

List of Publications by Citations

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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.

56 papers	8,172 citations	27 h-index	62 g-index
62 ext. papers	11,273 ext. citations	8.1 avg, IF	6.74 L-index

#	Paper	IF	Citations
56	The I-TASSER Suite: protein structure and function prediction. <i>Nature Methods</i> , 2015 , 12, 7-8	21.6	3430
55	I-TASSER server: new development for protein structure and function predictions. <i>Nucleic Acids Research</i> , 2015 , 43, W174-81	20.1	1059
54	Improved protein structure prediction using predicted interresidue orientations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 1496-1503	11.5	496
53	Protein-ligand binding site recognition using complementary binding-specific substructure comparison and sequence profile alignment. <i>Bioinformatics</i> , 2013 , 29, 2588-95	7.2	483
52	COFACTOR: an accurate comparative algorithm for structure-based protein function annotation. <i>Nucleic Acids Research</i> , 2012 , 40, W471-7	20.1	448
51	BioLiP: a semi-manually curated database for biologically relevant ligand-protein interactions. <i>Nucleic Acids Research</i> , 2013 , 41, D1096-103	20.1	348
50	Protein Structure and Function Prediction Using I-TASSER. <i>Current Protocols in Bioinformatics</i> , 2015 , 52, 5.8.1-5.8.15	24.2	214
49	PotentialNet for Molecular Property Prediction. <i>ACS Central Science</i> , 2018 , 4, 1520-1530	16.8	155
48	Advances in GPCR modeling evaluated by the GPCR Dock 2013 assessment: meeting new challenges. <i>Structure</i> , 2014 , 22, 1120-1139	5.2	136
47	A comparative assessment and analysis of 20 representative sequence alignment methods for protein structure prediction. <i>Scientific Reports</i> , 2013 , 3, 2619	4.9	128
46	GPCR-I-TASSER: A Hybrid Approach to G Protein-Coupled Receptor Structure Modeling and the Application to the Human Genome. <i>Structure</i> , 2015 , 23, 1538-1549	5.2	121
45	Prediction of protein structural classes by recurrence quantification analysis based on chaos game representation. <i>Journal of Theoretical Biology</i> , 2009 , 257, 618-26	2.3	97
44	COACH-D: improved protein-ligand binding sites prediction with refined ligand-binding poses through molecular docking. <i>Nucleic Acids Research</i> , 2018 , 46, W438-W442	20.1	77
43	ResQ: An Approach to Unified Estimation of B-Factor and Residue-Specific Error in Protein Structure Prediction. <i>Journal of Molecular Biology</i> , 2016 , 428, 693-701	6.5	76
42	Prediction of protein structural classes for low-homology sequences based on predicted secondary structure. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 1, S9	3.6	62
41	GLASS: a comprehensive database for experimentally validated GPCR-ligand associations. <i>Bioinformatics</i> , 2015 , 31, 3035-42	7.2	57
40	Recognizing metal and acid radical ion-binding sites by integrating ab initio modeling with template-based transferals. <i>Bioinformatics</i> , 2016 , 32, 3260-3269	7.2	56

39	Improving taxonomy-based protein fold recognition by using global and local features. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 2053-64	4.2	50
38	Integration of QUARK and I-TASSER for Ab Initio Protein Structure Prediction in CASP11. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 76-86	4.2	47
37	Structural and Sequence Similarity Makes a Significant Impact on Machine-Learning-Based Scoring Functions for Protein-Ligand Interactions. <i>Journal of Chemical Information and Modeling</i> , 2017 , 57, 1007-1012	6.1	46
36	Protein contact prediction using metagenome sequence data and residual neural networks. <i>Bioinformatics</i> , 2020 , 36, 41-48	7.2	43
35	Template-based protein structure prediction in CASP11 and retrospect of I-TASSER in the last decade. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 233-46	4.2	42
34	Super Spy variants implicate flexibility in chaperone action. <i>ELife</i> , 2014 , 3, e01584	8.9	38
33	The trRosetta server for fast and accurate protein structure prediction. <i>Nature Protocols</i> , 2021 , 16, 5634-5651	10.5	36
32	mTM-align: a server for fast protein structure database search and multiple protein structure alignment. <i>Nucleic Acids Research</i> , 2018 , 46, W380-W386	20.1	32
31	mTM-align: an algorithm for fast and accurate multiple protein structure alignment. <i>Bioinformatics</i> , 2018 , 34, 1719-1725	7.2	31
30	In various protein complexes, disordered protomers have large per-residue surface areas and area of protein-, DNA- and RNA-binding interfaces. <i>FEBS Letters</i> , 2015 , 589, 2561-9	3.8	30
29	An improved classification of G-protein-coupled receptors using sequence-derived features. <i>BMC Bioinformatics</i> , 2010 , 11, 420	3.6	27
28	Clustering structures of large proteins using multifractal analyses based on a 6-letter model and hydrophobicity scale of amino acids. <i>Chaos, Solitons and Fractals</i> , 2009 , 40, 607-620	9.3	22
27	Human Pol II promoter recognition based on primary sequences and free energy of dinucleotides. <i>BMC Bioinformatics</i> , 2008 , 9, 113	3.6	21
26	Computational Prediction of MoRFs, Short Disorder-to-order Transitioning Protein Binding Regions. <i>Computational and Structural Biotechnology Journal</i> , 2019 , 17, 454-462	6.8	20
25	Histatin 5 binds to Porphyromonas gingivalis hemagglutinin B (HagB) and alters HagB-induced chemokine responses. <i>Scientific Reports</i> , 2014 , 4, 3904	4.9	20
24	A large-scale comparative assessment of methods for residue-residue contact prediction. <i>Briefings in Bioinformatics</i> , 2018 , 19, 219-230	13.4	20
23	A small shared epitope-mimetic compound potentially accelerates osteoclast-mediated bone damage in autoimmune arthritis. <i>Journal of Immunology</i> , 2013 , 191, 2096-103	5.3	18
22	Improving the prediction of protein-nucleic acids binding residues via multiple sequence profiles and the consensus of complementary methods. <i>Bioinformatics</i> , 2019 , 35, 930-936	7.2	18

