Zhenling Peng

List of Publications by Year
in descending order

33 papers	2,901 citations	361413 20 h-index	414414 32 g-index
34 all docs	34 docs citations	34 times ranked	5816 citing authors

#	Article	IF	Citations
1	On Monomeric and Multimeric Structures-Based Protein-Ligand Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 569-574.	3.0	1
2	RNA inter-nucleotide 3D closeness prediction by deep residual neural networks. Bioinformatics, 2021, 37, 1093-1098.	4.1	24
3	Recognition of small molecule–RNA binding sites using RNA sequence and structure. Bioinformatics, 2021, 37, 36-42.	4.1	20
4	Codon selection reduces GC content bias in nucleic acids encoding for intrinsically disordered proteins. Cellular and Molecular Life Sciences, 2020, 77, 149-160.	5.4	8
5	Protein contact prediction using metagenome sequence data and residual neural networks. Bioinformatics, 2020, 36, 41-48.	4.1	68
6	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
7	CATHER: a novel threading algorithm with predicted contacts. Bioinformatics, 2020, 36, 2119-2125.	4.1	11
8	Disordered RNA-Binding Region Prediction with DisoRDPbind. Methods in Molecular Biology, 2020, 2106, 225-239.	0.9	16
9	OUP accepted manuscript. Bioinformatics, 2020, 36, i754-i761.	4.1	6
10	Endoplasmic reticulum and the microRNA environment in the cardiovascular system. Canadian Journal of Physiology and Pharmacology, 2019, 97, 515-527.	1.4	3
11	Computational Prediction of MoRFs, Short Disorder-to-order Transitioning Protein Binding Regions. Computational and Structural Biotechnology Journal, 2019, 17, 454-462.	4.1	50
12	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
13	Improving the prediction of protein–nucleic acids binding residues via multiple sequence profiles and the consensus of complementary methods. Bioinformatics, 2019, 35, 930-936.	4.1	50
14	mTM-align: an algorithm for fast and accurate multiple protein structure alignment. Bioinformatics, 2018, 34, 1719-1725.	4.1	75
15	CoABind: a novel algorithm for Coenzyme A (CoA)- and CoA derivatives-binding residues prediction. Bioinformatics, 2018, 34, 2598-2604.	4.1	13
16	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
17	COACH-D: improved protein–ligand binding sites prediction with refined ligand-binding poses through molecular docking. Nucleic Acids Research, 2018, 46, W438-W442.	14.5	164
18	Improving Sequence-Based Prediction of Protein–Peptide Binding Residues by Introducing Intrinsic Disorder and a Consensus Method. Journal of Chemical Information and Modeling, 2018, 58, 1459-1468.	5.4	33

#	Article	IF	Citations
19	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
20	Prediction of Disordered RNA, DNA, and Protein Binding Regions Using DisoRDPbind. Methods in Molecular Biology, 2017, 1484, 187-203.	0.9	59
21	Genes encoding intrinsic disorder in Eukaryota have high GC content. Intrinsically Disordered Proteins, 2016, 4, e1262225.	1.9	25
22	A large-scale comparative assessment of methods for residue–residue contact prediction. Briefings in Bioinformatics, 2016, 19, bbw106.	6.5	23
23	In various protein complexes, disordered protomers have large per‐residue surface areas and area of protein‐, DNA‐and RNA‐binding interfaces. FEBS Letters, 2015, 589, 2561-2569.	2.8	42
24	High-throughput prediction of RNA, DNA and protein binding regions mediated by intrinsic disorder. Nucleic Acids Research, 2015, 43, e121-e121.	14.5	131
25	Exceptionally abundant exceptions: comprehensive characterization of intrinsic disorder in all domains of life. Cellular and Molecular Life Sciences, 2015, 72, 137-151.	5.4	314
26	Intrinsic Disorder in the BK Channel and Its Interactome. PLoS ONE, 2014, 9, e94331.	2.5	16
27	Genome-wide analysis of thapsigargin-induced microRNAs and their targets in NIH3T3 cells. Genomics Data, 2014, 2, 325-327.	1.3	3
28	Genome-scale prediction of proteins with long intrinsically disordered regions. Proteins: Structure, Function and Bioinformatics, 2014, 82, 145-158.	2.6	104
29	A creature with a hundred waggly tails: intrinsically disordered proteins in the ribosome. Cellular and Molecular Life Sciences, 2014, 71, 1477-1504.	5.4	119
30	Interplay Between the Oxidoreductase PDIA6 and microRNA-322 Controls the Response to Disrupted Endoplasmic Reticulum Calcium Homeostasis. Science Signaling, 2014, 7, ra54.	3.6	92
31	On the intrinsic disorder status of the major players in programmed cell death pathways. F1000Research, 2013, 2, 190.	1.6	20
32	NOT THAT RIGID MIDGETS AND NOT SO FLEXIBLE GIANTS: ON THE ABUNDANCE AND ROLES OF INTRINSIC DISORDER IN SHORT AND LONG PROTEINS. Journal of Biological Systems, 2012, 20, 471-511.	1.4	19
33	More than just tails: intrinsic disorder in histone proteins. Molecular BioSystems, 2012, 8, 1886.	2.9	99