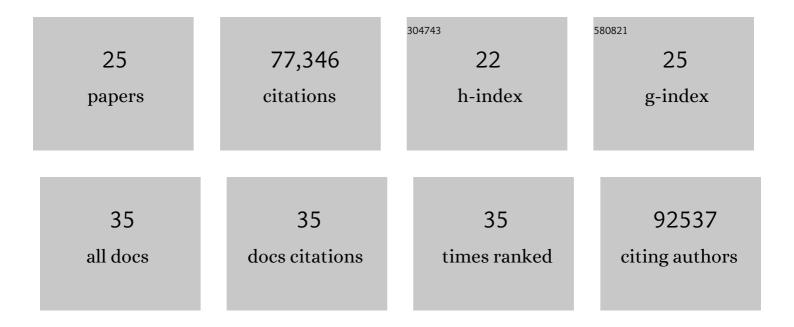
Robert C Edgar

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1127456/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Petabase-scale sequence alignment catalyses viral discovery. Nature, 2022, 602, 142-147.	27.8	213
2	Syncmers are more sensitive than minimizers for selecting conserved <i>k</i> ‑mers in biological sequences. PeerJ, 2021, 9, e10805.	2.0	48
3	Generation of recombinant hyperimmune globulins from diverse B-cell repertoires. Nature Biotechnology, 2021, 39, 989-999.	17.5	13
4	Massively parallel interrogation and mining of natively paired human TCRαβ repertoires. Nature Biotechnology, 2020, 38, 609-619.	17.5	34
5	URMAP, an ultra-fast read mapper. PeerJ, 2020, 8, e9338.	2.0	9
6	Antibody repertoire analysis of mouse immunization protocols using microfluidics and molecular genomics. MAbs, 2019, 11, 870-883.	5.2	29
7	Updating the 97% identity threshold for 16S ribosomal RNA OTUs. Bioinformatics, 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. MAbs, 2018, 10, 431-443.	5.2	28
9	Accuracy of taxonomy prediction for 16S rRNA and fungal ITS sequences. PeerJ, 2018, 6, e4652.	2.0	223
10	Taxonomy annotation and guide tree errors in 16S rRNA databases. PeerJ, 2018, 6, e5030.	2.0	157
11	Rare, high-affinity anti-pathogen antibodies from human repertoires, discovered using microfluidics and molecular genomics. MAbs, 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. MAbs, 2017, 9, 1270-1281.	5.2	26
13	Accuracy of microbial community diversity estimated by closed- and open-reference OTUs. PeerJ, 2017, 5, e3889.	2.0	138
14	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
15	Error filtering, pair assembly and error correction for next-generation sequencing reads. Bioinformatics, 2015, 31, 3476-3482.	4.1	1,102
16	UPARSE: highly accurate OTU sequences from microbial amplicon reads. Nature Methods, 2013, 10, 996-998.	19.0	13,193
17	Defining the core Arabidopsis thaliana root microbiome. Nature, 2012, 488, 86-90.	27.8	2,475
18	Quality measures for protein alignment benchmarks. Nucleic Acids Research, 2010, 38, 2145-2153.	14.5	103

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