

# Masahira Hattori

## List of Publications by Year in descending order

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310  
papers

76,247  
citations

2675

95  
h-index

529

266  
g-index

323  
all docs

323  
docs citations

323  
times ranked

74479  
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiple nutritional and gut microbial factors associated with allergic rhinitis: the Hitachi Health Study. <i>Scientific Reports</i> , 2022, 12, 3359.	3.3	8
2	A potential network structure of symbiotic bacteria involved in carbon and nitrogen metabolism of wood-utilizing insect larvae. <i>Science of the Total Environment</i> , 2022, 836, 155520.	8.0	14
3	Complete Genome Sequence of <i>Alistipes indistinctus</i> Strain 2BBH45, Isolated from the Feces of a Healthy Japanese Male. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
4	Rebamipide ameliorates indomethacin-induced small intestinal damage and proton pump inhibitor-induced exacerbation of this damage by modulation of small intestinal microbiota. <i>PLoS ONE</i> , 2021, 16, e0245995.	2.5	8
5	Pancreatic glycoprotein 2 is a first line of defense for mucosal protection in intestinal inflammation. <i>Nature Communications</i> , 2021, 12, 1067.	12.8	35
6	Alteration of oxidative-stress and related marker levels in mouse colonic tissues and fecal microbiota structures with chronic ethanol administration: Implications for the pathogenesis of ethanol-related colorectal cancer. <i>PLoS ONE</i> , 2021, 16, e0246580.	2.5	9
7	<i>Staphylococcus cohnii</i> is a potentially biotherapeutic skin commensal alleviating skin inflammation. <i>Cell Reports</i> , 2021, 35, 109052.	6.4	26
8	Hematopoietic Cell Transplantation Rescues Inflammatory Bowel Disease and Dysbiosis of Gut Microbiota in XIAP Deficiency. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2021, 9, 3767-3780.	3.8	15
9	Novel bile acid biosynthetic pathways are enriched in the microbiome of centenarians. <i>Nature</i> , 2021, 599, 458-464.	27.8	251
10	Long-read metagenomics of multiple displacement amplified DNA of low-biomass human gut phageomes by SACRA preprocessing chimeric reads. <i>DNA Research</i> , 2021, 28, .	3.4	11
11	Dysbiosis in the Salivary Microbiome Associated with IgA Nephropathy—Japanese Cohort Study. <i>Microbes and Environments</i> , 2021, 36, n/a.	1.6	7
12	Metagenomic analysis provides functional insights into seasonal change of a non-cyanobacterial prokaryotic community in temperate coastal waters. <i>PLoS ONE</i> , 2021, 16, e0257862.	2.5	5
13	<i>Lentilactobacillus kosonis</i> sp. nov., isolated from <i>kāñso</i> , a Japanese sugar-vegetable fermented beverage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	8
14	Dysregulation of the Intestinal Microbiome in Patients With Haploinsufficiency of A20. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 787667.	3.9	0
15	Japanese subgingival microbiota in health vs disease and their roles in predicted functions associated with periodontitis. <i>Odontology / the Society of the Nippon Dental University</i> , 2020, 108, 280-291.	1.9	44
16	Altered microbiota composition reflects enhanced communication in 15q11-13 CNV mice. <i>Neuroscience Research</i> , 2020, 161, 59-67.	1.9	8
17	Gut microbiota composition in obese and non-obese adult relatives from the highlands of Papua New Guinea. <i>FEMS Microbiology Letters</i> , 2020, 367, .	1.8	4
18	TH1 cell-inducing <i>Escherichia coli</i> strain identified from the small intestinal mucosa of patients with Crohn's disease. <i>Gut Microbes</i> , 2020, 12, 1788898.	9.8	40

