

Takuji Yamada

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

20,435
citations

236612

25
h-index

264894

42
g-index

49
all docs

49
docs citations

49
times ranked

24888
citing authors

#	ARTICLE	IF	CITATIONS
1	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
2	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
3	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014, 10, 766.	3.2	991
4	Metagenomic and metabolomic analyses reveal distinct stage-specific phenotypes of the gut microbiota in colorectal cancer. <i>Nature Medicine</i> , 2019, 25, 968-976.	15.2	748
5	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019, 25, 679-689.	15.2	734
6	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.	15.2	602
7	KEGG Atlas mapping for global analysis of metabolic pathways. <i>Nucleic Acids Research</i> , 2008, 36, W423-W426.	6.5	445
8	Evolution of biomolecular networks – lessons from metabolic and protein interactions. <i>Nature Reviews Molecular Cell Biology</i> , 2009, 10, 791-803.	16.1	257
9	iPath: interactive exploration of biochemical pathways and networks. <i>Trends in Biochemical Sciences</i> , 2008, 33, 101-103.	3.7	216
10	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
11	The transcription factor ATF7 mediates lipopolysaccharide-induced epigenetic changes in macrophages involved in innate immunological memory. <i>Nature Immunology</i> , 2015, 16, 1034-1043.	7.0	149
12	High-affinity monoclonal IgA regulates gut microbiota and prevents colitis in mice. <i>Nature Microbiology</i> , 2016, 1, 16103.	5.9	128
13	Classification and quantification of bacteriophage taxa in human gut metagenomes. <i>ISME Journal</i> , 2014, 8, 1391-1402.	4.4	127
14	Influence of gastrectomy for gastric cancer treatment on faecal microbiome and metabolome profiles. <i>Gut</i> , 2020, 69, 1404-1415.	6.1	84
15	<i>Bacteroides</i> spp. promotes branched-chain amino acid catabolism in brown fat and inhibits obesity. <i>IScience</i> , 2021, 24, 103342.	1.9	58
16	Significance of the gut microbiome in multistep colorectal carcinogenesis. <i>Cancer Science</i> , 2020, 111, 766-773.	1.7	51
17	Inter-Individual Differences in the Oral Bacteriome Are Greater than Intra-Day Fluctuations in Individuals. <i>PLoS ONE</i> , 2015, 10, e0131607.	1.1	47
18	High stability of faecal microbiome composition in guanidine thiocyanate solution at room temperature and robustness during colonoscopy. <i>Gut</i> , 2016, 65, 1574-1575.	6.1	43

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19	Identification of <i>Faecalibacterium prausnitzii</i> strains for gut microbiome-based intervention in Alzheimer's-type dementia. <i>Cell Reports Medicine</i> , 2021, 2, 100398.	3.3	42
20	Comprehensive microbiome analysis of tonsillar crypts in IgA nephropathy. <i>Nephrology Dialysis Transplantation</i> , 2017, 32, gfw343.	0.4	40
21	A possible beneficial effect of <i>Bacteroides</i> on faecal lipopolysaccharide activity and cardiovascular diseases. <i>Scientific Reports</i> , 2020, 10, 13009.	1.6	38
22	Variation and transmission of the human gut microbiota across multiple familial generations. <i>Nature Microbiology</i> , 2022, 7, 87-96.	5.9	32
23	FuncTree: Functional Analysis and Visualization for Large-Scale Omics Data. <i>PLoS ONE</i> , 2015, 10, e0126967.	1.1	30
24	Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. <i>Molecular Systems Biology</i> , 2012, 8, 581.	3.2	29
25	Minor taxa in human skin microbiome contribute to the personal identification. <i>PLoS ONE</i> , 2018, 13, e0199947.	1.1	26
26	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.	1.5	26
27	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.	3.0	23
28	Cecal Microbiome Analyses on Wild Japanese Rock Ptarmigans (<i>Lagopus muta japonica</i>) Reveals High Level of Coexistence of Lactic Acid Bacteria and Lactate-Utilizing Bacteria. <i>Microorganisms</i> , 2018, 6, 77.	1.6	21
29	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.	0.3	20
30	Identification of Enzyme Genes Using Chemical Structure Alignments of Substrate-Product Pairs. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 510-516.	2.5	17
31	FuncTree2: an interactive radial tree for functional hierarchies and omics data visualization. <i>Bioinformatics</i> , 2019, 35, 4519-4521.	1.8	15
32	CLAST: CUDA implemented large-scale alignment search tool. <i>BMC Bioinformatics</i> , 2014, 15, 406.	1.2	13
33	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.	1.6	11
34	<i>Gluconobacter</i> dominates the gut microbiome of the Asian palm civet <i>Paradoxurus hermaphroditus</i> that produces kopi luwak. <i>PeerJ</i> , 2020, 8, e9579.	0.9	10
35	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.	0.3	8
36	The Nutritional Efficacy of <i>Chlorella</i> Supplementation Depends on the Individual Gut Environment: A Randomised Control Study. <i>Frontiers in Nutrition</i> , 2021, 8, 648073.	1.6	7

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37	Essential role of the <i>Crk</i> family-dosage in DiGeorge-like anomaly and metabolic homeostasis. Life Science Alliance, 2020, 3, e201900635.	1.3	7
38	DomSign: a top-down annotation pipeline to enlarge enzyme space in the protein universe. BMC Bioinformatics, 2015, 16, 96.	1.2	6
39	Analysis of genomic characteristics and their influence on metabolism in <i>Aspergillus luchuensis</i> albino mutants using genome sequencing. Fungal Genetics and Biology, 2021, 155, 103601.	0.9	6
40	Resistant Maltodextrin Intake Reduces Virulent Metabolites in the Gut Environment: A Randomized Control Study in a Japanese Cohort. Frontiers in Microbiology, 2022, 13, .	1.5	4
41	Targeted enzyme gene re-positioning: A computational approach for discovering alternative bacterial enzymes for the synthesis of plant-specific secondary metabolites. Metabolic Engineering Communications, 2019, 9, e00102.	1.9	3
42	Surgical Treatment for Colorectal Cancer Partially Restores Gut Microbiome and Metabolome Traits. MSystems, 2022, 7, e0001822.	1.7	3