

Florent E Angly

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

7,314
citations

201674

27
h-index

454955

30
g-index

32
all docs

32
docs citations

32
times ranked

8780
citing authors

#	ARTICLE	IF	CITATIONS
1	Viruses in the faecal microbiota of monozygotic twins and their mothers. <i>Nature</i> , 2010, 466, 334-338.	27.8	1,054
2	The Marine Viromes of Four Oceanic Regions. <i>PLoS Biology</i> , 2006, 4, e368.	5.6	867
3	Functional metagenomic profiling of nine biomes. <i>Nature</i> , 2008, 452, 629-632.	27.8	842
4	Metagenomic analysis of stressed coral holobionts. <i>Environmental Microbiology</i> , 2009, 11, 2148-2163.	3.8	551
5	Viral and microbial community dynamics in four aquatic environments. <i>ISME Journal</i> , 2010, 4, 739-751.	9.8	387
6	Microbial Ecology of Four Coral Atolls in the Northern Line Islands. <i>PLoS ONE</i> , 2008, 3, e1584.	2.5	383
7	Metagenomic Analysis of Respiratory Tract DNA Viral Communities in Cystic Fibrosis and Non-Cystic Fibrosis Individuals. <i>PLoS ONE</i> , 2009, 4, e7370.	2.5	359
8	Viral diversity and dynamics in an infant gut. <i>Research in Microbiology</i> , 2008, 159, 367-373.	2.1	288
9	Biodiversity and biogeography of phages in modern stromatolites and thrombolites. <i>Nature</i> , 2008, 452, 340-343.	27.8	251
10	Comparative Metagenomics Reveals Host Specific Metavirulomes and Horizontal Gene Transfer Elements in the Chicken Cecum Microbiome. <i>PLoS ONE</i> , 2008, 3, e2945.	2.5	247
11	CopyRighter: a rapid tool for improving the accuracy of microbial community profiles through lineage-specific gene copy number correction. <i>Microbiome</i> , 2014, 2, 11.	11.1	225
12	Metagenomic analysis indicates that stressors induce production of herpes-like viruses in the coral <i>Porites compressa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18413-18418.	7.1	205
13	Next Generation Sequence Assembly with AMOS. <i>Current Protocols in Bioinformatics</i> , 2011, 33, Unit 11.8.	25.8	200
14	PHACCS, an online tool for estimating the structure and diversity of uncultured viral communities using metagenomic information. <i>BMC Bioinformatics</i> , 2005, 6, 41.	2.6	182
15	Grinder: a versatile amplicon and shotgun sequence simulator. <i>Nucleic Acids Research</i> , 2012, 40, e94-e94.	14.5	180
16	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.	3.2	177
17	Future reef decalcification under a business-as-usual CO ₂ emission scenario. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15342-15347.	7.1	152
18	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. <i>Environmental Microbiology</i> , 2012, 14, 207-227.	3.8	128

#	ARTICLE	IF	CITATIONS
19	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
20	Metagenomic analysis of DNA viruses in a wastewater treatment plant in tropical climate. Environmental Microbiology, 2012, 14, 441-452.	3.8	98
21	Oxygen minimum zones harbour novel viral communities with low diversity. Environmental Microbiology, 2012, 14, 3043-3065.	3.8	68
22	Genomic analysis of multiple Roseophage SIO1 strains. Environmental Microbiology, 2009, 11, 2863-2873.	3.8	64
23	Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. PLoS ONE, 2011, 6, e20095.	2.5	59
24	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
25	Power law rank-abundance models for marine phage communities. FEMS Microbiology Letters, 2007, 273, 224-228.	1.8	51
26	Wastewater treatment systems harbor specific and diverse yeast communities. Biochemical Engineering Journal, 2011, 58-59, 168-176.	3.6	40
27	Evaluation of viral genome assembly and diversity estimation in deep metagenomes. BMC Genomics, 2014, 15, 989.	2.8	31
28	The Bio-Community Perl toolkit for microbial ecology. Bioinformatics, 2014, 30, 1926-1927.	4.1	16
29	Diuron tolerance and potential degradation by pelagic microbiomes in the Great Barrier Reef lagoon. PeerJ, 2016, 4, e1758.	2.0	7