Nicolas Pinel

List of Publications by Year
in descending order

28 papers	2,096 citations	623734 14 h-index	642732 23 g-index
32 all docs	32 docs citations	32 times ranked	3321 citing authors

#	Article	IF	Citations
1	*Nitrosopumilus maritimus* genome reveals unique mechanisms for nitrification and autotrophy in globally distributed marine crenarchaea. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8818-8823.	7.1	853
2	Metabolic modeling of a mutualistic microbial community. Molecular Systems Biology, 2007, 3, 92.	7.2	441
3	Genes for the cytoskeletal protein tubulin in the bacterial genus Prosthecobacter. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 17049-17054.	7.1	158
4	IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. Genome Biology, 2016, 17, 260.	8.8	141
5	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. Nature Communications, 2014, 5, 5603.	12.8	75
6	Verminephrobacter eiseniae gen. nov., sp. nov., a nephridial symbiont of the earthworm Eisenia foetida (Savigny). International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 2147-2157.	1.7	70
7	Erosion of functional independence early in the evolution of a microbial mutualism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14822-14827.	7.1	63
8	Spatial and temporal variability in a stratified hypersaline microbial mat community. FEMS Microbiology Ecology, 2009, 68, 46-58.	2.7	58
9	Alignment-free Visualization of Metagenomic Data by Nonlinear Dimension Reduction. Scientific Reports, 2014, 4, 4516.	3.3	46
10	Genome Sequence of "Candidatus Microthrix parvicella" Bio17-1, a Long-Chain-Fatty-Acid-Accumulating Filamentous Actinobacterium from a Biological Wastewater Treatment Plant. Journal of Bacteriology, 2012, 194, 6670-6671.	2.2	27
11	Purifying Selection and Molecular Adaptation in the Genome of Verminephrobacter, the Heritable Symbiotic Bacteria of Earthworms. Genome Biology and Evolution, 2012, 4, 307-315.	2.5	25
12	Forecasting PM10 and PM2.5 in the Aburrá Valley (Medellín, Colombia) via EnKF based data assimilation. Atmospheric Environment, 2020, 232, 117507.	4.1	21
13	Contribution of mobile genetic elements to *Desulfovibrio vulgaris* genome plasticity. Environmental Microbiology, 2009, 11, 2244-2252.	3.8	20
14	Genome Sequence of the Thermophilic Cyanobacterium *Thermosynechococcus* sp. Strain NK55a. Genome Announcements, 2014, 2, .	0.8	20
15	Model Organisms Retain an "Ecological Memory" of Complex Ecologically Relevant Environmental Variation. Applied and Environmental Microbiology, 2014, 80, 1821-1831.	3.1	16
16	Recovery of temperate Desulfovibrio vulgaris bacteriophage using a novel host strain. Environmental Microbiology, 2006, 8, 1950-1959.	3.8	14
17	Urban Air Quality Modeling Using Low-Cost Sensor Network and Data Assimilation in the Aburrá Valley, Colombia. Atmosphere, 2021, 12, 91.	2.3	12
18	On the mathematical modelling and data assimilation for air pollution assessment in the Tropical Andes. Environmental Science and Pollution Research, 2020, 27, 35993-36012.	5.3	10

#	ARTICLE	IF	CITATIONS
19	Earthworm symbiont Verminephrobacter eiseniae mediates natural transformation within host egg capsules using type IV pili. Frontiers in Microbiology, 2014, 5, 546.	3.5	7
20	An efficient ensemble Kalman Filter implementation via shrinkage covariance matrix estimation: exploiting prior knowledge. Computational Geosciences, 2021, 25, 985-1003.	2.4	7
21	Standardized Approaches for Assessing Metagenomic Contig Binning Performance from Barnes-Hut t-Stochastic Neighbor Embeddings. IFMBE Proceedings, 2020, , 761-768.	0.3	3
22	Estimating NOx LOTOS-EUROS CTM Emission Parameters over the Northwest of South America through 4DEnVar TROPOMI NO2 Assimilation. Atmosphere, 2021, 12, 1633.	2.3	3
23	A Knowledge-Aided Robust Ensemble Kalman Filter Algorithm for Non-Linear and Non-Gaussian Large Systems. Frontiers in Applied Mathematics and Statistics, 2022, 8, .	1.3	3
24	Unsupervised fuzzy binning of metagenomic sequence fragments on three-dimensional Barnes-Hut t-Stochastic Neighbor Embeddings. , 2018, 2018, 1315-1318.		2
25	Verminephrobacter eiseniae gen. nov., sp. nov., a nephridial symbiont of the earthworm Eisenia foetida (Savigny). International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 796-796.	1.7	1
26	Data Assimilation as a Tool to Improve Chemical Transport Models Performance in Developing Countries. , 0, , .		0
27	Medellin Air Quality Initiative (MAUI). , 0, , .		0
28	An Entropy-Based Graph Construction Method for Representing and Clustering Biological Data. IFMBE Proceedings, 2020, , 315-321.	0.3	0