

Masahira Hattori

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298
papers

59,811
citations

87
h-index

244
g-index

323
ext. papers

69,294
ext. citations

9.9
avg, IF

6.7
L-index

#	Paper	IF	Citations
298	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001 , 409, 860-921	50.4	17366
297	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
296	A comprehensive two-hybrid analysis to explore the yeast protein interactome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 4569-74	11.5	2933
295	Treg induction by a rationally selected mixture of Clostridia strains from the human microbiota. <i>Nature</i> , 2013 , 500, 232-6	50.4	1795
294	Whole genome sequencing of meticillin-resistant <i>Staphylococcus aureus</i> . <i>Lancet, The</i> , 2001 , 357, 1225-40	40	1586
293	Dideoxy sequencing method using denatured plasmid templates. <i>Analytical Biochemistry</i> , 1986 , 152, 232-8	3.1	1493
292	Bifidobacteria can protect from enteropathogenic infection through production of acetate. <i>Nature</i> , 2011 , 469, 543-7	50.4	1423
291	Obesity-induced gut microbial metabolite promotes liver cancer through senescence secretome. <i>Nature</i> , 2013 , 499, 97-101	50.4	1298
290	Genome sequence of the endocellular bacterial symbiont of aphids <i>Buchnera</i> sp. APS. <i>Nature</i> , 2000 , 407, 81-6	50.4	1026
289	Complete genome sequence of enterohemorrhagic <i>Escherichia coli</i> O157:H7 and genomic comparison with a laboratory strain K-12. <i>DNA Research</i> , 2001 , 8, 11-22	4.5	986
288	Complete genome sequence and comparative analysis of the industrial microorganism <i>Streptomyces avermitilis</i> . <i>Nature Biotechnology</i> , 2003 , 21, 526-31	44.5	974
287	The DNA sequence of human chromosome 21. <i>Nature</i> , 2000 , 405, 311-9	50.4	911
286	Genome sequence of <i>Vibrio parahaemolyticus</i> : a pathogenic mechanism distinct from that of <i>V. cholerae</i> . <i>Lancet, The</i> , 2003 , 361, 743-9	40	740
285	A physical map of the human genome. <i>Nature</i> , 2001 , 409, 934-41	50.4	732
284	Comparative metagenomics revealed commonly enriched gene sets in human gut microbiomes. <i>DNA Research</i> , 2007 , 14, 169-81	4.5	673
283	Genome sequence of an industrial microorganism <i>Streptomyces avermitilis</i> : deducing the ability of producing secondary metabolites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 12215-20	11.5	672
282	Th17 Cell Induction by Adhesion of Microbes to Intestinal Epithelial Cells. <i>Cell</i> , 2015 , 163, 367-80	56.2	612

281	Complete genome sequence of <i>Clostridium perfringens</i> , an anaerobic flesh-eater. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 996-1001	11.5	588
280	Genome sequence of the endocellular obligate symbiont of tsetse flies, <i>Wigglesworthia glossinidia</i> . <i>Nature Genetics</i> , 2002 , 32, 402-7	36.3	491
279	Genome sequence of the streptomycin-producing microorganism <i>Streptomyces griseus</i> IFO 13350. <i>Journal of Bacteriology</i> , 2008 , 190, 4050-60	3.5	462
278	Two FOXP3(+)CD4(+) T cell subpopulations distinctly control the prognosis of colorectal cancers. <i>Nature Medicine</i> , 2016 , 22, 679-84	50.5	445
277	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	3.7	424
276	A defined commensal consortium elicits CD8 T cells and anti-cancer immunity. <i>Nature</i> , 2019 , 565, 600-605	50.4	417
275	The 160-kilobase genome of the bacterial endosymbiont <i>Carsonella</i> . <i>Science</i> , 2006 , 314, 267	33.3	403
274	A novel superoxide-producing NAD(P)H oxidase in kidney. <i>Journal of Biological Chemistry</i> , 2001 , 276, 1417-23	5.4	397
273	Continuum of overlapping clones spanning the entire human chromosome 21q. <i>Nature</i> , 1992 , 359, 380-7	50.4	394
272	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16	26.6	387
271	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017 , 35, 1069-1076	44.5	355
270	Ectopic colonization of oral bacteria in the intestine drives T1 cell induction and inflammation. <i>Science</i> , 2017 , 358, 359-365	33.3	341
269	Foxp3(+) T cells regulate immunoglobulin a selection and facilitate diversification of bacterial species responsible for immune homeostasis. <i>Immunity</i> , 2014 , 41, 152-65	32.3	333
268	Comparative genomics reveal the mechanism of the parallel evolution of O157 and non-O157 enterohemorrhagic <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 17939-44	11.5	273
267	Massive genome erosion and functional adaptations provide insights into the symbiotic lifestyle of <i>Sodalis glossinidius</i> in the tsetse host. <i>Genome Research</i> , 2006 , 16, 149-56	9.7	252
266	The complete genomic sequence of <i>Nocardia farcinica</i> IFM 10152. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 14925-30	11.5	234
265	Genome sequence of the lager brewing yeast, an interspecies hybrid. <i>DNA Research</i> , 2009 , 16, 115-29	4.5	233
264	Evolutionary origin of insect-Wolbachia nutritional mutualism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 10257-62	11.5	228

