# Alex L Mitchell

## List of Publications by Year in descending order

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

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 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. | 1.6 | 13 |
| 2 | Unifying the known and unknown microbial coding sequence space. ELife, 2022, 11, . | 2.8 | 41 |
| 3 | The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354. | 6.5 | 1,385 |
| 4 | MGnify: the microbiome analysis resource in 2020. Nucleic Acids Research, 2020, 48, D570-D578. | 6.5 | 296 |
| 5 | Estimating the quality of eukaryotic genomes recovered from metagenomic analysis with EukCC. Genome Biology, 2020, 21, 244. | 3.8 | 58 |
| 6 | Microbial composition of Kombucha determined using amplicon sequencing and shotgun metagenomics. Journal of Food Science, 2020, 85, 455-464. | 1.5 | 72 |
| 7 | Microbiota Characterization of Agricultural Green Waste-Based Suppressive Composts Using Omics and Classic Approaches. Agriculture (Switzerland), 2020, 10, 61. | 1.4 | 21 |
| 8 | The Evolution of Protein Family Databases. , 2019, , 34-45. |  | 1 |
| 9 | Microbial abundance, activity and population genomic profiling with mOTUs2. Nature Communications, 2019, 10, 1014. | 5.8 | 298 |
| 10 | A new genomic blueprint of the human gut microbiota. Nature, 2019, 568, 499-504. | 13.7 | 901 |
| 11 | InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360. | 6.5 | 1,291 |
| 12 | A human gut bacterial genome and culture collection for improved metagenomic analyses. Nature Biotechnology, 2019, 37, 186-192. | 9.4 | 420 |
| 13 | 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 |
| 14 | Benchmarking taxonomic assignments based on 16S rRNA gene profiling of the microbiota from commonly sampled environments. GigaScience, 2018, 7, . | 3.3 | 95 |
| 15 | InterPro in 2017â€"beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199. | 6.5 | 1,358 |
| 16 | The metagenomic data life-cycle: standards and best practices. GigaScience, 2017, 6, 1-11. | 3.3 | 42 |
| 17 | ELIXIR pilot action: Marine metagenomics â€" towards a domain specific set of sustainable services. F1000Research, 2017, 6, 70. | 0.8 | 8 |
| 18 | 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 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | 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 |
| 20 | The Pfam protein families database: towards a more sustainable future. Nucleic Acids Research, 2016, 44, D279-D285. | 6.5 | 5,391 |
| 21 | HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. Nucleic Acids Research, 2016, 44, D604-D609. | 6.5 | 60 |
| 22 | The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221. | 6.5 | 1,205 |
| 23 | EBI metagenomicsâ€"a new resource for the analysis and archiving of metagenomic data. Nucleic Acids Research, 2014, 42, D600-D606. | 6.5 | 127 |
| 24 | InterProScan 5: genome-scale protein function classification. Bioinformatics, 2014, 30, 1236-1240. | 1.8 | 6,553 |
| 25 | 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 |
| 26 | 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 |
| 27 | Metagenomic analysis: the challenge of the data bonanza. Briefings in Bioinformatics, 2012, 13, 743-746. | 3.2 | 23 |
| 28 | 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 |
| 29 | InterPro in 2011: new developments in the family and domain prediction database. Nucleic Acids Research, 2012, 40, D306-D312. | 6.5 | 921 |
| 30 | MINOTAUR. International Journal of Systems Biology and Biomedical Technologies, 2012, 1, 1-10. | 0.2 | 1 |
| 31 | InterPro: the integrative protein signature database. Nucleic Acids Research, 2009, 37, D211-D215. | 6.5 | 1,712 |
| 32 | New developments in the InterPro database. Nucleic Acids Research, 2007, 35, D224-D228. | 6.5 | 444 |
| 33 | Learning to extract relations for protein annotation. Bioinformatics, 2007, 23, i256-i263. | 1.8 | 11 |
| 34 | Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. BMC Genomics, 2007, 8, 325. | 1.2 | 44 |
| 35 | InterPro, progress and status in 2005. Nucleic Acids Research, 2004, 33, D201-D205. | 6.5 | 478 |