SÃ©bastien Monchy

List of Publications by Year
in descending order

42 papers	4,730 citations	218677 26 h-index	276875 41 g-index
42 all docs	42 docs citations	42 times ranked	6357 citing authors

#	Article	IF	Citations
1	A New Method for Microplastics Identification in Copepods. Frontiers in Environmental Chemistry, 2022, 3, .	1.6	2
2	Identification and quantification of plastic additives using pyrolysis-GC/MS: A review. Science of the Total Environment, 2021, 773, 145073.	8.0	63
3	Impacts of microplastics exposure on mussel (Mytilus edulis) gut microbiota. Science of the Total Environment, 2020, 745, 141018.	8.0	56
4	First Report on the Prevalence and Subtype Distribution of Blastocystis sp. in Edible Marine Fish and Marine Mammals: A Large Scale-Study Conducted in Atlantic Northeast and on the Coasts of Northern France. Microorganisms, 2020, 8, 460.	3.6	21
5	Ontogenetic shift in the energy allocation strategy and physiological condition of larval plaice (Pleuronectes platessa). PLoS ONE, 2019, 14, e0222261.	2.5	12
6	Major changes in the composition of a Southern Ocean bacterial community in response to diatom-derived dissolved organic matter. FEMS Microbiology Ecology, 2018, 94, .	2.7	25
7	Diversity and potential activity patterns of planktonic eukaryotic microbes in a mesoeutrophic coastal area (eastern English Channel). PLoS ONE, 2018, 13, e0196987.	2.5	13
8	Ontogenetic changes in the larval condition of Downs herring: use of a multi-index approach at an individual scale. Marine Biology, 2017, 164, 1.	1.5	6
9	Parasitic Eukaryotes in a Meso-Eutrophic Coastal System with Marked Phaeocystis globosa Blooms. Frontiers in Marine Science, 2017, 4, .	2.5	18
10	Molecular Epidemiology of Blastocystis sp. in Various Animal Groups from Two French Zoos and Evaluation of Potential Zoonotic Risk. PLoS ONE, 2017, 12, e0169659.	2.5	135
11	Mussel biofiltration effects on attached bacteria and unicellular eukaryotes in fish-rearing seawater. PeerJ, 2016, 4, e1829.	2.0	6
12	Molecular Diversity Studies in Lake Pavin Reveal the Ecological Importance of Parasitic True Fungi in the Plankton. , 2016, , 329-343.		4
13	Marine microbial community structure assessed from combined metagenomic analysis and ribosomal amplicon deep-sequencing. Marine Biology Research, 2016, 12, 30-42.	0.7	3
14	Shifts in bacterial community composition associated with increased carbon cycling in a mosaic of phytoplankton blooms. ISME Journal, 2016, 10, 39-50.	9.8	136
15	Small-scale variability of protistan planktonic communities relative to environmental pressures and biotic interactions at two adjacent coastal stations. Marine Ecology - Progress Series, 2016, 548, 61-75.	1.9	30
16	Seasonal variations of marine protist community structure based on taxon-specific traits using the eastern English Channel as a model coastal system. FEMS Microbiology Ecology, 2015, 91, .	2.7	53
17	Size-fractionated diversity of eukaryotic microbial communities in the Eastern Tropical North Pacific oxygen minimum zone. FEMS Microbiology Ecology, 2015, 91, .	2.7	34
18	Microzooplankton community associated with phytoplankton blooms in the naturally iron-fertilized Kerguelen area (Southern Ocean). FEMS Microbiology Ecology, 2015, 91, .	2.7	18

