

# Nicolas Terrapon

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

7,138  
citations

186265

28  
h-index

161849

54  
g-index

60  
all docs

60  
docs citations

60  
times ranked

8395  
citing authors

#	ARTICLE	IF	CITATIONS
1	Assembly and synthesis of the extracellular matrix in brown algae. <i>Seminars in Cell and Developmental Biology</i> , 2023, 134, 112-124.	5.0	6
2	The carbohydrate-active enzyme database: functions and literature. <i>Nucleic Acids Research</i> , 2022, 50, D571-D577.	14.5	813
3	Gut microbiome of the largest living rodent harbors unprecedented enzymatic systems to degrade plant polysaccharides. <i>Nature Communications</i> , 2022, 13, 629.	12.8	26
4	Phenotypic and Genomic Diversification in Complex Carbohydrate-Degrading Human Gut Bacteria. <i>MSystems</i> , 2022, 7, e0094721.	3.8	40
5	Mechanistic insights into consumption of the food additive xanthan gum by the human gut microbiota. <i>Nature Microbiology</i> , 2022, 7, 556-569.	13.3	21
6	Functional exploration of the glycoside hydrolase family GH113. <i>PLoS ONE</i> , 2022, 17, e0267509.	2.5	5
7	Microbial liberation of N-methylserotonin from orange fiber in gnotobiotic mice and humans. <i>Cell</i> , 2022, 185, 2495-2509.e11.	28.9	26
8	Strain-level functional variation in the human gut microbiota based on bacterial binding to artificial food particles. <i>Cell Host and Microbe</i> , 2021, 29, 664-673.e5.	11.0	27
9	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> , 2021, 14, 127.	6.2	10
10	Genome Features of <i>Asaia</i> sp. W12 Isolated from the Mosquito <i>Anopheles stephensi</i> Reveal Symbiotic Traits. <i>Genes</i> , 2021, 12, 752.	2.4	2
11	Bioinformatic Analysis of Lytic Polysaccharide Monooxygenases Reveals the Pan-Families Occurrence of Intrinsically Disordered C-Terminal Extensions. <i>Biomolecules</i> , 2021, 11, 1632.	4.0	25
12	Harvesting of Prebiotic Fructooligosaccharides by Nonbeneficial Human Gut Bacteria. <i>MSphere</i> , 2020, 5, .	2.9	12
13	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. <i>Nature Communications</i> , 2020, 11, 5773.	12.8	55
14	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. <i>GigaScience</i> , 2020, 9, .	6.4	35
15	Isolation and Characterization of Extracellular Vesicles Secreted In Vitro by Porcine Microbiota. <i>Microorganisms</i> , 2020, 8, 983.	3.6	9
16	Metabolism of multiple glycosaminoglycans by <i>Bacteroides thetaiotaomicron</i> is orchestrated by a versatile core genetic locus. <i>Nature Communications</i> , 2020, 11, 646.	12.8	58
17	Analysis of the diversity of the glycoside hydrolase family 130 in mammal gut microbiomes reveals a novel mannoside-phosphorylase function. <i>Microbial Genomics</i> , 2020, 6, .	2.0	6
18	Investigating host-microbiome interactions by droplet based microfluidics. <i>Microbiome</i> , 2020, 8, 141.	11.1	33

