Damiano Piovesan

List of Publications by Year in Descending Order

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	Databases for intrinsically disordered proteins.. *Acta Crystallographica Section D: Structural Biology*, **2022**, 78, 144-151	5.5	
61	FuzDB: a new phase in understanding fuzzy interactions. *Nucleic Acids Research*, **2021**,	20.1	5
60	ProSeqViewer: an interactive, responsive and efficient TypeScript library for visualization of sequences and alignments in web applications. *Bioinformatics*, **2021**,	7.2	1
59	PDBe-KB: collaboratively defining the biological context of structural data. *Nucleic Acids Research*, **2021**,	20.1	7
58	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. *Nucleic Acids Research*, **2021**,	20.1	13
57	FLIPPER: Predicting and Characterizing Linear Interacting Peptides in the Protein Data Bank. *Journal of Molecular Biology*, **2021**, 433, 166900	6.5	3
56	Critical assessment of protein intrinsic disorder prediction. *Nature Methods*, **2021**, 18, 472-481	21.6	60
55	Exploring Curated Conformational Ensembles of Intrinsically Disordered Proteins in the Protein Ensemble Database. *Current Protocols*, **2021**, 1, e192		1
54	DOME: recommendations for supervised machine learning validation in biology. *Nature Methods*, **2021**, 18, 1122-1127	21.6	25
53	MobiDB: intrinsically disordered proteins in 2021. *Nucleic Acids Research*, **2021**, 49, D361-D367	20.1	51
52	RepeatsDB in 2021: improved data and extended classification for protein tandem repeat structures. *Nucleic Acids Research*, **2021**, 49, D452-D457	20.1	10
51	APICURON: a database to credit and acknowledge the work of biocurators. *Database: the Journal of Biological Databases and Curation*, **2021**, 2021,	5	3
50	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. *Nucleic Acids Research*, **2021**, 49, D404-D411	20.1	31
49	Exploring Manually Curated Annotations of Intrinsically Disordered Proteins with DisProt. *Current Protocols in Bioinformatics*, **2020**, 72, e107	24.2	1
48	PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins. *Nucleic Acids Research*, **2020**, 48, W77-W84	20.1	33
47	Assessing predictors for new post translational modification sites: A case study on hydroxylation. *PLoS Computational Biology*, **2020**, 16, e1007967	5	6
46	Experimentally Determined Long Intrinsically Disordered Protein Regions Are Now Abundant in the Protein Data Bank. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	12

45	The Feature-Viewer: a visualization tool for positional annotations on a sequence. *Bioinformatics*, **2020**, 36, 3244-3245	7.2	8
44	DisProt: intrinsic protein disorder annotation in 2020. *Nucleic Acids Research*, **2020**, 48, D269-D276	20.1	91
43	Exploring Protein Intrinsic Disorder with MobiDB. *Methods in Molecular Biology*, **2020**, 2141, 127-143	1.4	0
42	The E3 ubiquitin-protein ligase MDM2 is a novel interactor of the von Hippel-Lindau tumor suppressor. *Scientific Reports*, **2020**, 10, 15850	4.9	0
41	A novel approach to investigate the evolution of structured tandem repeat protein families by exon duplication. *Journal of Structural Biology*, **2020**, 212, 107608	3.4	2
40	MobiDB-lite 3.0: fast consensus annotation of intrinsic disorder flavours in proteins. *Bioinformatics*, **2020**,	7.2	15
39	INGA 2.0: improving protein function prediction for the dark proteome. *Nucleic Acids Research*, **2019**, 47, W373-W378	20.1	11
38	An intrinsically disordered proteins community for ELIXIR. *F1000Research*, **2019**, 8,	3.6	7
37	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. *Genome Biology*, **2019**, 20, 244	18.3	111
36	The Pfam protein families database in 2019. *Nucleic Acids Research*, **2019**, 47, D427-D432	20.1	2298
35	A comprehensive assessment of long intrinsic protein disorder from the DisProt database. *Bioinformatics*, **2018**, 34, 445-452	7.2	42
34	Mobi 2.0: an improved method to define intrinsic disorder, mobility and linear binding regions in protein structures. *Bioinformatics*, **2018**, 34, 122-123	7.2	14
33	RepeatsDB-lite: a web server for unit annotation of tandem repeat proteins. *Nucleic Acids Research*, **2018**, 46, W402-W407	20.1	9
32	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. *Nucleic Acids Research*, **2018**, 46, D471-D476	20.1	143
31	PhytoTypeDB: a database of plant protein inter-cultivar variability and function. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018,	5	1
30	Where differences resemble: sequence-feature analysis in curated databases of intrinsically disordered proteins. *Database: the Journal of Biological Databases and Curation*, **2018**, 2018,	5	6
29	FELLS: fast estimator of latent local structure. *Bioinformatics*, **2017**, 33, 1889-1891	7.2	38
28	DisProt 7.0: a major update of the database of disordered proteins. *Nucleic Acids Research*, **2017**, 45, D219-D227	20.1	182