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19	Prebiotics protect against acute graft-versus-host disease and preserve the gut microbiota in stem cell transplantation. <i>Blood Advances</i> , 2020, 4, 4607-4617.	5.2	42
20	Genome Analysis of <i>Candidatus</i> Regiella insecticola Strain TUt, Facultative Bacterial Symbiont of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
21	The influences of low protein diet on the intestinal microbiota of mice. <i>Scientific Reports</i> , 2020, 10, 17077.	3.3	22
22	Gut microorganisms act together to exacerbate inflammation in spinal cords. <i>Nature</i> , 2020, 585, 102-106.	27.8	153
23	Alterations of the gut ecological and functional microenvironment in different stages of multiple sclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22402-22412.	7.1	103
24	Complete Genome Sequence of <i>Adlercreutzia</i> sp. Strain 8CFCBH1, a Potent Producer of Equol, Isolated from Healthy Japanese Feces. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
25	Ancient DNA analysis of food remains in human dental calculus from the Edo period, Japan. <i>PLoS ONE</i> , 2020, 15, e0226654.	2.5	24
26	Revealing the microbial assemblage structure in the human gut microbiome using latent Dirichlet allocation. <i>Microbiome</i> , 2020, 8, 95.	11.1	22
27	<i>Alistipes communis</i> sp. nov., <i>Alistipes dispar</i> sp. nov. and <i>Alistipes onderdonkii</i> subsp. <i>vulgaris</i> subsp. nov., isolated from human faeces, and creation of <i>Alistipes onderdonkii</i> subsp. <i>onderdonkii</i> subsp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 473-480.	1.7	27
28	5-Aminosalicylic acid intolerance is associated with a risk of adverse clinical outcomes and dysbiosis in patients with ulcerative colitis. <i>Intestinal Research</i> , 2020, 18, 69-78.	2.6	19
29	Effects of storage temperature, storage time, and Cary-Blair transport medium on the stability of the gut microbiota. <i>Drug Discoveries and Therapeutics</i> , 2019, 13, 256-260.	1.5	16
30	Repeated selective enrichment process of sediment microbiota occurred in sea cucumber guts. <i>Environmental Microbiology Reports</i> , 2019, 11, 797-807.	2.4	10
31	Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. <i>Microbiome</i> , 2019, 7, 119.	11.1	65
32	Mucin O-glycans facilitate symbiosynthesis to maintain gut immune homeostasis. <i>EBioMedicine</i> , 2019, 48, 513-525.	6.1	66
33	A defined commensal consortium elicits CD8 T cells and anti-cancer immunity. <i>Nature</i> , 2019, 565, 600-605.	27.8	741
34	Influence of <i>Porphyromonas gingivalis</i> in gut microbiota of streptozotocin-induced diabetic mice. <i>Oral Diseases</i> , 2019, 25, 868-880.	3.0	37
35	Complete Genome Sequence of <i>Phascolarctobacterium faecium</i> JCM 30894, a Succinate-Utilizing Bacterium Isolated from Human Feces. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	38
36	Genome Sequence of <i>Candidatus</i> Serratia symbiotica Strain IS, a Facultative Bacterial Symbiont of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	9

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37	Effects of bowel preparation on the human gut microbiome and metabolome. <i>Scientific Reports</i> , 2019, 9, 4042.	3.3	78
38	Draft Genome Sequence of <i>Sporolactobacillus inulinus</i> NBRC 111894, Isolated from KÅ'so, a Japanese Sugar-Vegetable Fermented Beverage. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
39	Optimization of Data-Independent Acquisition Mass Spectrometry for Deep and Highly Sensitive Proteomic Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5932.	4.1	73
40	Gastric acid inhibitor aggravates indomethacin-induced small intestinal injury via reducing <i>Lactobacillus johnsonii</i> . <i>Scientific Reports</i> , 2019, 9, 17490.	3.3	31
41	Gut pathobionts underlie intestinal barrier dysfunction and liver T helper 17 cell immune response in primary sclerosing cholangitis. <i>Nature Microbiology</i> , 2019, 4, 492-503.	13.3	270
42	Insights into the Evolution of Shells and Love Darts of Land Snails Revealed from Their Matrix Proteins. <i>Genome Biology and Evolution</i> , 2019, 11, 380-397.	2.5	25
43	Mapping the Environmental Microbiome. , 2019, , 17-28.		1
44	The <i>Parachlorella</i> Genome and Transcriptome Endorse Active RWP-RK, Meiosis and Flagellar Genes in Trebouxiophycean Algae. <i>Cytologia</i> , 2019, 84, 323-330.	0.6	6
45	Pyrosequencing Analysis of Bacterial Species Affected by Ethanol-Extract from Activated Sludge. <i>Journal of Water and Environment Technology</i> , 2019, 17, 9-17.	0.7	1
46	The effect of fecal microbiota transplantation on psychiatric symptoms among patients with irritable bowel syndrome, functional diarrhea and functional constipation: An open-label observational study. <i>Journal of Affective Disorders</i> , 2018, 235, 506-512.	4.1	134
47	Dysbiosis of the salivary microbiota in pediatric-onset primary sclerosing cholangitis and its potential as a biomarker. <i>Scientific Reports</i> , 2018, 8, 5480.	3.3	49
48	<i>Lactobacillus kosoi</i> sp. nov., a fructophilic species isolated from kÅ'so, a Japanese sugar-vegetable fermented beverage. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1149-1156.	1.7	24
49	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	13.3	717
50	Efficacy of Indigo Naturalis in a Multicenter Randomized Controlled Trial of Patients With Ulcerative Colitis. <i>Gastroenterology</i> , 2018, 154, 935-947.	1.3	139
51	Effects of Attached and Suspended Biomass on the Dynamics of the Microbial Community and Wastewater Characteristics in Sewers. <i>Journal of Water and Environment Technology</i> , 2018, 16, 233-244.	0.7	5
52	Gut microbiota-derived D-serine protects against acute kidney injury. <i>JCI Insight</i> , 2018, 3, .	5.0	99
53	Draft Genome Sequence of <i>Lactobacillus kosoi</i> NBRC 113063, Isolated from KÅ'so, a Japanese Sugar-Vegetable Fermented Beverage. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	2
54	Fecal microbiota transplantation with frozen capsules for a patient with refractory acute gut graft-versus-host disease. <i>Blood Advances</i> , 2018, 2, 3097-3101.	5.2	51

