Ian Walsh

List of Publications by Year
in descending order

38 papers	2,613 citations	236612 25 h-index	301761 39 g-index
43 all docs	43 docs citations	43 times ranked	3498 citing authors

#	Article	IF	Citations
1	ESpritz: accurate and fast prediction of protein disorder. Bioinformatics, 2012, 28, 503-509.	1.8	445
2	PASTA 2.0: an improved server for protein aggregation prediction. Nucleic Acids Research, 2014, 42, W301-W307.	6.5	349
3	MobiDB 2.0: an improved database of intrinsically disordered and mobile proteins. Nucleic Acids Research, 2015, 43, D315-D320.	6.5	177
4	Comprehensive large-scale assessment of intrinsic protein disorder. Bioinformatics, 2015, 31, 201-208.	1.8	154
5	MobiDB: a comprehensive database of intrinsic protein disorder annotations. Bioinformatics, 2012, 28, 2080-2081.	1.8	142
6	RING: networking interacting residues, evolutionary information and energetics in protein structures. Bioinformatics, 2011, 27, 2003-2005.	1.8	116
7	DOME: recommendations for supervised machine learning validation in biology. Nature Methods, 2021, 18, 1122-1127.	9.0	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.	1.2	85
9	NeEMO: a method using residue interaction networks to improve prediction of protein stability upon mutation. BMC Genomics, 2014, 15, S7.	1.2	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.	6.5	77
11	GlycoStore: a database of retention properties for glycan analysis. Bioinformatics, 2018, 34, 3231-3232.	1.8	77
12	A two-stage approach for improved prediction of residue contact maps. BMC Bioinformatics, 2006, 7, 180.	1.2	74
13	Bluues server: electrostatic properties of wild-type and mutated protein structures. Bioinformatics, 2012, 28, 2189-2190.	1.8	72
14	FELLS: fast estimator of latent local structure. Bioinformatics, 2017, 33, 1889-1891.	1.8	72
15	Plasma N-glycans in colorectal cancer risk. Scientific Reports, 2018, 8, 8655.	1.6	57
16	RepeatsDB: a database of tandem repeat protein structures. Nucleic Acids Research, 2014, 42, D352-D357.	6.5	53
17	Correct machine learning on protein sequences: a peer-reviewing perspective. Briefings in Bioinformatics, 2016, 17, 831-840.	3.2	53
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	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
20	MOBI: a web server to define and visualize structural mobility in NMR protein ensembles. Bioinformatics, 2010, 26, 2916-2917.	1.8	35
21	Serum *N*‑glycome alterations in breast cancer during multimodal treatment and follow‑up. Molecular Oncology, 2017, 11, 1361-1379.	2.1	32
22	Analysis and consensus of currently available intrinsic protein disorder annotation sources in the MobiDB database. BMC Bioinformatics, 2013, 14, S3.	1.2	30
23	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
24	Quantitative profiling of glycans and glycopeptides: an informatics' perspective. Current Opinion in Structural Biology, 2016, 40, 70-80.	2.6	29
25	RAPHAEL: recognition, periodicity and insertion assignment of solenoid protein structures. Bioinformatics, 2012, 28, 3257-3264.	1.8	27
26	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
27	RUBI: rapid proteomic-scale prediction of lysine ubiquitination and factors influencing predictor performance. Amino Acids, 2014, 46, 853-862.	1.2	24
28	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
29	GlycanAnalyzer: software for automated interpretation of *N*-glycan profiles after exoglycosidase digestions. Bioinformatics, 2019, 35, 688-690.	1.8	17
30	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
31	Ab initio and homology based prediction of protein domains by recursive neural networks. BMC Bioinformatics, 2009, 10, 195.	1.2	13
32	PANADA: Protein Association Network Annotation, Determination and Analysis. PLoS ONE, 2013, 8, e78383.	1.1	7
33	Recursive Neural Networks for Undirected Graphs for Learning Molecular Endpoints. Lecture Notes in Computer Science, 2009, , 391-403.	1.0	6
34	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
35	LONG-RANGE INFORMATION AND PHYSICALITY CONSTRAINTS IMPROVE PREDICTED PROTEIN CONTACT MAPS. Journal of Bioinformatics and Computational Biology, 2008, 06, 1001-1020.	0.3	3
36	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

#	Article	IF	Citations
37	In Silico Protein Motif Discovery and Structural Analysis. Methods in Molecular Biology, 2011, 760, 341-353.	0.4	2
38	Glycoinformatics Tools for Comprehensive Characterization of Glycans Enzymatically Released from Proteins. Methods in Molecular Biology, 2022, 2370, 3-23.	0.4	0