

# Xiaoyang Jing

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1050050/publications.pdf>

Version: 2024-02-01

11  
papers

198  
citations

1163117

8  
h-index

1474206

9  
g-index

14  
all docs

14  
docs citations

14  
times ranked

220  
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	Fast and effective protein model refinement using deep graph neural networks. Nature Computational Science, 2021, 1, 462-469.	8.0	28
3	EnACP: An Ensemble Learning Model for Identification of Anticancer Peptides. Frontiers in Genetics, 2020, 11, 760.	2.3	25
4	Sorting protein decoys by machine-learning-to-rank. Scientific Reports, 2016, 6, 31571.	3.3	22
5	MQAPRank: improved global protein model quality assessment by learning-to-rank. BMC Bioinformatics, 2017, 18, 275.	2.6	17
6	A Web-Based Protocol for Interprotein Contact Prediction by Deep Learning. Methods in Molecular Biology, 2020, 2074, 67-80.	0.9	13
7	Improved protein model quality assessment by integrating sequential and pairwise features using deep learning. Bioinformatics, 2021, 36, 5361-5367.	4.1	11
8	Protein Inter-Residue Contacts Prediction: Methods, Performances and Applications. Current Bioinformatics, 2019, 14, 178-189.	1.5	11
9	RRCRank: a fusion method using rank strategy for residue-residue contact prediction. BMC Bioinformatics, 2017, 18, 390.	2.6	2
10	Protein model quality assessment by learning-to-rank. , 2015, , .		1
11	Improved protein residue-residue contacts prediction using learning-to-rank. , 2016, , .		0