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55	Fecal microbiota transplantation for recurrent <i>Clostridium difficile</i> infection in a patient with ulcerative colitis. <i>Intestinal Research</i> , 2018, 16, 142.	2.6	6
56	Computer-guided design of optimal microbial consortia for immune system modulation. <i>ELife</i> , 2018, 7, .	6.0	65
57	Confounding effects of microbiome on the susceptibility of TNFSF15 to Crohn's disease in the Ryukyu Islands. <i>Human Genetics</i> , 2017, 136, 387-397.	3.8	14
58	A proliferative probiotic <i>Bifidobacterium</i> strain in the gut ameliorates progression of metabolic disorders via microbiota modulation and acetate elevation. <i>Scientific Reports</i> , 2017, 7, 43522.	3.3	150
59	Draft Genome Sequencing of the Highly Halotolerant and Allopolyploid Yeast <i>Zygosaccharomyces rouxii</i> NBRC 1876. <i>Genome Announcements</i> , 2017, 5, .	0.8	14
60	Comprehensive single-cell transcriptome analysis reveals heterogeneity in endometrioid adenocarcinoma tissues. <i>Scientific Reports</i> , 2017, 7, 14225.	3.3	23
61	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	17.5	581
62	Commensal <i>Lactobacillus</i> Controls Immune Tolerance during Acute Liver Injury in Mice. <i>Cell Reports</i> , 2017, 21, 1215-1226.	6.4	67
63	Ectopic colonization of oral bacteria in the intestine drives T <sub>H</sub> 1 cell induction and inflammation. <i>Science</i> , 2017, 358, 359-365.	12.6	612
64	Genomic structure and evolution of the mating type locus in the green seaweed <i>Ulva partita</i> . <i>Scientific Reports</i> , 2017, 7, 11679.	3.3	25
65	Small genome symbiont underlies cuticle hardness in beetles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8382-E8391.	7.1	127
66	Microbiome profile of the amniotic fluid as a predictive biomarker of perinatal outcome. <i>Scientific Reports</i> , 2017, 7, 12171.	3.3	86
67	Aging-related changes in the diversity of women's skin microbiomes associated with oral bacteria. <i>Scientific Reports</i> , 2017, 7, 10567.	3.3	148
68	Gallbladder-derived surfactant protein D regulates gut commensal bacteria for maintaining intestinal homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10178-10183.	7.1	52
69	Clinical impact of pre-transplant gut microbial diversity on outcomes of allogeneic hematopoietic stem cell transplantation. <i>Annals of Hematology</i> , 2017, 96, 1517-1523.	1.8	48
70	<i>Bifidobacterium</i> -Rich Fecal Donor May Be a Positive Predictor for Successful Fecal Microbiota Transplantation in Patients with Irritable Bowel Syndrome. <i>Digestion</i> , 2017, 96, 29-38.	2.3	266
71	Intestinal Dysbiosis and Biotin Deprivation Induce Alopecia through Overgrowth of <i>Lactobacillus murinus</i> in Mice. <i>Cell Reports</i> , 2017, 20, 1513-1524.	6.4	93
72	Changes in the bacterial community in the fermentation process of <i>kā'iso</i> , a Japanese sugar-vegetable fermented beverage. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 403-410.	1.3	11

