

# Julien Tap

## List of Publications by Year in descending order

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41  
papers

28,993  
citations

270111

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h-index

325983

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46  
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46  
docs citations

46  
times ranked

33749  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Human Gut Microbiota in all its States: From Disturbance to Resilience. , 2022, , 161-178.		4
2	Drinking Water Source and Intake Are Associated with Distinct Gut Microbiota Signatures in US and UK Populations. Journal of Nutrition, 2022, 152, 171-182.	1.3	24
3	A posteriori dietary patterns better explain variations of the gut microbiome than individual markers in the American Gut Project. American Journal of Clinical Nutrition, 2022, 115, 432-443.	2.2	28
4	Human gut metatranscriptome changes induced by a fermented milk product are associated with improved tolerance to a flatulogenic diet. Computational and Structural Biotechnology Journal, 2022, 20, 1632-1641.	1.9	0
5	A novel stepwise integrative analysis pipeline reveals distinct microbiota-host interactions and link to symptoms in irritable bowel syndrome. Scientific Reports, 2021, 11, 5521.	1.6	4
6	Diet and gut microbiome interactions of relevance for symptoms in irritable bowel syndrome. Microbiome, 2021, 9, 74.	4.9	25
7	A Fermented Milk Product Containing B. lactis CNCM I-2494 Improves the Tolerance of a Plant-Based Diet in Patients with Disorders of Gut-Brain Interactions. Nutrients, 2021, 13, 4542.	1.7	1
8	Safety and functional enrichment of gut microbiome in healthy subjects consuming a multi-strain fermented milk product: a randomised controlled trial. Scientific Reports, 2020, 10, 15974.	1.6	18
9	A Fermented Milk Product with B. lactis CNCM I-2494 and Lactic Acid Bacteria Improves Gastrointestinal Comfort in Response to a Challenge Diet Rich in Fermentable Residues in Healthy Subjects. Nutrients, 2020, 12, 320.	1.7	7
10	Effects of the long-term storage of human fecal microbiota samples collected in RNAlater. Scientific Reports, 2019, 9, 601.	1.6	36
11	Evidence for an association of gut microbial Clostridia with brain functional connectivity and gastrointestinal sensorimotor function in patients with irritable bowel syndrome, based on tripartite network analysis. Microbiome, 2019, 7, 45.	4.9	83
12	Fasting breath H <sub>2</sub> and gut microbiota metabolic potential are associated with the response to a fermented milk product in irritable bowel syndrome. PLoS ONE, 2019, 14, e0214273.	1.1	12
13	Prediction of the intestinal resistome by a three-dimensional structure-based method. Nature Microbiology, 2019, 4, 112-123.	5.9	129
14	Fecal chromogranins and secretogranins are linked to the fecal and mucosal intestinal bacterial composition of IBS patients and healthy subjects. Scientific Reports, 2018, 8, 16821.	1.6	10
15	Altered intestinal antibacterial gene expression response profile in irritable bowel syndrome is linked to bacterial composition and immune activation. Neurogastroenterology and Motility, 2018, 30, e13468.	1.6	15
16	Faecal microbiota study reveals specific dysbiosis in spondyloarthritis. Annals of the Rheumatic Diseases, 2017, 76, 1614-1622.	0.5	266
17	Clostridia from the Gut Microbiome are Associated with Brain Functional Connectivity and Evoked Symptoms in IBS. Gastroenterology, 2017, 152, S40.	0.6	6
18	Identification of an Intestinal Microbiota Signature Associated With Severity of Irritable Bowel Syndrome. Gastroenterology, 2017, 152, 111-123.e8.	0.6	470

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19	Reply. <i>Clinical Gastroenterology and Hepatology</i> , 2016, 14, 1222-1223.	2.4	0
20	Lactulose Challenge Determines Visceral Sensitivity and Severity of Symptoms in Patients With Irritable Bowel Syndrome. <i>Clinical Gastroenterology and Hepatology</i> , 2016, 14, 226-233.e3.	2.4	38
21	Gut microbiota richness promotes its stability upon increased dietary fibre intake in healthy adults. <i>Environmental Microbiology</i> , 2015, 17, 4954-4964.	1.8	279
22	Metagenomics of the human intestinal tract: from who is there to what is done there. <i>Current Opinion in Food Science</i> , 2015, 4, 64-68.	4.1	12
23	The Gut Microbiota for Health Experts Exchange: An Online Network for Sharing Knowledge. <i>FASEB Journal</i> , 2015, 29, 909.4.	0.2	0
24	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014, 10, 766.	3.2	991
25	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
26	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
27	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
28	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
29	Gut microbiota after gastric bypass in human obesity: increased richness and associations of bacterial genera with adipose tissue genes. <i>American Journal of Clinical Nutrition</i> , 2013, 98, 16-24.	2.2	351
30	Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2013, 45, 172-179.	9.4	264
31	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013, 493, 45-50.	13.7	783
32	Individuality and temporal stability of the human gut microbiome. <i>Central Asian Journal of Global Health</i> , 2013, 2, 120.	0.6	6
33	Microbial Dysbiosis in Colorectal Cancer (CRC) Patients. <i>PLoS ONE</i> , 2011, 6, e16393.	1.1	706
34	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
35	Identification of NF- $\kappa$ B Modulation Capabilities within Human Intestinal Commensal Bacteria. <i>Journal of Biomedicine and Biotechnology</i> , 2011, 2011, 1-9.	3.0	66
36	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342

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37	Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. <i>Genome Research</i> , 2010, 20, 1605-1612.	2.4	228
38	Functional Metagenomics: A High Throughput Screening Method to Decipher Microbiota-Driven NF- $\kappa$ B Modulation in the Human Gut. <i>PLoS ONE</i> , 2010, 5, e13092.	1.1	72
39	Differential Adaptation of Human Gut Microbiota to Bariatric Surgery-Induced Weight Loss. <i>Diabetes</i> , 2010, 59, 3049-3057.	0.3	1,065
40	Comparative assessment of human and farm animal faecal microbiota using real-time quantitative PCR. <i>FEMS Microbiology Ecology</i> , 2009, 68, 351-362.	1.3	322
41	Towards the human intestinal microbiota phylogenetic core. <i>Environmental Microbiology</i> , 2009, 11, 2574-2584.	1.8	773