Jianyi Yang

List of Publications by Year
in descending order

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58	13,189	126907	149698
papers	citations	33 h-index	56 g-index

62	62	62	21166
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The I-TASSER Suite: protein structure and function prediction. Nature Methods, 2015, 12, 7-8.	19.0	4,923
2	I-TASSER server: new development for protein structure and function predictions. Nucleic Acids Research, 2015, 43, W174-W181.	14.5	1,897
3	Improved protein structure prediction using predicted interresidue orientations. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1496-1503.	7.1	1,135
4	Proteinâ€“ligand binding site recognition using complementary binding-specific substructure comparison and sequence profile alignment. Bioinformatics, 2013, 29, 2588-2595.	4.1	739
5	COFACTOR: an accurate comparative algorithm for structure-based protein function annotation. Nucleic Acids Research, 2012, 40, W471-W477.	14.5	582
6	BioLiP: a semi-manually curated database for biologically relevant ligandâ€“protein interactions. Nucleic Acids Research, 2012, 41, D1096-D1103.	14.5	568
7	Protein Structure and Function Prediction Using Iâ€TASSER. Current Protocols in Bioinformatics, 2015, 52, 5.8.1-5.8.15.	25.8	367
8	The trRosetta server for fast and accurate protein structure prediction. Nature Protocols, 2021, 16, 5634-5651.	12.0	290
9	PotentialNet for Molecular Property Prediction. ACS Central Science, 2018, 4, 1520-1530.	11.3	278
10	A comparative assessment and analysis of 20 representative sequence alignment methods for protein structure prediction. Scientific Reports, 2013, 3, 2619.	3.3	171
11	COACH-D: improved proteinâ€“ligand binding sites prediction with refined ligand-binding poses through molecular docking. Nucleic Acids Research, 2018, 46, W438-W442.	14.5	164
12	GPCR-I-TASSER: A Hybrid Approach to G Protein-Coupled Receptor Structure Modeling and the Application to the Human Genome. Structure, 2015, 23, 1538-1549.	3.3	153
13	Advances in GPCR Modeling Evaluated by the GPCR Dock 2013 Assessment: Meeting New Challenges. Structure, 2014, 22, 1120-1139.	3.3	149
14	ResQ: An Approach to Unified Estimation of B -Factor and Residue-Specific Error in Protein Structure Prediction. Journal of Molecular Biology, 2016, 428, 693-701.	4.2	119
15	Prediction of protein structural classes by recurrence quantification analysis based on chaos game representation. Journal of Theoretical Biology, 2009, 257, 618-626.	1.7	113
16	Recognizing metal and acid radical ion-binding sites by integrating ab initio modeling with template-based transferals. Bioinformatics, 2016, 32, 3260-3269.	4.1	98
17	GLASS: a comprehensive database for experimentally validated GPCR-ligand associations. Bioinformatics, 2015, 31, 3035-3042.	4.1	92
18	Prediction of protein structural classes for low-homology sequences based on predicted secondary structure. BMC Bioinformatics, 2010, 11, S9.	2.6	76

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19	mTM-align: an algorithm for fast and accurate multiple protein structure alignment. Bioinformatics, 2018, 34, 1719-1725.	4.1	75
20	mTM-align: a server for fast protein structure database search and multiple protein structure alignment. Nucleic Acids Research, 2018, 46, W380-W386.	14.5	70
21	Protein contact prediction using metagenome sequence data and residual neural networks. Bioinformatics, 2020, 36, 41-48.	4.1	68
22	SARS-CoV-2 nucleocapsid protein binds host mRNAs and attenuates stress granules to impair host stress response. IScience, 2022, 25, 103562.	4.1	68
23	Structural and Sequence Similarity Makes a Significant Impact on Machine-Learning-Based Scoring Functions for Proteinâ€“Ligand Interactions. Journal of Chemical Information and Modeling, 2017, 57, 1007-1012.	5.4	67
24	Improving taxonomyâ€based protein fold recognition by using global and local features. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2053-2064.	2.6	66
25	Improved Protein Structure Prediction Using a New Multiâ€Scale Network and Homologous Templates. Advanced Science, 2021, 8, e2102592.	11.2	65
26	Integration of <scp>QUARK</scp> and <scp>Iâ€TASSER</scp> for Ab Initio Protein Structure Prediction in <scp>CASP11</scp>. Proteins: Structure, Function and Bioinformatics, 2016, 84, 76-86.	2.6	63
27	Computational Prediction of MoRFs, Short Disorder-to-order Transitioning Protein Binding Regions. Computational and Structural Biotechnology Journal, 2019, 17, 454-462.	4.1	50
28	Improving the prediction of proteinâ€“nucleic acids binding residues via multiple sequence profiles and the consensus of complementary methods. Bioinformatics, 2019, 35, 930-936.	4.1	50
29	Templateâ€based protein structure prediction in <scp>CASP11</scp> and retrospect of <scp>Iâ€TASSER</scp> in the last decade. Proteins: Structure, Function and Bioinformatics, 2016, 84, 233-246.	2.6	48
30	Super Spy variants implicate flexibility in chaperone action. ELife, 2014, 3, e01584.	6.0	48
31	In various protein complexes, disordered protomers have large perâ€residue surface areas and area of proteinâ€“DNAâ€and RNAâ€binding interfaces. FEBS Letters, 2015, 589, 2561-2569.	2.8	42
32	An ensemble approach to protein fold classification by integration of template-based assignment and support vector machine classifier. Bioinformatics, 2017, 33, 863-870.	4.1	37
33	An improved classification of G-protein-coupled receptors using sequence-derived features. BMC Bioinformatics, 2010, 11, 420.	2.6	36
34	Improving Sequence-Based Prediction of Proteinâ€“Peptide Binding Residues by Introducing Intrinsic Disorder and a Consensus Method. Journal of Chemical Information and Modeling, 2018, 58, 1459-1468.	5.4	33
35	Human Pol II promoter recognition based on primary sequences and free energy of dinucleotides. BMC Bioinformatics, 2008, 9, 113.	2.6	27
36	Histatin 5 binds to Porphyromonas gingivalis hemagglutinin B (HagB) and alters HagB-induced chemokine responses. Scientific Reports, 2014, 4, 3904.	3.3	27

