

Damiano Piovesan

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62

papers

5,843

citations

24

h-index

76

g-index

76

ext. papers

8,423

ext. citations

11.2

avg, IF

5.74

L-index

#	Paper	IF	Citations
62	The Pfam protein families database in 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D427-D432	20.1	2298
61	InterPro in 2017-beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017 , 45, D190-D199	20.1	970
60	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013 , 10, 221-7	21.6	587
59	The RING 2.0 web server for high quality residue interaction networks. <i>Nucleic Acids Research</i> , 2016 , 44, W367-74	20.1	259
58	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016 , 17, 184	18.3	218
57	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017 , 45, D219-D227	20.1	182
56	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 2018 , 46, D471-D476	20.1	143
55	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019 , 20, 244	18.3	111
54	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D269-D276	20.1	91
53	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017 , 13, 339-342	11.7	83
52	MobiDB-lite: fast and highly specific consensus prediction of intrinsic disorder in proteins. <i>Bioinformatics</i> , 2017 , 33, 1402-1404	7.2	72
51	Critical assessment of protein intrinsic disorder prediction. <i>Nature Methods</i> , 2021 , 18, 472-481	21.6	60
50	INGA: protein function prediction combining interaction networks, domain assignments and sequence similarity. <i>Nucleic Acids Research</i> , 2015 , 43, W134-40	20.1	59
49	MobiDB: intrinsically disordered proteins in 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D361-D367	20.1	51
48	RepeatsDB: a database of tandem repeat protein structures. <i>Nucleic Acids Research</i> , 2014 , 42, D352-7	20.1	47
47	A comprehensive assessment of long intrinsic protein disorder from the DisProt database. <i>Bioinformatics</i> , 2018 , 34, 445-452	7.2	42
46	FELLS: fast estimator of latent local structure. <i>Bioinformatics</i> , 2017 , 33, 1889-1891	7.2	38

45	FFPred 2.0: improved homology-independent prediction of gene ontology terms for eukaryotic protein sequences. <i>PLoS ONE</i> , 2013 , 8, e63754	3.7	37
44	Large-scale analysis of intrinsic disorder flavors and associated functions in the protein sequence universe. <i>Protein Science</i> , 2016 , 25, 2164-2174	6.3	34
43	PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins. <i>Nucleic Acids Research</i> , 2020 , 48, W77-W84	20.1	33
42	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021 , 49, D404-D411	20.1	31
41	SODA: prediction of protein solubility from disorder and aggregation propensity. <i>Nucleic Acids Research</i> , 2017 , 45, W236-W240	20.1	29
40	DOME: recommendations for supervised machine learning validation in biology. <i>Nature Methods</i> , 2021 , 18, 1122-1127	21.6	25
39	RepeatsDB 2.0: improved annotation, classification, search and visualization of repeat protein structures. <i>Nucleic Acids Research</i> , 2017 , 45, D308-D312	20.1	21
38	BAR-PLUS: the Bologna Annotation Resource Plus for functional and structural annotation of protein sequences. <i>Nucleic Acids Research</i> , 2011 , 39, W197-202	20.1	21
37	VHLdb: A database of von Hippel-Lindau protein interactors and mutations. <i>Scientific Reports</i> , 2016 , 6, 31128	4.9	20
36	Protein function prediction using guilty by association from interaction networks. <i>Amino Acids</i> , 2015 , 47, 2583-92	3.5	19
35	The human "magnesome": detecting magnesium binding sites on human proteins. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 14, S10	3.6	17
34	MobiDB-lite 3.0: fast consensus annotation of intrinsic disorder flavours in proteins. <i>Bioinformatics</i> , 2020 ,	7.2	15
33	Mobi 2.0: an improved method to define intrinsic disorder, mobility and linear binding regions in protein structures. <i>Bioinformatics</i> , 2018 , 34, 122-123	7.2	14
32	Identification of repetitive units in protein structures with ReUPred. <i>Amino Acids</i> , 2016 , 48, 1391-400	3.5	14
31	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2021 ,	20.1	13
30	Experimentally Determined Long Intrinsically Disordered Protein Regions Are Now Abundant in the Protein Data Bank. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	12
29	INGA 2.0: improving protein function prediction for the dark proteome. <i>Nucleic Acids Research</i> , 2019 , 47, W373-W378	20.1	11
28	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017 , 6,	3.6	10

