

Zhenling Peng

List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	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
3	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
4	High-throughput prediction of RNA, DNA and protein binding regions mediated by intrinsic disorder. Nucleic Acids Research, 2015, 43, e121-e121.	14.5	131
5	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
6	Genome-scale prediction of proteins with long intrinsically disordered regions. Proteins: Structure, Function and Bioinformatics, 2014, 82, 145-158.	2.6	104
7	More than just tails: intrinsic disorder in histone proteins. Molecular BioSystems, 2012, 8, 1886.	2.9	99
8	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
9	mTM-align: an algorithm for fast and accurate multiple protein structure alignment. Bioinformatics, 2018, 34, 1719-1725.	4.1	75
10	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
11	Protein contact prediction using metagenome sequence data and residual neural networks. Bioinformatics, 2020, 36, 41-48.	4.1	68
12	Prediction of Disordered RNA, DNA, and Protein Binding Regions Using DisoRDPbind. Methods in Molecular Biology, 2017, 1484, 187-203.	0.9	59
13	Computational Prediction of MoRFs, Short Disorder-to-order Transitioning Protein Binding Regions. Computational and Structural Biotechnology Journal, 2019, 17, 454-462.	4.1	50
14	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
15	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
16	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
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Genes encoding intrinsic disorder in Eukaryota have high GC content. <i>Intrinsically Disordered Proteins</i> , 2016, 4, e1262225.	1.9	25
20	RNA inter-nucleotide 3D closeness prediction by deep residual neural networks. <i>Bioinformatics</i> , 2021, 37, 1093-1098.	4.1	24
21	A large-scale comparative assessment of methods for residue-residue contact prediction. <i>Briefings in Bioinformatics</i> , 2016, 19, bbw106.	6.5	23
22	Recognition of small molecule-RNA binding sites using RNA sequence and structure. <i>Bioinformatics</i> , 2021, 37, 36-42.	4.1	20
23	On the intrinsic disorder status of the major players in programmed cell death pathways. <i>F1000Research</i> , 2013, 2, 190.	1.6	20
24	NOT THAT RIGID MIDGETS AND NOT SO FLEXIBLE GIANTS: ON THE ABUNDANCE AND ROLES OF INTRINSIC DISORDER IN SHORT AND LONG PROTEINS. <i>Journal of Biological Systems</i> , 2012, 20, 471-511.	1.4	19
25	Intrinsic Disorder in the BK Channel and Its Interactome. <i>PLoS ONE</i> , 2014, 9, e94331.	2.5	16
26	Disordered RNA-Binding Region Prediction with DisoRDPbind. <i>Methods in Molecular Biology</i> , 2020, 2106, 225-239.	0.9	16
27	CoABind: a novel algorithm for Coenzyme A (CoA)- and CoA derivatives-binding residues prediction. <i>Bioinformatics</i> , 2018, 34, 2598-2604.	4.1	13
28	CATHER: a novel threading algorithm with predicted contacts. <i>Bioinformatics</i> , 2020, 36, 2119-2125.	4.1	11
29	Codon selection reduces GC content bias in nucleic acids encoding for intrinsically disordered proteins. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 149-160.	5.4	8
30	OUP accepted manuscript. <i>Bioinformatics</i> , 2020, 36, i754-i761.	4.1	6
31	Genome-wide analysis of thapsigargin-induced microRNAs and their targets in NIH3T3 cells. <i>Genomics Data</i> , 2014, 2, 325-327.	1.3	3
32	Endoplasmic reticulum and the microRNA environment in the cardiovascular system. <i>Canadian Journal of Physiology and Pharmacology</i> , 2019, 97, 515-527.	1.4	3
33	On Monomeric and Multimeric Structures-Based Protein-Ligand Interactions. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 569-574.	3.0	1