

Alex L Mitchell

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

37 papers	15,222 citations	25 h-index	38 g-index
38 ext. papers	21,028 ext. citations	15.1 avg, IF	6.01 L-index

#	Paper	IF	Citations
37	The Pfam protein families database: towards a more sustainable future. <i>Nucleic Acids Research</i> , 2016 , 44, D279-85	20.1	3678
36	InterProScan 5: genome-scale protein function classification. <i>Bioinformatics</i> , 2014 , 30, 1236-40	7.2	3575
35	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009 , 37, D211-5	20.1	1379
34	InterPro in 2017-beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017 , 45, D190-D199	20.1	970
33	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015 , 43, D213-21	20.1	954
32	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012 , 40, D306-12	20.1	844
31	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019 , 47, D351-D360	20.1	835
30	A new genomic blueprint of the human gut microbiota. <i>Nature</i> , 2019 , 568, 499-504	50.4	484
29	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2005 , 33, D201-5	20.1	426
28	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007 , 35, D224-8	20.1	397
27	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021 , 49, D344-D354	20.1	358
26	A human gut bacterial genome and culture collection for improved metagenomic analyses. <i>Nature Biotechnology</i> , 2019 , 37, 186-192	44.5	224
25	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019 , 10, 1014	17.4	134
24	EBI Metagenomics in 2017: enriching the analysis of microbial communities, from sequence reads to assemblies. <i>Nucleic Acids Research</i> , 2018 , 46, D726-D735	20.1	130
23	MGNify: the microbiome analysis resource in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D570-D578	20.1	127
22	EBI metagenomics--a new resource for the analysis and archiving of metagenomic data. <i>Nucleic Acids Research</i> , 2014 , 42, D600-6	20.1	104
21	The PRINTS database: a fine-grained protein sequence annotation and analysis resource--its status in 2012. <i>Database: the Journal of Biological Databases and Curation</i> , 2012 , 2012, bas019	5	104

20	EBI metagenomics in 2016--an expanding and evolving resource for the analysis and archiving of metagenomic data. <i>Nucleic Acids Research</i> , 2016 , 44, D595-603	20.1	81
19	Manual GO annotation of predictive protein signatures: the InterPro approach to GO curation. <i>Database: the Journal of Biological Databases and Curation</i> , 2012 , 2012, bar068	5	70
18	Benchmarking taxonomic assignments based on 16S rRNA gene profiling of the microbiota from commonly sampled environments. <i>GigaScience</i> , 2018 , 7,	7.6	61
17	HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. <i>Nucleic Acids Research</i> , 2016 , 44, D604-9	20.1	50
16	Genome3D: a UK collaborative project to annotate genomic sequences with predicted 3D structures based on SCOP and CATH domains. <i>Nucleic Acids Research</i> , 2013 , 41, D499-507	20.1	48
15	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. <i>BMC Genomics</i> , 2007 , 8, 325	4.5	38
14	The metagenomic data life-cycle: standards and best practices. <i>GigaScience</i> , 2017 , 6, 1-11	7.6	29
13	Microbial composition of Kombucha determined using amplicon sequencing and shotgun metagenomics. <i>Journal of Food Science</i> , 2020 , 85, 455-464	3.4	28
12	Estimating the quality of eukaryotic genomes recovered from metagenomic analysis with EukCC. <i>Genome Biology</i> , 2020 , 21, 244	18.3	19
11	GO annotation in InterPro: why stability does not indicate accuracy in a sea of changing annotations. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	16
10	Metagenomic analysis: the challenge of the data bonanza. <i>Briefings in Bioinformatics</i> , 2012 , 13, 743-6	13.4	16
9	Microbiota Characterization of Agricultural Green Waste-Based Suppressive Composts Using Omics and Classic Approaches. <i>Agriculture (Switzerland)</i> , 2020 , 10, 61	3	14
8	Unifying the known and unknown microbial coding sequence space		9
7	Learning to extract relations for protein annotation. <i>Bioinformatics</i> , 2007 , 23, i256-63	7.2	6
6	ELIXIR pilot action: Marine metagenomics - towards a domain specific set of sustainable services. <i>F1000Research</i> , 2017 , 6,	3.6	6
5	Unifying the known and unknown microbial coding sequence space.. <i>ELife</i> , 2022 , 11,	8.9	4
4	Estimating the quality of eukaryotic genomes recovered from metagenomic analysis		3
3	The Evolution of Protein Family Databases 2019 , 34-45		1

- 2 MINOTAUR. *International Journal of Systems Biology and Biomedical Technologies*, **2012**, 1, 1-10 ○
- 1 Alteration of barrier properties, stratum corneum ceramides and microbiome composition in response to lotion application on cosmetic dry skin.. *Scientific Reports*, **2022**, 12, 5223 4.9 ○