

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9093515/publications.pdf>

Version: 2024-02-01

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 | ESpritz: accurate and fast prediction of protein disorder. <i>Bioinformatics</i> , 2012, 28, 503-509. | 1.8 | 445 |
| 2 | PASTA 2.0: an improved server for protein aggregation prediction. <i>Nucleic Acids Research</i> , 2014, 42, W301-W307. | 6.5 | 349 |
| 3 | MobiDB 2.0: an improved database of intrinsically disordered and mobile proteins. <i>Nucleic Acids Research</i> , 2015, 43, D315-D320. | 6.5 | 177 |
| 4 | Comprehensive large-scale assessment of intrinsic protein disorder. <i>Bioinformatics</i> , 2015, 31, 201-208. | 1.8 | 154 |
| 5 | MobiDB: a comprehensive database of intrinsic protein disorder annotations. <i>Bioinformatics</i> , 2012, 28, 2080-2081. | 1.8 | 142 |
| 6 | RING: networking interacting residues, evolutionary information and energetics in protein structures. <i>Bioinformatics</i> , 2011, 27, 2003-2005. | 1.8 | 116 |
| 7 | DOME: recommendations for supervised machine learning validation in biology. <i>Nature Methods</i> , 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. <i>BMC Bioinformatics</i> , 2006, 7, 402. | 1.2 | 85 |
| 9 | NeEMO: a method using residue interaction networks to improve prediction of protein stability upon mutation. <i>BMC Genomics</i> , 2014, 15, S7. | 1.2 | 83 |
| 10 | CSpritz: accurate prediction of protein disorder segments with annotation for homology, secondary structure and linear motifs. <i>Nucleic Acids Research</i> , 2011, 39, W190-W196. | 6.5 | 77 |
| 11 | GlycoStore: a database of retention properties for glycan analysis. <i>Bioinformatics</i> , 2018, 34, 3231-3232. | 1.8 | 77 |
| 12 | A two-stage approach for improved prediction of residue contact maps. <i>BMC Bioinformatics</i> , 2006, 7, 180. | 1.2 | 74 |
| 13 | FELLS: fast estimator of latent local structure. <i>Bioinformatics</i> , 2017, 33, 1889-1891. | 1.8 | 72 |
| 14 | RepeatsDB: a database of tandem repeat protein structures. <i>Nucleic Acids Research</i> , 2014, 42, D352-D357. | 6.5 | 53 |
| 15 | Correct machine learning on protein sequences: a peer-reviewing perspective. <i>Briefings in Bioinformatics</i> , 2016, 17, 831-840. | 3.2 | 53 |
| 16 | Toward an accurate prediction of inter-residue distances in proteins using 2D recursive neural networks. <i>BMC Bioinformatics</i> , 2014, 15, 6. | 1.2 | 51 |
| 17 | Ab initio and template-based prediction of multi-class distance maps by two-dimensional recursive neural networks. <i>BMC Structural Biology</i> , 2009, 9, 5. | 2.3 | 44 |
| 18 | MOBI: a web server to define and visualize structural mobility in NMR protein ensembles. <i>Bioinformatics</i> , 2010, 26, 2916-2917. | 1.8 | 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. | 1.2 | 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. | 3.2 | 30 |
| 21 | Quantitative profiling of glycans and glycopeptides: an informatics™ perspective. Current Opinion in Structural Biology, 2016, 40, 70-80. | 2.6 | 29 |
| 22 | RAPHAEL: recognition, periodicity and insertion assignment of solenoid protein structures. Bioinformatics, 2012, 28, 3257-3264. | 1.8 | 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. | 1.8 | 25 |
| 24 | RUBI: rapid proteomic-scale prediction of lysine ubiquitination and factors influencing predictor performance. Amino Acids, 2014, 46, 853-862. | 1.2 | 24 |
| 25 | Harnessing the potential of machine learning for advancing “Quality by Design” in biomanufacturing. MAb, 2022, 14, 2013593. | 2.6 | 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. | 2.5 | 18 |
| 27 | GlycanAnalyzer: software for automated interpretation of N-glycan profiles after exoglycosidase digestions. Bioinformatics, 2019, 35, 688-690. | 1.8 | 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. | 3.2 | 14 |
| 29 | Ab initio and homology based prediction of protein domains by recursive neural networks. BMC Bioinformatics, 2009, 10, 195. | 1.2 | 13 |
| 30 | PANADA: Protein Association Network Annotation, Determination and Analysis. PLoS ONE, 2013, 8, e78383. | 1.1 | 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. | 1.3 | 5 |
| 32 | LONG-RANGE INFORMATION AND PHYSICALITY CONSTRAINTS IMPROVE PREDICTED PROTEIN CONTACT MAPS. Journal of Bioinformatics and Computational Biology, 2008, 06, 1001-1020. | 0.3 | 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. | 1.8 | 3 |
| 34 | An Integrative Glycomic Approach for Quantitative Meat Species Profiling. Foods, 2022, 11, 1952. | 1.9 | 3 |
| 35 | In Silico Protein Motif Discovery and Structural Analysis. Methods in Molecular Biology, 2011, 760, 341-353. | 0.4 | 2 |
| 36 | Glycoinformatics Tools for Comprehensive Characterization of Glycans Enzymatically Released from Proteins. Methods in Molecular Biology, 2022, 2370, 3-23. | 0.4 | 0 |