

# Nicolas Pinel

## List of Publications by Year in descending order

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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	A Knowledge-Aided Robust Ensemble Kalman Filter Algorithm for Non-Linear and Non-Gaussian Large Systems. <i>Frontiers in Applied Mathematics and Statistics</i> , 2022, 8, .	1.3	3
2	Urban Air Quality Modeling Using Low-Cost Sensor Network and Data Assimilation in the Aburr� Valley, Colombia. <i>Atmosphere</i> , 2021, 12, 91.	2.3	12
3	An efficient ensemble Kalman Filter implementation via shrinkage covariance matrix estimation: exploiting prior knowledge. <i>Computational Geosciences</i> , 2021, 25, 985-1003.	2.4	7
4	Estimating NOx LOTOS-EUROS CTM Emission Parameters over the Northwest of South America through 4D-EnVar TROPOMI NO2 Assimilation. <i>Atmosphere</i> , 2021, 12, 1633.	2.3	3
5	Forecasting PM10 and PM2.5 in the Aburr� Valley (Medell�n, Colombia) via EnKF based data assimilation. <i>Atmospheric Environment</i> , 2020, 232, 117507.	4.1	21
6	On the mathematical modelling and data assimilation for air pollution assessment in the Tropical Andes. <i>Environmental Science and Pollution Research</i> , 2020, 27, 35993-36012.	5.3	10
7	An Entropy-Based Graph Construction Method for Representing and Clustering Biological Data. <i>IFMBE Proceedings</i> , 2020, , 315-321.	0.3	0
8	Standardized Approaches for Assessing Metagenomic Contig Binning Performance from Barnes-Hut t-Stochastic Neighbor Embeddings. <i>IFMBE Proceedings</i> , 2020, , 761-768.	0.3	3
9	Unsupervised fuzzy binning of metagenomic sequence fragments on three-dimensional Barnes-Hut t-Stochastic Neighbor Embeddings. , 2018, 2018, 1315-1318.		2
10	IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. <i>Genome Biology</i> , 2016, 17, 260.	8.8	141
11	Earthworm symbiont <i>Verminephrobacter eiseniae</i> mediates natural transformation within host egg capsules using type IV pili. <i>Frontiers in Microbiology</i> , 2014, 5, 546.	3.5	7
12	Model Organisms Retain an "Ecological Memory" of Complex Ecologically Relevant Environmental Variation. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1821-1831.	3.1	16
13	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. <i>Nature Communications</i> , 2014, 5, 5603.	12.8	75
14	Genome Sequence of the Thermophilic Cyanobacterium <i>Thermosynechococcus</i> sp. Strain NK55a. <i>Genome Announcements</i> , 2014, 2, .	0.8	20
15	Erosion of functional independence early in the evolution of a microbial mutualism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14822-14827.	7.1	63
16	Alignment-free Visualization of Metagenomic Data by Nonlinear Dimension Reduction. <i>Scientific Reports</i> , 2014, 4, 4516.	3.3	46
17	<i>Verminephrobacter eiseniae</i> gen. nov., sp. nov., a nephridial symbiont of the earthworm <i>Eisenia foetida</i> (Savigny). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 796-796.	1.7	1
18	Purifying Selection and Molecular Adaptation in the Genome of <i>Verminephrobacter</i> , the Heritable Symbiotic Bacteria of Earthworms. <i>Genome Biology and Evolution</i> , 2012, 4, 307-315.	2.5	25

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19	Genome Sequence of "Candidatus Microthrix parvicella" Bio17-1, a Long-Chain-Fatty-Acid-Accumulating Filamentous Actinobacterium from a Biological Wastewater Treatment Plant. <i>Journal of Bacteriology</i> , 2012, 194, 6670-6671.	2.2	27
20	"Nitrosopumilus maritimus" genome reveals unique mechanisms for nitrification and autotrophy in globally distributed marine crenarchaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8818-8823.	7.1	853
21	Spatial and temporal variability in a stratified hypersaline microbial mat community. <i>FEMS Microbiology Ecology</i> , 2009, 68, 46-58.	2.7	58
22	Contribution of mobile genetic elements to "Desulfovibrio vulgaris" genome plasticity. <i>Environmental Microbiology</i> , 2009, 11, 2244-2252.	3.8	20
23	<i>Verminephrobacter eiseniae</i> gen. nov., sp. nov., a nephridial symbiont of the earthworm <i>Eisenia foetida</i> (Savigny). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2147-2157.	1.7	70
24	Metabolic modeling of a mutualistic microbial community. <i>Molecular Systems Biology</i> , 2007, 3, 92.	7.2	441
25	Recovery of temperate <i>Desulfovibrio vulgaris</i> bacteriophage using a novel host strain. <i>Environmental Microbiology</i> , 2006, 8, 1950-1959.	3.8	14
26	Genes for the cytoskeletal protein tubulin in the bacterial genus <i>Prostheco bacter</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 17049-17054.	7.1	158
27	Data Assimilation as a Tool to Improve Chemical Transport Models Performance in Developing Countries. , 0, , .		0
28	Medellin Air Quality Initiative (MAUI). , 0, , .		0