

Gurvan Michel

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

95
papers

7,481
citations

44
h-index

86
g-index

100
ext. papers

9,509
ext. citations

7.8
avg, IF

5.58
L-index

#	Paper	IF	Citations
95	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> , 2021 , 201, 143-143	7.9	0
94	A single sulfatase is required to access colonic mucin by a gut bacterium. <i>Nature</i> , 2021 , 598, 332-337	50.4	16
93	Role and Evolution of the Extracellular Matrix in the Acquisition of Complex Multicellularity in Eukaryotes: A Macroalgal Perspective. <i>Genes</i> , 2021 , 12,	4.2	6
92	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	5.4	1
91	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	20.1	9
90	Alterocin, an Antibiofilm Protein Secreted by sp. Strain 3J6. <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	2
89	A subfamily roadmap of the evolutionarily diverse glycoside hydrolase family 16 (GH16). <i>Journal of Biological Chemistry</i> , 2019 , 294, 15973-15986	5.4	55
88	The agar-specific hydrolase AgaC from the marine bacterium defines a new GH16 protein subfamily. <i>Journal of Biological Chemistry</i> , 2019 , 294, 6923-6939	5.4	11
87	A marine bacterial enzymatic cascade degrades the algal polysaccharide ulvan. <i>Nature Chemical Biology</i> , 2019 , 15, 803-812	11.7	52
86	<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	2.2	8
85	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	4.9	10
84	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	16.6	30
83	Evolutionary Evidence of Algal Polysaccharide Degradation Acquisition by 9 to Adapt to Macroalgal Niches. <i>Frontiers in Microbiology</i> , 2018 , 9, 2740	5.7	26
82	The laterally acquired GH5 EngA from the marine bacterium is dedicated to hemicellulose hydrolysis. <i>Biochemical Journal</i> , 2018 , 475, 3609-3628	3.8	4
81	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	5.2	41
80	Innovating glycoside hydrolase activity on a same structural scaffold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 4857-4859	11.5	4
79	Structural insights into marine carbohydrate degradation by family GH16 β -carrageenases. <i>Journal of Biological Chemistry</i> , 2017 , 292, 19919-19934	5.4	22

78	Development of novel monoclonal antibodies against starch and ulvan - implications for antibody production against polysaccharides with limited immunogenicity. <i>Scientific Reports</i> , 2017 , 7, 9326	4.9	15
77	Insights into the red algae and eukaryotic evolution from the genome of (Bangiophyceae, Rhodophyta). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E6361-E6370	11.5	131
76	Carrageenan catabolism is encoded by a complex regulon in marine heterotrophic bacteria. <i>Nature Communications</i> , 2017 , 8, 1685	17.4	72
75	Insoluble (1- β), (1- α)-D-glucan is a component of cell walls in brown algae (Phaeophyceae) and is masked by alginates in tissues. <i>Scientific Reports</i> , 2017 , 7, 2880	4.9	46
74	The Complete Genome Sequence of the Fish Pathogen Provides Insights into Virulence Mechanisms. <i>Frontiers in Microbiology</i> , 2017 , 8, 1542	5.7	33
73	Gene Expression Analysis of during the Degradation of Algal Polysaccharides Reveals both Substrate-Specific and Shared Transcriptome-Wide Responses. <i>Frontiers in Microbiology</i> , 2017 , 8, 1808	5.7	25
72	Habitat and taxon as driving forces of carbohydrate catabolism in marine heterotrophic bacteria: example of the model algae-associated bacterium <i>Zobellia galactanivorans</i> Dsij. <i>Environmental Microbiology</i> , 2016 , 18, 4610-4627	5.2	72
71	The cell-wall active mannuronan C5-epimerases in the model brown alga <i>Ectocarpus</i> : From gene context to recombinant protein. <i>Glycobiology</i> , 2016 , 26, 973-983	5.8	22
70	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016 , 530, 331-5	50.4	276
69	Matching the Diversity of Sulfated Biomolecules: Creation of a Classification Database for Sulfatases Reflecting Their Substrate Specificity. <i>PLoS ONE</i> , 2016 , 11, e0164846	3.7	73
68	Unraveling the multivalent binding of a marine family 6 carbohydrate-binding module with its native laminarin ligand. <i>FEBS Journal</i> , 2016 , 283, 1863-79	5.7	10
67	Discovering novel enzymes by functional screening of plurigenomic libraries from alga-associated Flavobacteriia and Gammaproteobacteria. <i>Microbiological Research</i> , 2016 , 186-187, 52-61	5.3	22
66	Polysaccharide utilisation loci of Bacteroidetes from two contrasting open ocean sites in the North Atlantic. <i>Environmental Microbiology</i> , 2016 , 18, 4456-4470	5.2	35
65	Ruminococcal cellulosomes: molecular Lego to deconstruct microcrystalline cellulose in human gut. <i>Environmental Microbiology</i> , 2015 , 17, 3113-5	5.2	3
64	The Cultivable Surface Microbiota of the Brown Alga <i>Ascophyllum nodosum</i> is Enriched in Macroalgal-Polysaccharide-Degrading Bacteria. <i>Frontiers in Microbiology</i> , 2015 , 6, 1487	5.7	89
63	Sweet and sour sugars from the sea: the biosynthesis and remodeling of sulfated cell wall polysaccharides from marine macroalgae. <i>Perspectives in Phycology</i> , 2015 , 2, 51-64	3.1	38
62	The mannitol utilization system of the marine bacterium <i>Zobellia galactanivorans</i> . <i>Applied and Environmental Microbiology</i> , 2015 , 81, 1799-812	4.8	22
61	Structural and biochemical characterization of the laminarinase ZgLamCGH16 from <i>Zobellia galactanivorans</i> suggests preferred recognition of branched laminarin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 173-84		29

