

Mirjam Czjzek

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.

30
papers

824
citations

16
h-index

28
g-index

37
ext. papers

1,219
ext. citations

9.9
avg, IF

4.08
L-index

#	Paper	IF	Citations
30	A single sulfatase is required to access colonic mucin by a gut bacterium. <i>Nature</i> , 2021 , 598, 332-337	50.4	16
29	Structure-function analysis of a new PL17 oligoalginate lyase from the marine bacterium <i>Zobellia galactanivorans</i> DsijT. <i>Glycobiology</i> , 2021 , 31, 1364-1377	5.8	1
28	A novel thermostable prokaryotic fucoidan active sulfatase PsFucS1 with an unusual quaternary hexameric structure. <i>Scientific Reports</i> , 2021 , 11, 19523	4.9	1
27	Structural and enzymatic characterisation of the Type III effector NopAA (=GunA) from <i>Sinorhizobium fredii</i> USDA257 reveals a Xyloglucan hydrolase activity. <i>Scientific Reports</i> , 2020 , 10, 9932	4.9	2
26	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
25	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
24	X-ray Diffraction and Density Functional Theory Provide Insight into Vanadate Binding to Homohexameric Bromoperoxidase II and the Mechanism of Bromide Oxidation. <i>ACS Chemical Biology</i> , 2018 , 13, 1243-1259	4.9	1
23	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
22	A Novel Enzyme Portfolio for Red Algal Polysaccharide Degradation in the Marine Bacterium S66 Encoded in a Sizeable Polysaccharide Utilization Locus. <i>Frontiers in Microbiology</i> , 2018 , 9, 839	5.7	34
21	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
20	Discovery and screening of novel metagenome-derived GH107 enzymes targeting sulfated fucans from brown algae. <i>FEBS Journal</i> , 2018 , 285, 4281-4295	5.7	16
19	Continually emerging mechanistic complexity of the multi-enzyme cellulosome complex. <i>Current Opinion in Structural Biology</i> , 2017 , 44, 151-160	8.1	32
18	Probing the Complex Architecture of Multimodular Carbohydrate-Active Enzymes Using a Combination of Small Angle X-Ray Scattering and X-Ray Crystallography. <i>Methods in Molecular Biology</i> , 2017 , 1588, 239-253	1.4	3
17	Internal Water Dynamics Control the Transglycosylation/Hydrolysis Balance in the Agarase (AgaD) of <i>Zobellia galactanivorans</i> . <i>ACS Catalysis</i> , 2017 , 7, 3357-3367	13.1	15
16	Nigritoxin is a bacterial toxin for crustaceans and insects. <i>Nature Communications</i> , 2017 , 8, 1248	17.4	5
15	Structural insights into marine carbohydrate degradation by family GH16 Carrageenases. <i>Journal of Biological Chemistry</i> , 2017 , 292, 19919-19934	5.4	22
14	Carrageenan catabolism is encoded by a complex regulon in marine heterotrophic bacteria. <i>Nature Communications</i> , 2017 , 8, 1685	17.4	72

13	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	11.5	67
12	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
11	Online coupling of high-resolution chromatography with extreme UV photon activation tandem mass spectrometry: Application to the structural investigation of complex glycans by dissociative photoionization. <i>Analytica Chimica Acta</i> , 2016 , 933, 1-9	6.6	20
10	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
9	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
8	Nanoscale Engineering of Designer Cellulosomes. <i>Advanced Materials</i> , 2016 , 28, 5619-47	24	35
7	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
6	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
5	Large conformational fluctuations of the multi-domain xylanase Z of <i>Clostridium thermocellum</i> . <i>Journal of Structural Biology</i> , 2015 , 191, 68-75	3.4	13
4	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
3	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
2	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
1	A sweet new wave: structures and mechanisms of enzymes that digest polysaccharides from marine algae. <i>Current Opinion in Structural Biology</i> , 2014 , 28, 77-86	8.1	80