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73	Uremic Toxin-Producing Gut Microbiota in Rats with Chronic Kidney Disease. <i>Nephron</i> , 2017, 135, 51-60.	1.8	71
74	Circadian oscillations of microbial and functional composition in the human salivary microbiome. <i>DNA Research</i> , 2017, 24, 261-270.	3.4	85
75	Dysbiosis and compositional alterations with aging in the gut microbiota of patients with heart failure. <i>PLoS ONE</i> , 2017, 12, e0174099.	2.5	182
76	<i>Vibrio aphrogenes</i> sp. nov., in the Rumoiensis clade isolated from a seaweed. <i>PLoS ONE</i> , 2017, 12, e0180053.	2.5	15
77	Single fecal microbiota transplantation failed to change intestinal microbiota and had limited effectiveness against ulcerative colitis in Japanese patients. <i>Intestinal Research</i> , 2017, 15, 68.	2.6	32
78	A 3-dimensional mathematical model of microbial proliferation that generates the characteristic cumulative relative abundance distributions in gut microbiomes. <i>PLoS ONE</i> , 2017, 12, e0180863.	2.5	6
79	DNA hypermethylation and silencing of <i>PITX1</i> correlated with advanced stage and poor postoperative prognosis of esophageal squamous cell carcinoma. <i>Oncotarget</i> , 2017, 8, 84434-84448.	1.8	27
80	Polymicrobial Amniotic Fluid Infection with <i>Mycoplasma/Ureaplasma</i> and Other Bacteria Induces Severe Intra-Amniotic Inflammation Associated with Poor Perinatal Prognosis in Preterm Labor. <i>American Journal of Reproductive Immunology</i> , 2016, 75, 112-125.	1.2	51
81	Ecophysiological consequences of alcoholism on human gut microbiota: implications for ethanol-related pathogenesis of colon cancer. <i>Scientific Reports</i> , 2016, 6, 27923.	3.3	66
82	Fecal microbiota transplantation for patients with steroid-resistant acute graft-versus-host disease of the gut. <i>Blood</i> , 2016, 128, 2083-2088.	1.4	279
83	Unique pioneer microbial communities exposed to volcanic sulfur dioxide. <i>Scientific Reports</i> , 2016, 6, 19687.	3.3	22
84	First microbiota assessments of children's paddling pool waters evaluated using 16S rRNA gene-based metagenome analysis. <i>Journal of Infection and Public Health</i> , 2016, 9, 362-365.	4.1	7
85	<i>Vibrio ishigakensis</i> sp. nov., in Halioticoli clade isolated from seawater in Okinawa coral reef area, Japan. <i>Systematic and Applied Microbiology</i> , 2016, 39, 330-335.	2.8	20
86	Two FOXP3+CD4+ T cell subpopulations distinctly control the prognosis of colorectal cancers. <i>Nature Medicine</i> , 2016, 22, 679-684.	30.7	641
87	A Histone Methyltransferase ESET Is Critical for T Cell Development. <i>Journal of Immunology</i> , 2016, 197, 2269-2279.	0.8	33
88	Individual <i>Apostichopus japonicus</i> fecal microbiome reveals a link with polyhydroxybutyrate producers in host growth gaps. <i>Scientific Reports</i> , 2016, 6, 21631.	3.3	81
89	Deciphering the relationship among phosphate dynamics, electron-dense body and lipid accumulation in the green alga <i>Parachlorella kessleri</i> . <i>Scientific Reports</i> , 2016, 6, 25731.	3.3	53
90	Highly efficient lipid production in the green alga <i>Parachlorella kessleri</i> : draft genome and transcriptome endorsed by whole-cell 3D ultrastructure. <i>Biotechnology for Biofuels</i> , 2016, 9, 13.	6.2	56

