

# Lisanna Paladin

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7186850/publications.pdf>

Version: 2024-02-01

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	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
2	MobiDB: intrinsically disordered proteins in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D361-D367.	6.5	183
3	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
4	Pfam: The protein families database in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D412-D419.	6.5	3,068
5	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	6.5	141
6	Disentangling the complexity of low complexity proteins. <i>Briefings in Bioinformatics</i> , 2020, 21, 458-472.	3.2	70
7	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
8	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
9	The Feature-Viewer: a visualization tool for positional annotations on a sequence. <i>Bioinformatics</i> , 2020, 36, 3244-3245.	1.8	18
10	In silico Characterization of Human Prion-Like Proteins: Beyond Neurological Diseases. <i>Frontiers in Physiology</i> , 2019, 10, 314.	1.3	17
11	The Pfam protein families database in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D427-D432.	6.5	3,937
12	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
13	RepeatsDB-lite: a web server for unit annotation of tandem repeat proteins. <i>Nucleic Acids Research</i> , 2018, 46, W402-W407.	6.5	18
14	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
15	SODA: prediction of protein solubility from disorder and aggregation propensity. <i>Nucleic Acids Research</i> , 2017, 45, W236-W240.	6.5	47
16	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
17	Identification of repetitive units in protein structures with ReUPred. <i>Amino Acids</i> , 2016, 48, 1391-1400.	1.2	17
18	Comparison of protein repeat classifications based on structure and sequence families. <i>Biochemical Society Transactions</i> , 2015, 43, 832-837.	1.6	11

#	ARTICLE	IF	CITATIONS
19	Structural in silico dissection of the collagen V interactome to identify genotypeâ€“phenotype correlations in classic Ehlersâ€“Danlos Syndrome (EDS). FEBS Letters, 2015, 589, 3871-3878.	1.3	11