21	SARS-CoV-2 Nucleocapsid protein attenuates stress granule formation and alters gene expression via direct interaction with host mRNAs		17
20	Improved protein structure prediction using predicted inter-residue orientations		17
19	SARS-CoV-2 nucleocapsid protein binds host mRNAs and attenuates stress granules to impair host stress response.. <i>IScience</i> , 2022 , 25, 103562	6.1	15
18	An ensemble approach to protein fold classification by integration of template-based assignment and support vector machine classifier. <i>Bioinformatics</i> , 2017 , 33, 863-870	7.2	15
17	Improving Sequence-Based Prediction of Protein-Peptide Binding Residues by Introducing Intrinsic Disorder and a Consensus Method. <i>Journal of Chemical Information and Modeling</i> , 2018 , 58, 1459-1468	6.1	14
16	Improved Protein Structure Prediction Using a New Multi-Scale Network and Homologous Templates. <i>Advanced Science</i> , 2021 , e2102592	13.6	11
15	Identification of partially linear structure in additive models with an application to gene expression prediction from sequences. <i>Biometrics</i> , 2012 , 68, 437-45	1.8	10
14	Enhanced prediction of RNA solvent accessibility with long short-term memory neural networks and improved sequence profiles. <i>Bioinformatics</i> , 2019 , 35, 1686-1691	7.2	9
13	CoABind: a novel algorithm for Coenzyme A (CoA)- and CoA derivatives-binding residues prediction. <i>Bioinformatics</i> , 2018 , 34, 2598-2604	7.2	8
12	DLTree: efficient and accurate phylogeny reconstruction using the dynamical language method. <i>Bioinformatics</i> , 2017 , 33, 2214-2215	7.2	7
11	Antimicrobial Activity of Chemokine CXCL10 for Dermal and Oral Microorganisms. <i>Antibiotics</i> , 2014 , 3, 527-39	4.9	6
10	Correlations between designability and various structural characteristics of protein lattice models. <i>Journal of Chemical Physics</i> , 2007 , 126, 195101	3.9	6
9	CATHER: a novel threading algorithm with predicted contacts. <i>Bioinformatics</i> , 2020 , 36, 2119-2125	7.2	6
8	Constructing consensus genetic maps in comparative analysis. <i>Journal of Computational Biology</i> , 2010 , 17, 1561-73	1.7	5
7	Comprehensive Survey and Comparative Assessment of RNA-Binding Residue Predictions with Analysis by RNA Type. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	5
6	Recognition of small molecule-RNA binding sites using RNA sequence and structure. <i>Bioinformatics</i> , 2021 ,	7.2	5
5	RNA inter-nucleotide 3D closeness prediction by deep residual neural networks. <i>Bioinformatics</i> , 2021 , 37, 1093-1098	7.2	4
4	Toward the assessment of predicted inter-residue distance. <i>Bioinformatics</i> , 2021 ,	7.2	3

3	RNA Flexibility Prediction With Sequence Profile and Predicted Solvent Accessibility. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 2017-2022	3	3
2	Single-sequence protein structure prediction using supervised transformer protein language models		1
1	The structure of the large regulatory β subunit of phosphorylase kinase examined by modeling and hydrogen-deuterium exchange. <i>Protein Science</i> , 2018 , 27, 472-484	6.3	1