60	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, 209-23		16
59	Microorganisms living on macroalgae: diversity, interactions, and biotechnological applications. <i>Applied Microbiology and Biotechnology</i> , 2014 , 98, 2917-35	5.7	98
58	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, 2027-42	5.4	50
57	The Vanadium Iodoperoxidase 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, 7561-73	4.8	32
56	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, 1203-16	4.1	164
55	Genome and metabolic network of "Candidate Genus <i>Phaeomarinobacter ectocarpi</i> " Ec32, a new candidate genus of Alphaproteobacteria frequently associated with brown algae. <i>Frontiers in Genetics</i> , 2014 , 5, 241	4.5	23
54	<i>Chondrus crispus</i> A Present and Historical Model Organism for Red Seaweeds. <i>Advances in Botanical Research</i> , 2014 , 71, 53-89	2.2	22
53	<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, 2525-37	5.2	32
52	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, 4958-67	4.8	43
51	Mannitol metabolism in brown algae involves a new phosphatase family. <i>Journal of Experimental Botany</i> , 2014 , 65, 559-70	7	46
50	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, 23021-37	5.4	122
49	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, 5247-52	11.5	239
48	Polysaccharide-degrading enzymes from marine bacteria 2013 , 429-464		28
47	Purification, cloning, characterization and essential amino acid residues analysis of a new β -carrageenase from <i>Cellulophaga</i> sp. QY3. <i>PLoS ONE</i> , 2013 , 8, e64666	3.7	19
46	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. <i>Environmental Microbiology</i> , 2012 , 14, 2379-94	5.2	128
45	The Ectocarpus Genome and Brown Algal Genomics: The Ectocarpus Genome Consortium. <i>Advances in Botanical Research</i> , 2012 , 64, 141-184	2.2	10
44	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, 30571-84	5.4	85
43	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, 61-6	2.8	39

42	Environmental and gut bacteroidetes: the food connection. <i>Frontiers in Microbiology</i> , 2011 , 2, 93	5.7	605
41	Discovery and structural characterization of a novel glycosidase family of marine origin. <i>Environmental Microbiology</i> , 2011 , 13, 1253-70	5.2	70
40	Evolution and diversity of plant cell walls: from algae to flowering plants. <i>Annual Review of Plant Biology</i> , 2011 , 62, 567-90	30.7	455
39	Mannitol-1-phosphate dehydrogenase activity in <i>Ectocarpus siliculosus</i> , a key role for mannitol synthesis in brown algae. <i>Planta</i> , 2011 , 233, 261-73	4.7	48
38	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	9.8	129
37	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	9.8	297
36	Transfer of carbohydrate-active enzymes from marine bacteria to Japanese gut microbiota. <i>Nature</i> , 2010 , 464, 908-12	50.4	734
35	The <i>Ectocarpus</i> genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 2010 , 465, 617-21	50.4	645
34	Identification of catalytic residues and mechanistic analysis of family GH82 iota-carrageenases. <i>Biochemistry</i> , 2010 , 49, 7590-9	3.2	32
33	Carrageenan-induced innate immune response is modified by enzymes that hydrolyze distinct galactosidic bonds. <i>Journal of Nutritional Biochemistry</i> , 2010 , 21, 906-13	6.3	87
32	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	76
31	Life cycle analysis of the model organism <i>Rhodospirillum rubrum</i> SH 1(T) by transcriptome studies. <i>Microbial Biotechnology</i> , 2010 , 3, 583-94	6.3	14
30	Expression, purification and preliminary X-ray diffraction analysis of the catalytic module of a beta-agarase from the flavobacterium <i>Zobellia galactanivorans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 413-7		14
29	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	6.4	44
28	The family 6 carbohydrate-binding modules have coevolved with their appended catalytic modules toward similar substrate specificity. <i>Glycobiology</i> , 2009 , 19, 615-23	5.8	31
27	Analysis of nasturtium TmNXG1 complexes by crystallography and molecular dynamics provides detailed insight into substrate recognition by family GH16 xyloglucan endo-transglycosylases and endo-hydrolases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 820-36	4.2	47
26	Anion binding in biological systems. <i>Journal of Physics: Conference Series</i> , 2009 , 190, 012196	0.3	3
25	Development and physiology of the brown alga <i>Ectocarpus siliculosus</i> : two centuries of research. <i>New Phytologist</i> , 2008 , 177, 319-332	9.8	103

