

Robert Schmieder

List of Publications by Citations

Source: <https://exaly.com/author-pdf/12108646/robert-schmieder-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

25
papers

5,662
citations

23
h-index

25
g-index

25
ext. papers

7,214
ext. citations

5.9
avg, IF

6.24
L-index

#	Paper	IF	Citations
25	Quality control and preprocessing of metagenomic datasets. <i>Bioinformatics</i> , 2011 , 27, 863-4	7.2	2975
24	Fast identification and removal of sequence contamination from genomic and metagenomic datasets. <i>PLoS ONE</i> , 2011 , 6, e17288	3.7	471
23	Metagenomic analysis of respiratory tract DNA viral communities in cystic fibrosis and non-cystic fibrosis individuals. <i>PLoS ONE</i> , 2009 , 4, e7370	3.7	297
22	Insights into antibiotic resistance through metagenomic approaches. <i>Future Microbiology</i> , 2012 , 7, 73-89	2.9	199
21	Broad surveys of DNA viral diversity obtained through viral metagenomics of mosquitoes. <i>PLoS ONE</i> , 2011 , 6, e20579	3.7	168
20	The GAAS metagenomic tool and its estimations of viral and microbial average genome size in four major biomes. <i>PLoS Computational Biology</i> , 2009 , 5, e1000593	5	162
19	TagCleaner: Identification and removal of tag sequences from genomic and metagenomic datasets. <i>BMC Bioinformatics</i> , 2010 , 11, 341	3.6	157
18	Identification and removal of ribosomal RNA sequences from metatranscriptomes. <i>Bioinformatics</i> , 2012 , 28, 433-5	7.2	148
17	Spatial distribution of microbial communities in the cystic fibrosis lung. <i>ISME Journal</i> , 2012 , 6, 471-4	11.9	135
16	Metagenomics and metatranscriptomics: windows on CF-associated viral and microbial communities. <i>Journal of Cystic Fibrosis</i> , 2013 , 12, 154-64	4.1	118
15	Metagenomic detection of phage-encoded platelet-binding factors in the human oral cavity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108 Suppl 1, 4547-53	11.5	103
14	Clinical insights from metagenomic analysis of sputum samples from patients with cystic fibrosis. <i>Journal of Clinical Microbiology</i> , 2014 , 52, 425-37	9.7	96
13	Abrolhos bank reef health evaluated by means of water quality, microbial diversity, benthic cover, and fish biomass data. <i>PLoS ONE</i> , 2012 , 7, e36687	3.7	93
12	Breath gas metabolites and bacterial metagenomes from cystic fibrosis airways indicate active pH neutral 2,3-butanedione fermentation. <i>ISME Journal</i> , 2014 , 8, 1247-58	11.9	92
11	Case studies of the spatial heterogeneity of DNA viruses in the cystic fibrosis lung. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2012 , 46, 127-31	5.7	87
10	Allelic variation contributes to bacterial host specificity. <i>Nature Communications</i> , 2015 , 6, 8754	17.4	54
9	Reference-independent comparative metagenomics using cross-assembly: crAss. <i>Bioinformatics</i> , 2012 , 28, 3225-31	7.2	52

8	SEQanswers: an open access community for collaboratively decoding genomes. <i>Bioinformatics</i> , 2012 , 28, 1272-3	7.2	49
7	Species-specific viromes in the ancestral holobiont Hydra. <i>PLoS ONE</i> , 2014 , 9, e109952	3.7	43
6	Combining de novo and reference-guided assembly with scaffold_builder. <i>Source Code for Biology and Medicine</i> , 2013 , 8, 23	1.9	39
5	Mechanistic model of <i>Rothia mucilaginosa</i> adaptation toward persistence in the CF lung, based on a genome reconstructed from metagenomic data. <i>PLoS ONE</i> , 2013 , 8, e64285	3.7	38
4	Genomic Comparison of the Closely-Related <i>Salmonella enterica</i> Serovars Enteritidis, Dublin and Gallinarum. <i>PLoS ONE</i> , 2015 , 10, e0126883	3.7	27
3	Big data challenges and opportunities in high-throughput sequencing. <i>Systems Biomedicine (Austin, Tex)</i> , 2013 , 1, 29-34		27
2	Comparative genomics of 274 <i>Vibrio cholerae</i> genomes reveals mobile functions structuring three niche dimensions. <i>BMC Genomics</i> , 2014 , 15, 654	4.5	21
1	Microfluidic PCR combined with pyrosequencing for identification of allelic variants with phenotypic associations among targeted <i>Salmonella</i> genes. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 7480-2	4.8	11