

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	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
2	The carbohydrate-active enzyme database: functions and literature. <i>Nucleic Acids Research</i> , 2022, 50, D571-D577.	14.5	813
3	Complex pectin metabolism by gut bacteria reveals novel catalytic functions. <i>Nature</i> , 2017, 544, 65-70.	27.8	447
4	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	17.5	414
5	Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014, 5, 3636.	12.8	371
6	Glycan complexity dictates microbial resource allocation in the large intestine. <i>Nature Communications</i> , 2015, 6, 7481.	12.8	328
7	Dietary pectic glycans are degraded by coordinated enzyme pathways in human colonic <i>Bacteroides</i> . <i>Nature Microbiology</i> , 2018, 3, 210-219.	13.3	263
8	<i>Bacteroidetes</i> use thousands of enzyme combinations to break down glycans. <i>Nature Communications</i> , 2019, 10, 2043.	12.8	238
9	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
10	Interspecies Competition Impacts Targeted Manipulation of Human Gut Bacteria by Fiber-Derived Glycans. <i>Cell</i> , 2019, 179, 59-73.e13.	28.9	224
11	Automatic prediction of polysaccharide utilization loci in <i>Bacteroidetes</i> species. <i>Bioinformatics</i> , 2015, 31, 647-655.	4.1	195
12	PULDB: the expanded database of Polysaccharide Utilization Loci. <i>Nucleic Acids Research</i> , 2018, 46, D677-D683.	14.5	191
13	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> , 2019, 116, 6063-6068.	7.1	154
14	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. <i>ISME Journal</i> , 2017, 11, 2538-2551.	9.8	120
15	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
16	A surface endogalactanase in <i>Bacteroides thetaiotaomicron</i> confers keystone status for arabinogalactan degradation. <i>Nature Microbiology</i> , 2018, 3, 1314-1326.	13.3	103
17	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.	7.1	99
18	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

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19	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
20	A bioinformatics analysis of 3400 lytic polysaccharide oxidases from family AA9. <i>Carbohydrate Research</i> , 2017, 448, 166-174.	2.3	55
21	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. <i>Nature Communications</i> , 2020, 11, 5773.	12.8	55
22	DoMosaics: software for domain arrangement visualization and domain-centric analysis of proteins. <i>Bioinformatics</i> , 2014, 30, 282-283.	4.1	52
23	Phenotypic and Genomic Diversification in Complex Carbohydrate-Degrading Human Gut Bacteria. <i>MSystems</i> , 2022, 7, e0094721.	3.8	40
24	A fibrolytic potential in the human ileum mucosal microbiota revealed by functional metagenomic. <i>Scientific Reports</i> , 2017, 7, 40248.	3.3	38
25	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> , 2017, 114, 4936-4941.	7.1	38
26	Detection of new protein domains using co-occurrence: application to <i>Plasmodium falciparum</i> . <i>Bioinformatics</i> , 2009, 25, 3077-3083.	4.1	37
27	Rapid similarity search of proteins using alignments of domain arrangements. <i>Bioinformatics</i> , 2014, 30, 274-281.	4.1	37
28	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
29	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
30	Investigating host-microbiome interactions by droplet based microfluidics. <i>Microbiome</i> , 2020, 8, 141.	11.1	33
31	The CAZy Database/the Carbohydrate-Active Enzyme (CAZy) Database: Principles and Usage Guidelines. , 2017, , 117-131.		27
32	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
33	An evolutionarily distinct family of polysaccharide lyases removes rhamnose capping of complex arabinogalactan proteins. <i>Journal of Biological Chemistry</i> , 2017, 292, 13271-13283.	3.4	26
34	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
35	Microbial liberation of N-methylserotonin from orange fiber in gnotobiotic mice and humans. <i>Cell</i> , 2022, 185, 2495-2509.e11.	28.9	26
36	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

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37	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. <i>Frontiers in Microbiology</i> , 2017, 8, 2504.	3.5	24
38	How do gut microbes break down dietary fiber?. <i>Trends in Biochemical Sciences</i> , 2014, 39, 156-158.	7.5	21
39	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
40	Comparative genomic analyses reveal diverse virulence factors and antimicrobial resistance mechanisms in clinical <i>Elizabethkingia meningoseptica</i> strains. <i>PLoS ONE</i> , 2019, 14, e0222648.	2.5	15
41	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
42	Harvesting of Prebiotic Fructooligosaccharides by Nonbeneficial Human Gut Bacteria. <i>MSphere</i> , 2020, 5, .	2.9	12
43	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
44	Isolation and Characterization of Extracellular Vesicles Secreted In Vitro by Porcine Microbiota. <i>Microorganisms</i> , 2020, 8, 983.	3.6	9
45	EuPathDomains: The divergent domain database for eukaryotic pathogens. <i>Infection, Genetics and Evolution</i> , 2011, 11, 698-707.	2.3	8
46	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
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	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
49	Functional exploration of the glycoside hydrolase family GH113. <i>PLoS ONE</i> , 2022, 17, e0267509.	2.5	5
50	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