

Nicolas Palopoli

List of Publications by Year in descending order

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26
papers

1,003
citations

687363

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610901

24
g-index

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. Nucleic Acids Research, 2022, 50, D480-D487.	14.5	117
2	Impact of protein conformational diversity on AlphaFold predictions. Bioinformatics, 2022, 38, 2742-2748.	4.1	57
3	CoDNAS-RNA: a database of conformational diversity in the native state of RNA. Bioinformatics, 2022, 38, 1745-1748.	4.1	1
4	Intrinsically Disordered Protein Ensembles Shape Evolutionary Rates Revealing Conformational Patterns. Journal of Molecular Biology, 2021, 433, 166751.	4.2	3
5	“Protein” no longer means what it used to. Current Research in Structural Biology, 2021, 3, 146-152.	2.2	3
6	ELM—the eukaryotic linear motif resource in 2020. Nucleic Acids Research, 2020, 48, D296-D306.	14.5	195
7	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	14.5	141
8	ProtMiscuity: a database of promiscuous proteins. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	7
9	Bioinformatics calls the school: Use of smartphones to introduce Python for bioinformatics in high schools. PLoS Computational Biology, 2019, 15, e1006473.	3.2	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. Protein Engineering, Design and Selection, 2018, 31, 69-77.	2.1	33
12	The eukaryotic linear motif resource “ 2018 update. Nucleic Acids Research, 2018, 46, D428-D434.	14.5	183
13	Starch Synthesis in <i>Ostreococcus tauri</i> : The Starch-Binding Domains of Starch Synthase III-B Are Essential for Catalytic Activity. Frontiers in Plant Science, 2018, 9, 1541.	3.6	9
14	A report on the “International Society for Computational Biology - Latin America (ISCB-LA)” Bioinformatics Conference 2016. EMBnet Journal, 2017, 23, 883.	0.6	1
15	Second ISCB Latin American Student Council Symposium (LA-SCS) 2016. F1000Research, 2017, 6, 1491.	1.6	5
16	ISCB-Student Council Narratives: Strategic development of the ISCB-Regional Student Groups in 2016. F1000Research, 2016, 5, 2882.	1.6	6
17	Addressing the Role of Conformational Diversity in Protein Structure Prediction. PLoS ONE, 2016, 11, e0154923.	2.5	14
18	A report on the “International Society for Computational Biology - Latin America (ISCB-LA)” Bioinformatics Conference 2016. EMBnet Journal, 2016, 22, 883.	0.6	0

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19	QSLiMFinder: improved short linear motif prediction using specific query protein data. <i>Bioinformatics</i> , 2015, 31, 2284-2293.	4.1	19
20	Computational Prediction of Short Linear Motifs from Protein Sequences. <i>Methods in Molecular Biology</i> , 2015, 1268, 89-141.	0.9	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.	1.6	1
22	BeEP Server: using evolutionary information for quality assessment of protein structure models. <i>Nucleic Acids Research</i> , 2013, 41, W398-W405.	14.5	5
23	Protein Conformational Diversity Modulates Sequence Divergence. <i>Molecular Biology and Evolution</i> , 2013, 30, 79-87.	8.9	31
24	MetaBase--the wiki-database of biological databases. <i>Nucleic Acids Research</i> , 2012, 40, D1250-D1254.	14.5	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.	2.6	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.	2.6	35