

Christine Orengo

List of Publications by Year in descending order

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Version: 2024-02-01

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	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019, 47, D351-D360.	14.5	1,291
2	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	14.5	1,205
3	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
4	Gene3D: Extensive prediction of globular domains in proteins. <i>Nucleic Acids Research</i> , 2018, 46, D435-D439.	14.5	129
5	Gene3D: a domain-based resource for comparative genomics, functional annotation and protein network analysis. <i>Nucleic Acids Research</i> , 2012, 40, D465-D471.	14.5	98
6	Landscape of activating cancer mutations in FGFR kinases and their differential responses to inhibitors in clinical use. <i>Oncotarget</i> , 2016, 7, 24252-24268.	1.8	83
7	Emerging concepts in pseudoenzyme classification, evolution, and signaling. <i>Science Signaling</i> , 2019, 12, .	3.6	80
8	Transmission of SARS-CoV-2 from humans to animals and potential host adaptation. <i>Nature Communications</i> , 2022, 13, .	12.8	67
9	GeMMA: functional subfamily classification within superfamilies of predicted protein structural domains. <i>Nucleic Acids Research</i> , 2010, 38, 720-737.	14.5	65
10	Protein CoAlation and antioxidant function of coenzyme A in prokaryotic cells. <i>Biochemical Journal</i> , 2018, 475, 1909-1937.	3.7	60
11	Gene3D: merging structure and function for a Thousand genomes. <i>Nucleic Acids Research</i> , 2010, 38, D296-D300.	14.5	50
12	A fast and automated solution for accurately resolving protein domain architectures. <i>Bioinformatics</i> , 2010, 26, 745-751.	4.1	47
13	An overview of comparative modelling and resources dedicated to large-scale modelling of genome sequences. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 628-640.	2.3	46
14	Genome-Wide Transcriptional Profiling of Skin and Dorsal Root Ganglia after Ultraviolet-B-Induced Inflammation. <i>PLoS ONE</i> , 2014, 9, e93338.	2.5	46
15	Comprehensive analysis of long noncoding RNA expression in dorsal root ganglion reveals cell-type specificity and dysregulation after nerve injury. <i>Pain</i> , 2019, 160, 463-485.	4.2	45
16	Integration of biological data by kernels on graph nodes allows prediction of new genes involved in mitotic chromosome condensation. <i>Molecular Biology of the Cell</i> , 2014, 25, 2522-2536.	2.1	44
17	Genome3D: exploiting structure to help users understand their sequences. <i>Nucleic Acids Research</i> , 2015, 43, D382-D386.	14.5	42
18	Contrastive learning on protein embeddings enlightens midnight zone. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	3.2	38

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19	Structural and Functional View of Polypharmacology. <i>Scientific Reports</i> , 2017, 7, 10102.	3.3	33
20	Clustering FunFams using sequence embeddings improves EC purity. <i>Bioinformatics</i> , 2021, 37, 3449-3455.	4.1	25
21	Novel Computational Protocols for Functionally Classifying and Characterising Serine Beta-Lactamases. <i>PLoS Computational Biology</i> , 2016, 12, e1004926.	3.2	24
22	Finding the "Dark Matter" in Human and Yeast Protein Network Prediction and Modelling. <i>PLoS Computational Biology</i> , 2010, 6, e1000945.	3.2	21
23	FunFam protein families improve residue level molecular function prediction. <i>BMC Bioinformatics</i> , 2019, 20, 400.	2.6	20
24	CATH functional families predict functional sites in proteins. <i>Bioinformatics</i> , 2021, 37, 1099-1106.	4.1	19
25	Characterizing and explaining the impact of disease-associated mutations in proteins without known structures or structural homologs. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	18
26	Metagenome Mining: A Sequence Directed Strategy for the Retrieval of Enzymes for Biocatalysis. <i>ChemistrySelect</i> , 2016, 1, 2217-2220.	1.5	16
27	Tracing Evolution Through Protein Structures: Nature Captured in a Few Thousand Folds. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 668184.	3.5	16
28	Gene Function Prediction from Functional Association Networks Using Kernel Partial Least Squares Regression. <i>PLoS ONE</i> , 2015, 10, e0134668.	2.5	15
29	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. <i>Nucleic Acids Research</i> , 2020, 48, D314-D319.	14.5	13
30	Unique signalling connectivity of FGFR3-TACC3 oncoprotein revealed by quantitative phosphoproteomics and differential network analysis. <i>Oncotarget</i> , 2017, 8, 102898-102911.	1.8	10
31	FUN-L: gene prioritization for RNAi screens: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 2052-2053.	4.1	9
32	Assigning protein function from domain-function associations using DomFun. <i>BMC Bioinformatics</i> , 2022, 23, 43.	2.6	8
33	Arthropod Ectoparasites Have Potential to Bind SARS-CoV-2 via ACE. <i>Viruses</i> , 2021, 13, 708.	3.3	7
34	Choosing the Best Enzyme Complex Structure Made Easy. <i>Structure</i> , 2018, 26, 528-530.	3.3	4
35	Transcriptional Profiling of Dendritic Cells in a Mouse Model of Food Antigen-Induced Anaphylaxis Reveals the Upregulation of Multiple Immune-Related Pathways. <i>Molecular Nutrition and Food Research</i> , 2019, 63, e1800759.	3.3	4
36	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. <i>Methods in Molecular Biology</i> , 2020, 2165, 27-67.	0.9	3

#	ARTICLE	IF	CITATIONS
37	Assessing Protein Function Through Structural Similarities with CATH. <i>Methods in Molecular Biology</i> , 2020, 2112, 43-57.	0.9	2
38	Exploiting protein family and protein network data to identify novel drug targets for bladder cancer. <i>Oncotarget</i> , 2022, 13, 105-117.	1.8	2
39	Srinivasan (1962â€“2021) in Bioinformatics and beyond. <i>Bioinformatics</i> , 2022, 38, 2377-2379.	4.1	2
40	Three-dimensional Structure Databases of Biological Macromolecules. <i>Methods in Molecular Biology</i> , 2022, 2449, 43-91.	0.9	2