

Gurvan Michel

List of Publications by Year in descending order

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97
papers

10,544
citations

38742

50
h-index

38395

95
g-index

100
all docs

100
docs citations

100
times ranked

10550
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic comparison of eight methods for preparation of high purity sulfated fucans extracted from the brown alga <i>Pelvetia canaliculata</i> . <i>International Journal of Biological Macromolecules</i> , 2022, 201, 143-157.	7.5	1
2	In-depth structural characterization of oligosaccharides released by GH107 endofucanase <i>FcnA</i> reveals enzyme subsite specificity and sulfated fucan substructural features. <i>Glycobiology</i> , 2022, 32, 276-288.	2.5	2
3	Connecting Algal Polysaccharide Degradation to Formaldehyde Detoxification. <i>ChemBioChem</i> , 2022, 23, .	2.6	3
4	Role and Evolution of the Extracellular Matrix in the Acquisition of Complex Multicellularity in Eukaryotes: A Macroalgal Perspective. <i>Genes</i> , 2021, 12, 1059.	2.4	34
5	In silico and in vitro analysis of an <i>Aspergillus niger</i> chitin deacetylase to decipher its subsite sugar preferences. <i>Journal of Biological Chemistry</i> , 2021, 297, 101129.	3.4	9
6	A single sulfatase is required to access colonic mucin by a gut bacterium. <i>Nature</i> , 2021, 598, 332-337.	27.8	87
7	Alterocin, an Antibiofilm Protein Secreted by <i>Pseudoalteromonas</i> sp. Strain 3J6. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	7
8	Regulation of alginate catabolism involves a GntR family repressor in the marine flavobacterium <i>Zobellia galactanivorans</i> DsijT. <i>Nucleic Acids Research</i> , 2020, 48, 7786-7800.	14.5	18
9	Erratum for Jouault et al., "Alterocin, an Antibiofilm Protein Secreted by <i>Pseudoalteromonas</i> sp. Strain 3J6". <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	0
10	A marine bacterial enzymatic cascade degrades the algal polysaccharide ulvan. <i>Nature Chemical Biology</i> , 2019, 15, 803-812.	8.0	97
11	A subfamily roadmap of the evolutionarily diverse glycoside hydrolase family 16 (GH16). <i>Journal of Biological Chemistry</i> , 2019, 294, 15973-15986.	3.4	118
12	The agar-specific hydrolase ZgAgaC from the marine bacterium <i>Zobellia galactanivorans</i> defines a new GH16 protein subfamily. <i>Journal of Biological Chemistry</i> , 2019, 294, 6923-6939.	3.4	32
13	<i>Alteromonas fortis</i> sp. nov., a non-flagellated bacterium specialized in the degradation of iota-carrageenan, and emended description of the genus <i>Alteromonas</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2514-2521.	1.7	20
14	Double blind microarray-based polysaccharide profiling enables parallel identification of uncharacterized polysaccharides and carbohydrate-binding proteins with unknown specificities. <i>Scientific Reports</i> , 2018, 8, 2500.	3.3	18
15	Seasonal and algal diet-driven patterns of the digestive microbiota of the European abalone <i>Haliotis tuberculata</i> , a generalist marine herbivore. <i>Microbiome</i> , 2018, 6, 60.	11.1	50
16	Evolutionary Evidence of Algal Polysaccharide Degradation Acquisition by <i>Pseudoalteromonas carrageenovora</i> 9T to Adapt to Macroalgal Niches. <i>Frontiers in Microbiology</i> , 2018, 9, 2740.	3.5	54
17	The laterally acquired GH5 <i>ZgEngAGH5_4</i> from the marine bacterium <i>Zobellia galactanivorans</i> is dedicated to hemicellulose hydrolysis. <i>Biochemical Journal</i> , 2018, 475, 3609-3628.	3.7	7
18	Genetic analyses unravel the crucial role of a horizontally acquired alginate lyase for brown algal biomass degradation by <i>Zobellia galactanivorans</i> . <i>Environmental Microbiology</i> , 2017, 19, 2164-2181.	3.8	84