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19	Protist community composition during early phytoplankton blooms in the naturally iron-fertilized Kerguelen area (Southern Ocean). Biogeosciences, 2014, 11, 5847-5863.	3.3	25
20	Winterâ€“Summer Succession of Unicellular Eukaryotes in a Meso-eutrophic Coastal System. Microbial Ecology, 2014, 67, 13-23.	2.8	39
21	Molecular diversity reveals previously undetected air-dispersed protist colonists in a Mediterranean area. Science of the Total Environment, 2014, 478, 70-79.	8.0	21
22	The Airway Microbiota in Cystic Fibrosis: A Complex Fungal and Bacterial Communityâ€”Implications for Therapeutic Management. PLoS ONE, 2012, 7, e36313.	2.5	312
23	Microplanktonic Community Structure in a Coastal System Relative to a Phaeocystis Bloom Inferred from Morphological and Tag Pyrosequencing Methods. PLoS ONE, 2012, 7, e39924.	2.5	68
24	Exploring and quantifying fungal diversity in freshwater lake ecosystems using rDNA cloning/sequencing and SSU tag pyrosequencing. Environmental Microbiology, 2011, 13, 1433-1453.	3.8	161
25	Comparative genomics and functional analysis of niche-specific adaptation inPseudomonas putida. FEMS Microbiology Reviews, 2011, 35, 299-323.	8.6	281
26	The Complete Genome Sequence of Cupriavidus metallidurans Strain CH34, a Master Survivalist in Harsh and Anthropogenic Environments. PLoS ONE, 2010, 5, e10433.	2.5	275
27	Genome Sequence of the Plant Growth Promoting Endophytic Bacterium Enterobacter sp. 638. PLoS Genetics, 2010, 6, e1000943.	3.5	282
28	Lead(II) resistance in Cupriavidus metallidurans CH34: interplay between plasmid and chromosomally-located functions. Antonie Van Leeuwenhoek, 2009, 96, 171-182.	1.7	81
29	ArsR arsenic-resistance regulatory protein from Cupriavidus metallidurans CH34. Antonie Van Leeuwenhoek, 2009, 96, 161-170.	1.7	46
30	New mobile genetic elements in Cupriavidus metallidurans CH34, their possible roles and occurrence in other bacteria. Antonie Van Leeuwenhoek, 2009, 96, 205-226.	1.7	98
31	Bioprospecting metagenomes: glycosyl hydrolases for converting biomass. Biotechnology for Biofuels, 2009, 2, 10.	6.2	146
32	The versatility and adaptation of bacteria from the genus Stenotrophomonas. Nature Reviews Microbiology, 2009, 7, 514-525.	28.6	641
33	Poplar and its Bacterial Endophytes: Coexistence and Harmony. Critical Reviews in Plant Sciences, 2009, 28, 346-358.	5.7	97
34	Genome Survey and Characterization of Endophytic Bacteria Exhibiting a Beneficial Effect on Growth and Development of Poplar Trees. Applied and Environmental Microbiology, 2009, 75, 748-757.	3.1	524
35	Megaplasmids in Cupriavidus Genus and Metal Resistance. Microbiology Monographs, 2009, , 209-238.	0.6	19
36	Plasmids pMOL28 and pMOL30 of Cupriavidus metallidurans Are Specialized in the Maximal Viable Response to Heavy Metals. Journal of Bacteriology, 2007, 189, 7417-7425.	2.2	231

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37	Transcriptomic and proteomic analyses of the pMOL30-encoded copper resistance in Cupriavidus metallidurans strain CH34. Microbiology (United Kingdom), 2006, 152, 1765-1776.	1.8	118
38	Metal transport ATPase genes fromCupriavidus metalliduransCH34: a transcriptomic approach. International Journal of Environmental Analytical Chemistry, 2006, 86, 677-692.	3.3	24
39	Characterization of Ni-tolerant methylobacteria associated with the hyperaccumulating plant Thlaspi goesingense and description of Methylobacterium goesingense sp. nov.. Systematic and Applied Microbiology, 2006, 29, 634-644.	2.8	81
40	Global analysis of the Ralstonia metallidurans proteome: Prelude for the largeâ€scale study of heavy metal response. Proteomics, 2004, 4, 151-179.	2.2	38
41	Ralstonia metallidurans, a bacterium specifically adapted to toxic metals: towards a catalogue of metal-responsive genes. FEMS Microbiology Reviews, 2003, 27, 385-410.	8.6	386
42	The Biphenyl- and 4-Chlorobiphenyl-Catabolic Transposon Tn4371, a Member of a New Family of Genomic Islands Related to IncP and Ti Plasmids. Applied and Environmental Microbiology, 2003, 69, 4837-4845.	3.1	101