Takuji Yamada

List of Publications by Citations

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	A human gut microbial gene catalogue established by metagenomic sequencing. *Nature*, **2010**, 464, 59-65	50.4	7044
41	Enterotypes of the human gut microbiome. *Nature*, **2011**, 473, 174-80	50.4	4240
40	Potential of fecal microbiota for early-stage detection of colorectal cancer. *Molecular Systems Biology*, **2014**, 10, 766	12.2	575
39	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. *Nature Medicine*, **2019**, 25, 679-689	50.5	353
38	KEGG Atlas mapping for global analysis of metabolic pathways. *Nucleic Acids Research*, **2008**, 36, W423-6	20.1	343
37	Metagenomic and metabolomic analyses reveal distinct stage-specific phenotypes of the gut microbiota in colorectal cancer. *Nature Medicine*, **2019**, 25, 968-976	50.5	328
36	Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. *Nature Medicine*, **2019**, 25, 667-678	50.5	289
35	Evolution of biomolecular networks: lessons from metabolic and protein interactions. *Nature Reviews Molecular Cell Biology*, **2009**, 10, 791-803	48.7	210
34	iPath: interactive exploration of biochemical pathways and networks. *Trends in Biochemical Sciences* , **2008**, 33, 101-3	10.3	156
33	The transcription factor ATF7 mediates lipopolysaccharide-induced epigenetic changes in macrophages involved in innate immunological memory. *Nature Immunology*, **2015**, 16, 1034-43	19.1	113
32	Classification and quantification of bacteriophage taxa in human gut metagenomes. *ISME Journal*, **2014**, 8, 1391-402	11.9	102
31	High-affinity monoclonal IgA regulates gut microbiota and prevents colitis in mice. *Nature Microbiology*, **2016**, 1, 16103	26.6	96
30	Inter-Individual Differences in the Oral Bacteriome Are Greater than Intra-Day Fluctuations in Individuals. *PLoS ONE*, **2015**, 10, e0131607	3.7	38
29	High stability of faecal microbiome composition in guanidine thiocyanate solution at room temperature and robustness during colonoscopy. *Gut*, **2016**, 65, 1574-5	19.2	31
28	Influence of gastrectomy for gastric cancer treatment on faecal microbiome and metabolome profiles. *Gut*, **2020**, 69, 1404-1415	19.2	29
27	Comprehensive microbiome analysis of tonsillar crypts in IgA nephropathy. *Nephrology Dialysis Transplantation*, **2017**, 32, 2072-2079	4.3	28
26	Significance of the gut microbiome in multistep colorectal carcinogenesis. *Cancer Science*, **2020**, 111, 766-773	6.9	27

25	Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. *Molecular Systems Biology*, **2012**, 8, 581	12.2	25
24	FuncTree: Functional Analysis and Visualization for Large-Scale Omics Data. *PLoS ONE*, **2015**, 10, e0126967	3.7	23
23	Reporting guidelines for human microbiome research: the STORMS checklist. *Nature Medicine*, **2021** , 27, 1885-1892	50.5	19
22	A possible beneficial effect of Bacteroides on faecal lipopolysaccharide activity and cardiovascular diseases. *Scientific Reports*, **2020**, 10, 13009	4.9	16
21	Minor taxa in human skin microbiome contribute to the personal identification. *PLoS ONE*, **2018**, 13, e0199947	3.7	14
20	VITCOMIC2: visualization tool for the phylogenetic composition of microbial communities based on 16S rRNA gene amplicons and metagenomic shotgun sequencing. *BMC Systems Biology*, **2018**, 12, 30	3.5	11
19	Role of coprophagy in the cecal microbiome development of an herbivorous bird Japanese rock ptarmigan. *Journal of Veterinary Medical Science*, **2019**, 81, 1389-1399	1.1	11
18	Evolution of Aspergillus oryzae before and after domestication inferred by large-scale comparative genomic analysis. *DNA Research*, **2019**, 26, 465-472	4.5	10
17	Identification of Enzyme Genes Using Chemical Structure Alignments of Substrate-Product Pairs. *Journal of Chemical Information and Modeling*, **2016**, 56, 510-6	6.1	8
16	CLAST: CUDA implemented large-scale alignment search tool. *BMC Bioinformatics*, **2014**, 15, 406	3.6	7
15	FuncTree2: an interactive radial tree for functional hierarchies and omics data visualization. *Bioinformatics*, **2019**, 35, 4519-4521	7.2	6
14	DomSign: a top-down annotation pipeline to enlarge enzyme space in the protein universe. *BMC Bioinformatics*, **2015**, 16, 96	3.6	6
13	spp. promotes branched-chain amino acid catabolism in brown fat and inhibits obesity. *IScience*, **2021**, 24, 103342	6.1	6
12	Identification of strains for gut microbiome-based intervention in Alzheimer's-type dementia. *Cell Reports Medicine*, **2021**, 2, 100398	18	5
11	Cecal Microbiome Analyses on Wild Japanese Rock Ptarmigans () Reveals High Level of Coexistence of Lactic Acid Bacteria and Lactate-Utilizing Bacteria. *Microorganisms*, **2018**, 6,	4.9	4
10	dominates the gut microbiome of the Asian palm civet that produces kopi luwak. *PeerJ*, **2020**, 8, e9579	3.1	4
9	Variation and transmission of the human gut microbiota across multiple familial generations.. *Nature Microbiology*, **2021**,	26.6	4
8	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. *Journal of Veterinary Medical Science*, **2020**, 82, 1165-1172	1.1	2

7	Essential role of the family-dosage in DiGeorge-like anomaly and metabolic homeostasis. *Life Science Alliance*, **2020**, 3,	5.8	2
6	Resistant maltodextrin intake reduces virulent metabolites in the gut environment: randomized control study in a Japanese cohort		2
5	The relationships between microbiota and the amino acids and organic acids in commercial vegetable pickle fermented in rice-bran beds. *Scientific Reports*, **2021**, 11, 1791	4.9	2
4	Surgical Treatment for Colorectal Cancer Partially Restores Gut Microbiome and Metabolome Traits.. *MSystems*, **2022**, e0001822	7.6	2
3	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	6.5	1
2	Analysis of genomic characteristics and their influence on metabolism in Aspergillus luchuensis albino mutants using genome sequencing. *Fungal Genetics and Biology*, **2021**, 155, 103601	3.9	1
1	The Nutritional Efficacy of Supplementation Depends on the Individual Gut Environment: A Randomised Control Study. *Frontiers in Nutrition*, **2021**, 8, 648073	6.2	0