Hiroshi Mori

List of Publications by Year
in descending order

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	Metagenomics reveals global-scale contrasts in nitrogen cycling and cyanobacterial light-harvesting mechanisms in glacier cryoconite. Microbiome, 2022, 10, 50.	11.1	10
2	Distinct responsiveness to rifaximin in patients with hepatic encephalopathy depends on functional gut microbial species. Hepatology Communications, 2022, 6, 2090-2104.	4.3	15
3	Paleogenomics reveals independent and hybrid origins of two morphologically distinct wolf lineages endemic to Japan. Current Biology, 2022, 32, 2494-2504.e5.	3.9	5
4	PZLAST: an ultra-fast sequence similarity search tool implemented on a MIMD processor. International Journal of Networking and Computing, 2022, 12, 446-466.	0.4	1
5	Aberrant mucosal immunoreaction to tonsillar microbiota in immunoglobulin A nephropathy. Nephrology Dialysis Transplantation, 2021, 36, 75-86.	0.7	9
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	Coprobacter secundus subsp. similis subsp. nov. and Solibaculum mannosilyticum gen. nov., sp. nov., isolated from human feces. Microbiology and Immunology, 2021, 65, 245-256.	1.4	19
8	PZLAST: an ultra-fast amino acid sequence similarity search server against public metagenomes. Bioinformatics, 2021, 37, 3944-3946.	4.1	5
9	Ancient DNA reveals multiple origins and migration waves of extinct Japanese brown bear lineages. Royal Society Open Science, 2021, 8, 210518.	2.4	8
10	Comprehensive discovery of CRISPR-targeted terminally redundant sequences in the human gut metagenome: Viruses, plasmids, and more. PLoS Computational Biology, 2021, 17, e1009428.	3.2	7
11	Adlercreutzia hattorii sp. nov., an equol non-producing bacterium isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	10
12	PZLAST: an ultra-fast sequence similarity search tool implemented on a MIMD processor. , 2021, , .		0
13	Redox stratification within cryoconite granules influences the nitrogen cycle on glaciers. FEMS Microbiology Ecology, 2020, 96, .	2.7	19
14	Gut Bacterial Species Distinctively Impact Host Purine Metabolites during Aging in Drosophila. IScience, 2020, 23, 101477.	4.1	28
15	Local Necrotic Cells Trigger Systemic Immune Activation via Gut Microbiome Dysbiosis in Drosophila. Cell Reports, 2020, 32, 107938.	6.4	20
16	Microbial interaction between the succinate‒utilizing bacterium *Phascolarctobacterium faecium* and the gut commensal *Bacteroides thetaiotaomicron*. MicrobiologyOpen, 2020, 9, e1111.	3.0	54
17	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
18	Meta‒Analysis of Gut Dysbiosis in Parkinson's Disease. Movement Disorders, 2020, 35, 1626-1635.	3.9	208

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19	Dialister hominis sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 589-595.	1.7	18
20	BioHackathon 2015: Semantics of data for life sciences and reproducible research. F1000Research, 2020, 9, 136.	1.6	5
21	Amedibacterium intestinale gen. nov., sp. nov., isolated from human faeces, and reclassification of Eubacterium dolichum Moore et al. 1976 (Approved Lists 1980) as Amedibacillus dolichus gen. nov., comb. nov. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3656-3664.	1.7	18
22	Complete Genome Sequence of <i>Faecalibacillus intestinalis</i> JCM 34082, Isolated from Feces from a Healthy Japanese Female. Microbiology Resource Announcements, 2020, 9, .	0.6	1
23	Hadean Primordial Metabolism Pathway Driven by a Nuclear Geyser. Journal of Geography (Chigaku) Tj ETQq1 1 0.784314 rgBT /Overlo	0.3	2
24	Blastochloris tepida, sp. nov., a thermophilic species of the bacteriochlorophyll b-containing genus Blastochloris. Archives of Microbiology, 2019, 201, 1351-1359.	2.2	18
25	Genomic Analyses of Bifidobacterium moukalabense Reveal Adaptations to Frugivore/Folivore Feeding Behavior. Microorganisms, 2019, 7, 99.	3.6	6
26	TogoGenome/TogoStanza: modularized Semantic Web genome database. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	6
27	Draft Genome Sequence of Clostridium tagluense Strain A121 ^T, Isolated from a Permafrost Core in the Canadian High Arctic. Microbiology Resource Announcements, 2019, 8, .	0.6	3
28	Comparative genomics of Parolsenella catena and Libanicoccus massiliensis: Reclassification of Libanicoccus massiliensis as Parolsenella massiliensis comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1123-1129.	1.7	11
29	Quantification of hydrogen production by intestinal bacteria that are specifically dysregulated in Parkinson's disease. PLoS ONE, 2018, 13, e0208313.	2.5	41
30	The Relationship Between Microbial Community Structures and Environmental Parameters Revealed by Metagenomic Analysis of Hot Spring Water in the Kirishima Area, Japan. Frontiers in Bioengineering and Biotechnology, 2018, 6, 202.	4.1	26
31	Bipolar dispersal of red-snow algae. Nature Communications, 2018, 9, 3094.	12.8	75
32	Minor taxa in human skin microbiome contribute to the personal identification. PLoS ONE, 2018, 13, e0199947.	2.5	26
33	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.	3.0	23
34	Latent environment allocation of microbial community data. PLoS Computational Biology, 2018, 14, e1006143.	3.2	10
35	Comprehensive microbiome analysis of tonsillar crypts in IgA nephropathy. Nephrology Dialysis Transplantation, 2017, 32, gfw343.	0.7	40
36	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

