Robert C Edgar

List of Publications by Year
in descending order

25 papers	77,346 citations	304743 22 h-index	580821 25 g-index
35 all docs	35 docs citations	35 times ranked	92537 citing authors

#	Article	IF	Citations
1	MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Research, 2004, 32, 1792-1797.	14.5	36,947
2	Search and clustering orders of magnitude faster than BLAST. Bioinformatics, 2010, 26, 2460-2461.	4.1	18,572
3	UPARSE: highly accurate OTU sequences from microbial amplicon reads. Nature Methods, 2013, 10, 996-998.	19.0	13,193
4	Defining the core Arabidopsis thaliana root microbiome. Nature, 2012, 488, 86-90.	27.8	2,475
5	Error filtering, pair assembly and error correction for next-generation sequencing reads. Bioinformatics, 2015, 31, 3476-3482.	4.1	1,102
6	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038
7	Updating the 97% identity threshold for 16S ribosomal RNA OTUs. Bioinformatics, 2018, 34, 2371-2375.	4.1	513
8	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. Microbes and Environments, 2015, 30, 145-150.	1.6	231
9	Accuracy of taxonomy prediction for 16S rRNA and fungal ITS sequences. PeerJ, 2018, 6, e4652.	2.0	223
10	Petabase-scale sequence alignment catalyses viral discovery. Nature, 2022, 602, 142-147.	27.8	213
11	Taxonomy annotation and guide tree errors in 16S rRNA databases. PeerJ, 2018, 6, e5030.	2.0	157
12	Accuracy of microbial community diversity estimated by closed- and open-reference OTUs. PeerJ, 2017, 5, e3889.	2.0	138
13	Local homology recognition and distance measures in linear time using compressed amino acid alphabets. Nucleic Acids Research, 2004, 32, 380-385.	14.5	112
14	Characterization and distribution of retrotransposons and simple sequence repeats in the bovine genome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12855-12860.	7.1	108
15	Quality measures for protein alignment benchmarks. Nucleic Acids Research, 2010, 38, 2145-2153.	14.5	103
16	Improved repeat identification and masking in Dipterans. Gene, 2007, 389, 1-9.	2.2	87
17	Syncmers are more sensitive than minimizers for selecting conserved k‑mers in biological sequences. PeerJ, 2021, 9, e10805.	2.0	48
18	Multiple alignment of protein sequences with repeats and rearrangements. Nucleic Acids Research, 2006, 34, 5932-5942.	14.5	40

#	Article	IF	Citations
19	Massively parallel interrogation and mining of natively paired human TCRαβ repertoires. Nature Biotechnology, 2020, 38, 609-619.	17.5	34
20	Rare, high-affinity anti-pathogen antibodies from human repertoires, discovered using microfluidics and molecular genomics. MAbs, 2017, 9, 1282-1296.	5.2	32
21	Antibody repertoire analysis of mouse immunization protocols using microfluidics and molecular genomics. MAbs, 2019, 11, 870-883.	5.2	29
22	A natively paired antibody library yields drug leads with higher sensitivity and specificity than a randomly paired antibody library. MAbs, 2018, 10, 431-443.	5.2	28
23	Rare, high-affinity mouse anti-PD-1 antibodies that function in checkpoint blockade, discovered using microfluidics and molecular genomics. MAbs, 2017, 9, 1270-1281.	5.2	26
24	Generation of recombinant hyperimmune globulins from diverse B-cell repertoires. Nature Biotechnology, 2021, 39, 989-999.	17.5	13
25	URMAP, an ultra-fast read mapper. PeerJ, 2020, 8, e9338.	2.0	9