

Vincent Lombard

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

12,220
citations

516215

16
h-index

752256

20
g-index

22
all docs

22
docs citations

22
times ranked

16092
citing authors

#	ARTICLE	IF	CITATIONS
1	The carbohydrate-active enzymes database (CAZy) in 2013. <i>Nucleic Acids Research</i> , 2014, 42, D490-D495.	6.5	5,443
2	The Carbohydrate-Active EnZymes database (CAZy): an expert resource for Glycogenomics. <i>Nucleic Acids Research</i> , 2009, 37, D233-D238.	6.5	4,854
3	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	9.4	414
4	Gut microbiota richness promotes its stability upon increased dietary fibre intake in healthy adults. <i>Environmental Microbiology</i> , 2015, 17, 4954-4964.	1.8	279
5	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae). <i>Scientific Reports</i> , 2018, 8, 1931.	1.6	215
6	PULDB: the expanded database of Polysaccharide Utilization Loci. <i>Nucleic Acids Research</i> , 2018, 46, D677-D683.	6.5	191
7	Dividing the Large Glycoside Hydrolase Family 43 into Subfamilies: a Motivation for Detailed Enzyme Characterization. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1686-1692.	1.4	173
8	Feed in summer, rest in winter: microbial carbon utilization in forest topsoil. <i>Microbiome</i> , 2017, 5, 122.	4.9	121
9	A subfamily roadmap of the evolutionarily diverse glycoside hydrolase family 16 (GH16). <i>Journal of Biological Chemistry</i> , 2019, 294, 15973-15986.	1.6	118
10	How members of the human gut microbiota overcome the sulfation problem posed by glycosaminoglycans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7037-7042.	3.3	99
11	Evaluating microbiome-directed fibre snacks in gnotobiotic mice and humans. <i>Nature</i> , 2021, 595, 91-95.	13.7	70
12	A bioinformatics analysis of 3400 lytic polysaccharide oxidases from family AA9. <i>Carbohydrate Research</i> , 2017, 448, 166-174.	1.1	55
13	Role of Glycoside Phosphorylases in Mannose Foraging by Human Gut Bacteria. <i>Journal of Biological Chemistry</i> , 2013, 288, 32370-32383.	1.6	50
14	Broad phylogeny and functionality of cellulosomal components in the bovine rumen microbiome. <i>Environmental Microbiology</i> , 2017, 19, 185-197.	1.8	32
15	Bioinformatic Analysis of Lytic Polysaccharide Monooxygenases Reveals the Pan-Families Occurrence of Intrinsically Disordered C-Terminal Extensions. <i>Biomolecules</i> , 2021, 11, 1632.	1.8	25
16	Comparative Metagenomics of Cellulose- and Poplar Hydrolysate-Degrading Microcosms from Gut Microflora of the Canadian Beaver (<i>Castor canadensis</i>) and North American Moose (<i>Alces americanus</i>) after Long-Term Enrichment. <i>Frontiers in Microbiology</i> , 2017, 8, 2504.	1.5	24
17	Gut microbiome contributions to altered metabolism in a pig model of undernutrition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
18	<i>Trichoderma reesei</i> Dehydrogenase, a Pyrroloquinoline Quinone-Dependent Member of Auxiliary Activity Family 12 of the Carbohydrate-Active Enzymes Database: Functional and Structural Characterization. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	13

#	ARTICLE	IF	CITATIONS
19	Characterization of three bacterial glycoside hydrolase family 9 endoglucanases with different modular architectures isolated from a compost metagenome. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129848.	1.1	11
20	Composting-Like Conditions Are More Efficient for Enrichment and Diversity of Organisms Containing Cellulase-Encoding Genes than Submerged Cultures. <i>PLoS ONE</i> , 2016, 11, e0167216.	1.1	11