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19	Comparative genomic analyses reveal diverse virulence factors and antimicrobial resistance mechanisms in clinical <i>Elizabethkingia meningoseptica</i> strains. PLoS ONE, 2019, 14, e0222648.	2.5	15
20	A subfamily roadmap of the evolutionarily diverse glycoside hydrolase family 16 (GH16). Journal of Biological Chemistry, 2019, 294, 15973-15986.	3.4	118
21	Interspecies Competition Impacts Targeted Manipulation of Human Gut Bacteria by Fiber-Derived Glycans. Cell, 2019, 179, 59-73.e13.	28.9	224
22	Bacteroidetes use thousands of enzyme combinations to break down glycans. Nature Communications, 2019, 10, 2043.	12.8	238
23	Discovery of novel carbohydrate-active enzymes through the rational exploration of the protein sequences space. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6063-6068.	7.1	154
24	PULDB: the expanded database of Polysaccharide Utilization Loci. Nucleic Acids Research, 2018, 46, D677-D683.	14.5	191
25	Dietary pectic glycans are degraded by coordinated enzyme pathways in human colonic Bacteroides. Nature Microbiology, 2018, 3, 210-219.	13.3	263
26	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. Nature Biotechnology, 2018, 36, 359-367.	17.5	414
27	A surface endogalactanase in <i>Bacteroides thetaiotaomicron</i> confers keystone status for arabinogalactan degradation. Nature Microbiology, 2018, 3, 1314-1326.	13.3	103
28	A fibrolytic potential in the human ileum mucosal microbiota revealed by functional metagenomic. Scientific Reports, 2017, 7, 40248.	3.3	38
29	Unusual active site location and catalytic apparatus in a glycoside hydrolase family. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4936-4941.	7.1	38
30	A bioinformatics analysis of 3400 lytic polysaccharide oxidases from family AA9. Carbohydrate Research, 2017, 448, 166-174.	2.3	55
31	An evolutionarily distinct family of polysaccharide lyases removes rhamnose capping of complex arabinogalactan proteins. Journal of Biological Chemistry, 2017, 292, 13271-13283.	3.4	26
32	Complex pectin metabolism by gut bacteria reveals novel catalytic functions. Nature, 2017, 544, 65-70.	27.8	447
33	The CAZy Database/the Carbohydrate-Active Enzyme (CAZy) Database: Principles and Usage Guidelines. , 2017, , 117-131.		27
34	Ninety-nine <i>de novo</i> assembled genomes from the moose ( <i>Alces alces</i> ) rumen microbiome provide new insights into microbial plant biomass degradation. ISME Journal, 2017, 11, 2538-2551.	9.8	120
35	How members of the human gut microbiota overcome the sulfation problem posed by glycosaminoglycans. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7037-7042.	7.1	99
36	Comparative Metagenomics of Cellulose- and Poplar Hydrolysate-Degrading Microcosms from Gut Microflora of the Canadian Beaver ( <i>Castor canadensis</i> ) and North American Moose ( <i>Alces americanus</i> ) after Long-Term Enrichment. Frontiers in Microbiology, 2017, 8, 2504.	3.5	24

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37	A Dietary Fiber-Deprived Gut Microbiota Degrades the Colonic Mucus Barrier and Enhances Pathogen Susceptibility. <i>Cell</i> , 2016, 167, 1339-1353.e21.	28.9	1,882
38	Xylan degradation by the human gut <i>Bacteroides xylanisolvens</i> XB1AT involves two distinct gene clusters that are linked at the transcriptional level. <i>BMC Genomics</i> , 2016, 17, 326.	2.8	81
39	Unraveling the pectinolytic function of <i>Bacteroides xylanisolvens</i> using a RNA-seq approach and mutagenesis. <i>BMC Genomics</i> , 2016, 17, 147.	2.8	33
40	Glycan complexity dictates microbial resource allocation in the large intestine. <i>Nature Communications</i> , 2015, 6, 7481.	12.8	328
41	Genetic determinants of in vivo fitness and diet responsiveness in multiple human gut <i>Bacteroides</i> . <i>Science</i> , 2015, 350, aac5992.	12.6	229
42	Automatic prediction of polysaccharide utilization loci in <i>Bacteroidetes</i> species. <i>Bioinformatics</i> , 2015, 31, 647-655.	4.1	195
43	Rapid similarity search of proteins using alignments of domain arrangements. <i>Bioinformatics</i> , 2014, 30, 274-281.	4.1	37
44	DoMosaics: software for domain arrangement visualization and domain-centric analysis of proteins. <i>Bioinformatics</i> , 2014, 30, 282-283.	4.1	52
45	How do gut microbes break down dietary fiber?. <i>Trends in Biochemical Sciences</i> , 2014, 39, 156-158.	7.5	21
46	Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014, 5, 3636.	12.8	371
47	Identification of Divergent Protein Domains by Combining HMM-HMM Comparisons and Co-Occurrence Detection. <i>PLoS ONE</i> , 2014, 9, e95275.	2.5	6
48	Fitting hidden Markov models of protein domains to a target species: application to <i>Plasmodium falciparum</i> . <i>BMC Bioinformatics</i> , 2012, 13, 67.	2.6	14
49	EuPathDomains: The divergent domain database for eukaryotic pathogens. <i>Infection, Genetics and Evolution</i> , 2011, 11, 698-707.	2.3	8
50	Detection of new protein domains using co-occurrence: application to <i>Plasmodium falciparum</i> . <i>Bioinformatics</i> , 2009, 25, 3077-3083.	4.1	37