Gurvan Michel

List of Publications by Year
in descending order

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97	10,544	38742	38395
papers	citations	50 h-index	95 g-index

100	100	100	10550
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Environmental and Gut Bacteroidetes: The Food Connection. Frontiers in Microbiology, 2011, 2, 93.	3.5	989
2	Transfer of carbohydrate-active enzymes from marine bacteria to Japanese gut microbiota. Nature, 2010, 464, 908-912.	27.8	905
3	The Ectocarpus genome and the independent evolution of multicellularity in brown algae. Nature, 2010, 465, 617-621.	27.8	774
4	Evolution and Diversity of Plant Cell Walls: From Algae to Flowering Plants. Annual Review of Plant Biology, 2011, 62, 567-590.	18.7	613
5	The genome of the seagrass Zostera marina reveals angiosperm adaptation to the sea. Nature, 2016, 530, 331-335.	27.8	460
6	The cell wall polysaccharide metabolism of the brown alga Ectocarpus siliculosus. Insights into the evolution of extracellular matrix polysaccharides in Eukaryotes. New Phytologist, 2010, 188, 82-97.	7.3	381
7	Genome structure and metabolic features in the red seaweed Chondrus crispus shed light on evolution of the Archaeplastida. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5247-5252.	7.1	307
8	Bioconversion of red seaweed galactans: a focus on bacterial agarases and carrageenases. Applied Microbiology and Biotechnology, 2006, 71, 23-33.	3.6	238
9	Structural Evidence for the Evolution of Xyloglucanase Activity from Xyloglucan Endo-Transglycosylases: Biological Implications for Cell Wall Metabolism. Plant Cell, 2007, 19, 1947-1963.	6.6	234
10	Insights into the red algae and eukaryotic evolution from the genome of Porphyra umbilicalis (Bangiophyceae, Rhodophyta). Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6361-E6370.	7.1	233
11	Chemical and enzymatic fractionation of cell walls from Fucales: insights into the structure of the extracellular matrix of brown algae. Annals of Botany, 2014, 114, 1203-1216.	2.9	219
12	Characterization of the first alginolytic operons in a marine bacterium: from their emergence in marine Flavobacteriia to their independent transfers to marine Proteobacteria and human gut Bacteroides. Environmental Microbiology, 2012, 14, 2379-2394.	3.8	201
13	The Î²-carrageenase of P. carrageenovora Features a Tunnel-Shaped Active Site. Structure, 2001, 9, 513-525.	3.3	193
14	Comparative Characterization of Two Marine Alginate Lyases from Zobellia galactanivorans Reveals Distinct Modes of Action and Exquisite Adaptation to Their Natural Substrate. Journal of Biological Chemistry, 2013, 288, 23021-23037.	3.4	175
15	Central and storage carbon metabolism of the brown alga Ectocarpus siliculosus: insights into the origin and evolution of storage carbohydrates in Eukaryotes. New Phytologist, 2010, 188, 67-81.	7.3	172
16	The Cultivable Surface Microbiota of the Brown Alga Ascophyllum nodosum is Enriched in Macroalgal-Polysaccharide-Degrading Bacteria. Frontiers in Microbiology, 2015, 6, 1487.	3.5	172
17	Microorganisms living on macroalgae: diversity, interactions, and biotechnological applications. Applied Microbiology and Biotechnology, 2014, 98, 2917-2935.	3.6	171
18	Matching the Diversity of Sulfated Biomolecules: Creation of a Classification Database for Sulfatases Reflecting Their Substrate Specificity. PLoS ONE, 2016, 11, e0164846.	2.5	147

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19	Biochemical and Structural Characterization of the Complex Agarolytic Enzyme System from the Marine Bacterium Zobellia galactanivorans. Journal of Biological Chemistry, 2012, 287, 30571-30584.	3.4	139
