

Damiano Piovesan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1537821/publications.pdf>

Version: 2024-02-01

66
papers

9,735
citations

159358

30
h-index

110170

64
g-index

76
all docs

76
docs citations

76
times ranked

16219
citing authors

#	ARTICLE	IF	CITATIONS
1	The Pfam protein families database in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D427-D432.	6.5	3,937
2	InterPro in 2017â€”beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
3	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
4	The RING 2.0 web server for high quality residue interaction networks. <i>Nucleic Acids Research</i> , 2016, 44, W367-W374.	6.5	369
5	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	3.8	308
6	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.	3.8	261
7	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	6.5	242
8	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 2018, 46, D471-D476.	6.5	190
9	Critical assessment of protein intrinsic disorder prediction. <i>Nature Methods</i> , 2021, 18, 472-481.	9.0	187
10	MobiDB: intrinsically disordered proteins in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D361-D367.	6.5	183
11	MobiDB-lite: fast and highly specific consensus prediction of intrinsic disorder in proteins. <i>Bioinformatics</i> , 2017, 33, 1402-1404.	1.8	161
12	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	6.5	141
13	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	6.5	117
14	Simultaneous quantification of protein order and disorder. <i>Nature Chemical Biology</i> , 2017, 13, 339-342.	3.9	113
15	DOME: recommendations for supervised machine learning validation in biology. <i>Nature Methods</i> , 2021, 18, 1122-1127.	9.0	105
16	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021, 49, D404-D411.	6.5	95
17	RING 3.0: fast generation of probabilistic residue interaction networks from structural ensembles. <i>Nucleic Acids Research</i> , 2022, 50, W651-W656.	6.5	75
18	INGA: protein function prediction combining interaction networks, domain assignments and sequence similarity. <i>Nucleic Acids Research</i> , 2015, 43, W134-W140.	6.5	73

#	ARTICLE	IF	CITATIONS
19	FELLS: fast estimator of latent local structure. <i>Bioinformatics</i> , 2017, 33, 1889-1891.	1.8	72
20	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.	6.5	71
21	RepeatsDB: a database of tandem repeat protein structures. <i>Nucleic Acids Research</i> , 2014, 42, D352-D357.	6.5	53
22	A comprehensive assessment of long intrinsic protein disorder from the DisProt database. <i>Bioinformatics</i> , 2018, 34, 445-452.	1.8	53
23	Large-scale analysis of intrinsic disorder flavors and associated functions in the protein sequence universe. <i>Protein Science</i> , 2016, 25, 2164-2174.	3.1	52
24	SODA: prediction of protein solubility from disorder and aggregation propensity. <i>Nucleic Acids Research</i> , 2017, 45, W236-W240.	6.5	47
25	MobiDB-lite 3.0: fast consensus annotation of intrinsic disorder flavors in proteins. <i>Bioinformatics</i> , 2021, 36, 5533-5534.	1.8	47
26	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2022, 50, D534-D542.	6.5	46
27	FFPred 2.0: Improved Homology-Independent Prediction of Gene Ontology Terms for Eukaryotic Protein Sequences. <i>PLoS ONE</i> , 2013, 8, e63754.	1.1	40
28	Protein function prediction using guilty by association from interaction networks. <i>Amino Acids</i> , 2015, 47, 2583-2592.	1.2	40
29	RepeatsDB in 2021: improved data and extended classification for protein tandem repeat structures. <i>Nucleic Acids Research</i> , 2021, 49, D452-D457.	6.5	37
30	VHLdb: A database of von Hippel-Lindau protein interactors and mutations. <i>Scientific Reports</i> , 2016, 6, 31128.	1.6	36
31	RepeatsDB 2.0: improved annotation, classification, search and visualization of repeat protein structures. <i>Nucleic Acids Research</i> , 2017, 45, D308-D312.	6.5	33
32	The human "magnesome": detecting magnesium binding sites on human proteins. <i>BMC Bioinformatics</i> , 2012, 13, S10.	1.2	26
33	Experimentally Determined Long Intrinsically Disordered Protein Regions Are Now Abundant in the Protein Data Bank. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4496.	1.8	25
34	FuzDB: a new phase in understanding fuzzy interactions. <i>Nucleic Acids Research</i> , 2022, 50, D509-D517.	6.5	25
35	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.	1.8	24
36	INGA 2.0: improving protein function prediction for the dark proteome. <i>Nucleic Acids Research</i> , 2019, 47, W373-W378.	6.5	24