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37	Enhanced prediction of RNA solvent accessibility with long short-term memory neural networks and improved sequence profiles. Bioinformatics, 2019, 35, 1686-1691.	4.1	26
38	Clustering structures of large proteins using multifractal analyses based on a 6-letter model and hydrophobicity scale of amino acids. Chaos, Solitons and Fractals, 2009, 40, 607-620.	5.1	25
39	RNA inter-nucleotide 3D closeness prediction by deep residual neural networks. Bioinformatics, 2021, 37, 1093-1098.	4.1	24
40	A large-scale comparative assessment of methods for residueâ€“residue contact prediction. Briefings in Bioinformatics, 2016, 19, bbw106.	6.5	23
41	A Small Shared Epitopeâ€“Mimetic Compound Potently Accelerates Osteoclast-Mediated Bone Damage in Autoimmune Arthritis. Journal of Immunology, 2013, 191, 2096-2103.	0.8	22
42	Recognition of small moleculeâ€“RNA binding sites using RNA sequence and structure. Bioinformatics, 2021, 37, 36-42.	4.1	20
43	Identification of Partially Linear Structure in Additive Models with an Application to Gene Expression Prediction from Sequences. Biometrics, 2012, 68, 437-445.	1.4	15
44	CoABind: a novel algorithm for Coenzyme A (CoA)- and CoA derivatives-binding residues prediction. Bioinformatics, 2018, 34, 2598-2604.	4.1	13
45	Comprehensive Survey and Comparative Assessment of RNA-Binding Residue Predictions with Analysis by RNA Type. International Journal of Molecular Sciences, 2020, 21, 6879.	4.1	13
46	RNALigands: a database and web server for RNAâ€“ligand interactions. Rna, 2022, 28, 115-122.	3.5	12
47	CATHER: a novel threading algorithm with predicted contacts. Bioinformatics, 2020, 36, 2119-2125.	4.1	11
48	Human host status inference from temporal microbiome changes via recurrent neural networks. Briefings in Bioinformatics, 2021, 22, .	6.5	11
49	Correlations between designability and various structural characteristics of protein lattice models. Journal of Chemical Physics, 2007, 126, 195101.	3.0	9
50	Improved estimation of model quality using predicted inter-residue distance. Bioinformatics, 2021, 37, 3752-3759.	4.1	9
51	Antimicrobial Activity of Chemokine CXCL10 for Dermal and Oral Microorganisms. Antibiotics, 2014, 3, 527-539.	3.7	8
52	DLTree: efficient and accurate phylogeny reconstruction using the dynamical language method. Bioinformatics, 2017, 33, 2214-2215.	4.1	8
53	Toward the assessment of predicted inter-residue distance. Bioinformatics, 2022, 38, 962-969.	4.1	8
54	Constructing Consensus Genetic Maps in Comparative Analysis. Journal of Computational Biology, 2010, 17, 1561-1573.	1.6	5

#	Article	IF	Citations
55	RNA Flexibility Prediction With Sequence Profile and Predicted Solvent Accessibility. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2017-2022.	3.0	4
56	The structure of the large regulatory Î± subunit of phosphorylase kinase examined by modeling and hydrogenâ€deuterium exchange. Protein Science, 2018, 27, 472-484.	7.6	3
57	On Monomeric and Multimeric Structures-Based Protein-Ligand Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 569-574.	3.0	1
58	Accurate Sequence-Based Prediction of Deleterious nsSNPs with Multiple Sequence Profiles and Putative Binding Residues. Biomolecules, 2021, 11, 1337.	4.0	1