20	Habitat and taxon as driving forces of carbohydrate catabolism in marine heterotrophic bacteria: example of the model algaeâ€associated bacterium Zobellia galactanivorans Dsij^T. Environmental Microbiology, 2016, 18, 4610-4627.	3.8	131
21	Carrageenan catabolism is encoded by a complex regulon in marine heterotrophic bacteria. Nature Communications, 2017, 8, 1685.	12.8	131
22	The endo-Î²-agarases AgaA and AgaB from the marine bacterium Zobellia galactanivorans: two paralogue enzymes with different molecular organizations and catalytic behaviours. Biochemical Journal, 2005, 385, 703-713.	3.7	130
23	Development and physiology of the brown alga Ectocarpus siliculosus: two centuries of research. New Phytologist, 2008, 177, 319-332.	7.3	128
24	A subfamily roadmap of the evolutionarily diverse glycoside hydrolase family 16 (GH16). Journal of Biological Chemistry, 2019, 294, 15973-15986.	3.4	118
25	Î¹-Carrageenases Constitute a Novel Family of Glycoside Hydrolases, Unrelated to That of Îº-Carrageenases. Journal of Biological Chemistry, 2000, 275, 35499-35505.	3.4	113
26	Structures of Shikimate Dehydrogenase AroE and Its Paralog YdiB. Journal of Biological Chemistry, 2003, 278, 19463-19472.	3.4	111
27	A marine bacterial enzymatic cascade degrades the algal polysaccharide ulvan. Nature Chemical Biology, 2019, 15, 803-812.	8.0	97
28	Carrageenan-induced innate immune response is modified by enzymes that hydrolyze distinct galactosidic bonds. Journal of Nutritional Biochemistry, 2010, 21, 906-913.	4.2	96
29	Cloning and biochemical characterization of the fucanase FcnA: definition of a novel glycoside hydrolase family specific for sulfated fucans. Glycobiology, 2006, 16, 1021-1032.	2.5	95
30	Chlorophyll-binding proteins revisited - a multigenic family of light-harvesting and stress proteins from a brown algal perspective. BMC Evolutionary Biology, 2010, 10, 365.	3.2	93
31	The Structure of the RlmB 23S rRNA Methyltransferase Reveals a New Methyltransferase Fold with a Unique Knot. Structure, 2002, 10, 1303-1315.	3.3	92
32	The Structure of Chondroitin B Lyase Complexed with Glycosaminoglycan Oligosaccharides Unravels a Calcium-dependent Catalytic Machinery. Journal of Biological Chemistry, 2004, 279, 32882-32896.	3.4	91
33	A single sulfatase is required to access colonic mucin by a gut bacterium. Nature, 2021, 598, 332-337.	27.8	87
34	Vanadium-dependent iodoperoxidases in Laminaria digitata, a novel biochemical function diverging from brown algal bromoperoxidases. Journal of Biological Inorganic Chemistry, 2005, 10, 156-166.	2.6	84
35	Genetic analyses unravel the crucial role of a horizontally acquired alginate lyase for brown algal biomass degradation by <scp>Z</scp>obellia galactanivorans. Environmental Microbiology, 2017, 19, 2164-2181.	3.8	84
36	Degradation of Î»-carrageenan by Pseudoalteromonas carrageenovora Î»-carrageenase: a new family of glycoside hydrolases unrelated to Îº- and Î¹-carrageenases. Biochemical Journal, 2007, 404, 105-114.	3.7	83

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37	Discovery and structural characterization of a novel glycosidase family of marine origin. Environmental Microbiology, 2011, 13, 1253-1270.	3.8	76
38	The Î²-Glucanase ZgLamA from Zobellia galactanivorans Evolved a Bent Active Site Adapted for Efficient Degradation of Algal Laminarin. Journal of Biological Chemistry, 2014, 289, 2027-2042.	3.4	75
39	The Î¹-Carrageenase of Alteromonas fortis. Journal of Biological Chemistry, 2001, 276, 40202-40209.	3.4	71
40	Mannitol metabolism in brown algae involves a new phosphatase family. Journal of Experimental Botany, 2014, 65, 559-570.	4.8	67
