List of Publications by Year in descending order

36 papers	2,467 citations	304743 22 h-index	361022 35 g-index
38 all docs	38 docs citations	38 times ranked	3193 citing authors

#	Article	IF	Citations
1	ESpritz: accurate and fast prediction of protein disorder. Bioinformatics, 2012, 28, 503-509.	4.1	445
2	PASTA 2.0: an improved server for protein aggregation prediction. Nucleic Acids Research, 2014, 42, W301-W307.	14.5	349
3	MobiDB 2.0: an improved database of intrinsically disordered and mobile proteins. Nucleic Acids Research, 2015, 43, D315-D320.	14.5	177
4	Comprehensive large-scale assessment of intrinsic protein disorder. Bioinformatics, 2015, 31, 201-208.	4.1	154
5	MobiDB: a comprehensive database of intrinsic protein disorder annotations. Bioinformatics, 2012, 28, 2080-2081.	4.1	142
6	RING: networking interacting residues, evolutionary information and energetics in protein structures. Bioinformatics, 2011, 27, 2003-2005.	4.1	116
7	DOME: recommendations for supervised machine learning validation in biology. Nature Methods, 2021, 18, 1122-1127.	19.0	105
8	Distill: a suite of web servers for the prediction of one-, two- and three-dimensional structural features of proteins. BMC Bioinformatics, 2006, 7, 402.	2.6	85
9	NeEMO: a method using residue interaction networks to improve prediction of protein stability upon mutation. BMC Genomics, 2014, 15, S7.	2.8	83
10	CSpritz: accurate prediction of protein disorder segments with annotation for homology, secondary structure and linear motifs. Nucleic Acids Research, 2011, 39, W190-W196.	14.5	77
11	GlycoStore: a database of retention properties for glycan analysis. Bioinformatics, 2018, 34, 3231-3232.	4.1	77
12	A two-stage approach for improved prediction of residue contact maps. BMC Bioinformatics, 2006, 7, 180.	2.6	74
13	FELLS: fast estimator of latent local structure. Bioinformatics, 2017, 33, 1889-1891.	4.1	72
14	RepeatsDB: a database of tandem repeat protein structures. Nucleic Acids Research, 2014, 42, D352-D357.	14.5	53
15	Correct machine learning on protein sequences: a peer-reviewing perspective. Briefings in Bioinformatics, 2016, 17, 831-840.	6.5	53
16	Toward an accurate prediction of inter-residue distances in proteins using 2D recursive neural networks. BMC Bioinformatics, 2014, 15, 6.	2.6	51
17	Ab initio and template-based prediction of multi-class distance maps by two-dimensional recursive neural networks. BMC Structural Biology, 2009, 9, 5.	2.3	44
18	MOBI: a web server to define and visualize structural mobility in NMR protein ensembles. Bioinformatics, 2010, 26, 2916-2917.	4.1	35

#	Article	IF	Citations
19	Analysis and consensus of currently available intrinsic protein disorder annotation sources in the MobiDB database. BMC Bioinformatics, 2013, 14, S3.	2.6	30
20	Utility of Ion-Mobility Spectrometry for Deducing Branching of Multiply Charged Glycans and Glycopeptides in a High-Throughput Positive ion LC-FLR-IMS-MS Workflow. Analytical Chemistry, 2020, 92, 15323-15335.	6.5	30
21	Quantitative profiling of glycans and glycopeptides: an informaticsâ€™ perspective. Current Opinion in Structural Biology, 2016, 40, 70-80.	5.7	29
22	RAPHAEL: recognition, periodicity and insertion assignment of solenoid protein structures. Bioinformatics, 2012, 28, 3257-3264.	4.1	27
23	Experimentally Determined Long Intrinsically Disordered Protein Regions Are Now Abundant in the Protein Data Bank. International Journal of Molecular Sciences, 2020, 21, 4496.	4.1	25
24	RUBI: rapid proteomic-scale prediction of lysine ubiquitination and factors influencing predictor performance. Amino Acids, 2014, 46, 853-862.	2.7	24
25	Harnessing the potential of machine learning for advancing â€œQuality by Designâ€•in biomanufacturing. MAbs, 2022, 14, 2013593.	5.2	21
26	A Robust and Versatile Automated Glycoanalytical Technology for Serum Antibodies and Acute Phase Proteins: Ovarian Cancer Case Study. Molecular and Cellular Proteomics, 2019, 18, 2191-2206.	3.8	18
27	GlycanAnalyzer: software for automated interpretation of N-glycan profiles after exoglycosidase digestions. Bioinformatics, 2019, 35, 688-690.	4.1	17
28	Combining Glucose Units, m/z, and Collision Cross Section Values: Multiattribute Data for Increased Accuracy in Automated Glycosphingolipid Glycan Identifications and Its Application in Triple Negative Breast Cancer. Analytical Chemistry, 2019, 91, 9078-9085.	6.5	14
29	Ab initio and homology based prediction of protein domains by recursive neural networks. BMC Bioinformatics, 2009, 10, 195.	2.6	13
30	PANADA: Protein Association Network Annotation, Determination and Analysis. PLoS ONE, 2013, 8, e78383.	2.5	7
31	Clustering and curation of electropherograms: an efficient method for analyzing large cohorts of capillary electrophoresis glycomic profiles for bioprocessing operations. Beilstein Journal of Organic Chemistry, 2020, 16, 2087-2099.	2.2	5
32	LONG-RANGE INFORMATION AND PHYSICALITY CONSTRAINTS IMPROVE PREDICTED PROTEIN CONTACT MAPS. Journal of Bioinformatics and Computational Biology, 2008, 06, 1001-1020.	0.8	3
33	Semi-Automated Glycoproteomic Data Analysis of LC-MS Data Using GlycopeptideGraphMS in Process Development of Monoclonal Antibody Biologics. Frontiers in Chemistry, 2021, 9, 661406.	3.6	3
34	An Integrative Glycomic Approach for Quantitative Meat Species Profiling. Foods, 2022, 11, 1952.	4.3	3
35	In Silico Protein Motif Discovery and Structural Analysis. Methods in Molecular Biology, 2011, 760, 341-353.	0.9	2
36	Glycoinformatics Tools for Comprehensive Characterization of Glycans Enzymatically Released from Proteins. Methods in Molecular Biology, 2022, 2370, 3-23.	0.9	0