Ian Sillitoe

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7703844/publications.pdf

Version: 2024-02-01

35 papers	8,258 citations	236925 25 h-index	345221 36 g-index
41 all docs	41 docs citations	41 times ranked	14512 citing authors

#	Article	IF	Citations
1	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	14.5	1,385
2	InterPro in 2017â€"beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	14.5	1,358
3	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	14.5	1,291
4	The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221.	14.5	1,205
5	CATH: comprehensive structural and functional annotations for genome sequences. Nucleic Acids Research, 2015, 43, D376-D381.	14.5	399
6	CATH: an expanded resource to predict protein function through structure and sequence. Nucleic Acids Research, 2017, 45, D289-D295.	14.5	344
7	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
8	CATH: increased structural coverage of functional space. Nucleic Acids Research, 2021, 49, D266-D273.	14.5	270
9	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
10	New functional families (FunFams) in CATH to improve the mapping of conserved functional sites to 3D structures. Nucleic Acids Research, 2012, 41, D490-D498.	14.5	188
11	MSAViewer: interactive JavaScript visualization of multiple sequence alignments. Bioinformatics, 2016, 32, 3501-3503.	4.1	156
12	CATH: expanding the horizons of structure-based functional annotations for genome sequences. Nucleic Acids Research, 2019, 47, D280-D284.	14.5	131
13	Gene3D: Extensive prediction of globular domains in proteins. Nucleic Acids Research, 2018, 46, D435-D439.	14.5	129
14	Functional classification of CATH superfamilies: a domain-based approach for protein function annotation. Bioinformatics, 2015, 31, 3460-3467.	4.1	93
15	VarSite: Disease variants and protein structure. Protein Science, 2020, 29, 111-119.	7.6	77
16	Gene3D: expanding the utility of domain assignments. Nucleic Acids Research, 2016, 44, D404-D409.	14.5	64
17	CATH FunFHMMer web server: protein functional annotations using functional family assignments. Nucleic Acids Research, 2015, 43, W148-W153.	14.5	59
18	Genome3D: a UK collaborative project to annotate genomic sequences with predicted 3D structures based on SCOP and CATH domains. Nucleic Acids Research, 2012, 41, D499-D507.	14.5	53

#	Article	IF	Citations
19	Functional innovation from changes in protein domains and their combinations. Current Opinion in Structural Biology, 2016, 38, 44-52.	5.7	51
20	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
21	Genome3D: exploiting structure to help users understand their sequences. Nucleic Acids Research, 2015, 43, D382-D386.	14.5	42
22	Contrastive learning on protein embeddings enlightens midnight zone. NAR Genomics and Bioinformatics, 2022, 4, .	3.2	38
23	Understanding enzyme function evolution from a computational perspective. Current Opinion in Structural Biology, 2017, 47, 131-139.	5.7	36
24	The evolution of enzyme function in the isomerases. Current Opinion in Structural Biology, 2014, 26, 121-130.	5.7	33
25	Anatomy of BioJS, an open source community for the life sciences. ELife, 2015, 4, .	6.0	29
26	CATH-Gene3D: Generation of the Resource and Its Use in Obtaining Structural and Functional Annotations for Protein Sequences. Methods in Molecular Biology, 2017, 1558, 79-110.	0.9	24
27	Assessing strategies for improved superfamily recognition. Protein Science, 2005, 14, 1800-1810.	7.6	20
28	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
29	Tracing Evolution Through Protein Structures: Nature Captured in a Few Thousand Folds. Frontiers in Molecular Biosciences, 2021, 8, 668184.	3.5	16
30	The Classification of Protein Domains. Methods in Molecular Biology, 2017, 1525, 137-164.	0.9	14
31	FunTree: advances in a resource for exploring and contextualising protein function evolution. Nucleic Acids Research, 2016, 44, D317-D323.	14.5	13
32	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
33	Exploring Enzyme Evolution from Changes in Sequence, Structure, and Function. Methods in Molecular Biology, 2019, 1851, 263-275.	0.9	8
34	Assigning protein function from domain-function associations using DomFun. BMC Bioinformatics, 2022, 23, 43.	2.6	8
35	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. Methods in Molecular Biology, 2020, 2165, 27-67.	0.9	3