Alex L Mitchell

List of Publications by Year
in descending order

35 papers	23,877 citations	218592 26 h-index	395590 33 g-index
38 all docs	38 docs citations	38 times ranked	38500 citing authors

#	Article	IF	Citations
1	InterProScan 5: genome-scale protein function classification. Bioinformatics, 2014, 30, 1236-1240.	1.8	6,553
2	The Pfam protein families database: towards a more sustainable future. Nucleic Acids Research, 2016, 44, D279-D285.	6.5	5,391
3	InterPro: the integrative protein signature database. Nucleic Acids Research, 2009, 37, D211-D215.	6.5	1,712
4	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	6.5	1,385
5	InterPro in 2017â€"beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	6.5	1,358
6	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	6.5	1,291
7	The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221.	6.5	1,205
8	InterPro in 2011: new developments in the family and domain prediction database. Nucleic Acids Research, 2012, 40, D306-D312.	6.5	921
9	A new genomic blueprint of the human gut microbiota. Nature, 2019, 568, 499-504.	13.7	901
10	InterPro, progress and status in 2005. Nucleic Acids Research, 2004, 33, D201-D205.	6.5	478
11	New developments in the InterPro database. Nucleic Acids Research, 2007, 35, D224-D228.	6.5	444
12	A human gut bacterial genome and culture collection for improved metagenomic analyses. Nature Biotechnology, 2019, 37, 186-192.	9.4	420
13	Microbial abundance, activity and population genomic profiling with mOTUs2. Nature Communications, 2019, 10, 1014.	5.8	298
14	MGnify: the microbiome analysis resource in 2020. Nucleic Acids Research, 2020, 48, D570-D578.	6.5	296
15	EBI Metagenomics in 2017: enriching the analysis of microbial communities, from sequence reads to assemblies. Nucleic Acids Research, 2018, 46, D726-D735.	6.5	175
16	The PRINTS database: a fine-grained protein sequence annotation and analysis resource--its status in 2012. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas019-bas019.	1.4	138
17	EBI metagenomicsâ€"a new resource for the analysis and archiving of metagenomic data. Nucleic Acids Research, 2014, 42, D600-D606.	6.5	127
18	Manual GO annotation of predictive protein signatures: the InterPro approach to GO curation. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar068-bar068.	1.4	108

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19	EBI metagenomics in 2016 - an expanding and evolving resource for the analysis and archiving of metagenomic data. Nucleic Acids Research, 2016, 44, D595-D603.	6.5	97
20	Benchmarking taxonomic assignments based on 16S rRNA gene profiling of the microbiota from commonly sampled environments. GigaScience, 2018, 7, .	3.3	95
21	Microbial composition of Kombucha determined using amplicon sequencing and shotgun metagenomics. Journal of Food Science, 2020, 85, 455-464.	1.5	72
22	HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. Nucleic Acids Research, 2016, 44, D604-D609.	6.5	60
23	Estimating the quality of eukaryotic genomes recovered from metagenomic analysis with EukCC. Genome Biology, 2020, 21, 244.	3.8	58
24	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.	6.5	53
25	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. BMC Genomics, 2007, 8, 325.	1.2	44
26	The metagenomic data life-cycle: standards and best practices. GigaScience, 2017, 6, 1-11.	3.3	42
27	Unifying the known and unknown microbial coding sequence space. ELife, 2022, 11, .	2.8	41
28	Metagenomic analysis: the challenge of the data bonanza. Briefings in Bioinformatics, 2012, 13, 743-746.	3.2	23
29	Microbiota Characterization of Agricultural Green Waste-Based Suppressive Composts Using Omics and Classic Approaches. Agriculture (Switzerland), 2020, 10, 61.	1.4	21
30	GO annotation in InterPro: why stability does not indicate accuracy in a sea of changing annotations. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw027.	1.4	19
31	Alteration of barrier properties, stratum corneum ceramides and microbiome composition in response to lotion application on cosmetic dry skin. Scientific Reports, 2022, 12, 5223.	1.6	13
32	Learning to extract relations for protein annotation. Bioinformatics, 2007, 23, i256-i263.	1.8	11
33	ELIXIR pilot action: Marine metagenomics â€" towards a domain specific set of sustainable services. F1000Research, 2017, 6, 70.	0.8	8
34	MINOTAUR. International Journal of Systems Biology and Biomedical Technologies, 2012, 1, 1-10.	0.2	1
35	The Evolution of Protein Family Databases. , 2019, , 34-45.		1