27	RepeatsDB in 2021: improved data and extended classification for protein tandem repeat structures. <i>Nucleic Acids Research</i> , 2021 , 49, D452-D457	20.1	10
26	RepeatsDB-lite: a web server for unit annotation of tandem repeat proteins. <i>Nucleic Acids Research</i> , 2018 , 46, W402-W407	20.1	9
25	The Feature-Viewer: a visualization tool for positional annotations on a sequence. <i>Bioinformatics</i> , 2020 , 36, 3244-3245	7.2	8
24	How to inherit statistically validated annotation within BAR+ protein clusters. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 3, S4	3.6	8
23	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019 , 8,	3.6	7
22	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	7
21	Critical Assessment of Protein Intrinsic Disorder Prediction		7
20	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7
19	Assessing predictors for new post translational modification sites: A case study on hydroxylation. <i>PLoS Computational Biology</i> , 2020 , 16, e1007967	5	6
18	Where differences resemble: sequence-feature analysis in curated databases of intrinsically disordered proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	6
17	The Victor C++ library for protein representation and advanced manipulation. <i>Bioinformatics</i> , 2015 , 31, 1138-40	7.2	5
16	FuzDB: a new phase in understanding fuzzy interactions. <i>Nucleic Acids Research</i> , 2021 ,	20.1	5
15	SUS-BAR: a database of pig proteins with statistically validated structural and functional annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat065	5	3
14	FLIPPER: Predicting and Characterizing Linear Interacting Peptides in the Protein Data Bank. <i>Journal of Molecular Biology</i> , 2021 , 433, 166900	6.5	3
13	APICURON: a database to credit and acknowledge the work of biocurators. <i>Database: the Journal of Biological Databases and Curation</i> , 2021 , 2021,	5	3
12	Mapping and annotating obesity-related genes in pig and human genomes. <i>Protein and Peptide Letters</i> , 2014 , 21, 840-6	1.9	2
11	Machine-Learning Methods to Predict Protein Interaction Sites in Folded Proteins. <i>Lecture Notes in Computer Science</i> , 2012 , 127-135	0.9	2
10	A novel approach to investigate the evolution of structured tandem repeat protein families by exon duplication. <i>Journal of Structural Biology</i> , 2020 , 212, 107608	3.4	2

9	Exploring Manually Curated Annotations of Intrinsically Disordered Proteins with DisProt. <i>Current Protocols in Bioinformatics</i> , 2020 , 72, e107	24.2	1
8	Extended and Robust Protein Sequence Annotation over Conservative Nonhierarchical Clusters. <i>ACM Journal on Emerging Technologies in Computing Systems</i> , 2013 , 9, 1-8	1.7	1
7	ProSeqViewer: an interactive, responsive and efficient TypeScript library for visualization of sequences and alignments in web applications. <i>Bioinformatics</i> , 2021 ,	7.2	1
6	Exploring Curated Conformational Ensembles of Intrinsically Disordered Proteins in the Protein Ensemble Database. <i>Current Protocols</i> , 2021 , 1, e192		1
5	PhytoTypeDB: a database of plant protein inter-cultivar variability and function. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	1
4	Exploring Protein Intrinsic Disorder with MobiDB. <i>Methods in Molecular Biology</i> , 2020 , 2141, 127-143	1.4	0
3	The E3 ubiquitin-protein ligase MDM2 is a novel interactor of the von Hippel-Lindau tumor suppressor. <i>Scientific Reports</i> , 2020 , 10, 15850	4.9	0
2	Extended and robust protein sequence annotation over conservative non hierarchical clusters. The Bologna Annotation Resource v 2.0. <i>Journal of Biotechnology</i> , 2010 , 150, 547-548	3.7	
1	Databases for intrinsically disordered proteins.. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022 , 78, 144-151	5.5	