

# Nicolas Terrapon

## List of Publications by Citations

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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.

50  
papers

3,784  
citations

25  
h-index

60  
g-index

60  
ext. papers

5,575  
ext. citations

14.9  
avg, IF

5.19  
L-index

#	Paper	IF	Citations
50	A Dietary Fiber-Deprived Gut Microbiota Degrades the Colonic Mucus Barrier and Enhances Pathogen Susceptibility. <i>Cell</i> , <b>2016</b> , 167, 1339-1353.e21	56.2	1149
49	Complex pectin metabolism by gut bacteria reveals novel catalytic functions. <i>Nature</i> , <b>2017</b> , 544, 65-70	50.4	291
48	Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , <b>2014</b> , 5, 3636	17.4	250
47	Glycan complexity dictates microbial resource allocation in the large intestine. <i>Nature Communications</i> , <b>2015</b> , 6, 7481	17.4	241
46	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , <b>2018</b> , 36, 359-367	44.5	207
45	Dietary pectic glycans are degraded by coordinated enzyme pathways in human colonic Bacteroides. <i>Nature Microbiology</i> , <b>2018</b> , 3, 210-219	26.6	142
44	Genetic determinants of in vivo fitness and diet responsiveness in multiple human gut Bacteroides. <i>Science</i> , <b>2015</b> , 350, aac5992	33.3	138
43	Automatic prediction of polysaccharide utilization loci in Bacteroidetes species. <i>Bioinformatics</i> , <b>2015</b> , 31, 647-55	7.2	131
42	Bacteroidetes use thousands of enzyme combinations to break down glycans. <i>Nature Communications</i> , <b>2019</b> , 10, 2043	17.4	109
41	PULDB: the expanded database of Polysaccharide Utilization Loci. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D6772-D6683	10.4	104
40	Interspecies Competition Impacts Targeted Manipulation of Human Gut Bacteria by Fiber-Derived Glycans. <i>Cell</i> , <b>2019</b> , 179, 59-73.e13	56.2	103
39	Discovery of novel carbohydrate-active enzymes through the rational exploration of the protein sequences space. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 6063-6068	11.5	88
38	The carbohydrate-active enzyme database: functions and literature. <i>Nucleic Acids Research</i> , <b>2021</b> ,	20.1	81
37	Ninety-nine de novo assembled genomes from the moose ( <i>Alces alces</i> ) rumen microbiome provide new insights into microbial plant biomass degradation. <i>ISME Journal</i> , <b>2017</b> , 11, 2538-2551	11.9	70
36	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> , <b>2017</b> , 114, 7037-7042	11.5	67
35	A surface endogalactanase in <i>Bacteroides thetaiotaomicron</i> confers keystone status for arabinogalactan degradation. <i>Nature Microbiology</i> , <b>2018</b> , 3, 1314-1326	26.6	57
34	A subfamily roadmap of the evolutionarily diverse glycoside hydrolase family 16 (GH16). <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 15973-15986	5.4	55