263	The gut microbiome of healthy Japanese and its microbial and functional uniqueness. <i>DNA Research</i> , 2016 , 23, 125-33	4.5	226
262	Insights into the evolution of Archaea and eukaryotic protein modifier systems revealed by the genome of a novel archaeal group. <i>Nucleic Acids Research</i> , 2011 , 39, 3204-23	20.1	222
261	Comparative genome analysis of <i>Lactobacillus reuteri</i> and <i>Lactobacillus fermentum</i> reveal a genomic island for reuterin and cobalamin production. <i>DNA Research</i> , 2008 , 15, 151-61	4.5	215
260	Genome sequence of an M3 strain of <i>Streptococcus pyogenes</i> reveals a large-scale genomic rearrangement in invasive strains and new insights into phage evolution. <i>Genome Research</i> , 2003 , 13, 1042-55	9.7	213
259	Dysbiosis of salivary microbiota in inflammatory bowel disease and its association with oral immunological biomarkers. <i>DNA Research</i> , 2014 , 21, 15-25	4.5	212
258	L1 family of repetitive DNA sequences in primates may be derived from a sequence encoding a reverse transcriptase-related protein. <i>Nature</i> , 1986 , 321, 625-8	50.4	205
257	Fecal microbiota transplantation for patients with steroid-resistant acute graft-versus-host disease of the gut. <i>Blood</i> , 2016 , 128, 2083-2088	2.2	201
256	Robustness of gut microbiota of healthy adults in response to probiotic intervention revealed by high-throughput pyrosequencing. <i>DNA Research</i> , 2013 , 20, 241-53	4.5	200
255	Determination of the genome sequence of <i>Porphyromonas gingivalis</i> strain ATCC 33277 and genomic comparison with strain W83 revealed extensive genome rearrangements in <i>P. gingivalis</i> . <i>DNA Research</i> , 2008 , 15, 215-25	4.5	200
254	Construction and analysis of a human-chimpanzee comparative clone map. <i>Science</i> , 2002 , 295, 131-4	33.3	199
253	A large-scale full-length cDNA analysis to explore the budding yeast transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 17846-51	11.5	198
252	Defensive bacteriome symbiont with a drastically reduced genome. <i>Current Biology</i> , 2013 , 23, 1478-84	6.3	197
251	Genomic analysis of <i>Bacteroides fragilis</i> reveals extensive DNA inversions regulating cell surface adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 14919-24	11.5	195
250	Genome sequence of the tsetse fly (<i>Glossina morsitans</i>): vector of African trypanosomiasis. <i>Science</i> , 2014 , 344, 380-6	33.3	192
249	Whole genome sequence of <i>Staphylococcus saprophyticus</i> reveals the pathogenesis of uncomplicated urinary tract infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 13272-7	11.5	192
248	The human intestinal microbiome: a new frontier of human biology. <i>DNA Research</i> , 2009 , 16, 1-12	4.5	190
247	Accelerated evolution in the protein-coding regions is universal in crotalinae snake venom gland phospholipase A2 isozyme genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995 , 92, 5605-9	11.5	186
246	Complete genome of the uncultured Termite Group 1 bacteria in a single host protist cell. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 5555-60	11.5	184