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19	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
20	Structural insights into marine carbohydrate degradation by family GH16 β -carrageenases. Journal of Biological Chemistry, 2017, 292, 19919-19934.	3.4	38
21	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangiophyceae, Rhodophyta). Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6361-E6370.	7.1	233
22	Carrageenan catabolism is encoded by a complex regulon in marine heterotrophic bacteria. Nature Communications, 2017, 8, 1685.	12.8	131
23	Insoluble (1 \rightarrow 3), (1 \rightarrow 4)-D-glucan is a component of cell walls in brown algae (Phaeophyceae) and is masked by alginates in tissues. Scientific Reports, 2017, 7, 2880.	3.3	64
24	The Complete Genome Sequence of the Fish Pathogen <i>Tenacibaculum maritimum</i> Provides Insights into Virulence Mechanisms. Frontiers in Microbiology, 2017, 8, 1542.	3.5	57
25	Gene Expression Analysis of <i>Zobellia galactanivorans</i> during the Degradation of Algal Polysaccharides Reveals both Substrate-Specific and Shared Transcriptome-Wide Responses. Frontiers in Microbiology, 2017, 8, 1808.	3.5	58
26	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
27	Unraveling the multivalent binding of a marine family 6 carbohydrate-binding module with its native laminarin ligand. FEBS Journal, 2016, 283, 1863-1879.	4.7	16
28	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
29	Polysaccharide utilisation loci of <i>Bacteroidetes</i> from two contrasting open ocean sites in the North Atlantic. Environmental Microbiology, 2016, 18, 4456-4470.	3.8	56
30	Habitat and taxon as driving forces of carbohydrate catabolism in marine heterotrophic bacteria: example of the model alga-associated bacterium <i>Zobellia galactanivorans</i> . Environmental Microbiology, 2016, 18, 4610-4627.	3.8	131
31	The cell-wall active mannuronan C5-epimerases in the model brown alga <i>Ectocarpus</i> : From gene context to recombinant protein. Glycobiology, 2016, 26, 973-983.	2.5	38
32	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. Nature, 2016, 530, 331-335.	27.8	460
33	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
34	α -mannanococcal cellulosomes: molecular biology to deconstruct microcrystalline cellulose in human gut. Environmental Microbiology, 2015, 17, 3113-3115.	3.8	3
35	The Cultivable Surface Microbiota of the Brown Alga <i>Ascophyllum nodosum</i> is Enriched in Macroalgal-Polysaccharide-Degrading Bacteria. Frontiers in Microbiology, 2015, 6, 1487.	3.5	172
36	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