41	Insoluble (1â€‰â†’â€‰3), (1â€‰â†’â€‰4)-Î²-D-glucan is a component of cell walls in brown algae (Phaeophyceae) and is masked by alginates in tissues. Scientific Reports, 2017, 7, 2880.	3.8	64
42	The Structural Bases of the Processive Degradation of Î¹-Carrageenan, a Main Cell Wall Polysaccharide of Red Algae. Journal of Molecular Biology, 2003, 334, 421-433.	4.2	60
43	Evaluation of reference genes for real-time quantitative PCR in the marine flavobacterium Zobellia galactanivorans. Journal of Microbiological Methods, 2011, 84, 61-66.	1.6	60
44	Sweet and sour sugars from the sea: the biosynthesis and remodeling of sulfated cell wall polysaccharides from marine macroalgae. Perspectives in Phycology, 2015, 2, 51-64.	1.9	58
45	Gene Expression Analysis of Zobellia galactanivorans during the Degradation of Algal Polysaccharides Reveals both Substrate-Specific and Shared Transcriptome-Wide Responses. Frontiers in Microbiology, 2017, 8, 1808.	3.5	58
46	Alpha-Agarases Define a New Family of Glycoside Hydrolases, Distinct from Beta-Agarase Families. Applied and Environmental Microbiology, 2007, 73, 4691-4694.	3.1	57
47	The Complete Genome Sequence of the Fish Pathogen Tenacibaculum maritimum Provides Insights into Virulence Mechanisms. Frontiers in Microbiology, 2017, 8, 1542.	3.5	57
48	Polysaccharide utilisation loci of Bacteroidetes from two contrasting open ocean sites in the North Atlantic. Environmental Microbiology, 2016, 18, 4456-4470.	3.8	56
49	MARINE-EXPRESS: taking advantage of high throughput cloning and expression strategies for the post-genomic analysis of marine organisms. Microbial Cell Factories, 2010, 9, 45.	4.0	55
50	Evolutionary Evidence of Algal Polysaccharide Degradation Acquisition by Pseudoalteromonas carrageenovora 9T to Adapt to Macroalgal Niches. Frontiers in Microbiology, 2018, 9, 2740.	3.5	54
51	Analysis of nasturtium TmNXG1 complexes by crystallography and molecular dynamics provides detailed insight into substrate recognition by family GH16 xyloglucan endoâ€transglycosylases and endoâ€hydrolases. Proteins: Structure, Function and Bioinformatics, 2009, 75, 820-836.	2.6	53
52	Mannitol-1-phosphate dehydrogenase activity in Ectocarpus siliculosus, a key role for mannitol synthesis in brown algae. Planta, 2011, 233, 261-273.	3.2	52
53	Identification and Characterization of a Halotolerant, Cold-Active Marine Endo-Î²-1,4-Glucanase by Using Functional Metagenomics of Seaweed-Associated Microbiota. Applied and Environmental Microbiology, 2014, 80, 4958-4967.	3.1	52
54	Seasonal and algal diet-driven patterns of the digestive microbiota of the European abalone Haliotis tuberculata, a generalist marine herbivore. Microbiome, 2018, 6, 60.	11.1	50

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55	Description of Maribacter forsetii sp. nov., a marine Flavobacteriaceae isolated from North Sea water, and emended description of the genus Maribacter. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 790-797.	1.7	47
56	The Vanadium Iodoperoxidase from the Marine Flavobacteriaceae Species Zobellia galactanivorans Reveals Novel Molecular and Evolutionary Features of Halide Specificity in the Vanadium Haloperoxidase Enzyme Family. Applied and Environmental Microbiology, 2014, 80, 7561-7573.	3.1	46
57	Genome and metabolic network of Ã¢â‚¬Å“Candidatus Phaeomarinobacter ectocarpiÃ¢â‚¬Â•Ec32, a new candidate genus of Alphaproteobacteria frequently associated with brown algae. Frontiers in Genetics, 2014, 5, 241.	2.3	43
