

Hiroshi Mori

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

3,854
citations

257450

24
h-index

133252

59
g-index

62
all docs

62
docs citations

62
times ranked

6187
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Metagenomics Revealed Commonly Enriched Gene Sets in Human Gut Microbiomes. DNA Research, 2007, 14, 169-181.	3.4	760
2	Klebsormidium flaccidum genome reveals primary factors for plant terrestrial adaptation. Nature Communications, 2014, 5, 3978.	12.8	532
3	Design and Experimental Application of a Novel Non-Degenerate Universal Primer Set that Amplifies Prokaryotic 16S rRNA Genes with a Low Possibility to Amplify Eukaryotic rRNA Genes. DNA Research, 2014, 21, 217-227.	3.4	432
4	A key genetic factor for fucosyllactose utilization affects infant gut microbiota development. Nature Communications, 2016, 7, 11939.	12.8	284
5	<scp>Meta-Analysis</scp> of Gut Dysbiosis in Parkinson's Disease. Movement Disorders, 2020, 35, 1626-1635.	3.9	208
6	Key bacterial taxa and metabolic pathways affecting gut short-chain fatty acid profiles in early life. ISME Journal, 2021, 15, 2574-2590.	9.8	131
7	High-affinity monoclonal IgA regulates gut microbiota and prevents colitis in mice. Nature Microbiology, 2016, 1, 16103.	13.3	128
8	Phylogenomics and Morphology of Extinct Paleognaths Reveal the Origin and Evolution of the Ratites. Current Biology, 2017, 27, 68-77.	3.9	123
9	Genome-Organizing Factors Top2 and Hmo1 Prevent Chromosome Fragility at Sites of S phase Transcription. Cell, 2009, 138, 870-884.	28.9	101
10	R-Spondin1 expands Paneth cells and prevents dysbiosis induced by graft-versus-host disease. Journal of Experimental Medicine, 2017, 214, 3507-3518.	8.5	96
11	Bipolar dispersal of red-snow algae. Nature Communications, 2018, 9, 3094.	12.8	75
12	Short-Chain Fatty Acid-Producing Gut Microbiota Is Decreased in Parkinson's Disease but Not in Rapid-Eye-Movement Sleep Behavior Disorder. MSystems, 2020, 5, .	3.8	63
13	Microbial interaction between the succinate-utilizing bacterium <i>Phascolarctobacterium faecium</i> and the gut commensal <i>Bacteroides thetaiotaomicron</i> . MicrobiologyOpen, 2020, 9, e1111.	3.0	54
14	High-resolution genetic analysis of the requirements for horizontal transmission of the ESBL plasmid from Escherichia coli O104:H4. Nucleic Acids Research, 2015, 43, 348-360.	14.5	53
15	Differently localized lysophosphatidic acid acyltransferases crucial for triacylglycerol biosynthesis in the oleaginous alga <i>Nannochloropsis</i> . Plant Journal, 2017, 90, 547-559.	5.7	52
16	Intestinal IgA as a modulator of the gut microbiota. Gut Microbes, 2017, 8, 486-492.	9.8	49
17	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. Journal of Biomedical Semantics, 2014, 5, 5.	1.6	47
18	Quantification of hydrogen production by intestinal bacteria that are specifically dysregulated in Parkinson's disease. PLoS ONE, 2018, 13, e0208313.	2.5	41

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19	Comprehensive microbiome analysis of tonsillar crypts in IgA nephropathy. <i>Nephrology Dialysis Transplantation</i> , 2017, 32, gfw343.	0.7	40
20	Time-series metagenomic analysis reveals robustness of soil microbiome against chemical disturbance. <i>DNA Research</i> , 2015, 22, 413-424.	3.4	39
21	Ecophysiology of <i>Thioploca ingrica</i> as revealed by the complete genome sequence supplemented with proteomic evidence. <i>ISME Journal</i> , 2015, 9, 1166-1176.	9.8	35
22	Establishment of a multi-species biofilm model and metatranscriptomic analysis of biofilm and planktonic cell communities. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 7263-7279.	3.6	34
23	FuncTree: Functional Analysis and Visualization for Large-Scale Omics Data. <i>PLoS ONE</i> , 2015, 10, e0126967.	2.5	30
24	Gut Bacterial Species Distinctively Impact Host Purine Metabolites during Aging in <i>Drosophila</i> . <i>IScience</i> , 2020, 23, 101477.	4.1	28
25	The Relationship Between Microbial Community Structures and Environmental Parameters Revealed by Metagenomic Analysis of Hot Spring Water in the Kirishima Area, Japan. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 202.	4.1	26
26	Minor taxa in human skin microbiome contribute to the personal identification. <i>PLoS ONE</i> , 2018, 13, e0199947.	2.5	26
27	VITCOMIC: visualization tool for taxonomic compositions of microbial communities based on 16S rRNA gene sequences. <i>BMC Bioinformatics</i> , 2010, 11, 332.	2.6	25
28	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
29	Next-Generation Sequencing of an 88-Year-Old Specimen of the Poorly Known Species <i>Liagora japonica</i> (Nemaliales, Rhodophyta) Supports the Recognition of <i>Otohimella</i> gen. nov.. <i>PLoS ONE</i> , 2016, 11, e0158944.	2.5	21
30	Local Necrotic Cells Trigger Systemic Immune Activation via Gut Microbiome Dysbiosis in <i>Drosophila</i> . <i>Cell Reports</i> , 2020, 32, 107938.	6.4	20
31	Redox stratification within cryoconite granules influences the nitrogen cycle on glaciers. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	19
32	<i>Coprobacter secundus</i> subsp. <i>similis</i> subsp. nov. and <i>Solibaculum mannosilyticum</i> gen. nov., sp. nov., isolated from human feces. <i>Microbiology and Immunology</i> , 2021, 65, 245-256.	1.4	19
33	Asymmetric reproductive isolation during simultaneous reciprocal mating in pulmonates. <i>Biology Letters</i> , 2009, 5, 240-243.	2.3	18
34	<i>Blastochloris tepida</i> , sp. nov., a thermophilic species of the bacteriochlorophyll b-containing genus <i>Blastochloris</i> . <i>Archives of Microbiology</i> , 2019, 201, 1351-1359.	2.2	18
35	<i>Dialister hominis</i> sp. nov., isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 589-595.	1.7	18
36	<i>Amedibacterium intestinale</i> gen. nov., sp. nov., isolated from human faeces, and reclassification of <i>Eubacterium dolichum</i> Moore et al. 1976 (Approved Lists 1980) as <i>Amedibacillus dolichus</i> gen. nov., comb. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3656-3664.	1.7	18

