

Takuji Yamada

List of Publications by Year in Descending Order

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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.

42
papers

14,195
citations

19
h-index

49
g-index

49
ext. papers

17,954
ext. citations

15.2
avg, IF

5.05
L-index

#	Paper	IF	Citations
42	Surgical Treatment for Colorectal Cancer Partially Restores Gut Microbiome and Metabolome Traits.. <i>MSystems</i> , 2022 , e0001822	7.6	2
41	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
40	spp. promotes branched-chain amino acid catabolism in brown fat and inhibits obesity. <i>IScience</i> , 2021 , 24, 103342	6.1	6
39	The Nutritional Efficacy of Supplementation Depends on the Individual Gut Environment: A Randomised Control Study. <i>Frontiers in Nutrition</i> , 2021 , 8, 648073	6.2	0
38	The relationships between microbiota and the amino acids and organic acids in commercial vegetable pickle fermented in rice-bran beds. <i>Scientific Reports</i> , 2021 , 11, 1791	4.9	2
37	Identification of strains for gut microbiome-based intervention in Alzheimer's-type dementia. <i>Cell Reports Medicine</i> , 2021 , 2, 100398	18	5
36	Analysis of genomic characteristics and their influence on metabolism in <i>Aspergillus luchuensis</i> albino mutants using genome sequencing. <i>Fungal Genetics and Biology</i> , 2021 , 155, 103601	3.9	1
35	Variation and transmission of the human gut microbiota across multiple familial generations.. <i>Nature Microbiology</i> , 2021 ,	26.6	4
34	Metabolomic LC-MS/MS analyses and meta 16S rRNA gene analyses on cecal feces of Japanese rock ptarmigans reveal fundamental differences between semi-wild and captive raised individuals. <i>Journal of Veterinary Medical Science</i> , 2020 , 82, 1165-1172	1.1	2
33	Significance of the gut microbiome in multistep colorectal carcinogenesis. <i>Cancer Science</i> , 2020 , 111, 766-773	6.9	27
32	Influence of gastrectomy for gastric cancer treatment on faecal microbiome and metabolome profiles. <i>Gut</i> , 2020 , 69, 1404-1415	19.2	29
31	Essential role of the family-dosage in DiGeorge-like anomaly and metabolic homeostasis. <i>Life Science Alliance</i> , 2020 , 3,	5.8	2
30	dominates the gut microbiome of the Asian palm civet that produces kopi luwak. <i>PeerJ</i> , 2020 , 8, e9579	3.1	4
29	A possible beneficial effect of <i>Bacteroides</i> on faecal lipopolysaccharide activity and cardiovascular diseases. <i>Scientific Reports</i> , 2020 , 10, 13009	4.9	16
28	Targeted enzyme gene re-positioning: A computational approach for discovering alternative bacterial enzymes for the synthesis of plant-specific secondary metabolites. <i>Metabolic Engineering Communications</i> , 2019 , 9, e00102	6.5	1
27	Metagenomic and metabolomic analyses reveal distinct stage-specific phenotypes of the gut microbiota in colorectal cancer. <i>Nature Medicine</i> , 2019 , 25, 968-976	50.5	328
26	FuncTree2: an interactive radial tree for functional hierarchies and omics data visualization. <i>Bioinformatics</i> , 2019 , 35, 4519-4521	7.2	6

25	Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. <i>Nature Medicine</i> , 2019 , 25, 667-678	50.5	289
24	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019 , 25, 679-689	50.5	353
23	Role of coprophagy in the cecal microbiome development of an herbivorous bird Japanese rock ptarmigan. <i>Journal of Veterinary Medical Science</i> , 2019 , 81, 1389-1399	1.1	11
22	Evolution of <i>Aspergillus oryzae</i> before and after domestication inferred by large-scale comparative genomic analysis. <i>DNA Research</i> , 2019 , 26, 465-472	4.5	10
21	Minor taxa in human skin microbiome contribute to the personal identification. <i>PLoS ONE</i> , 2018 , 13, e0199947	3.7	14
20	Cecal Microbiome Analyses on Wild Japanese Rock Ptarmigans () Reveals High Level of Coexistence of Lactic Acid Bacteria and Lactate-Utilizing Bacteria. <i>Microorganisms</i> , 2018 , 6,	4.9	4
19	VITCOMIC2: visualization tool for the phylogenetic composition of microbial communities based on 16S rRNA gene amplicons and metagenomic shotgun sequencing. <i>BMC Systems Biology</i> , 2018 , 12, 30	3.5	11
18	Comprehensive microbiome analysis of tonsillar crypts in IgA nephropathy. <i>Nephrology Dialysis Transplantation</i> , 2017 , 32, 2072-2079	4.3	28
17	High-affinity monoclonal IgA regulates gut microbiota and prevents colitis in mice. <i>Nature Microbiology</i> , 2016 , 1, 16103	26.6	96
16	Identification of Enzyme Genes Using Chemical Structure Alignments of Substrate-Product Pairs. <i>Journal of Chemical Information and Modeling</i> , 2016 , 56, 510-6	6.1	8
15	High stability of faecal microbiome composition in guanidine thiocyanate solution at room temperature and robustness during colonoscopy. <i>Gut</i> , 2016 , 65, 1574-5	19.2	31
14	DomSign: a top-down annotation pipeline to enlarge enzyme space in the protein universe. <i>BMC Bioinformatics</i> , 2015 , 16, 96	3.6	6
13	The transcription factor ATF7 mediates lipopolysaccharide-induced epigenetic changes in macrophages involved in innate immunological memory. <i>Nature Immunology</i> , 2015 , 16, 1034-43	19.1	113
12	FuncTree: Functional Analysis and Visualization for Large-Scale Omics Data. <i>PLoS ONE</i> , 2015 , 10, e0126967	6.7	23
11	Inter-Individual Differences in the Oral Bacteriome Are Greater than Intra-Day Fluctuations in Individuals. <i>PLoS ONE</i> , 2015 , 10, e0131607	3.7	38
10	Classification and quantification of bacteriophage taxa in human gut metagenomes. <i>ISME Journal</i> , 2014 , 8, 1391-402	11.9	102
9	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014 , 10, 766	12.2	575
8	CLAST: CUDA implemented large-scale alignment search tool. <i>BMC Bioinformatics</i> , 2014 , 15, 406	3.6	7

7	Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. <i>Molecular Systems Biology</i> , 2012 , 8, 581	12.2	25
6	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
5	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010 , 464, 59-65	50.4	7044
4	Evolution of biomolecular networks: lessons from metabolic and protein interactions. <i>Nature Reviews Molecular Cell Biology</i> , 2009 , 10, 791-803	48.7	210
3	iPath: interactive exploration of biochemical pathways and networks. <i>Trends in Biochemical Sciences</i> , 2008 , 33, 101-3	10.3	156
2	KEGG Atlas mapping for global analysis of metabolic pathways. <i>Nucleic Acids Research</i> , 2008 , 36, W423-620.1	20.1	343
1	Resistant maltodextrin intake reduces virulent metabolites in the gut environment: randomized control study in a Japanese cohort		2