24	Mariniflexile fucanivorans 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, 2107-13	2.2	30
23	Description of Maribacter forsetii sp. nov., a marine Flavobacteriaceae isolated from North Sea water, and emended description of the genus Maribacter. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 790-7	2.2	38
22	Expression, purification, crystallization and preliminary X-ray analysis of the polysaccharide lyase RB5312 from the marine planctomycete Rhodopirellula baltica. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 224-7		11
21	Structural evidence for the evolution of xyloglucanase activity from xyloglucan endo-transglycosylases: biological implications for cell wall metabolism. <i>Plant Cell</i> , 2007 , 19, 1947-63	11.6	178
20	Alpha-agarases define a new family of glycoside hydrolases, distinct from beta-agarase families. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 4691-4	4.8	51
19	Degradation of lambda-carrageenan by Pseudoalteromonas carrageenovora lambda-carrageenase: a new family of glycoside hydrolases unrelated to kappa- and iota-carrageenases. <i>Biochemical Journal</i> , 2007 , 404, 105-14	3.8	34
18	Degradation of E-carrageenan by Pseudoalteromonas carrageenovora E-carrageenase: a new family of glycoside hydrolases unrelated to D and F-carrageenases. <i>Biochemical Journal</i> , 2007 , 404, 105-114	3.8	64
17	Bioconversion of red seaweed galactans: a focus on bacterial agarases and carrageenases. <i>Applied Microbiology and Biotechnology</i> , 2006 , 71, 23-33	5.7	186
16	Cloning and biochemical characterization of the fucanase FcnA: definition of a novel glycoside hydrolase family specific for sulfated fucans. <i>Glycobiology</i> , 2006 , 16, 1021-32	5.8	66
15	Bromine is an endogenous component of a vanadium bromoperoxidase. <i>Journal of the American Chemical Society</i> , 2005 , 127, 15340-1	16.4	29
14	Microscopic and Molecular Insights into Heterogeneous Phase Degradation of Agars and Carrageenans by Marine Bacterial Galactanases. <i>Macromolecular Symposia</i> , 2005 , 231, 11-15	0.8	
13	The endo-beta-agarases AgaA and AgaB from the marine bacterium Zobellia galactanivorans: two paralogue enzymes with different molecular organizations and catalytic behaviours. <i>Biochemical Journal</i> , 2005 , 385, 703-13	3.8	108
12	Vanadium-dependent iodoperoxidases in Laminaria digitata, a novel biochemical function diverging from brown algal bromoperoxidases. <i>Journal of Biological Inorganic Chemistry</i> , 2005 , 10, 156-66	3.7	72
11	Site-directed mutagenesis of the active site region in the quinate/shikimate 5-dehydrogenase YdiB of Escherichia coli. <i>Journal of Biological Chemistry</i> , 2005 , 280, 7162-9	5.4	20
10	The structure of chondroitin B lyase complexed with glycosaminoglycan oligosaccharides unravels a calcium-dependent catalytic machinery. <i>Journal of Biological Chemistry</i> , 2004 , 279, 32882-96	5.4	76
9	The structural bases of the processive degradation of iota-carrageenan, a main cell wall polysaccharide of red algae. <i>Journal of Molecular Biology</i> , 2003 , 334, 421-33	6.5	51
8	Structures of shikimate dehydrogenase AroE and its Paralog YdiB. A common structural framework for different activities. <i>Journal of Biological Chemistry</i> , 2003 , 278, 19463-72	5.4	81
7	The structure of the RlmB 23S rRNA methyltransferase reveals a new methyltransferase fold with a unique knot. <i>Structure</i> , 2002 , 10, 1303-15	5.2	84

6	The kappa-carrageenase of <i>P. carrageenovora</i> features a tunnel-shaped active site: a novel insight in the evolution of Clan-B glycoside hydrolases. <i>Structure</i> , 2001 , 9, 513-25	5.2	167
5	The iota-carrageenase of <i>Alteromonas fortis</i> . A beta-helix fold-containing enzyme for the degradation of a highly polyanionic polysaccharide. <i>Journal of Biological Chemistry</i> , 2001 , 276, 40202-9	5.4	62
4	Expression, purification, crystallization and preliminary X-ray analysis of the iota-carrageenase from <i>Alteromonas fortis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 766-8		20
3	iota-Carrageenases constitute a novel family of glycoside hydrolases, unrelated to that of kappa-carrageenases. <i>Journal of Biological Chemistry</i> , 2000 , 275, 35499-505	5.4	97
2	Expression, purification, crystallization and preliminary x-ray analysis of the kappa-carrageenase from <i>Pseudoalteromonas carrageenovora</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 918-20		14
1	A single bacterial sulfatase is required for metabolism of colonic mucin O-glycans and intestinal colonization by a symbiotic human gut bacterium		2