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List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

59
papers

3,261
citations

26
h-index

57
g-index

63
ext. papers

3,996
ext. citations

9.3
avg, IF

5.11
L-index

#	Paper	IF	Citations
59	Phage display identification of nanomolar ligands for human NEDD4-WW3: Energetic and dynamic implications for the development of broad-spectrum antivirals.. <i>International Journal of Biological Macromolecules</i> , 2022 , 207, 308-323	7.9	
58	Deep generative modeling for protein design.. <i>Current Opinion in Structural Biology</i> , 2021 , 72, 226-236	8.1	2
57	Computational Design of Potent D-Peptide Inhibitors of SARS-CoV-2. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 14955-14967	8.3	5
56	ELASPIC2 (EL2): Combining Contextualized Language Models and Graph Neural Networks to Predict Effects of Mutations. <i>Journal of Molecular Biology</i> , 2021 , 433, 166810	6.5	5
55	Computational generation of proteins with predetermined three-dimensional shapes using ProteinSolver. <i>STAR Protocols</i> , 2021 , 2, 100505	1.4	1
54	Large-scale survey and database of high affinity ligands for peptide recognition modules. <i>Molecular Systems Biology</i> , 2020 , 16, e9310	12.2	11
53	A Method to Calculate the Relative Binding Free Energy Differences of β -Helical Stapled Peptides. <i>Journal of Organic Chemistry</i> , 2020 , 85, 1644-1651	4.2	3
52	Fast and Flexible Protein Design Using Deep Graph Neural Networks. <i>Cell Systems</i> , 2020 , 11, 402-411.e4	10.6	37
51	The geometric influence on the Cys2His2 zinc finger domain and functional plasticity. <i>Nucleic Acids Research</i> , 2020 , 48, 6382-6402	20.1	1
50	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAG15 challenge. <i>Human Mutation</i> , 2019 , 40, 1392-1399	4.7	11
49	A Multireporter Bacterial 2-Hybrid Assay for the High-Throughput and Dynamic Assay of PDZ Domain-Peptide Interactions. <i>ACS Synthetic Biology</i> , 2019 , 8, 918-928	5.7	5
48	Predicting changes in protein stability caused by mutation using sequence-and structure-based methods in a CAG15 blind challenge. <i>Human Mutation</i> , 2019 , 40, 1414-1423	4.7	14
47	Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. <i>Journal of Molecular Biology</i> , 2019 , 431, 336-350	6.5	11
46	Rapid and accurate structure-based therapeutic peptide design using GPU accelerated thermodynamic integration. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 236-244	4.2	5
45	Predicting the Effect of Mutations on Protein Folding and Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2019 , 1851, 1-17	1.4	9
44	Method to generate highly stable D-amino acid analogs of bioactive helical peptides using a mirror image of the entire PDB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 1505-1510	11.5	54
43	The Chemical Fluctuation Theorem governing gene expression. <i>Nature Communications</i> , 2018 , 9, 297	17.4	18

42	The present and the future of motif-mediated protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2018 , 50, 162-170	8.1	15
41	A PxL motif promotes timely cell cycle substrate dephosphorylation by the Cdc14 phosphatase. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 1093-1102	17.6	21
40	A computational approach for designing D-proteins with non-canonical amino acid optimised binding affinity. <i>PLoS ONE</i> , 2017 , 12, e0187524	3.7	5
39	Data driven flexible backbone protein design. <i>PLoS Computational Biology</i> , 2017 , 13, e1005722	5	8
38	Comprehensive Analysis of the Human SH3 Domain Family Reveals a Wide Variety of Non-canonical Specificities. <i>Structure</i> , 2017 , 25, 1598-1610.e3	5.2	56
37	Large-Scale Interaction Profiling of Protein Domains Through Proteomic Peptide-Phage Display Using Custom Peptidomes. <i>Methods in Molecular Biology</i> , 2017 , 1518, 213-226	1.4	1
36	Strategies to Develop Inhibitors of Motif-Mediated Protein-Protein Interactions as Drug Leads. <i>Annual Review of Pharmacology and Toxicology</i> , 2017 , 57, 39-60	17.9	27
35	Non-base-contacting residues enable kaleidoscopic evolution of metazoan C2H2 zinc finger DNA binding. <i>Genome Biology</i> , 2017 , 18, 167	18.3	20
34	Protein engineering by highly parallel screening of computationally designed variants. <i>Science Advances</i> , 2016 , 2, e1600692	14.3	21
33	PAT: predictor for structured units and its application for the optimization of target molecules for the generation of synthetic antibodies. <i>BMC Bioinformatics</i> , 2016 , 17, 150	3.6	
32	Motif mediated protein-protein interactions as drug targets. <i>Cell Communication and Signaling</i> , 2016 , 14, 8	7.5	52
31	ELASPIC web-server: proteome-wide structure-based prediction of mutation effects on protein stability and binding affinity. <i>Bioinformatics</i> , 2016 , 32, 1589-91	7.2	37
30	Proteomic peptide phage display uncovers novel interactions of the PDZ1-2 supramodule of syntenin. <i>FEBS Letters</i> , 2016 , 590, 3-12	3.8	18
29	Pooled screening for antiproliferative inhibitors of protein-protein interactions. <i>Nature Chemical Biology</i> , 2016 , 12, 275-81	11.7	26
28	A high-throughput pipeline for the production of synthetic antibodies for analysis of ribonucleoprotein complexes. <i>Rna</i> , 2016 , 22, 636-55	5.8	16
27	JBASE: Joint Bayesian Analysis of Subphenotypes and Epistasis. <i>Bioinformatics</i> , 2016 , 32, 203-10	7.2	4
26	A structural approach reveals how neighbouring C2H2 zinc fingers influence DNA binding specificity. <i>Nucleic Acids Research</i> , 2015 , 43, 9147-57	20.1	30
25	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. <i>Cell Reports</i> , 2015 , 12, 183-9	10.6	17

