List of Publications by Year in descending order

36 papers	2,467 citations	304368 22 h-index	360668 35 g-index
38 all docs	38 docs citations	38 times ranked	3193 citing authors

#	Article	IF	Citations
1	Glycoinformatics Tools for Comprehensive Characterization of Glycans Enzymatically Released from Proteins. Methods in Molecular Biology, 2022, 2370, 3-23.	0.4	0
2	Harnessing the potential of machine learning for advancing â€œQuality by Designâ€•in biomanufacturing. MAbs, 2022, 14, 2013593.	2.6	21
3	An Integrative Glycomic Approach for Quantitative Meat Species Profiling. Foods, 2022, 11, 1952.	1.9	3
4	Semi-Automated Glycoproteomic Data Analysis of LC-MS Data Using GlycopeptideGraphMS in Process Development of Monoclonal Antibody Biologics. Frontiers in Chemistry, 2021, 9, 661406.	1.8	3
5	DOME: recommendations for supervised machine learning validation in biology. Nature Methods, 2021, 18, 1122-1127.	9.0	105
6	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.	1.3	5
7	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.	3.2	30
8	Experimentally Determined Long Intrinsically Disordered Protein Regions Are Now Abundant in the Protein Data Bank. International Journal of Molecular Sciences, 2020, 21, 4496.	1.8	25
9	GlycanAnalyzer: software for automated interpretation of N-glycan profiles after exoglycosidase digestions. Bioinformatics, 2019, 35, 688-690.	1.8	17
10	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.	3.2	14
11	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.	2.5	18
12	GlycoStore: a database of retention properties for glycan analysis. Bioinformatics, 2018, 34, 3231-3232.	1.8	77
13	FELLS: fast estimator of latent local structure. Bioinformatics, 2017, 33, 1889-1891.	1.8	72
14	Quantitative profiling of glycans and glycopeptides: an informaticsâ€™ perspective. Current Opinion in Structural Biology, 2016, 40, 70-80.	2.6	29
15	Correct machine learning on protein sequences: a peer-reviewing perspective. Briefings in Bioinformatics, 2016, 17, 831-840.	3.2	53
16	MobiDB 2.0: an improved database of intrinsically disordered and mobile proteins. Nucleic Acids Research, 2015, 43, D315-D320.	6.5	177
17	Comprehensive large-scale assessment of intrinsic protein disorder. Bioinformatics, 2015, 31, 201-208.	1.8	154
18	Toward an accurate prediction of inter-residue distances in proteins using 2D recursive neural networks. BMC Bioinformatics, 2014, 15, 6.	1.2	51

#	Article	IF	Citations
19	RUBI: rapid proteomic-scale prediction of lysine ubiquitination and factors influencing predictor performance. Amino Acids, 2014, 46, 853-862.	1.2	24
20	RepeatsDB: a database of tandem repeat protein structures. Nucleic Acids Research, 2014, 42, D352-D357.	6.5	53
21	PASTA 2.0: an improved server for protein aggregation prediction. Nucleic Acids Research, 2014, 42, W301-W307.	6.5	349
22	NeEMO: a method using residue interaction networks to improve prediction of protein stability upon mutation. BMC Genomics, 2014, 15, S7.	1.2	83
23	Analysis and consensus of currently available intrinsic protein disorder annotation sources in the MobiDB database. BMC Bioinformatics, 2013, 14, S3.	1.2	30
24	PANADA: Protein Association Network Annotation, Determination and Analysis. PLoS ONE, 2013, 8, e78383.	1.1	7
25	ESpritz: accurate and fast prediction of protein disorder. Bioinformatics, 2012, 28, 503-509.	1.8	445
26	RAPHAEL: recognition, periodicity and insertion assignment of solenoid protein structures. Bioinformatics, 2012, 28, 3257-3264.	1.8	27
27	MobiDB: a comprehensive database of intrinsic protein disorder annotations. Bioinformatics, 2012, 28, 2080-2081.	1.8	142
28	RING: networking interacting residues, evolutionary information and energetics in protein structures. Bioinformatics, 2011, 27, 2003-2005.	1.8	116
29	CSpritz: accurate prediction of protein disorder segments with annotation for homology, secondary structure and linear motifs. Nucleic Acids Research, 2011, 39, W190-W196.	6.5	77
30	In Silico Protein Motif Discovery and Structural Analysis. Methods in Molecular Biology, 2011, 760, 341-353.	0.4	2
31	MOBI: a web server to define and visualize structural mobility in NMR protein ensembles. Bioinformatics, 2010, 26, 2916-2917.	1.8	35
32	Ab initio and homology based prediction of protein domains by recursive neural networks. BMC Bioinformatics, 2009, 10, 195.	1.2	13
33	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
34	LONG-RANGE INFORMATION AND PHYSICALITY CONSTRAINTS IMPROVE PREDICTED PROTEIN CONTACT MAPS. Journal of Bioinformatics and Computational Biology, 2008, 06, 1001-1020.	0.3	3
35	A two-stage approach for improved prediction of residue contact maps. BMC Bioinformatics, 2006, 7, 180.	1.2	74
36	Distill: a suite of web servers for the prediction of one-, two- and three-dimensional structural features of proteins. BMC Bioinformatics, 2006, 7, 402.	1.2	85