Lisanna Paladin

List of Publications by Year
in descending order

19 papers	7,890 citations	686830 13 h-index	752256 20 g-index
20 all docs	20 docs citations	20 times ranked	12565 citing authors

#	Article	IF	Citations
1	The Pfam protein families database in 2019. Nucleic Acids Research, 2019, 47, D427-D432.	6.5	3,937
2	Pfam: The protein families database in 2021. Nucleic Acids Research, 2021, 49, D412-D419.	6.5	3,068
3	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	6.5	190
4	MobiDB: intrinsically disordered proteins in 2021. Nucleic Acids Research, 2021, 49, D361-D367.	6.5	183
5	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	6.5	141
6	PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins. Nucleic Acids Research, 2020, 48, W77-W84.	6.5	71
7	Disentangling the complexity of low complexity proteins. Briefings in Bioinformatics, 2020, 21, 458-472.	3.2	70
8	SODA: prediction of protein solubility from disorder and aggregation propensity. Nucleic Acids Research, 2017, 45, W236-W240.	6.5	47
9	RepeatsDB in 2021: improved data and extended classification for protein tandem repeat structures. Nucleic Acids Research, 2021, 49, D452-D457.	6.5	37
10	RepeatsDB 2.0: improved annotation, classification, search and visualization of repeat protein structures. Nucleic Acids Research, 2017, 45, D308-D312.	6.5	33
11	RepeatsDB-lite: a web server for unit annotation of tandem repeat proteins. Nucleic Acids Research, 2018, 46, W402-W407.	6.5	18
12	The Feature-Viewer: a visualization tool for positional annotations on a sequence. Bioinformatics, 2020, 36, 3244-3245.	1.8	18
13	Identification of repetitive units in protein structures with ReUPred. Amino Acids, 2016, 48, 1391-1400.	1.2	17
14	In silico Characterization of Human Prion-Like Proteins: Beyond Neurological Diseases. Frontiers in Physiology, 2019, 10, 314.	1.3	17
15	Comparison of protein repeat classifications based on structure and sequence families. Biochemical Society Transactions, 2015, 43, 832-837.	1.6	11
16	Structural in silico dissection of the collagen V interactome to identify genotype–phenotype correlations in classic Ehlers–Danlos Syndrome (EDS). FEBS Letters, 2015, 589, 3871-3878.	1.3	11
17	A novel approach to investigate the evolution of structured tandem repeat protein families by exon duplication. Journal of Structural Biology, 2020, 212, 107608.	1.3	8
18	ProSeqViewer: an interactive, responsive and efficient TypeScript library for visualization of sequences and alignments in web applications. Bioinformatics, 2022, 38, 1129-1130.	1.8	4

#	Article	IF	Citations
19	PhytoTypeDB: a database of plant protein inter-cultivar variability and function. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	1