

Nicolas Palopoli

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

1,003
citations

686830

13
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610482

24
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39
all docs

39
docs citations

39
times ranked

1880
citing authors

#	ARTICLE	IF	CITATIONS
1	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	6.5	117
2	Impact of protein conformational diversity on AlphaFold predictions. <i>Bioinformatics</i> , 2022, 38, 2742-2748.	1.8	57
3	CoDNaS-RNA: a database of conformational diversity in the native state of RNA. <i>Bioinformatics</i> , 2022, 38, 1745-1748.	1.8	1
4	Intrinsically Disordered Protein Ensembles Shape Evolutionary Rates Revealing Conformational Patterns. <i>Journal of Molecular Biology</i> , 2021, 433, 166751.	2.0	3
5	“Protein” no longer means what it used to. <i>Current Research in Structural Biology</i> , 2021, 3, 146-152.	1.1	3
6	ELM—the eukaryotic linear motif resource in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D296-D306.	6.5	195
7	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	6.5	141
8	ProtMiscuity: a database of promiscuous proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	7
9	Bioinformatics calls the school: Use of smartphones to introduce Python for bioinformatics in high schools. <i>PLoS Computational Biology</i> , 2019, 15, e1006473.	1.5	2
10	Assessment of Structure Quality (RNA and Protein). , 2019, , 586-605.		0
11	Short linear motif core and flanking regions modulate retinoblastoma protein binding affinity and specificity. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 69-77.	1.0	33
12	The eukaryotic linear motif resource “ 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D428-D434.	6.5	183
13	Starch Synthesis in <i>Ostreococcus tauri</i> : The Starch-Binding Domains of Starch Synthase III-B Are Essential for Catalytic Activity. <i>Frontiers in Plant Science</i> , 2018, 9, 1541.	1.7	9
14	A report on the “International Society for Computational Biology - Latin America (ISCB-LA)” Bioinformatics Conference 2016. <i>EMBnet Journal</i> , 2017, 23, 883.	0.2	1
15	Second ISCB Latin American Student Council Symposium (LA-SCS) 2016. <i>F1000Research</i> , 2017, 6, 1491.	0.8	5
16	ISCB-Student Council Narratives: Strategic development of the ISCB-Regional Student Groups in 2016. <i>F1000Research</i> , 2016, 5, 2882.	0.8	6
17	Addressing the Role of Conformational Diversity in Protein Structure Prediction. <i>PLoS ONE</i> , 2016, 11, e0154923.	1.1	14
18	A report on the “International Society for Computational Biology - Latin America (ISCB-LA)” Bioinformatics Conference 2016. <i>EMBnet Journal</i> , 2016, 22, 883.	0.2	0

#	ARTICLE	IF	CITATIONS
19	QSLiMFinder: improved short linear motif prediction using specific query protein data. <i>Bioinformatics</i> , 2015, 31, 2284-2293.	1.8	19
20	Computational Prediction of Short Linear Motifs from Protein Sequences. <i>Methods in Molecular Biology</i> , 2015, 1268, 89-141.	0.4	39
21	SLiMScape 3.x: a Cytoscape 3 app for discovery of Short Linear Motifs in protein interaction networks. <i>F1000Research</i> , 2015, 4, 477.	0.8	1
22	BeEP Server: using evolutionary information for quality assessment of protein structure models. <i>Nucleic Acids Research</i> , 2013, 41, W398-W405.	6.5	5
23	Protein Conformational Diversity Modulates Sequence Divergence. <i>Molecular Biology and Evolution</i> , 2013, 30, 79-87.	3.5	31
24	MetaBase--the wiki-database of biological databases. <i>Nucleic Acids Research</i> , 2012, 40, D1250-D1254.	6.5	40
25	Functional and structural characterization of the catalytic domain of the starch synthase III from <i>Arabidopsis thaliana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 31-40.	1.5	42
26	Starch-synthase III family encodes a tandem of three starch-binding domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 27-31.	1.5	35