Alex L Mitchell

List of Publications by Year in Descending Order

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	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	0
36	Unifying the known and unknown microbial coding sequence space.. *ELife*, **2022**, 11,	8.9	4
35	The InterPro protein families and domains database: 20 years on. *Nucleic Acids Research*, **2021**, 49, D344-D354	20.1	358
34	Microbial composition of Kombucha determined using amplicon sequencing and shotgun metagenomics. *Journal of Food Science*, **2020**, 85, 455-464	3.4	28
33	Microbiota Characterization of Agricultural Green Waste-Based Suppressive Composts Using Omics and Classic Approaches. *Agriculture (Switzerland)*, **2020**, 10, 61	3	14
32	MGnify: the microbiome analysis resource in 2020. *Nucleic Acids Research*, **2020**, 48, D570-D578	20.1	127
31	Estimating the quality of eukaryotic genomes recovered from metagenomic analysis with EukCC. *Genome Biology*, **2020**, 21, 244	18.3	19
30	Microbial abundance, activity and population genomic profiling with mOTUs2. *Nature Communications*, **2019**, 10, 1014	17.4	134
29	A new genomic blueprint of the human gut microbiota. *Nature*, **2019**, 568, 499-504	50.4	484
28	The Evolution of Protein Family Databases **2019**, 34-45		1
27	A human gut bacterial genome and culture collection for improved metagenomic analyses. *Nature Biotechnology*, **2019**, 37, 186-192	44.5	224
26	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. *Nucleic Acids Research*, **2019**, 47, D351-D360	20.1	835
25	EBI Metagenomics in 2017: enriching the analysis of microbial communities, from sequence reads to assemblies. *Nucleic Acids Research*, **2018**, 46, D726-D735	20.1	130
24	Benchmarking taxonomic assignments based on 16S rRNA gene profiling of the microbiota from commonly sampled environments. *GigaScience*, **2018**, 7,	7.6	61
23	InterPro in 2017-beyond protein family and domain annotations. *Nucleic Acids Research*, **2017**, 45, D190-D199	20.1	970
22	The metagenomic data life-cycle: standards and best practices. *GigaScience*, **2017**, 6, 1-11	7.6	29
21	ELIXIR pilot action: Marine metagenomics - towards a domain specific set of sustainable services. *F1000Research*, **2017**, 6,	3.6	6

20	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,	5	16
19	The Pfam protein families database: towards a more sustainable future. *Nucleic Acids Research*, **2016**, 44, D279-85	20.1	3678
18	HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. *Nucleic Acids Research*, **2016**, 44, D604-9	20.1	50
17	EBI metagenomics in 2016--an expanding and evolving resource for the analysis and archiving of metagenomic data. *Nucleic Acids Research*, **2016**, 44, D595-603	20.1	81
16	The InterPro protein families database: the classification resource after 15 years. *Nucleic Acids Research*, **2015**, 43, D213-21	20.1	954
15	EBI metagenomics--a new resource for the analysis and archiving of metagenomic data. *Nucleic Acids Research*, **2014**, 42, D600-6	20.1	104
14	InterProScan 5: genome-scale protein function classification. *Bioinformatics*, **2014**, 30, 1236-40	7.2	3575
13	Genome3D: a UK collaborative project to annotate genomic sequences with predicted 3D structures based on SCOP and CATH domains. *Nucleic Acids Research*, **2013**, 41, D499-507	20.1	48
12	MINOTAUR. *International Journal of Systems Biology and Biomedical Technologies*, **2012**, 1, 1-10		0
11	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	5	104
10	Manual GO annotation of predictive protein signatures: the InterPro approach to GO curation. *Database: the Journal of Biological Databases and Curation*, **2012**, 2012, bar068	5	70
9	Metagenomic analysis: the challenge of the data bonanza. *Briefings in Bioinformatics*, **2012**, 13, 743-6	13.4	16
8	InterPro in 2011: new developments in the family and domain prediction database. *Nucleic Acids Research*, **2012**, 40, D306-12	20.1	844
7	InterPro: the integrative protein signature database. *Nucleic Acids Research*, **2009**, 37, D211-5	20.1	1379
6	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. *BMC Genomics*, **2007**, 8, 325	4.5	38
5	New developments in the InterPro database. *Nucleic Acids Research*, **2007**, 35, D224-8	20.1	397
4	Learning to extract relations for protein annotation. *Bioinformatics*, **2007**, 23, i256-63	7.2	6
3	InterPro, progress and status in 2005. *Nucleic Acids Research*, **2005**, 33, D201-5	20.1	426

2 Estimating the quality of eukaryotic genomes recovered from metagenomic analysis 3

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