

# Qiwen Dong

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

981  
citations

687363

13  
h-index

580821

25  
g-index

30  
all docs

30  
docs citations

30  
times ranked

1033  
citing authors

#	ARTICLE	IF	CITATIONS
1	Combining evolutionary information extracted from frequency profiles with sequence-based kernels for protein remote homology detection. <i>Bioinformatics</i> , 2014, 30, 472-479.	4.1	266
2	A discriminative method for protein remote homology detection and fold recognition combining Top-n-grams and latent semantic analysis. <i>BMC Bioinformatics</i> , 2008, 9, 510.	2.6	129
3	Protein Remote Homology Detection by Combining Chou's Pseudo Amino Acid Composition and Profile-Based Protein Representation. <i>Molecular Informatics</i> , 2013, 32, 775-782.	2.5	103
4	Recognizing metal and acid radical ion-binding sites by integrating <i>ab initio</i> modeling with template-based transfers. <i>Bioinformatics</i> , 2016, 32, 3260-3269.	4.1	98
5	Predicting protein-ligand binding residues with deep convolutional neural networks. <i>BMC Bioinformatics</i> , 2019, 20, 93.	2.6	57
6	Amino Acid Encoding Methods for Protein Sequences: A Comprehensive Review and Assessment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 1918-1931.	3.0	55
7	Exploiting residue-level and profile-level interface propensities for usage in binding sites prediction of proteins. <i>BMC Bioinformatics</i> , 2007, 8, 147.	2.6	42
8	Novel knowledge-based mean force potential at the profile level. <i>BMC Bioinformatics</i> , 2006, 7, 324.	2.6	26
9	Protein ligand-specific binding residue predictions by an ensemble classifier. <i>BMC Bioinformatics</i> , 2016, 17, 470.	2.6	25
10	Identification of DNA-binding proteins by auto-cross covariance transformation. , 2015, , .		23
11	Sorting protein decoys by machine-learning-to-rank. <i>Scientific Reports</i> , 2016, 6, 31571.	3.3	22
12	Domain boundary prediction based on profile domain linker propensity index. <i>Computational Biology and Chemistry</i> , 2006, 30, 127-133.	2.3	17
13	MQAPRank: improved global protein model quality assessment by learning-to-rank. <i>BMC Bioinformatics</i> , 2017, 18, 275.	2.6	17
14	Structural Bioinformatics Inspection of neXtProt PE5 Proteins in the Human Proteome. <i>Journal of Proteome Research</i> , 2015, 14, 3750-3761.	3.7	13
15	Analysis and prediction of protein local structure based on structure alphabets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 163-172.	2.6	12
16	Prediction of protein protein interactions from primary sequences. <i>International Journal of Data Mining and Bioinformatics</i> , 2010, 4, 211.	0.1	12
17	Novel Nonlinear Knowledge-Based Mean Force Potentials Based on Machine Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 476-486.	3.0	11
18	Protein Inter-Residue Contacts Prediction: Methods, Performances and Applications. <i>Current Bioinformatics</i> , 2019, 14, 178-189.	1.5	11

#	ARTICLE	IF	CITATIONS
19	A seqlet-based maximum entropy Markov approach for protein secondary structure prediction. Science in China Series C: Life Sciences, 2005, 48, 394.	1.3	8
20	Prediction of protein local structures and folding fragments based on building a block library. Proteins: Structure, Function and Bioinformatics, 2008, 72, 353-366.	2.6	6
21	CSSSketch2Code. , 2018, , .		6
22	A Novel Application of Educational Management Information System based on Micro Frontends. Procedia Computer Science, 2020, 176, 1567-1576.	2.0	6
23	Characterization and Prediction of Protein Flexibility Based on Structural Alphabets. BioMed Research International, 2016, 2016, 1-7.	1.9	5
24	A machine learning-based method for protein global model quality assessment. International Journal of General Systems, 2011, 40, 417-425.	2.5	4
25	Identifying the missing proteins in human proteome by biological language model. BMC Systems Biology, 2016, 10, 113.	3.0	2
26	RRCRank: a fusion method using rank strategy for residue-residue contact prediction. BMC Bioinformatics, 2017, 18, 390.	2.6	2
27	A novel application integration architecture for the education industry. Procedia Computer Science, 2020, 176, 1813-1822.	2.0	2
28	Protein model quality assessment by learning-to-rank. , 2015, , .		1
29	Improving Prediction of the Contact Numbers of Residues in Proteins from Primary Sequences. , 2009, , .		0
30	Protein Backbone Dihedral Angle Prediction Based on Probabilistic Models. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	0