusion index, pseudo hydrophobicity and electron-ion interaction pseudopotential features. Oncotarget, 2016, 7, 18065-18075.	0.8	21
136	Computational Prediction of Protein Hot Spot Residues. Current Pharmaceutical Design, 2012, 18, 1255-1265.	0.9	86
137	Decoding Protein-protein Interactions: An Overview. Current Topics in Medicinal Chemistry, 2020, 20, 855-882.	1.0	13
138	A Sequence-segment Neighbor Encoding Schema for Protein Hotspot Residue Prediction. Current Bioinformatics, 2020, 15, 445-454.	0.7	9
140	Computational Analyses of Docosahexaenoic Acid (DHA, C22:6, n-3) with Alzheimerâ€™s Disease-Causing Amyloid Peptide A<i>Î²</i>₁₋₄₂ Reassures Its Therapeutic Utility. Advances in Alzheimer's Disease, 2016, 05, 73-86.	0.3	2
141	IFACE: A BIOINFORMATICS TOOL FOR THE ANALYSIS OF PROTEIN-PROTEIN INTERFACE. International Journal for Computational Biology, 2012, 1, 37.	0.1	0
142	Comparative Assessment of Data Sets of Protein Interaction Hot Spots Used in the Computational Method. Lecture Notes in Computer Science, 2014, , 478-486.	1.0	0
143	Prediction of Hot Spots in Dimer Interface of Green Fluorescent Protein. Lecture Notes in Electrical Engineering, 2018, , 349-355.	0.3	0
153	Developing a machine learning model to identify proteinâ€“protein interaction hotspots to facilitate drug discovery. PeerJ, 2020, 8, e10381.	0.9	2
156	In silico Techniques for Prospecting and Characterizing Monoclonal Antibodies. , 0, , .		1
158	The Increased Level of Serum p53 in Hepatitis B-Associated Liver Cirrhosis. Iranian Journal of Medical Sciences, 2014, 39, 446-51.	0.3	6
159	Identifying mutation specific cancer pathways using a structurally resolved protein interaction network. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 84-95.	0.7	7
160	In-silico design of peptides for inhibition of HLA-A*03-KLIETYFSK complex as a new drug design for treatment of multiples sclerosis disease. Journal of Molecular Graphics and Modelling, 2022, 111, 108079.	1.3	1
162	Sequence Divergence and Functional Specializations of the Ancient Spliceosomal SF3b: Implications in Flexibility and Adaptations of the Multi-Protein Complex. Frontiers in Genetics, 2021, 12, 747344.	1.1	1
163	Artificial intelligence based methods for hot spot prediction. Current Opinion in Structural Biology, 2022, 72, 209-218.	2.6	16

#	Article	IF	Citations
164	Comparative study of SARS-CoV-2 infection in different cell types: Biophysical-computational approach to the role of potential receptors. Computers in Biology and Medicine, 2022, 142, 105245.	3.9	3
165	Using machineâ€learningâ€driven approaches to boost hotâ€spot's knowledge. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, .	6.2	2
166	PPI-Hotspot^{DB}: Database of Proteinâ€“Protein Interaction Hot Spots. Journal of Chemical Information and Modeling, 2022, 62, 1052-1060.	2.5	12
167	A structural model of the human plasminogen and Aspergillus fumigatus enolase complex. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1509-1520.	1.5	0
179	Molecular Docking and In Silico Simulation of Trichinella spiralis Membrane-Associated Progesterone Receptor Component 2 (Ts-MAPRC2) and Its Interaction with Human PGRMC1. BioMed Research International, 2022, 2022, 1-10.	0.9	3
180	The free energy folding penalty accompanying binding of intrinsically disordered Î±â€helical motifs. Protein Science, 2022, 31, .	3.1	5
181	C. elegans ribosomal protein S3 protects against H2O2-induced DNA damage and suppresses spontaneous mutations in yeast. DNA Repair, 2022, 117, 103359.	1.3	1
182	Identification of Small-Molecule Inhibitors of Fibroblast Growth Factor 23 Signaling via In Silico Hot Spot Prediction and Molecular Docking to Î±-Klotho. Journal of Chemical Information and Modeling, 2022, 62, 3627-3637.	2.5	5
183	Quaternary organization of the human eEF1B complex reveals unique multi-GEF domain assembly. Nucleic Acids Research, 2022, 50, 9490-9504.	6.5	4
185	Structural and functional characterization of NEMO cleavage by SARS-CoV-2 3CLpro. Nature Communications, 2022, 13, .	5.8	12
187	A novel deleterious oxytocin variant is associated with the lower twinning ratio in Awassi ewes. Animal Biotechnology, 0, , 1-12.	0.7	4
188	Analysis of critical proteinâ€“protein interactions of SARS-CoV-2 capping and proofreading molecular machineries towards designing dual target inhibitory peptides. Scientific Reports, 2023, 13, .	1.6	3
190	Molecular Interactions of the Copper Chaperone Atx1 of Paracoccidioides brasiliensis with Fungal Proteins Suggest a Crosstalk between Iron and Copper Homeostasis. Microorganisms, 2023, 11, 248.	1.6	0
191	Initiation of fatty acid biosynthesis in Pseudomonas putida KT2440. Metabolic Engineering, 2023, 76, 193-203.	3.6	6
192	Molecular Simulation Study on the Interaction between Porcine CR1-like and C3b. Molecules, 2023, 28, 2183.	1.7	1
193	Computational design of a cyclic peptide that inhibits the CTLA4 immune checkpoint. RSC Medicinal Chemistry, 2023, 14, 658-670.	1.7	7
198	Techniques for Developing Reliable Machine Learning Classifiers Applied to Understanding and Predicting Protein:Protein Interaction Hot Spots. Methods in Molecular Biology, 2024, , 235-268.	0.4	0