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37	The Mannitol Utilization System of the Marine Bacterium <i>Zobellia galactanivorans</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 1799-1812.	3.1	38
38	Structural and biochemical characterization of the laminarinase ZgLamC _{GH16} from <i>Zobellia galactanivorans</i> suggests preferred recognition of branched laminarin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 173-184.	2.5	34
39	Biochemical and structural investigation of two paralogous glycoside hydrolases from <i>Zobellia galactanivorans</i> : novel insights into the evolution, dimerization plasticity and catalytic mechanism of the GH117 family. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 209-223.	2.5	18
40	Genome and metabolic network of <i>Candidatus Phaeomarinobacter ectocarpi</i> Ec32, a new candidate genus of Alphaproteobacteria frequently associated with brown algae. <i>Frontiers in Genetics</i> , 2014, 5, 241.	2.3	43
41	<i>Chondrus crispus</i> – A Present and Historical Model Organism for Red Seaweeds. <i>Advances in Botanical Research</i> , 2014, 71, 53-89.	1.1	37
42	<i>Halorhabdus tiamatea</i> : proteogenomics and glycosidase activity measurements identify the first cultivated euryarchaeon from a deep-sea anoxic brine lake as potential polysaccharide degrader. <i>Environmental Microbiology</i> , 2014, 16, 2525-2537.	3.8	41
43	Identification and Characterization of a Halotolerant, Cold-Active Marine Endo- β -1,4-Glucanase by Using Functional Metagenomics of Seaweed-Associated Microbiota. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4958-4967.	3.1	52
44	Mannitol metabolism in brown algae involves a new phosphatase family. <i>Journal of Experimental Botany</i> , 2014, 65, 559-570.	4.8	67
45	Microorganisms living on macroalgae: diversity, interactions, and biotechnological applications. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 2917-2935.	3.6	171
46	The β -Glucanase ZgLamA from <i>Zobellia galactanivorans</i> Evolved a Bent Active Site Adapted for Efficient Degradation of Algal Laminarin. <i>Journal of Biological Chemistry</i> , 2014, 289, 2027-2042.	3.4	75
47	The Vanadium Haloperoxidase from the Marine Flavobacteriaceae Species <i>Zobellia galactanivorans</i> Reveals Novel Molecular and Evolutionary Features of Halide Specificity in the Vanadium Haloperoxidase Enzyme Family. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7561-7573.	3.1	46
48	Chemical and enzymatic fractionation of cell walls from Fucales: insights into the structure of the extracellular matrix of brown algae. <i>Annals of Botany</i> , 2014, 114, 1203-1216.	2.9	219
49	Comparative Characterization of Two Marine Alginate Lyases from <i>Zobellia galactanivorans</i> Reveals Distinct Modes of Action and Exquisite Adaptation to Their Natural Substrate. <i>Journal of Biological Chemistry</i> , 2013, 288, 23021-23037.	3.4	175
50	Genome structure and metabolic features in the red seaweed <i>Chondrus crispus</i> shed light on evolution of the Archaeplastida. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5247-5252.	7.1	307
51	Polysaccharide-degrading enzymes from marine bacteria. , 2013, , 429-464.		33
52	Purification, Cloning, Characterization and Essential Amino Acid Residues Analysis of a New β -1-Carrageenase from <i>Cellulophaga</i> sp. QY3. <i>PLoS ONE</i> , 2013, 8, e64666.	2.5	22
53	Biochemical and Structural Characterization of the Complex Agarolytic Enzyme System from the Marine Bacterium <i>Zobellia galactanivorans</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 30571-30584.	3.4	139
54	The <i>Ectocarpus</i> Genome and Brown Algal Genomics. <i>Advances in Botanical Research</i> , 2012, 64, 141-184.	1.1	18