33	Xylan degradation by the human gut <i>Bacteroides xylanisolvens</i> XB1A(T) involves two distinct gene clusters that are linked at the transcriptional level. <i>BMC Genomics</i> , <b>2016</b> , 17, 326	4.5	44
32	A bioinformatics analysis of 3400 lytic polysaccharide oxidases from family AA9. <i>Carbohydrate Research</i> , <b>2017</b> , 448, 166-174	2.9	41
31	DoMosaics: software for domain arrangement visualization and domain-centric analysis of proteins. <i>Bioinformatics</i> , <b>2014</b> , 30, 282-3	7.2	34
30	Rapid similarity search of proteins using alignments of domain arrangements. <i>Bioinformatics</i> , <b>2014</b> , 30, 274-81	7.2	31
29	Unusual active site location and catalytic apparatus in a glycoside hydrolase family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 4936-4941	11.5	30
28	A fibrolytic potential in the human ileum mucosal microbiota revealed by functional metagenomic. <i>Scientific Reports</i> , <b>2017</b> , 7, 40248	4.9	27
27	Metabolism of multiple glycosaminoglycans by <i>Bacteroides thetaiotaomicron</i> is orchestrated by a versatile core genetic locus. <i>Nature Communications</i> , <b>2020</b> , 11, 646	17.4	27
26	Unraveling the pectinolytic function of <i>Bacteroides xylanisolvens</i> using a RNA-seq approach and mutagenesis. <i>BMC Genomics</i> , <b>2016</b> , 17, 147	4.5	26
25	Detection of new protein domains using co-occurrence: application to <i>Plasmodium falciparum</i> . <i>Bioinformatics</i> , <b>2009</b> , 25, 3077-83	7.2	25
24	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. <i>Nature Communications</i> , <b>2020</b> , 11, 5773	17.4	24
23	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. <i>GigaScience</i> , <b>2020</b> , 9,	7.6	21
22	An evolutionarily distinct family of polysaccharide lyases removes rhamnose capping of complex arabinogalactan proteins. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 13271-13283	5.4	20
21	The CAZy Database/the Carbohydrate-Active Enzyme (CAZy) Database: Principles and Usage Guidelines <b>2017</b> , 117-131		18
20	How do gut microbes break down dietary fiber?. <i>Trends in Biochemical Sciences</i> , <b>2014</b> , 39, 156-8	10.3	18
19	Investigating host-microbiome interactions by droplet based microfluidics. <i>Microbiome</i> , <b>2020</b> , 8, 141	16.6	15
18	Comparative Metagenomics of Cellulose- and Poplar Hydrolysate-Degrading Microcosms from Gut Microflora of the Canadian Beaver () and North American Moose () after Long-Term Enrichment. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 2504	5.7	14
17	Fitting hidden Markov models of protein domains to a target species: application to <i>Plasmodium falciparum</i> . <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 67	3.6	10
16	Comparative genomic analyses reveal diverse virulence factors and antimicrobial resistance mechanisms in clinical <i>Elizabethkingia meningoseptica</i> strains. <i>PLoS ONE</i> , <b>2019</b> , 14, e0222648	3.7	9

15	Harvesting of Prebiotic Fructooligosaccharides by Nonbeneficial Human Gut Bacteria. <i>MSphere</i> , <b>2020</b> , 5,	5	7
14	EuPathDomains: the divergent domain database for eukaryotic pathogens. <i>Infection, Genetics and Evolution</i> , <b>2011</b> , 11, 698-707	4.5	6
13	Isolation and Characterization of Extracellular Vesicles Secreted In Vitro by Porcine Microbiota. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	4
12	Identification of divergent protein domains by combining HMM-HMM comparisons and co-occurrence detection. <i>PLoS ONE</i> , <b>2014</b> , 9, e95275	3.7	4
11	Strain-level functional variation in the human gut microbiota based on bacterial binding to artificial food particles. <i>Cell Host and Microbe</i> , <b>2021</b> , 29, 664-673.e5	23.4	4
10	Phenotypic and Genomic Diversification in Complex Carbohydrate-Degrading Human Gut Bacteria.. <i>MSystems</i> , <b>2022</b> , e0094721	7.6	4
9	Gut microbiome of the largest living rodent harbors unprecedented enzymatic systems to degrade plant polysaccharides.. <i>Nature Communications</i> , <b>2022</b> , 13, 629	17.4	3
8	Bioinformatic Analysis of Lytic Polysaccharide Monooxygenases Reveals the Pan-Families Occurrence of Intrinsically Disordered C-Terminal Extensions. <i>Biomolecules</i> , <b>2021</b> , 11,	5.9	3
7	Analysis of the diversity of the glycoside hydrolase family 130 in mammal gut microbiomes reveals a novel mannoside-phosphorylase function. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	3
6	Mechanistic insights into consumption of the food additive xanthan gum by the human gut microbiota.. <i>Nature Microbiology</i> , <b>2022</b> , 7, 556-569	26.6	3
5	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment		1
4	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut		1
3	Polysaccharide utilization loci-driven enzyme discovery reveals BD-FAE: a bifunctional feruloyl and acetyl xylan esterase active on complex natural xylans. <i>Biotechnology for Biofuels</i> , <b>2021</b> , 14, 127	7.8	1
2	The Food Additive Xanthan Gum Drives Adaptation of the Human Gut Microbiota		1
1	Functional exploration of the glycoside hydrolase family GH113.. <i>PLoS ONE</i> , <b>2022</b> , 17, e0267509	3.7	1