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91	Draft Genome Sequence of <i>Lactobacillus farciminis</i> NBRC 111452, Isolated from K�so, a Japanese Sugar-Vegetable Fermented Beverage. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
92	Major Anaerobic Bacteria Responsible for the Production of Carcinogenic Acetaldehyde from Ethanol in the Colon and Rectum. <i>Alcohol and Alcoholism</i> , 2016, 51, 395-401.	1.6	46
93	Interferon��3 constrains cytokine production of group 2 innate lymphoid cells. <i>Immunology</i> , 2016, 147, 21-29.	4.4	32
94	The gut microbiome of healthy Japanese and its microbial and functional uniqueness. <i>DNA Research</i> , 2016, 23, 125-133.	3.4	387
95	Distribution and Evolution of Nitrogen Fixation Genes in the Phylum &Bacteroidetes. <i>Microbes and Environments</i> , 2015, 30, 44-50.	1.6	67
96	Proteome analysis of shell matrix proteins in the brachiopod <i>Laqueus rubellus</i> . <i>Proteome Science</i> , 2015, 13, 21.	1.7	24
97	Comparative Genomic Insights into Ecophysiology of Neutrophilic, Microaerophilic Iron Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2015, 6, 1265.	3.5	78
98	Genome Analysis of a Novel Bradyrhizobium sp. DOA9 Carrying a Symbiotic Plasmid. <i>PLoS ONE</i> , 2015, 10, e0117392.	2.5	52
99	Dysbiosis in the Gut Microbiota of Patients with Multiple Sclerosis, with a Striking Depletion of Species Belonging to Clostridia XIVa and IV Clusters. <i>PLoS ONE</i> , 2015, 10, e0137429.	2.5	609
100	Advanced Microbial Taxonomy Combined with Genome-Based-Approaches Reveals that <i>Vibrio astriarenae</i> sp. nov., an Agarolytic Marine Bacterium, Forms a New Clade in Vibrionaceae. <i>PLoS ONE</i> , 2015, 10, e0136279.	2.5	47
101	Time-series metagenomic analysis reveals robustness of soil microbiome against chemical disturbance. <i>DNA Research</i> , 2015, 22, 413-424.	3.4	39
102	Complete genome sequence of <i>Bifidobacterium angulatum</i> JCM 7096T isolated from human feces. <i>Journal of Biotechnology</i> , 2015, 211, 10-11.	3.8	5
103	Complete Genome Sequence of <i>Bifidobacterium scardovii</i> Strain JCM 12489 T , Isolated from Human Blood. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
104	Complete genome sequence of <i>Bifidobacterium bifidum</i> JCM 1255T isolated from feces of a breast-fed infant. <i>Journal of Biotechnology</i> , 2015, 210, 66-67.	3.8	4
105	Complete genome sequence of <i>Bifidobacterium breve</i> JCM 1192T isolated from infant feces. <i>Journal of Biotechnology</i> , 2015, 210, 81-82.	3.8	5
106	Complete genome sequence of <i>Bifidobacterium catenulatum</i> JCM 1194T isolated from human feces. <i>Journal of Biotechnology</i> , 2015, 210, 25-26.	3.8	7
107	Complete genome sequence of <i>Bifidobacterium pseudocatenulatum</i> JCM 1200T isolated from infant feces. <i>Journal of Biotechnology</i> , 2015, 210, 68-69.	3.8	7
108	Influence of Proton-Pump Inhibitors on the Luminal Microbiota in the Gastrointestinal Tract. <i>Clinical and Translational Gastroenterology</i> , 2015, 6, e89.	2.5	132