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55	Characterization of the first alginolytic operons in a marine bacterium: from their emergence in marine <i>Flavobacteriia</i> to their independent transfers to marine <i>Proteobacteria</i> and human gut <i>Bacteroides</i> . <i>Environmental Microbiology</i> , 2012, 14, 2379-2394.	3.8	201
56	Evaluation of reference genes for real-time quantitative PCR in the marine flavobacterium <i>Zobellia galactanivorans</i> . <i>Journal of Microbiological Methods</i> , 2011, 84, 61-66.	1.6	60
57	Environmental and Gut Bacteroidetes: The Food Connection. <i>Frontiers in Microbiology</i> , 2011, 2, 93.	3.5	989
58	Discovery and structural characterization of a novel glycosidase family of marine origin. <i>Environmental Microbiology</i> , 2011, 13, 1253-1270.	3.8	76
59	Evolution and Diversity of Plant Cell Walls: From Algae to Flowering Plants. <i>Annual Review of Plant Biology</i> , 2011, 62, 567-590.	18.7	613
60	Mannitol-1-phosphate dehydrogenase activity in <i>Ectocarpus siliculosus</i> , a key role for mannitol synthesis in brown algae. <i>Planta</i> , 2011, 233, 261-273.	3.2	52
61	Carrageenan-induced innate immune response is modified by enzymes that hydrolyze distinct galactosidic bonds. <i>Journal of Nutritional Biochemistry</i> , 2010, 21, 906-913.	4.2	96
62	Chlorophyll-binding proteins revisited - a multigenic family of light-harvesting and stress proteins from a brown algal perspective. <i>BMC Evolutionary Biology</i> , 2010, 10, 365.	3.2	93
63	Life cycle analysis of the model organism <i>Rhodospirillum rubrum</i> SH 1 by transcriptome studies. <i>Microbial Biotechnology</i> , 2010, 3, 583-594.	4.2	15
64	Expression, purification and preliminary X-ray diffraction analysis of the catalytic module of a β -agarase from the flavobacterium <i>Zobellia galactanivorans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 413-417.	0.7	14
65	MARINE-EXPRESS: taking advantage of high throughput cloning and expression strategies for the post-genomic analysis of marine organisms. <i>Microbial Cell Factories</i> , 2010, 9, 45.	4.0	55
66	Central and storage carbon metabolism of the brown alga <i>Ectocarpus siliculosus</i> : insights into the origin and evolution of storage carbohydrates in Eukaryotes. <i>New Phytologist</i> , 2010, 188, 67-81.	7.3	172
67	The cell wall polysaccharide metabolism of the brown alga <i>Ectocarpus siliculosus</i> . Insights into the evolution of extracellular matrix polysaccharides in Eukaryotes. <i>New Phytologist</i> , 2010, 188, 82-97.	7.3	381
68	Transfer of carbohydrate-active enzymes from marine bacteria to Japanese gut microbiota. <i>Nature</i> , 2010, 464, 908-912.	27.8	905
69	The <i>Ectocarpus</i> genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010, 465, 617-621.	27.8	774
70	Identification of Catalytic Residues and Mechanistic Analysis of Family GH82 β -Carrageenases. <i>Biochemistry</i> , 2010, 49, 7590-7599.	2.5	34
71	The family 6 carbohydrate-binding modules have coevolved with their appended catalytic modules toward similar substrate specificity. <i>Glycobiology</i> , 2009, 19, 615-623.	2.5	36
72	Analysis of nasturtium <i>NXG1</i> complexes by crystallography and molecular dynamics provides detailed insight into substrate recognition by family GH16 xyloglucan β -transglycosylases and β -hydrolases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 820-836.	2.6	53

