

Robert C Edgar

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1127456/publications.pdf>

Version: 2024-02-01

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	Petabase-scale sequence alignment catalyses viral discovery. <i>Nature</i> , 2022, 602, 142-147.	27.8	213
2	Syncmers are more sensitive than minimizers for selecting conserved k -mers in biological sequences. <i>PeerJ</i> , 2021, 9, e10805.	2.0	48
3	Generation of recombinant hyperimmune globulins from diverse B-cell repertoires. <i>Nature Biotechnology</i> , 2021, 39, 989-999.	17.5	13
4	Massively parallel interrogation and mining of natively paired human TCR $\alpha\beta$ repertoires. <i>Nature Biotechnology</i> , 2020, 38, 609-619.	17.5	34
5	URMAP, an ultra-fast read mapper. <i>PeerJ</i> , 2020, 8, e9338.	2.0	9
6	Antibody repertoire analysis of mouse immunization protocols using microfluidics and molecular genomics. <i>MAbs</i> , 2019, 11, 870-883.	5.2	29
7	Updating the 97% identity threshold for 16S ribosomal RNA OTUs. <i>Bioinformatics</i> , 2018, 34, 2371-2375.	4.1	513
8	A natively paired antibody library yields drug leads with higher sensitivity and specificity than a randomly paired antibody library. <i>MAbs</i> , 2018, 10, 431-443.	5.2	28
9	Accuracy of taxonomy prediction for 16S rRNA and fungal ITS sequences. <i>PeerJ</i> , 2018, 6, e4652.	2.0	223
10	Taxonomy annotation and guide tree errors in 16S rRNA databases. <i>PeerJ</i> , 2018, 6, e5030.	2.0	157
11	Rare, high-affinity anti-pathogen antibodies from human repertoires, discovered using microfluidics and molecular genomics. <i>MAbs</i> , 2017, 9, 1282-1296.	5.2	32
12	Rare, high-affinity mouse anti-PD-1 antibodies that function in checkpoint blockade, discovered using microfluidics and molecular genomics. <i>MAbs</i> , 2017, 9, 1270-1281.	5.2	26
13	Accuracy of microbial community diversity estimated by closed- and open-reference OTUs. <i>PeerJ</i> , 2017, 5, e3889.	2.0	138
14	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. <i>Microbes and Environments</i> , 2015, 30, 145-150.	1.6	231
15	Error filtering, pair assembly and error correction for next-generation sequencing reads. <i>Bioinformatics</i> , 2015, 31, 3476-3482.	4.1	1,102
16	UPARSE: highly accurate OTU sequences from microbial amplicon reads. <i>Nature Methods</i> , 2013, 10, 996-998.	19.0	13,193
17	Defining the core <i>Arabidopsis thaliana</i> root microbiome. <i>Nature</i> , 2012, 488, 86-90.	27.8	2,475
18	Quality measures for protein alignment benchmarks. <i>Nucleic Acids Research</i> , 2010, 38, 2145-2153.	14.5	103

#	ARTICLE	IF	CITATIONS
19	Search and clustering orders of magnitude faster than BLAST. <i>Bioinformatics</i> , 2010, 26, 2460-2461.	4.1	18,572
20	Characterization and distribution of retrotransposons and simple sequence repeats in the bovine genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12855-12860.	7.1	108
21	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
22	Improved repeat identification and masking in Dipterans. <i>Gene</i> , 2007, 389, 1-9.	2.2	87
23	Multiple alignment of protein sequences with repeats and rearrangements. <i>Nucleic Acids Research</i> , 2006, 34, 5932-5942.	14.5	40
24	Local homology recognition and distance measures in linear time using compressed amino acid alphabets. <i>Nucleic Acids Research</i> , 2004, 32, 380-385.	14.5	112
25	MUSCLE: multiple sequence alignment with high accuracy and high throughput. <i>Nucleic Acids Research</i> , 2004, 32, 1792-1797.	14.5	36,947