Christine Orengo

List of Publications by Year
in descending order

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40 papers	4,630 citations	394421 19 h-index	276875 41 g-index
67 all docs	67 docs citations	67 times ranked	10099 citing authors

#	Article	IF	Citations
1	Exploiting protein family and protein network data to identify novel drug targets for bladder cancer. Oncotarget, 2022, 13, 105-117.	1.8	2
2	Assigning protein function from domain-function associations using DomFun. BMC Bioinformatics, 2022, 23, 43.	2.6	8
3	Srinivasan (1962â€“2021) in Bioinformatics and beyond. Bioinformatics, 2022, 38, 2377-2379.	4.1	2
4	Characterizing and explaining the impact of disease-associated mutations in proteins without known structures or structural homologs. Briefings in Bioinformatics, 2022, 23, .	6.5	18
5	Three-dimensional Structure Databases of Biological Macromolecules. Methods in Molecular Biology, 2022, 2449, 43-91.	0.9	2
6	Transmission of SARS-CoV-2 from humans to animals and potential host adaptation. Nature Communications, 2022, 13, .	12.8	67
7	Contrastive learning on protein embeddings enlightens midnight zone. NAR Genomics and Bioinformatics, 2022, 4, .	3.2	38
8	Arthropod Ectoparasites Have Potential to Bind SARS-CoV-2 via ACE. Viruses, 2021, 13, 708.	3.3	7
9	Tracing Evolution Through Protein Structures: Nature Captured in a Few Thousand Folds. Frontiers in Molecular Biosciences, 2021, 8, 668184.	3.5	16
10	Clustering FunFams using sequence embeddings improves EC purity. Bioinformatics, 2021, 37, 3449-3455.	4.1	25
11	CATH functional families predict functional sites in proteins. Bioinformatics, 2021, 37, 1099-1106.	4.1	19
12	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. Nucleic Acids Research, 2020, 48, D314-D319.	14.5	13
13	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. Methods in Molecular Biology, 2020, 2165, 27-67.	0.9	3
14	Assessing Protein Function Through Structural Similarities with CATH. Methods in Molecular Biology, 2020, 2112, 43-57.	0.9	2
15	Emerging concepts in pseudoenzyme classification, evolution, and signaling. Science Signaling, 2019, 12, .	3.6	80
16	FunFam protein families improve residue level molecular function prediction. BMC Bioinformatics, 2019, 20, 400.	2.6	20
17	Comprehensive analysis of long noncoding RNA expression in dorsal root ganglion reveals cell-type specificity and dysregulation after nerve injury. Pain, 2019, 160, 463-485.	4.2	45
18	Transcriptional Profiling of Dendritic Cells in a Mouse Model of Foodâ€Antigenâ€Induced Anaphylaxis Reveals the Upregulation of Multiple Immuneâ€Related Pathways. Molecular Nutrition and Food Research, 2019, 63, e1800759.	3.3	4

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19	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	14.5	1,291
20	Choosing the Best Enzyme Complex Structure Made Easy. Structure, 2018, 26, 528-530.	3.3	4
21	Protein CoAlation and antioxidant function of coenzyme A in prokaryotic cells. Biochemical Journal, 2018, 475, 1909-1937.	3.7	60
22	Gene3D: Extensive prediction of globular domains in proteins. Nucleic Acids Research, 2018, 46, D435-D439.	14.5	129
23	Structural and Functional View of Polypharmacology. Scientific Reports, 2017, 7, 10102.	3.3	33
24	An overview of comparative modelling and resources dedicated to large-scale modelling of genome sequences. Acta Crystallographica Section D: Structural Biology, 2017, 73, 628-640.	2.3	46
25	Unique signalling connectivity of FGFR3-TACC3 oncoprotein revealed by quantitative phosphoproteomics and differential network analysis. Oncotarget, 2017, 8, 102898-102911.	1.8	10
26	Landscape of activating cancer mutations in FGFR kinases and their differential responses to inhibitors in clinical use. Oncotarget, 2016, 7, 24252-24268.	1.8	83
27	Metagenome Mining: A Sequence Directed Strategy for the Retrieval of Enzymes for Biocatalysis. ChemistrySelect, 2016, 1, 2217-2220.	1.5	16
28	Novel Computational Protocols for Functionally Classifying and Characterising Serine Beta-Lactamases. PLoS Computational Biology, 2016, 12, e1004926.	3.2	24
29	Genome3D: exploiting structure to help users understand their sequences. Nucleic Acids Research, 2015, 43, D382-D386.	14.5	42
30	The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221.	14.5	1,205
31	FUN-L: gene prioritization for RNAi screens: Fig. 1.. Bioinformatics, 2015, 31, 2052-2053.	4.1	9
32	Gene Function Prediction from Functional Association Networks Using Kernel Partial Least Squares Regression. PLoS ONE, 2015, 10, e0134668.	2.5	15
33	Integration of biological data by kernels on graph nodes allows prediction of new genes involved in mitotic chromosome condensation. Molecular Biology of the Cell, 2014, 25, 2522-2536.	2.1	44
34	Genome-Wide Transcriptional Profiling of Skin and Dorsal Root Ganglia after Ultraviolet-B-Induced Inflammation. PLoS ONE, 2014, 9, e93338.	2.5	46
35	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	19.0	789
36	Gene3D: a domain-based resource for comparative genomics, functional annotation and protein network analysis. Nucleic Acids Research, 2012, 40, D465-D471.	14.5	98

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37	Gene3D: merging structure and function for a Thousand genomes. Nucleic Acids Research, 2010, 38, D296-D300.	14.5	50
38	GeMMA: functional subfamily classification within superfamilies of predicted protein structural domains. Nucleic Acids Research, 2010, 38, 720-737.	14.5	65
39	A fast and automated solution for accurately resolving protein domain architectures. Bioinformatics, 2010, 26, 745-751.	4.1	47
40	Finding the â€œDark Matterâ€•in Human and Yeast Protein Network Prediction and Modelling. PLoS Computational Biology, 2010, 6, e1000945.	3.2	21