Florent E Angly

List of Publications by Year in descending order

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Version: 2024-02-01

201674 454955 7,314 29 27 30 h-index citations g-index papers 32 32 32 8780 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Marine microbial communities of the Great Barrier Reef lagoon are influenced by riverine floodwaters and seasonal weather events. PeerJ, 2016, 4, e1511.	2.0	53
2	Diuron tolerance and potential degradation by pelagic microbiomes in the Great Barrier Reef lagoon. PeerJ, 2016, 4, e1758.	2.0	7
3	Evaluation of viral genome assembly and diversity estimation in deep metagenomes. BMC Genomics, 2014, 15, 989.	2.8	31
4	The Bio-Community Perl toolkit for microbial ecology. Bioinformatics, 2014, 30, 1926-1927.	4.1	16
5	CopyRighter: a rapid tool for improving the accuracy of microbial community profiles through lineage-specific gene copy number correction. Microbiome, 2014, 2, 11.	11.1	225
6	Future reef decalcification under a business-as-usual CO ₂ emission scenario. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15342-15347.	7.1	152
7	Grinder: a versatile amplicon and shotgun sequence simulator. Nucleic Acids Research, 2012, 40, e94-e94.	14.5	180
8	Oxygen minimum zones harbour novel viral communities with low diversity. Environmental Microbiology, 2012, 14, 3043-3065.	3.8	68
9	Phage–bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. Environmental Microbiology, 2012, 14, 207-227.	3.8	128
10	Metagenomic analysis of DNA viruses in a wastewater treatment plant in tropical climate. Environmental Microbiology, 2012, 14, 441-452.	3.8	98
11	Next Generation Sequence Assembly with AMOS. Current Protocols in Bioinformatics, 2011, 33, Unit 11.8.	25.8	200
12	Wastewater treatment systems harbor specific and diverse yeast communities. Biochemical Engineering Journal, 2011, 58-59, 168-176.	3 . 6	40
13	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
14	Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. PLoS ONE, 2011, 6, e20095.	2.5	59
15	Viral and microbial community dynamics in four aquatic environments. ISME Journal, 2010, 4, 739-751.	9.8	387
16	Viruses in the faecal microbiota of monozygotic twins and their mothers. Nature, 2010, 466, 334-338.	27.8	1,054
17	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
18	Metagenomic analysis of stressed coral holobionts. Environmental Microbiology, 2009, 11, 2148-2163.	3.8	551

#	Article	IF	Citations
19	Genomic analysis of multiple Roseophage SIO1 strains. Environmental Microbiology, 2009, 11, 2863-2873.	3.8	64
20	Metagenomic Analysis of Respiratory Tract DNA Viral Communities in Cystic Fibrosis and Non-Cystic Fibrosis Individuals. PLoS ONE, 2009, 4, e7370.	2.5	359
21	Biodiversity and biogeography of phages in modern stromatolites and thrombolites. Nature, 2008, 452, 340-343.	27.8	251
22	Functional metagenomic profiling of nine biomes. Nature, 2008, 452, 629-632.	27.8	842
23	Viral diversity and dynamics in an infant gut. Research in Microbiology, 2008, 159, 367-373.	2.1	288
24	Metagenomic analysis indicates that stressors induce production of herpes-like viruses in the coral <i>Porites compressa</i> . Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18413-18418.	7.1	205
25	Microbial Ecology of Four Coral Atolls in the Northern Line Islands. PLoS ONE, 2008, 3, e1584.	2.5	383
26	Comparative Metagenomics Reveals Host Specific Metavirulomes and Horizontal Gene Transfer Elements in the Chicken Cecum Microbiome. PLoS ONE, 2008, 3, e2945.	2.5	247
27	Power law rank–abundance models for marine phage communities. FEMS Microbiology Letters, 2007, 273, 224-228.	1.8	51
28	The Marine Viromes of Four Oceanic Regions. PLoS Biology, 2006, 4, e368.	5.6	867
29	PHACCS, an online tool for estimating the structure and diversity of uncultured viral communities using metagenomic information. BMC Bioinformatics, 2005, 6, 41.	2.6	182