

# Julien Tap

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

28,993  
citations

236925

25  
h-index

289244

40  
g-index

46  
all docs

46  
docs citations

46  
times ranked

31065  
citing authors

#	ARTICLE	IF	CITATIONS
1	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	27.8	9,342
2	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	27.8	5,800
3	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	27.8	3,641
4	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	17.5	1,664
5	Differential Adaptation of Human Gut Microbiota to Bariatric Surgery-Induced Weight Loss. <i>Diabetes</i> , 2010, 59, 3049-3057.	0.6	1,065
6	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014, 10, 766.	7.2	991
7	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	17.5	909
8	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013, 493, 45-50.	27.8	783
9	Towards the human intestinal microbiota phylogenetic core. <i>Environmental Microbiology</i> , 2009, 11, 2574-2584.	3.8	773
10	Microbial Dysbiosis in Colorectal Cancer (CRC) Patients. <i>PLoS ONE</i> , 2011, 6, e16393.	2.5	706
11	Identification of an Intestinal Microbiota Signature Associated With Severity of Irritable Bowel Syndrome. <i>Gastroenterology</i> , 2017, 152, 111-123.e8.	1.3	470
12	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	19.0	442
13	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.	4.7	351
14	Comparative assessment of human and farm animal faecal microbiota using real-time quantitative PCR. <i>FEMS Microbiology Ecology</i> , 2009, 68, 351-362.	2.7	322
15	Gut microbiota richness promotes its stability upon increased dietary fibre intake in healthy adults. <i>Environmental Microbiology</i> , 2015, 17, 4954-4964.	3.8	279
16	Faecal microbiota study reveals specific dysbiosis in spondyloarthritis. <i>Annals of the Rheumatic Diseases</i> , 2017, 76, 1614-1622.	0.9	266
17	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.	21.4	264
18	Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. <i>Genome Research</i> , 2010, 20, 1605-1612.	5.5	228

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19	Prediction of the intestinal resistome by a three-dimensional structure-based method. <i>Nature Microbiology</i> , 2019, 4, 112-123.	13.3	129
20	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. <i>Microbiome</i> , 2019, 7, 45.	11.1	83
21	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.	2.5	72
22	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
23	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.	4.4	38
24	Effects of the long-term storage of human fecal microbiota samples collected in RNAlater. <i>Scientific Reports</i> , 2019, 9, 601.	3.3	36
25	A posteriori dietary patterns better explain variations of the gut microbiome than individual markers in the American Gut Project. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 432-443.	4.7	28
26	Diet and gut microbiome interactions of relevance for symptoms in irritable bowel syndrome. <i>Microbiome</i> , 2021, 9, 74.	11.1	25
27	Drinking Water Source and Intake Are Associated with Distinct Gut Microbiota Signatures in US and UK Populations. <i>Journal of Nutrition</i> , 2022, 152, 171-182.	2.9	24
28	Safety and functional enrichment of gut microbiome in healthy subjects consuming a multi-strain fermented milk product: a randomised controlled trial. <i>Scientific Reports</i> , 2020, 10, 15974.	3.3	18
29	Altered intestinal antibacterial gene expression response profile in irritable bowel syndrome is linked to bacterial composition and immune activation. <i>Neurogastroenterology and Motility</i> , 2018, 30, e13468.	3.0	15
30	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.	8.0	12
31	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. <i>PLoS ONE</i> , 2019, 14, e0214273.	2.5	12
32	Fecal chromogranins and secretogranins are linked to the fecal and mucosal intestinal bacterial composition of IBS patients and healthy subjects. <i>Scientific Reports</i> , 2018, 8, 16821.	3.3	10
33	A Fermented Milk Product with <i>B. lactis</i> CNCM I-2494 and Lactic Acid Bacteria Improves Gastrointestinal Comfort in Response to a Challenge Diet Rich in Fermentable Residues in Healthy Subjects. <i>Nutrients</i> , 2020, 12, 320.	4.1	7
34	Clostridia from the Gut Microbiome are Associated with Brain Functional Connectivity and Evoked Symptoms in IBS. <i>Gastroenterology</i> , 2017, 152, S40.	1.3	6
35	Individuality and temporal stability of the human gut microbiome. <i>Central Asian Journal of Global Health</i> , 2013, 2, 120.	0.6	6
36	The Human Gut Microbiota in all its States: From Disturbance to Resilience. , 2022, , 161-178.		4

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37	A novel stepwise integrative analysis pipeline reveals distinct microbiota-host interactions and link to symptoms in irritable bowel syndrome. <i>Scientific Reports</i> , 2021, 11, 5521.	3.3	4
38	A Fermented Milk Product Containing <i>B. lactis</i> CNCM I-2494 Improves the Tolerance of a Plant-Based Diet in Patients with Disorders of Gut-Brain Interactions. <i>Nutrients</i> , 2021, 13, 4542.	4.1	1
39	Reply. <i>Clinical Gastroenterology and Hepatology</i> , 2016, 14, 1222-1223.	4.4	0
40	The Gut Microbiota for Health Experts Exchange: An Online Network for Sharing Knowledge. <i>FASEB Journal</i> , 2015, 29, 909.4.	0.5	0
41	Human gut metatranscriptome changes induced by a fermented milk product are associated with improved tolerance to a flatulogenic diet. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1632-1641.	4.1	0