245	DNA sequence and comparative analysis of chimpanzee chromosome 22. <i>Nature</i> , 2004 , 429, 382-8	50.4	182
244	Genome of an endosymbiont coupling N2 fixation to cellulolysis within protist cells in termite gut. <i>Science</i> , 2008 , 322, 1108-9	33.3	157
243	Accelerated evolution of Trimeresurus flavoviridis venom gland phospholipase A2 isozymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993 , 90, 5964-8	11.5	155
242	The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans. <i>Nucleic Acids Research</i> , 2002 , 30, 5293-300	20.1	154
241	Inhibition of Dectin-1 Signaling Ameliorates Colitis by Inducing Lactobacillus-Mediated Regulatory T Cell Expansion in the Intestine. <i>Cell Host and Microbe</i> , 2015 , 18, 183-97	23.4	153
240	Whole-genome screening indicates a possible burst of formation of processed pseudogenes and Alu repeats by particular L1 subfamilies in ancestral primates. <i>Genome Biology</i> , 2003 , 4, R74	18.3	138
239	Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA. <i>Nucleic Acids Research</i> , 2000 , 28, 2311-4	20.1	138
238	Efficient and stable transformation of Lactuca sativa L. cv. Cisco (lettuce) plastids. <i>Transgenic Research</i> , 2006 , 15, 205-17	3.3	131
237	Characterization of the 17 strains of regulatory T cell-inducing human-derived Clostridia. <i>Gut Microbes</i> , 2014 , 5, 333-9	8.8	130
236	Sequence analysis of a KpnI family member near the 3P end of human beta-globin gene. <i>Nucleic Acids Research</i> , 1985 , 13, 7813-27	20.1	130
235	Acetate-producing bifidobacteria protect the host from enteropathogenic infection via carbohydrate transporters. <i>Gut Microbes</i> , 2012 , 3, 449-54	8.8	128
234	Cd1d-dependent regulation of bacterial colonization in the intestine of mice. <i>Journal of Clinical Investigation</i> , 2009 , 119, 1241-50	15.9	128
233	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	26.6	126
232	The Whole-genome sequencing of the obligate intracellular bacterium Orientia tsutsugamushi revealed massive gene amplification during reductive genome evolution. <i>DNA Research</i> , 2008 , 15, 185-94.5	11.5	125
231	Genome sequence of Symbiobacterium thermophilum, an uncultivable bacterium that depends on microbial commensalism. <i>Nucleic Acids Research</i> , 2004 , 32, 4937-44	20.1	125
230	The human and mouse Period1 genes: five well-conserved E-boxes additively contribute to the enhancement of mPer1 transcription. <i>Genomics</i> , 2000 , 65, 224-33	4.3	123
229	A simplified method for the preparation of transcriptionally active liver nuclear extracts. <i>DNA and Cell Biology</i> , 1990 , 9, 777-81	3.6	120
228	The genome sequence of Clostridium botulinum type C neurotoxin-converting phage and the molecular mechanisms of unstable lysogeny. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 17472-7	11.5	119