58	<scp>H</scp>alorhabdus tiamatea: proteogenomics and glycosidase activity measurements identify the first cultivated euryarchaeon from a deepâ€sea anoxic brine lake as potential polysaccharide degrader. Environmental Microbiology, 2014, 16, 2525-2537.	3.8	41
59	Mariniflexile fucanivorans sp. nov., a marine member of the Flavobacteriaceae that degrades sulphated fucans from brown algae. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 2107-2113.	1.7	39
60	Degradation of Î»-carrageenan by Pseudoalteromonas carrageenovora Î»-carrageenase: a new family of glycoside hydrolases unrelated to Îº- and Î¹-carrageenases. Biochemical Journal, 2007, 404, 105.	3.7	38
61	The Mannitol Utilization System of the Marine Bacterium Zobellia galactanivorans. Applied and Environmental Microbiology, 2015, 81, 1799-1812.	3.1	38
62	The cell-wall active mannuronan C5-epimerases in the model brown algaEctocarpus: From gene context to recombinant protein. Glycobiology, 2016, 26, 973-983.	2.5	38
63	Structural insights into marine carbohydrate degradation by family GH16 Îº-carrageenases. Journal of Biological Chemistry, 2017, 292, 19919-19934.	3.4	38
64	Chondrus crispus â€“ A Present and Historical Model Organism for Red Seaweeds. Advances in Botanical Research, 2014, 71, 53-89.	1.1	37
65	The family 6 carbohydrate-binding modules have coevolved with their appended catalytic modules toward similar substrate specificity. Glycobiology, 2009, 19, 615-623.	2.5	36
66	Identification of Catalytic Residues and Mechanistic Analysis of Family GH82 Î¹-Carrageenases. Biochemistry, 2010, 49, 7590-7599.	2.5	34
67	Structural and biochemical characterization of the laminarinaseZgLamC_{GH16}fromZobellia galactanivoranssuggests preferred recognition of branched laminarin. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 173-184.	2.5	34
68	Discovering novel enzymes by functional screening of plurigenomic libraries from alga-associated Flavobacteriia and Gammaproteobacteria. Microbiological Research, 2016, 186-187, 52-61.	5.3	34
69	Role and Evolution of the Extracellular Matrix in the Acquisition of Complex Multicellularity in Eukaryotes: A Macroalgal Perspective. Genes, 2021, 12, 1059.	2.4	34
70	Polysaccharide-degrading enzymes from marine bacteria. , 2013, , 429-464.		33
71	The agar-specific hydrolase ZgAgaC from the marine bacterium Zobellia galactanivorans defines a new GH16 protein subfamily. Journal of Biological Chemistry, 2019, 294, 6923-6939.	3.4	32
72	Bromine is an Endogenous Component of a Vanadium Bromoperoxidase. Journal of the American Chemical Society, 2005, 127, 15340-15341.	13.7	30

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73	Site-directed Mutagenesis of the Active Site Region in the Quinate/Shikimate 5-Dehydrogenase YdiB of Escherichia coli. Journal of Biological Chemistry, 2005, 280, 7162-7169.	3.4	27
74	Expression, purification, crystallization and preliminary X-ray analysis of the Î²-carrageenase from Pseudoalteromonas carrageenovora. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 918-920.	2.5	24
75	Expression, purification, crystallization and preliminary X-ray analysis of the Î¹-carrageenase fromAlteromonas fortis. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 766-768.	2.5	23
76	Purification, Cloning, Characterization and Essential Amino Acid Residues Analysis of a New Î¹-Carrageenase from Cellulophaga sp. QY3. PLoS ONE, 2013, 8, e64666.	2.5	22
77	Alteromonas fortis sp. nov., a non-flagellated bacterium specialized in the degradation of iota-carrageenan, and emended description of the genus Alteromonas. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2514-2521.	1.7	20
78	The Ectocarpus Genome and Brown Algal Genomics. Advances in Botanical Research, 2012, 64, 141-184.	1.1	18