27   InterPro in 2017-beyond protein family and domain annotations. *Nucleic Acids Research*, **2017**, 45, D190-D199   20.1   970

26   Simultaneous quantification of protein order and disorder. *Nature Chemical Biology*, **2017**, 13, 339-342   11.7   83

25   MobiDB-lite: fast and highly specific consensus prediction of intrinsic disorder in proteins. *Bioinformatics*, **2017**, 33, 1402-1404   7.2   72

24   SODA: prediction of protein solubility from disorder and aggregation propensity. *Nucleic Acids Research*, **2017**, 45, W236-W240   20.1   29

23   RepeatsDB 2.0: improved annotation, classification, search and visualization of repeat protein structures. *Nucleic Acids Research*, **2017**, 45, D308-D312   20.1   21

22   A community proposal to integrate proteomics activities in ELIXIR. *F1000Research*, **2017**, 6,   3.6   10

21   Large-scale analysis of intrinsic disorder flavors and associated functions in the protein sequence universe. *Protein Science*, **2016**, 25, 2164-2174   6.3   34

20   The RING 2.0 web server for high quality residue interaction networks. *Nucleic Acids Research*, **2016**, 44, W367-74   20.1   259

19   Identification of repetitive units in protein structures with ReUPred. *Amino Acids*, **2016**, 48, 1391-400   3.5   14

18   VHLdb: A database of von Hippel-Lindau protein interactors and mutations. *Scientific Reports*, **2016**, 6, 31128   4.9   20

17   An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biology*, **2016**, 17, 184   18.3   218

16   Protein function prediction using guilty by association from interaction networks. *Amino Acids*, **2015**, 47, 2583-92   3.5   19

15   INGA: protein function prediction combining interaction networks, domain assignments and sequence similarity. *Nucleic Acids Research*, **2015**, 43, W134-40   20.1   59

14   The Victor C++ library for protein representation and advanced manipulation. *Bioinformatics*, **2015**, 31, 1138-40   7.2   5

13   RepeatsDB: a database of tandem repeat protein structures. *Nucleic Acids Research*, **2014**, 42, D352-7   20.1   47

12   Mapping and annotating obesity-related genes in pig and human genomes. *Protein and Peptide Letters*, **2014**, 21, 840-6   1.9   2

11   How to inherit statistically validated annotation within BAR+ protein clusters. *BMC Bioinformatics*, **2013**, 14 Suppl 3, S4   3.6   8

10   A large-scale evaluation of computational protein function prediction. *Nature Methods*, **2013**, 10, 221-7   21.6   587

LIST OF PUBLICATIONS

9	Extended and Robust Protein Sequence Annotation over Conservative Nonhierarchical Clusters. *ACM Journal on Emerging Technologies in Computing Systems*, **2013**, 9, 1-8	1.7	1
8	SUS-BAR: a database of pig proteins with statistically validated structural and functional annotation. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat065	5	3
7	FFPred 2.0: improved homology-independent prediction of gene ontology terms for eukaryotic protein sequences. *PLoS ONE*, **2013**, 8, e63754	3.7	37
6	The human "magnesome": detecting magnesium binding sites on human proteins. *BMC Bioinformatics*, **2012**, 13 Suppl 14, S10	3.6	17
5	Machine-Learning Methods to Predict Protein Interaction Sites in Folded Proteins. *Lecture Notes in Computer Science*, **2012**, 127-135	0.9	2
4	BAR-PLUS: the Bologna Annotation Resource Plus for functional and structural annotation of protein sequences. *Nucleic Acids Research*, **2011**, 39, W197-202	20.1	21
3	Extended and robust protein sequence annotation over conservative non hierarchical clusters. The Bologna Annotation Resource v 2.0. *Journal of Biotechnology*, **2010**, 150, 547-548	3.7	
2	Critical Assessment of Protein Intrinsic Disorder Prediction		7
1	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7