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109	<i>Tepidicaulis marinus</i> gen. nov., sp. nov., a marine bacterium that reduces nitrate to nitrous oxide under strictly microaerobic conditions. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1749-1754.	1.7	16
110	Mutual reinforcement of inflammation and carcinogenesis by the <i>Helicobacter pylori</i> CagA oncoprotein. <i>Scientific Reports</i> , 2015, 5, 10024.	3.3	52
111	Th17 Cell Induction by Adhesion of Microbes to Intestinal Epithelial Cells. <i>Cell</i> , 2015, 163, 367-380.	28.9	846
112	CTRP6 is an endogenous complement regulator that can effectively treat induced arthritis. <i>Nature Communications</i> , 2015, 6, 8483.	12.8	58
113	Complete Genome Sequence of a Phenanthrene Degradar, <i>Mycobacterium</i> sp. Strain EPA45 (NBRC) Tj ETQq1 1 0.784314 rgBT /Overlaid	0.8	7
114	Complete Genome Sequence of <i>Bifidobacterium kashiwanohense</i> JCM 15439 <sup>T</sup> , Isolated from Feces from a Healthy Japanese Infant. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
115	Inhibition of Dectin-1 Signaling Ameliorates Colitis by Inducing <i>Lactobacillus</i> -Mediated Regulatory T Cell Expansion in the Intestine. <i>Cell Host and Microbe</i> , 2015, 18, 183-197.	11.0	215
116	Complete Nucleotide Sequence of the IncN Plasmid Encoding IMP-6 and CTX-M-2 from Emerging Carbapenem-Resistant Enterobacteriaceae in Japan. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 1356-1359.	3.2	39
117	Draft Genome Sequence of <i>Bacteroides reticulotermitis</i> Strain JCM 10512 <sup>T</sup> , Isolated from the Gut of a Termite. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
118	Draft Genome Sequence of <i>Cytophaga fermentans</i> JCM 21142 <sup>T</sup> , a Facultative Anaerobe Isolated from Marine Mud. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
119	Complete Genome Sequence of <i>Winogradskyella</i> sp. Strain PG-2, a Proteorhodopsin-Containing Marine Flavobacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
120	Draft Genome Sequence of the Betaproteobacterial Endosymbiont Associated with the Fungus <i>Mortierella elongata</i> FMR23-6. <i>Genome Announcements</i> , 2014, 2, .	0.8	46
121	Multiple Omics Uncovers Host-Gut Microbial Mutualism During Prebiotic Fructooligosaccharide Supplementation. <i>DNA Research</i> , 2014, 21, 469-480.	3.4	101
122	Genome Evolution and Plasticity of <i>Serratia marcescens</i> , an Important Multidrug-Resistant Nosocomial Pathogen. <i>Genome Biology and Evolution</i> , 2014, 6, 2096-2110.	2.5	155
123	Characterization of the 17 strains of regulatory T cell-inducing human-derived <i>Clostridia</i> . <i>Gut Microbes</i> , 2014, 5, 333-339.	9.8	182
124	Genome Sequence of the Tsetse Fly ( <i>Glossina morsitans</i> ): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	12.6	254
125	Evolutionary origin of insect-Wolbachia nutritional mutualism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10257-10262.	7.1	327
126	<i>Methyloceanibacter caenitepidi</i> gen. nov., sp. nov., a facultatively methylotrophic bacterium isolated from marine sediments near a hydrothermal vent. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 462-468.	1.7	54

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127	Foxp3+ T Cells Regulate Immunoglobulin A Selection and Facilitate Diversification of Bacterial Species Responsible for Immune Homeostasis. <i>Immunity</i> , 2014, 41, 152-165.	14.3	431
128	Dysbiosis of Salivary Microbiota in Inflammatory Bowel Disease and Its Association With Oral Immunological Biomarkers. <i>DNA Research</i> , 2014, 21, 15-25.	3.4	307
129	<i>Methylocaldum marinum</i> sp. nov., a thermotolerant, methane-oxidizing bacterium isolated from marine sediments, and emended description of the genus <i>Methylocaldum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 3240-3246.	1.7	63
130	CTRP3 plays an important role in the development of collagen-induced arthritis in mice. <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 42-48.	2.1	58
131	3. Microbial community analysis of aquaculture habitat using next generation sequencer. <i>Nippon Suisan Gakkaishi</i> , 2014, 80, 1005-1005.	0.1	0
132	Characterization of Early Microbial Communities on Volcanic Deposits along a Vegetation Gradient on the Island of Miyake, Japan. <i>Microbes and Environments</i> , 2014, 29, 38-49.	1.6	26
133	HMGJ (Japan)., 2014, , 1-5.		0
134	Human Intestinal Microbiome. , 2014, , 1-7.		0
135	Treg induction by a rationally selected mixture of Clostridia strains from the human microbiota. <i>Nature</i> , 2013, 500, 232-236.	27.8	2,339
136	Defensive Bacteriome Symbiont with a Drastically Reduced Genome. <i>Current Biology</i> , 2013, 23, 1478-1484.	3.9	314
137	Qualitative Rather than Quantitative Changes Are Hallmarks of Fibroblasts in Bleomycin-Induced Pulmonary Fibrosis. <i>American Journal of Pathology</i> , 2013, 183, 758-773.	3.8	73
138	Evolutionary changes of multiple visual pigment genes in the complete genome of Pacific bluefin tuna. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11061-11066.	7.1	106
139	Comparative analysis of proteolytic enzymes need for processing of antihypertensive peptides between <i>Lactobacillus helveticus</i> CM4 and DPC4571. <i>Journal of Bioscience and Bioengineering</i> , 2013, 115, 246-252.	2.2	13
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