79	Biochemical and structural investigation of two paralogous glycoside hydrolases fromZobellia galactanivorans: novel insights into the evolution, dimerization plasticity and catalytic mechanism of the GH117 family. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 209-223.	2.5	18
80	Development of novel monoclonal antibodies against starch and ulvan - implications for antibody production against polysaccharides with limited immunogenicity. Scientific Reports, 2017, 7, 9326.	3.3	18
81	Double blind microarray-based polysaccharide profiling enables parallel identification of uncharacterized polysaccharides and carbohydrate-binding proteins with unknown specificities. Scientific Reports, 2018, 8, 2500.	3.3	18
82	Regulation of alginate catabolism involves a GntR family repressor in the marine flavobacterium Zobellia galactanivorans DsijT. Nucleic Acids Research, 2020, 48, 7786-7800.	14.5	18
83	Unraveling the multivalent binding of a marine family 6 carbohydrateâ€binding module with its native laminarin ligand. FEBS Journal, 2016, 283, 1863-1879.	4.7	16
84	Life cycle analysis of the model organism Rhodopirellula baltica SH 1^T by transcriptome studies. Microbial Biotechnology, 2010, 3, 583-594.	4.2	15
85	Expression, purification and preliminary X-ray diffraction analysis of the catalytic module of a Î²-agarase from the flavobacteriumZobellia galactanivorans. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 413-417.	0.7	14
86	Expression, purification, crystallization and preliminary X-ray analysis of the polysaccharide lyase RB5312 from the marine planctomyceteRhodopirellula baltica. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 224-227.	0.7	11
87	In silico and inÂvitro analysis of an Aspergillus niger chitin deacetylase to decipher its subsite sugar preferences. Journal of Biological Chemistry, 2021, 297, 101129.	3.4	9
88	The laterally acquired GH5 ZgEngAGH5_4 from the marine bacterium Zobellia galactanivorans is dedicated to hemicellulose hydrolysis. Biochemical Journal, 2018, 475, 3609-3628.	3.7	7
89	Alterocin, an Antibiofilm Protein Secreted by Pseudoalteromonas sp. Strain 3J6. Applied and Environmental Microbiology, 2020, 86, .	3.1	7
90	Innovating glycoside hydrolase activity on a same structural scaffold. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4857-4859.	7.1	5

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91	Anion binding in biological systems. Journal of Physics: Conference Series, 2009, 190, 012196.	0.4	3
92	<scp>R</scp>uminococcal cellulosomes: molecular <scp>L</scp>ego to deconstruct microcrystalline cellulose in human gut. Environmental Microbiology, 2015, 17, 3113-3115.	3.8	3
93	Connecting Algal Polysaccharide Degradation to Formaldehyde Detoxification. ChemBioChem, 2022, 23, .	2.6	3
94	In-depth structural characterization of oligosaccharides released by GH107 endofucanase MfFcnA reveals enzyme subsite specificity and sulfated fucan substructural features. Glycobiology, 2022, 32, 276-288.	2.5	2
95	Systematic comparison of eight methods for preparation of high purity sulfated fucans extracted from the brown alga Pelvetia canaliculata. International Journal of Biological Macromolecules, 2022, 201, 143-157.	7.5	1
96	Microscopic and Molecular Insights into Heterogeneous Phase Degradation of Agars and Carrageenans by Marine Bacterial Galactanases. Macromolecular Symposia, 2005, 231, 11-15.	0.7	0
97	Erratum for Jouault et al., â€œAlterocin, an Antibiofilm Protein Secreted by Pseudoalteromonas sp. Strain 3J6â€. Applied and Environmental Microbiology, 2020, 86, .	3.1	0