Ian Sillitoe

List of Publications by Year
in descending order

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	Assigning protein function from domain-function associations using DomFun. BMC Bioinformatics, 2022, 23, 43.	2.6	8
2	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
3	Contrastive learning on protein embeddings enlightens midnight zone. NAR Genomics and Bioinformatics, 2022, 4, .	3.2	38
4	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	14.5	1,385
5	CATH: increased structural coverage of functional space. Nucleic Acids Research, 2021, 49, D266-D273.	14.5	270
6	Tracing Evolution Through Protein Structures: Nature Captured in a Few Thousand Folds. Frontiers in Molecular Biosciences, 2021, 8, 668184.	3.5	16
7	VarSite: Disease variants and protein structure. Protein Science, 2020, 29, 111-119.	7.6	77
8	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
9	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. Methods in Molecular Biology, 2020, 2165, 27-67.	0.9	3
10	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
11	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	14.5	1,291
12	CATH: expanding the horizons of structure-based functional annotations for genome sequences. Nucleic Acids Research, 2019, 47, D280-D284.	14.5	131
13	Exploring Enzyme Evolution from Changes in Sequence, Structure, and Function. Methods in Molecular Biology, 2019, 1851, 263-275.	0.9	8
14	Gene3D: Extensive prediction of globular domains in proteins. Nucleic Acids Research, 2018, 46, D435-D439.	14.5	129
15	The Classification of Protein Domains. Methods in Molecular Biology, 2017, 1525, 137-164.	0.9	14
16	InterPro in 2017â€"beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	14.5	1,358
17	Understanding enzyme function evolution from a computational perspective. Current Opinion in Structural Biology, 2017, 47, 131-139.	5.7	36
18	CATH: an expanded resource to predict protein function through structure and sequence. Nucleic Acids Research, 2017, 45, D289-D295.	14.5	344

#	Article	IF	Citations
19	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
20	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
21	FunTree: advances in a resource for exploring and contextualising protein function evolution. Nucleic Acids Research, 2016, 44, D317-D323.	14.5	13
22	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
23	Functional innovation from changes in protein domains and their combinations. Current Opinion in Structural Biology, 2016, 38, 44-52.	5.7	51
24	MSAViewer: interactive JavaScript visualization of multiple sequence alignments. Bioinformatics, 2016, 32, 3501-3503.	4.1	156
25	Gene3D: expanding the utility of domain assignments. Nucleic Acids Research, 2016, 44, D404-D409.	14.5	64
26	CATH FunFHMMer web server: protein functional annotations using functional family assignments. Nucleic Acids Research, 2015, 43, W148-W153.	14.5	59
27	Genome3D: exploiting structure to help users understand their sequences. Nucleic Acids Research, 2015, 43, D382-D386.	14.5	42
28	CATH: comprehensive structural and functional annotations for genome sequences. Nucleic Acids Research, 2015, 43, D376-D381.	14.5	399
29	The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221.	14.5	1,205
30	Functional classification of CATH superfamilies: a domain-based approach for protein function annotation. Bioinformatics, 2015, 31, 3460-3467.	4.1	93
31	Anatomy of BioJS, an open source community for the life sciences. ELife, 2015, 4, .	6.0	29
32	The evolution of enzyme function in the isomerases. Current Opinion in Structural Biology, 2014, 26, 121-130.	5.7	33
33	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
34	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
35	Assessing strategies for improved superfamily recognition. Protein Science, 2005, 14, 1800-1810.	7.6	20