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37	Intestinal IgA as a modulator of the gut microbiota. Gut Microbes, 2017, 8, 486-492.	9.8	49
38	Phylogenomics and Morphology of Extinct Paleognaths Reveal the Origin and Evolution of the Ratites. Current Biology, 2017, 27, 68-77.	3.9	123
39	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
40	Establishment of a multi-species biofilm model and metatranscriptomic analysis of biofilm and planktonic cell communities. Applied Microbiology and Biotechnology, 2016, 100, 7263-7279.	3.6	34
41	High-affinity monoclonal IgA regulates gut microbiota and prevents colitis in mice. Nature Microbiology, 2016, 1, 16103.	13.3	128
42	A key genetic factor for fucosyllactose utilization affects infant gut microbiota development. Nature Communications, 2016, 7, 11939.	12.8	284
43	Next-Generation Sequencing of an 88-Year-Old Specimen of the Poorly Known Species Liagora japonica (Nemaliales, Rhodophyta) Supports the Recognition of Otohimella gen. nov.. PLoS ONE, 2016, 11, e0158944.	2.5	21
44	FuncTree: Functional Analysis and Visualization for Large-Scale Omics Data. PLoS ONE, 2015, 10, e0126967.	2.5	30
45	Time-series metagenomic analysis reveals robustness of soil microbiome against chemical disturbance. DNA Research, 2015, 22, 413-424.	3.4	39
46	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
47	DomSign: a top-down annotation pipeline to enlarge enzyme space in the protein universe. BMC Bioinformatics, 2015, 16, 96.	2.6	6
48	Complete Genome Sequence of a Phenanthrene Degrader, Mycobacterium sp. Strain EPa45 (NBRC) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.8	7
49	Ecophysiology of <i>Thioploca ingrica</i> as revealed by the complete genome sequence supplemented with proteomic evidence. ISME Journal, 2015, 9, 1166-1176.	9.8	35
50	CLAST: CUDA implemented large-scale alignment search tool. BMC Bioinformatics, 2014, 15, 406.	2.6	13
51	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
52	Klebsormidium flaccidum genome reveals primary factors for plant terrestrial adaptation. Nature Communications, 2014, 5, 3978.	12.8	532
53	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
54	Whole-Genome Sequence of the Purple Photosynthetic Bacterium Rhodovulum sulfidophilum Strain W4. Genome Announcements, 2013, 1, .	0.8	16

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55	Meeting Report: Hackathon-Workshop on Darwin Core and MIxS Standards Alignment (February 2012). Standards in Genomic Sciences, 2012, 7, 166-170.	1.5	8
56	VITCOMIC: visualization tool for taxonomic compositions of microbial communities based on 16S rRNA gene sequences. BMC Bioinformatics, 2010, 11, 332.	2.6	25
57	Genome-Organizing Factors Top2 and Hmo1 Prevent Chromosome Fragility at Sites of S phase Transcription. Cell, 2009, 138, 870-884.	28.9	101
58	Asymmetric reproductive isolation during simultaneous reciprocal mating in pulmonates. Biology Letters, 2009, 5, 240-243.	2.3	18
59	Comparative Metagenomics Revealed Commonly Enriched Gene Sets in Human Gut Microbiomes. DNA Research, 2007, 14, 169-181.	3.4	760
60	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 0, 8, 1677.	1.6	0