#	ARTICLE	IF	CITATIONS
37	BAR-PLUS: the Bologna Annotation Resource Plus for functional and structural annotation of protein sequences. <i>Nucleic Acids Research</i> , 2011, 39, W197-W202.	6.5	22
38	RepeatsDB-lite: a web server for unit annotation of tandem repeat proteins. <i>Nucleic Acids Research</i> , 2018, 46, W402-W407.	6.5	18
39	The Feature-Viewer: a visualization tool for positional annotations on a sequence. <i>Bioinformatics</i> , 2020, 36, 3244-3245.	1.8	18
40	Identification of repetitive units in protein structures with ReUPred. <i>Amino Acids</i> , 2016, 48, 1391-1400.	1.2	17
41	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017, 6, 875.	0.8	13
42	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
43	Assessing predictors for new post translational modification sites: A case study on hydroxylation. <i>PLoS Computational Biology</i> , 2020, 16, e1007967.	1.5	10
44	APICURON: a database to credit and acknowledge the work of biocurators. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	10
45	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, .	1.4	9
46	How to inherit statistically validated annotation within BAR+ protein clusters. <i>BMC Bioinformatics</i> , 2013, 14, S4.	1.2	8
47	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.	1.3	8
48	FLIPPER: Predicting and Characterizing Linear Interacting Peptides in the Protein Data Bank. <i>Journal of Molecular Biology</i> , 2021, 433, 166900.	2.0	8
49	The Victor C++ library for protein representation and advanced manipulation. <i>Bioinformatics</i> , 2015, 31, 1138-1140.	1.8	6
50	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-bat065.	1.4	4
51	Exploring Curated Conformational Ensembles of Intrinsically Disordered Proteins in the Protein Ensemble Database. <i>Current Protocols</i> , 2021, 1, e192.	1.3	4
52	ProSeqViewer: an interactive, responsive and efficient TypeScript library for visualization of sequences and alignments in web applications. <i>Bioinformatics</i> , 2022, 38, 1129-1130.	1.8	4
53	Databases for intrinsically disordered proteins. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 144-151.	1.1	3
54	Molecular Determinants of Selectivity in Disordered Complexes May Shed Light on Specificity in Protein Condensates. <i>Biomolecules</i> , 2022, 12, 92.	1.8	3

#	ARTICLE	IF	CITATIONS
55	Editorial: Fuzzy Interactions: Many Facets of Protein Binding. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	3
56	The E3 ubiquitin-protein ligase MDM2 is a novel interactor of the von Hippelâ€Lindau tumor suppressor. <i>Scientific Reports</i> , 2020, 10, 15850.	1.6	2
57	Exploring Manually Curated Annotations of Intrinsically Disordered Proteins with DisProt. <i>Current Protocols in Bioinformatics</i> , 2020, 72, e107.	25.8	2
58	Machine-Learning Methods to Predict Protein Interaction Sites in Folded Proteins. <i>Lecture Notes in Computer Science</i> , 2012, , 127-135.	1.0	2
59	Mapping and Annotating Obesity-Related Genes in Pig And Human Genomes. <i>Protein and Peptide Letters</i> , 2013, 21, 840-846.	0.4	2
60	Exploring Protein Intrinsic Disorder with MobiDB. <i>Methods in Molecular Biology</i> , 2020, 2141, 127-143.	0.4	2
61	Exploring Manually Curated Annotations of Intrinsically Disordered Proteins with DisProt. <i>Current Protocols</i> , 2022, 2, .	1.3	2
62	Extended and Robust Protein Sequence Annotation over Conservative Nonhierarchical Clusters. <i>ACM Journal on Emerging Technologies in Computing Systems</i> , 2013, 9, 1-8.	1.8	1
63	PhytoTypeDB: a database of plant protein inter-cultivar variability and function. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	1
64	Unconventional training for neural network predictions of inter-residue contacts. , 2009, , .		0
65	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.	1.9	0
66	Protein Sequence Annotation by Means of Community Detection. <i>Current Bioinformatics</i> , 2015, 10, 139-143.	0.7	0