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73	Anion binding in biological systems. <i>Journal of Physics: Conference Series</i> , 2009, 190, 012196.	0.4	3
74	Expression, purification, crystallization and preliminary X-ray analysis of the polysaccharide lyase RB5312 from the marine planctomycete <i>Rhodopirellula baltica</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 224-227.	0.7	11
75	Development and physiology of the brown alga <i>Ectocarpus siliculosus</i> : two centuries of research. <i>New Phytologist</i> , 2008, 177, 319-332.	7.3	128
76	<i>Mariniflexile fucanivorans</i> sp. nov., a marine member of the Flavobacteriaceae that degrades sulphated fucans from brown algae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2107-2113.	1.7	39
77	Description of <i>Maribacter forsetii</i> sp. nov., a marine Flavobacteriaceae isolated from North Sea water, and emended description of the genus <i>Maribacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 790-797.	1.7	47
78	Structural Evidence for the Evolution of Xyloglucanase Activity from Xyloglucan Endo-Transglycosylases: Biological Implications for Cell Wall Metabolism. <i>Plant Cell</i> , 2007, 19, 1947-1963.	6.6	234
79	Alpha-Agarases Define a New Family of Glycoside Hydrolases, Distinct from Beta-Agarase Families. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4691-4694.	3.1	57
80	Degradation of $\hat{\nu}$ -carrageenan by <i>Pseudoalteromonas carrageenovora</i> $\hat{\nu}$ -carrageenase: a new family of glycoside hydrolases unrelated to $\hat{\rho}$ - and $\hat{\iota}$ -carrageenases. <i>Biochemical Journal</i> , 2007, 404, 105.	3.7	38
81	Degradation of $\hat{\nu}$ -carrageenan by <i>Pseudoalteromonas carrageenovora</i> $\hat{\nu}$ -carrageenase: a new family of glycoside hydrolases unrelated to $\hat{\rho}$ - and $\hat{\iota}$ -carrageenases. <i>Biochemical Journal</i> , 2007, 404, 105-114.	3.7	83
82	Cloning and biochemical characterization of the fucanase FcnA: definition of a novel glycoside hydrolase family specific for sulfated fucans. <i>Glycobiology</i> , 2006, 16, 1021-1032.	2.5	95
83	Bioconversion of red seaweed galactans: a focus on bacterial agarases and carrageenases. <i>Applied Microbiology and Biotechnology</i> , 2006, 71, 23-33.	3.6	238
84	Microscopic and Molecular Insights into Heterogeneous Phase Degradation of Agars and Carrageenans by Marine Bacterial Galactanases. <i>Macromolecular Symposia</i> , 2005, 231, 11-15.	0.7	0
85	The endo- $\hat{\iota}$ -agarases AgaA and AgaB from the marine bacterium <i>Zobellia galactanivorans</i> : two paralogous enzymes with different molecular organizations and catalytic behaviours. <i>Biochemical Journal</i> , 2005, 385, 703-713.	3.7	130
86	Vanadium-dependent iodoperoxidases in <i>Laminaria digitata</i> , a novel biochemical function diverging from brown algal bromoperoxidases. <i>Journal of Biological Inorganic Chemistry</i> , 2005, 10, 156-166.	2.6	84
87	Site-directed Mutagenesis of the Active Site Region in the Quinate/Shikimate 5-Dehydrogenase YdiB of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 7162-7169.	3.4	27
88	Bromine is an Endogenous Component of a Vanadium Bromoperoxidase. <i>Journal of the American Chemical Society</i> , 2005, 127, 15340-15341.	13.7	30
89	The Structure of Chondroitin B Lyase Complexed with Glycosaminoglycan Oligosaccharides Unravels a Calcium-dependent Catalytic Machinery. <i>Journal of Biological Chemistry</i> , 2004, 279, 32882-32896.	3.4	91
90	The Structural Bases of the Processive Degradation of $\hat{\iota}$ -Carrageenan, a Main Cell Wall Polysaccharide of Red Algae. <i>Journal of Molecular Biology</i> , 2003, 334, 421-433.	4.2	60

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91	Structures of Shikimate Dehydrogenase AroE and Its Paralog YdiB. <i>Journal of Biological Chemistry</i> , 2003, 278, 19463-19472.	3.4	111
92	The Structure of the RlmB 23S rRNA Methyltransferase Reveals a New Methyltransferase Fold with a Unique Knot. <i>Structure</i> , 2002, 10, 1303-1315.	3.3	92
93	The $\hat{1}^9$ -carrageenase of <i>P. carrageenovora</i> Features a Tunnel-Shaped Active Site. <i>Structure</i> , 2001, 9, 513-525.	3.3	193
94	The $\hat{1}^1$ -Carrageenase of <i>Alteromonas fortis</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 40202-40209.	3.4	71
95	Expression, purification, crystallization and preliminary X-ray analysis of the $\hat{1}^1$ -carrageenase from <i>Alteromonas fortis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 766-768.	2.5	23
96	$\hat{1}^1$ -Carrageenases Constitute a Novel Family of Glycoside Hydrolases, Unrelated to That of $\hat{1}^9$ -Carrageenases. <i>Journal of Biological Chemistry</i> , 2000, 275, 35499-35505.	3.4	113
97	Expression, purification, crystallization and preliminary X-ray analysis of the $\hat{1}^9$ -carrageenase from <i>Pseudoalteromonas carrageenovora</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 918-920.	2.5	24