Robert Schmieder

List of Publications by Year
in descending order

25 papers	7,820 citations	279778 23 h-index	580810 25 g-index
25 all docs	25 docs citations	25 times ranked	15260 citing authors

#	ARTICLE	IF	CITATIONS
1	Allelic variation contributes to bacterial host specificity. Nature Communications, 2015, 6, 8754.	12.8	100
2	Genomic Comparison of the Closely-Related Salmonella enterica Serovars Enteritidis, Dublin and Gallinarum. PLoS ONE, 2015, 10, e0126883.	2.5	39
3	Species-Specific Viromes in the Ancestral Holobiont Hydra. PLoS ONE, 2014, 9, e109952.	2.5	53
4	Breath gas metabolites and bacterial metagenomes from cystic fibrosis airways indicate active pH neutral 2,3-butanedione fermentation. ISME Journal, 2014, 8, 1247-1258.	9.8	114
5	Clinical Insights from Metagenomic Analysis of Sputum Samples from Patients with Cystic Fibrosis. Journal of Clinical Microbiology, 2014, 52, 425-437.	3.9	120
6	Comparative genomics of 274 Vibrio cholerae genomes reveals mobile functions structuring three niche dimensions. BMC Genomics, 2014, 15, 654.	2.8	24
7	Metagenomics and metatranscriptomics: Windows on CF-associated viral and microbial communities. Journal of Cystic Fibrosis, 2013, 12, 154-164.	0.7	142
8	Combining de novo and reference-guided assembly with scaffold_builder. Source Code for Biology and Medicine, 2013, 8, 23.	1.7	59
9	Big data challenges and opportunities in high-throughput sequencing. Systems Biomedicine (Austin,) Tj ETQq1 1 0.784314 rgBT /Overlo	0.7	34
10	Mechanistic Model of Rothia mucilaginosa Adaptation toward Persistence in the CF Lung, Based on a Genome Reconstructed from Metagenomic Data. PLoS ONE, 2013, 8, e64285.	2.5	51
11	Spatial distribution of microbial communities in the cystic fibrosis lung. ISME Journal, 2012, 6, 471-474.	9.8	156
12	Identification and removal of ribosomal RNA sequences from metatranscriptomes. Bioinformatics, 2012, 28, 433-435.	4.1	212
13	SEQanswers: an open access community for collaboratively decoding genomes. Bioinformatics, 2012, 28, 1272-1273.	4.1	54
14	Microfluidic PCR Combined with Pyrosequencing for Identification of Allelic Variants with Phenotypic Associations among Targeted Salmonella Genes. Applied and Environmental Microbiology, 2012, 78, 7480-7482.	3.1	14
15	Case Studies of the Spatial Heterogeneity of DNA Viruses in the Cystic Fibrosis Lung. American Journal of Respiratory Cell and Molecular Biology, 2012, 46, 127-131.	2.9	102
16	Reference-independent comparative metagenomics using cross-assembly: crAss. Bioinformatics, 2012, 28, 3225-3231.	4.1	87
17	Insights into antibiotic resistance through metagenomic approaches. Future Microbiology, 2012, 7, 73-89.	2.0	251
18	Abrolhos Bank Reef Health Evaluated by Means of Water Quality, Microbial Diversity, Benthic Cover, and Fish Biomass Data. PLoS ONE, 2012, 7, e36687.	2.5	125

#	Article	IF	Citations
19	Fast Identification and Removal of Sequence Contamination from Genomic and Metagenomic Datasets. PLoS ONE, 2011, 6, e17288.	2.5	630
20	Broad Surveys of DNA Viral Diversity Obtained through Viral Metagenomics of Mosquitoes. PLoS ONE, 2011, 6, e20579.	2.5	185
21	Quality control and preprocessing of metagenomic datasets. Bioinformatics, 2011, 27, 863-864.	4.1	4,402
22	Metagenomic detection of phage-encoded platelet-binding factors in the human oral cavity. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4547-4553.	7.1	123
23	TagCleaner: Identification and removal of tag sequences from genomic and metagenomic datasets. BMC Bioinformatics, 2010, 11, 341.	2.6	207
24	The GAAS Metagenomic Tool and Its Estimations of Viral and Microbial Average Genome Size in Four Major Biomes. PLoS Computational Biology, 2009, 5, e1000593.	3.2	177
25	Metagenomic Analysis of Respiratory Tract DNA Viral Communities in Cystic Fibrosis and Non-Cystic Fibrosis Individuals. PLoS ONE, 2009, 4, e7370.	2.5	359