Andreas Wilke

List of Publications by Year
in descending order

22 papers	12,452 citations	623734 14 h-index	839539 18 g-index
22 all docs	22 docs citations	22 times ranked	17673 citing authors

#	Article	IF	Citations
1	The RAST Server: Rapid Annotations using Subsystems Technology. BMC Genomics, 2008, 9, 75.	2.8	9,977
2	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. GigaScience, 2012, 1, 7.	6.4	671
3	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
4	The M5nr: a novel non-redundant database containing protein sequences and annotations from multiple sources and associated tools. BMC Bioinformatics, 2012, 13, 141.	2.6	291
5	The MG-RAST metagenomics database and portal in 2015. Nucleic Acids Research, 2016, 44, D590-D594.	14.5	187
6	MIxS-BE: a MIxS extension defining a minimum information standard for sequence data from the built environment. ISME Journal, 2014, 8, 1-3.	9.8	127
7	MG-RAST version 4—lessons learned from a decade of low-budget ultra-high-throughput metagenome analysis. Briefings in Bioinformatics, 2019, 20, 1151-1159.	6.5	98
8	A Platform-Independent Method for Detecting Errors in Metagenomic Sequencing Data: DRISEE. PLoS Computational Biology, 2012, 8, e1002541.	3.2	83
9	A RESTful API for Accessing Microbial Community Data for MG-RAST. PLoS Computational Biology, 2015, 11, e1004008.	3.2	83
10	Skyport - Container-Based Execution Environment Management for Multi-cloud Scientific Workflows. , 2014, , .		70
11	The complete genome sequence for putative H_2—and S—oxidizer Candidatus Sulfuricurvum sp., assembled de novo from an aquifer—derived metagenome. Environmental Microbiology, 2014, 16, 3443-3462.	3.8	69
12	Short-read reading-frame predictors are not created equal: sequence error causes loss of signal. BMC Bioinformatics, 2012, 13, 183.	2.6	39
13	Using clouds for metagenomics: A case study. , 2009, , .		32
14	Bioinformatics support for high-throughput proteomics. Journal of Biotechnology, 2003, 106, 147-156.	3.8	31
15	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. Journal of Biotechnology, 2003, 106, 157-167.	3.8	22
16	A Metagenomics Portal for a Democratized Sequencing World. Methods in Enzymology, 2013, 531, 487-523.	1.0	16
17	An experience report: porting the MG-RAST rapid metagenomics analysis pipeline to the cloud. Concurrency Computation Practice and Experience, 2011, 23, 2250-2257.	2.2	13
18	The MG-RAST API explorer: an on-ramp for RESTful query composition. BMC Bioinformatics, 2019, 20, 561.	2.6	10

#	Article	IF	Citations
19	Shock: Active Storage for Multicloud Streaming Data Analysis. , 2015, , .		8
20	SAMPI: Protein Identification with Mass Spectra Alignments. BMC Bioinformatics, 2007, 8, 102.	2.6	7
21	Workload characterization for MG-RAST metagenomic data analytics service in the cloud. , 2014, , .		5
22	Metazen â€" metadata capture for metagenomes. Standards in Genomic Sciences, 2014, 9, 18.	1.5	5