## Paul Igor Costea

## List of Publications by Citations

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Version: 2024-04-09

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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.

22 7,572 21 24 g-index

24 10,863 20.5 5.03 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
22	Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , <b>2015</b> , 348, 1261359	33.3	1261
21	Environment dominates over host genetics in shaping human gut microbiota. <i>Nature</i> , <b>2018</b> , 555, 210-2	<b>15</b> 50.4	1170
20	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , <b>2015</b> , 528, 262-266	50.4	1107
19	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. <i>Science</i> , <b>2016</b> , 353, 78-82	33.3	944
18	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 766	12.2	575
17	Salt-responsive gut commensal modulates T17 axis and disease. <i>Nature</i> , <b>2017</b> , 551, 585-589	50.4	553
16	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , <b>2018</b> , 3, 8-16	26.6	387
15	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 1069-1076	44.5	355
14	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , <b>2016</b> , 352, 586-9	33.3	326
13	Extensive transmission of microbes along the gastrointestinal tract. ELife, 2019, 8,	8.9	158
12	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , <b>2019</b> , 10, 1014	17.4	134
11	Similarity of the dog and human gut microbiomes in gene content and response to diet. <i>Microbiome</i> , <b>2018</b> , 6, 72	16.6	117
10	Temporal and technical variability of human gut metagenomes. <i>Genome Biology</i> , <b>2015</b> , 16, 73	18.3	108
9	Subspecies in the global human gut microbiome. <i>Molecular Systems Biology</i> , <b>2017</b> , 13, 960	12.2	69
8	metaSNV: A tool for metagenomic strain level analysis. <i>PLoS ONE</i> , <b>2017</b> , 12, e0182392	3.7	64
7	The microbiomes of blowflies and houseflies as bacterial transmission reservoirs. <i>Scientific Reports</i> , <b>2017</b> , 7, 16324	4.9	63
6	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , <b>2019</b> , 68, 1781-1790	19.2	33

135, 71-79

5	A fair comparison. <i>Nature Methods</i> , <b>2014</b> , 11, 359	21.6	33
4	TagGD: fast and accurate software for DNA Tag generation and demultiplexing. <i>PLoS ONE</i> , <b>2013</b> , 8, e57	′5 <del>2.†</del>	33
3	Comprehensive analysis of the genome transcriptome and proteome landscapes of three tumor cell lines. <i>Genome Medicine</i> , <b>2012</b> , 4, 86	14.4	31
2	Metagenomic analysis of gut microbial communities from a Central Asian population. <i>BMJ Open</i> , <b>2018</b> , 8, e021682	3	23
1	Microbial induced mineral precipitations caused by nitrate treatment for souring control during microbial enhanced oil recovery (MEOR). International Biodeterioration and Biodegradation, 2018,	4.8	14