

# 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	Amino Acid Encoding Methods for Protein Sequences: A Comprehensive Review and Assessment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1918-1931.	3.0	55
2	A novel application integration architecture for the education industry. Procedia Computer Science, 2020, 176, 1813-1822.	2.0	2
3	A Novel Application of Educational Management Information System based on Micro Frontends. Procedia Computer Science, 2020, 176, 1567-1576.	2.0	6
4	Predicting protein-ligand binding residues with deep convolutional neural networks. BMC Bioinformatics, 2019, 20, 93.	2.6	57
5	Protein Inter-Residue Contacts Prediction: Methods, Performances and Applications. Current Bioinformatics, 2019, 14, 178-189.	1.5	11
6	CSSSketch2Code. , 2018, , .		6
7	MQAPRank: improved global protein model quality assessment by learning-to-rank. BMC Bioinformatics, 2017, 18, 275.	2.6	17
8	RRCRank: a fusion method using rank strategy for residue-residue contact prediction. BMC Bioinformatics, 2017, 18, 390.	2.6	2
9	Characterization and Prediction of Protein Flexibility Based on Structural Alphabets. BioMed Research International, 2016, 2016, 1-7.	1.9	5
10	Recognizing metal and acid radical ion-binding sites by integrating <i>ab initio</i> modeling with template-based transfers. Bioinformatics, 2016, 32, 3260-3269.	4.1	98
11	Protein ligand-specific binding residue predictions by an ensemble classifier. BMC Bioinformatics, 2016, 17, 470.	2.6	25
12	Sorting protein decoys by machine-learning-to-rank. Scientific Reports, 2016, 6, 31571.	3.3	22
13	Identifying the missing proteins in human proteome by biological language model. BMC Systems Biology, 2016, 10, 113.	3.0	2
14	Protein model quality assessment by learning-to-rank. , 2015, , .		1
15	Identification of DNA-binding proteins by auto-cross covariance transformation. , 2015, , .		23
16	Structural Bioinformatics Inspection of neXtProt PE5 Proteins in the Human Proteome. Journal of Proteome Research, 2015, 14, 3750-3761.	3.7	13
17	Combining evolutionary information extracted from frequency profiles with sequence-based kernels for protein remote homology detection. Bioinformatics, 2014, 30, 472-479.	4.1	266
18	Protein Remote Homology Detection by Combining Chou's Pseudo Amino Acid Composition and Profile-Based Protein Representation. Molecular Informatics, 2013, 32, 775-782.	2.5	103

#	ARTICLE	IF	CITATIONS
19	Novel Nonlinear Knowledge-Based Mean Force Potentials Based on Machine Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 476-486.	3.0	11
20	A machine learning-based method for protein global model quality assessment. International Journal of General Systems, 2011, 40, 417-425.	2.5	4
21	Prediction of protein protein interactions from primary sequences. International Journal of Data Mining and Bioinformatics, 2010, 4, 211.	0.1	12
22	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
23	Improving Prediction of the Contact Numbers of Residues in Proteins from Primary Sequences. , 2009, , .		0
24	Analysis and prediction of protein local structure based on structure alphabets. Proteins: Structure, Function and Bioinformatics, 2008, 72, 163-172.	2.6	12
25	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
26	A discriminative method for protein remote homology detection and fold recognition combining Top-n-grams and latent semantic analysis. BMC Bioinformatics, 2008, 9, 510.	2.6	129
27	Exploiting residue-level and profile-level interface propensities for usage in binding sites prediction of proteins. BMC Bioinformatics, 2007, 8, 147.	2.6	42
28	Domain boundary prediction based on profile domain linker propensity index. Computational Biology and Chemistry, 2006, 30, 127-133.	2.3	17
29	Novel knowledge-based mean force potential at the profile level. BMC Bioinformatics, 2006, 7, 324.	2.6	26
30	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