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37	Whole-Genome Sequence of the Purple Photosynthetic Bacterium <i>Rhodovulum sulfidophilum</i> Strain W4. <i>Genome Announcements</i> , 2013, 1, .	0.8	16
38	Distinct responsiveness to rifaximin in patients with hepatic encephalopathy depends on functional gut microbial species. <i>Hepatology Communications</i> , 2022, 6, 2090-2104.	4.3	15
39	CLAST: CUDA implemented large-scale alignment search tool. <i>BMC Bioinformatics</i> , 2014, 15, 406.	2.6	13
40	Comparative genomics of <i>Parolsenella catena</i> and <i>Libanicoccus massiliensis</i> : Reclassification of <i>Libanicoccus massiliensis</i> as <i>Parolsenella massiliensis</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1123-1129.	1.7	11
41	Latent environment allocation of microbial community data. <i>PLoS Computational Biology</i> , 2018, 14, e1006143.	3.2	10
42	<i>Adlercreutzia hattorii</i> sp. nov., an equol non-producing bacterium isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	10
43	Metagenomics reveals global-scale contrasts in nitrogen cycling and cyanobacterial light-harvesting mechanisms in glacier cryoconite. <i>Microbiome</i> , 2022, 10, 50.	11.1	10
44	Aberrant mucosal immunoreaction to tonsillar microbiota in immunoglobulin A nephropathy. <i>Nephrology Dialysis Transplantation</i> , 2021, 36, 75-86.	0.7	9
45	Meeting Report: Hackathon-Workshop on Darwin Core and MIxS Standards Alignment (February 2012). <i>Standards in Genomic Sciences</i> , 2012, 7, 166-170.	1.5	8
46	Ancient DNA reveals multiple origins and migration waves of extinct Japanese brown bear lineages. <i>Royal Society Open Science</i> , 2021, 8, 210518.	2.4	8
47	Complete Genome Sequence of a Phenanthrene Degradar, <i>Mycobacterium</i> sp. Strain EPa45 (NBRC) Tj ETQq1 1 0.784314 rgBT /Overlaid	0.8	7
48	Comprehensive discovery of CRISPR-targeted terminally redundant sequences in the human gut metagenome: Viruses, plasmids, and more. <i>PLoS Computational Biology</i> , 2021, 17, e1009428.	3.2	7
49	DomSign: a top-down annotation pipeline to enlarge enzyme space in the protein universe. <i>BMC Bioinformatics</i> , 2015, 16, 96.	2.6	6
50	Genomic Analyses of <i>Bifidobacterium moukalabense</i> Reveal Adaptations to Frugivore/Folivore Feeding Behavior. <i>Microorganisms</i> , 2019, 7, 99.	3.6	6
51	TogoGenome/TogoStanza: modularized Semantic Web genome database. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	6
52	PZLAST: an ultra-fast amino acid sequence similarity search server against public metagenomes. <i>Bioinformatics</i> , 2021, 37, 3944-3946.	4.1	5
53	BioHackathon 2015: Semantics of data for life sciences and reproducible research. <i>F1000Research</i> , 2020, 9, 136.	1.6	5
54	Paleogenomics reveals independent and hybrid origins of two morphologically distinct wolf lineages endemic to Japan. <i>Current Biology</i> , 2022, 32, 2494-2504.e5.	3.9	5

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55	Draft Genome Sequence of <i>Clostridium tagluense</i> Strain A121 ^T , Isolated from a Permafrost Core in the Canadian High Arctic. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
56	Hadean Primordial Metabolism Pathway Driven by a Nuclear Geysir. <i>Journal of Geography (Chigaku)</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.3	2
57	Complete Genome Sequence of <i>Faecalibacillus intestinalis</i> JCM 34082, Isolated from Feces from a Healthy Japanese Female. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
58	PZLAST: an ultra-fast sequence similarity search tool implemented on a MIMD processor. <i>International Journal of Networking and Computing</i> , 2022, 12, 446-466.	0.4	1
59	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , 0, 8, 1677.	1.6	0
60	PZLAST: an ultra-fast sequence similarity search tool implemented on a MIMD processor. , 2021, , .		0