Geoffrey McMullan

List of Publications by Year
in descending order

33 papers	5,205 citations	393982 19 h-index	414034 32 g-index
34 all docs	34 docs citations	34 times ranked	6555 citing authors

#	Article	IF	Citations
1	Response to methodologic variables that impact growth of Clostridium difficile in a broth culture medium without requirement for anaerobic culture conditions. Anaerobe, 2019, 56, 135.	1.0	0
2	Increased sporulation underpins adaptation of Clostridium difficile strain 630 to a biologicallyâ€“relevant faecal environment, with implications for pathogenicity. Scientific Reports, 2018, 8, 16691.	1.6	7
3	Development of an optimized broth enrichment culture medium for the isolation of Clostridium difficile. Anaerobe, 2018, 54, 92-99.	1.0	5
4	NaCl-saturated brines are thermodynamically moderate, rather than extreme, microbial habitats. FEMS Microbiology Reviews, 2018, 42, 672-693.	3.9	54
5	Inactivation of the dnaK gene in Clostridium difficile 630 Î”erm yields a temperature-sensitive phenotype and increases biofilm-forming ability. Scientific Reports, 2017, 7, 17522.	1.6	38
6	Evaluation of bactericidal and anti-biofilm properties of a novel surface-active organosilane biocide against healthcare associated pathogens and Pseudomonas aeruginosa biolfilm. PLoS ONE, 2017, 12, e0182624.	1.1	15
7	Semiquantitative Analysis of Clinical Heat Stress in Clostridium difficile Strain 630 Using a GeLC/MS Workflow with emPAI Quantitation. PLoS ONE, 2014, 9, e88960.	1.1	20
8	The quantitative proteomic response of Synechocystis sp. PCC6803 to phosphate acclimation. Aquatic Biosystems, 2013, 9, 5.	1.8	22
9	Comparative Transcriptional Analysis of Clinically Relevant Heat Stress Response in Clostridium difficile Strain 630. PLoS ONE, 2012, 7, e42410.	1.1	33
10	Quantitative Proteomic Analysis of the Heat Stress Response in Clostridium difficile Strain 630. Journal of Proteome Research, 2011, 10, 3880-3890.	1.8	67
11	Proteomics in the microbial sciences. Bioengineered Bugs, 2011, 2, 17-30.	2.0	21
12	Comparative genomics and proteomics of Helicobacter mustelae, an ulcerogenic and carcinogenic gastric pathogen. BMC Genomics, 2010, 11, 164.	1.2	40
13	Proteomic analysis of the insoluble subproteome of Clostridium difficile strain 630. FEMS Microbiology Letters, 2010, 312, 151-159.	0.7	10
14	Elucidation of trends within venom components from the snake families Elapidae and Viperidae using gel filtration chromatography. Toxicon, 2008, 51, 121-129.	0.8	10
15	A semi-quantitative GeLC-MS analysis of temporal proteome expression in the emerging nosocomial pathogen Ochrobactrum anthropi. Genome Biology, 2007, 8, R110.	13.9	23
16	Microbial proteomics: a mass spectrometry primer for biologists. Microbial Cell Factories, 2007, 6, 26.	1.9	52
17	Multidimensional analysis of the insoluble sub-proteome ofOceanobacillus iheyensis HTE831, an alkaliphilic and halotolerant deep-sea bacterium isolated from the Iheya ridge. Proteomics, 2007, 7, 82-91.	1.3	23
18	A Combined Shotgun and Multidimensional Proteomic Analysis of the Insoluble Subproteome of the Obligate Thermophile,GeobacillusthermoleovoransT80. Journal of Proteome Research, 2006, 5, 2465-2473.	1.8	13

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19	Top-Down Proteomic Analysis of the Soluble Sub-Proteome of the Obligate Thermophile,GeobacillusthermoleovoransT80:Â Insights into Its Cellular Processes. Journal of Proteome Research, 2006, 5, 822-828.	1.8	16
20	Multidimensional Proteomic Analysis of the Soluble Subproteome of the Emerging Nosocomial PathogenOchrobactrumanthropi. Journal of Proteome Research, 2006, 5, 3145-3153.	1.8	13
21	Detection of phosphonoacetate degradation and phnA genes in soil bacteria from distinct geographical origins suggest its possible biogenic origin. Environmental Microbiology, 2006, 8, 939-945.	1.8	25
22	A role for carbon catabolite repression in the metabolism of phosphonoacetate byAgromyces fucosusVs2. FEMS Microbiology Letters, 2006, 261, 133-140.	0.7	13
23	High growth rate and substrate exhaustion results in rapid cell death and lysis in the thermophilic bacteriumGeobacillus thermoleovorans. Biotechnology and Bioengineering, 2006, 95, 84-95.	1.7	22
24	Organophosphonate Utilization by the Thermophile Geobacillus caldoxylosilyticus T20. Applied and Environmental Microbiology, 2002, 68, 2081-2084.	1.4	85
25	Iminodiacetate and Nitrilotriacetate Degradation by Kluyveromyces marxianus IMB3. Biochemical and Biophysical Research Communications, 2002, 290, 802-805.	1.0	12
26	Remediation of dyes in textile effluent: a critical review on current treatment technologies with a proposed alternative. Bioresource Technology, 2001, 77, 247-255.	4.8	4,185
27	Effect of environmental conditions on biological decolorization of textile dyestuff by C. versicolor. Enzyme and Microbial Technology, 2000, 26, 381-387.	1.6	141
28	The utilization of 4-aminobutylphosphonate as sole nitrogen source by a strain ofKluyveromyces fragilis. FEMS Microbiology Letters, 2000, 184, 237-240.	0.7	16
29	Organophosphonate metabolism by a moderately halophilic bacterial isolate. FEMS Microbiology Letters, 2000, 186, 171-175.	0.7	22
30	Decolorization of textile dyestuffs by a mixed bacterial consortium. Biotechnology Letters, 2000, 22, 1179-1181.	1.1	55
31	The effect of phenolic acids and molasses spent wash concentration on distillery wastewater remediation by fungi. Process Biochemistry, 1998, 33, 799-803.	1.8	67
32	Bioremediation of textile industry wastewater by white-rot fungi. Studies in Environmental Science, 1997, , 711-718.	0.0	8
33	The Purification and Properties of Phosphonoacetate Hydrolase, a Novel Carbon-Phosphorus Bond-Cleavage Enzyme from Pseudomonas Fluorescens 23F. FEBS Journal, 1995, 234, 225-230.	0.2	70