Renaud Berlemont

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2032820/publications.pdf

Version: 2024-02-01

30 papers 1,704 citations

430874 18 h-index 28 g-index

30 all docs 30 docs citations

30 times ranked

2449 citing authors

#	Article	IF	CITATIONS
1	Phylogenetic Distribution of Potential Cellulases in Bacteria. Applied and Environmental Microbiology, 2013, 79, 1545-1554.	3.1	267
2	Genomic Potential for Polysaccharide Deconstruction in Bacteria. Applied and Environmental Microbiology, 2015, 81, 1513-1519.	3.1	155
3	Elemental stoichiometry of Fungi and Bacteria strains from grassland leaf litter. Soil Biology and Biochemistry, 2014, 76, 278-285.	8.8	133
4	Microbial response to simulated global change is phylogenetically conserved and linked with functional potential. ISME Journal, 2016, 10, 109-118.	9.8	123
5	Temporal variation overshadows the response of leaf litter microbial communities to simulated global change. ISME Journal, 2015, 9, 2477-2489.	9.8	112
6	Microbial legacies alter decomposition in response to simulated global change. ISME Journal, 2017, 11, 490-499.	9.8	112
7	Function, distribution, and annotation of characterized cellulases, xylanases, and chitinases from CAZy. Applied Microbiology and Biotechnology, 2018, 102, 1629-1637.	3.6	109
8	Distribution and diversity of enzymes for polysaccharide degradation in fungi. Scientific Reports, 2017, 7, 222.	3.3	96
9	Glycoside Hydrolases across Environmental Microbial Communities. PLoS Computational Biology, 2016, 12, e1005300.	3.2	93
10	Natural diversity of cellulases, xylanases, and chitinases in bacteria. Biotechnology for Biofuels, 2016, 9, 133.	6.2	82
11	Evidence for Ecological Flexibility in the Cosmopolitan Genus Curtobacterium. Frontiers in Microbiology, 2016, 7, 1874.	3 . 5	66
12	Cellulolytic potential under environmental changes in microbial communities from grassland litter. Frontiers in Microbiology, 2014, 5, 639.	3 . 5	61
13	Nitrogen Cycling Potential of a Grassland Litter Microbial Community. Applied and Environmental Microbiology, 2015, 81, 7012-7022.	3.1	51
14	Insights into bacterial cellulose biosynthesis by functional metagenomics on Antarctic soil samples. ISME Journal, 2009, 3, 1070-1081.	9.8	48
15	Exploring the Antarctic soil metagenome as a source of novel cold-adapted enzymes and genetic mobile elements. Revista Argentina De Microbiologia, 2011, 43, 94-103.	0.7	39
16	Drought increases the frequencies of fungal functional genes related to carbon and nitrogen acquisition. PLoS ONE, 2018, 13, e0206441.	2.5	24
17	Novel Cold-Adapted Esterase MHlip from an Antarctic Soil Metagenome. Biology, 2013, 2, 177-188.	2.8	19
18	A Novel Extended-Spectrum TEM-Type \hat{l}^2 -Lactamase, TEM-138, from Salmonella enterica Serovar Infantis. Antimicrobial Agents and Chemotherapy, 2006, 50, 3183-3185.	3.2	18

#	Article	IF	CITATIONS
19	Nitrogen enrichment shifts functional genes related to nitrogen and carbon acquisition in the fungal community. Soil Biology and Biochemistry, 2018, 123, 87-96.	8.8	17
20	Life at the Frozen Limit: Microbial Carbon Metabolism Across a Late Pleistocene Permafrost Chronosequence. Frontiers in Microbiology, 2020, 11, 1753.	3.5	16
21	Novel organic solvent-tolerant esterase isolated by metagenomics: insights into the lipase/esterase classification. Revista Argentina De Microbiologia, 2013, 45, 3-12.	0.7	16
22	GeneHunt for rapid domain-specific annotation of glycoside hydrolases. Scientific Reports, 2019, 9, 10137.	3.3	15
23	Three-dimensional structure of RBcell, a metagenome-derived psychrotolerant family GH5 endoglucanase. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 828-833.	0.7	9
24	Crystal structure determination of <i>Pseudomonas stutzeri</i> Al501 endoglucanase Cel5A: the search for a molecular basis for glycosynthesis in GH5_5 enzymes. Acta Crystallographica Section D: Structural Biology, 2019, 75, 605-615.	2.3	8
25	MetaGeneHunt for protein domain annotation in short-read metagenomes. Scientific Reports, 2020, 10, 7712.	3.3	5
26	Draft Genome Sequences of Nine New Carnobacterium maltaromaticum Strains Isolated from Diseased Sharks. Genome Announcements, 2018, 6, .	0.8	4
27	Phylosymbiosis in the Rhizosphere Microbiome Extends to Nitrogen Cycle Functional Potential. Microorganisms, 2021, 9, 2476.	3.6	2
28	The Potential for Cellulose Deconstruction in Fungal Genomes. Encyclopedia, 2022, 2, 990-1003.	4.5	2
29	<i>Carnobacterium maltaromaticum</i> associated with meningoencephalitis and otitis in stranded common thresher sharks (<i>Alopias vulpinus</i>). Veterinary Pathology, 2022, 59, 850-859.	1.7	2
30	Antarctic Soil Metagenome. , 2013, , 1-7.		0