24	C2H2 zinc finger proteins greatly expand the human regulatory lexicon. <i>Nature Biotechnology</i> , 2015 , 33, 555-62	44.5	194
23	A systematic approach to identify novel cancer drug targets using machine learning, inhibitor design and high-throughput screening. <i>Genome Medicine</i> , 2014 , 6, 57	14.4	67
22	Combining structural modeling with ensemble machine learning to accurately predict protein fold stability and binding affinity effects upon mutation. <i>PLoS ONE</i> , 2014 , 9, e107353	3.7	53
21	Large-scale interaction profiling of PDZ domains through proteomic peptide-phage display using human and viral phage peptidomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 2542-7	11.5	82
20	Quantitative genome-wide genetic interaction screens reveal global epistatic relationships of protein complexes in Escherichia coli. <i>PLoS Genetics</i> , 2014 , 10, e1004120	6	71
19	Distinct types of disorder in the human proteome: functional implications for alternative splicing. <i>PLoS Computational Biology</i> , 2013 , 9, e1003030	5	48
18	Computational analysis of interactomes: current and future perspectives for bioinformatics approaches to model the host-pathogen interaction space. <i>Methods</i> , 2012 , 57, 508-18	4.6	35
17	Elucidation of the binding preferences of peptide recognition modules: SH3 and PDZ domains. <i>FEBS Letters</i> , 2012 , 586, 2631-7	3.8	39
16	An omics perspective of protein disorder. <i>Molecular BioSystems</i> , 2012 , 8, 185-93		10
15	Computational structural analysis of protein interactions and networks. <i>Proteomics</i> , 2012 , 12, 1697-705	4.8	13
14	Network evolution: rewiring and signatures of conservation in signaling. <i>PLoS Computational Biology</i> , 2012 , 8, e1002411	5	27
13	The multiple-specificity landscape of modular peptide recognition domains. <i>Molecular Systems Biology</i> , 2011 , 7, 484	12.2	67
12	Identification of specificity determining residues in peptide recognition domains using an information theoretic approach applied to large-scale binding maps. <i>BMC Biology</i> , 2011 , 9, 53	7.3	14
11	Coevolution of PDZ domain-ligand interactions analyzed by high-throughput phage display and deep sequencing. <i>Molecular BioSystems</i> , 2010 , 6, 1782-90		85
10	Deciphering protein kinase specificity through large-scale analysis of yeast phosphorylation site motifs. <i>Science Signaling</i> , 2010 , 3, ra12	8.8	262
9	MOTIPS: automated motif analysis for predicting targets of modular protein domains. <i>BMC Bioinformatics</i> , 2010 , 11, 243	3.6	25
8	Bayesian modeling of the yeast SH3 domain interactome predicts spatiotemporal dynamics of endocytosis proteins. <i>PLoS Biology</i> , 2009 , 7, e1000218	9.7	151
7	The role of disorder in interaction networks: a structural analysis. <i>Molecular Systems Biology</i> , 2008 , 4, 179	12.2	167

6	Analysis of copy number variants and segmental duplications in the human genome: Evidence for a change in the process of formation in recent evolutionary history. <i>Genome Research</i> , 2008 , 18, 1865-74	9-7	114
5	The importance of bottlenecks in protein networks: correlation with gene essentiality and expression dynamics. <i>PLoS Computational Biology</i> , 2007 , 3, e59	5	657
4	Positive selection at the protein network periphery: evaluation in terms of structural constraints and cellular context. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 20274-9	11-5	111
3	Relating three-dimensional structures to protein networks provides evolutionary insights. <i>Science</i> , 2006 , 314, 1938-41	33-3	388
2	Fast and flexible design of novel proteins using graph neural networks		6
1	PepNN: a deep attention model for the identification of peptide binding sites		3