227	Dysbiosis and compositional alterations with aging in the gut microbiota of patients with heart failure. <i>PLoS ONE</i> , 2017 , 12, e0174099	3.7	115
226	Genome evolution and plasticity of <i>Serratia marcescens</i> , an important multidrug-resistant nosocomial pathogen. <i>Genome Biology and Evolution</i> , 2014 , 6, 2096-110	3.9	114
225	Architecture and anatomy of the genomic locus encoding the human leukemia-associated transcription factor RUNX1/AML1. <i>Gene</i> , 2001 , 262, 23-33	3.8	114
224	Reductive evolution of bacterial genome in insect gut environment. <i>Genome Biology and Evolution</i> , 2011 , 3, 702-14	3.9	108
223	Evolution in an oncogenic bacterial species with extreme genome plasticity: <i>Helicobacter pylori</i> East Asian genomes. <i>BMC Microbiology</i> , 2011 , 11, 104	4.5	107
222	A 2-Mb sequence-ready contig map and a novel immunoglobulin superfamily gene IGSF4 in the LOH region of chromosome 11q23.2. <i>Genomics</i> , 1999 , 62, 139-46	4.3	106
221	Anammox organism KSU-1 expresses a NirK-type copper-containing nitrite reductase instead of a NirS-type with cytochrome cd1. <i>FEBS Letters</i> , 2012 , 586, 1658-63	3.8	104
220	Chromosome-wide assessment of replication timing for human chromosomes 11q and 21q: disease-related genes in timing-switch regions. <i>Human Molecular Genetics</i> , 2002 , 11, 13-21	5.6	103
219	Identification of an internal cis-element essential for the human L1 transcription and a nuclear factor(s) binding to the element. <i>Nucleic Acids Research</i> , 1992 , 20, 3139-45	20.1	98
218	Complete genome sequences of rat and mouse segmented filamentous bacteria, a potent inducer of th17 cell differentiation. <i>Cell Host and Microbe</i> , 2011 , 10, 273-84	23.4	96
217	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, 11061-6 ^{11.5}		93
216	A deeply branching thermophilic bacterium with an ancient acetyl-CoA pathway dominates a subsurface ecosystem. <i>PLoS ONE</i> , 2012 , 7, e30559	3.7	93
215	Cloning and characterization of mevalonate pathway genes in a natural rubber producing plant, <i>Hevea brasiliensis</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2008 , 72, 2049-60	2.1	93
214	Comparative analysis of chimpanzee and human Y chromosomes unveils complex evolutionary pathway. <i>Nature Genetics</i> , 2006 , 38, 158-67	36.3	92
213	Influence of Proton-Pump Inhibitors on the Luminal Microbiota in the Gastrointestinal Tract. <i>Clinical and Translational Gastroenterology</i> , 2015 , 6, e89	4.2	91
212	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	4.9	89
211	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	6.6	87
210	Efficacy of Indigo Naturalis in a Multicenter Randomized Controlled Trial of Patients With Ulcerative Colitis. <i>Gastroenterology</i> , 2018 , 154, 935-947	13.3	85

209	Unusually high conservation of untranslated sequences in cDNAs for Trimeresurus flavoviridis phospholipase A2 isozymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992 , 89, 8557-61	11.5	84
208	Aging-related changes in the diversity of women's skin microbiomes associated with oral bacteria. <i>Scientific Reports</i> , 2017 , 7, 10567	4.9	83
207	Tonoplast- and plasma membrane-localized aquaporin-family transporters in blue hydrangea sepals of aluminum hyperaccumulating plant. <i>PLoS ONE</i> , 2012 , 7, e43189	3.7	83
206	Genome sequence of the cat pathogen, <i>Chlamydomonas felis</i> . <i>DNA Research</i> , 2006 , 13, 15-23	4.5	83
205	Microbial populations responsive to denitrification-inducing conditions in rice paddy soil, as revealed by comparative 16S rRNA gene analysis. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 7070-8	4.8	82
204	An Improved DNA Isolation Method for Metagenomic Analysis of the Microbial Flora of the Human Intestine. <i>Microbes and Environments</i> , 2007 , 22, 214-222	2.6	77
203	Contribution of Asian mouse subspecies <i>Mus musculus molossinus</i> to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis. <i>Genome Research</i> , 2004 , 14, 2439-47	9.7	77
202	Bifidobacterium-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	3.6	76
201	Insight into the transmission biology and species-specific functional capabilities of tsetse (Diptera: glossinidae) obligate symbiont <i>Wigglesworthia</i> . <i>MBio</i> , 2012 , 3,	7.8	76
200	Identification and characterization of a 500-kb homozygously deleted region at 1p36.2-p36.3 in a neuroblastoma cell line. <i>Oncogene</i> , 2000 , 19, 4302-7	9.2	76
199	Complete genome sequence and comparative analysis of the wild-type commensal <i>Escherichia coli</i> strain SE11 isolated from a healthy adult. <i>DNA Research</i> , 2008 , 15, 375-86	4.5	72
198	The lifestyle of the segmented filamentous bacterium: a non-culturable gut-associated immunostimulating microbe inferred by whole-genome sequencing. <i>DNA Research</i> , 2011 , 18, 291-303	4.5	71
197	Complete nucleotide sequence of the prophage VT1-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic <i>Escherichia coli</i> O157:H7 strain derived from the Sakai outbreak. <i>Gene</i> , 2000 , 258, 127-39	3.8	70
196	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	11.5	69
195	Genomic adaptation of the <i>Lactobacillus casei</i> group. <i>PLoS ONE</i> , 2013 , 8, e75073	3.7	67
194	Complete genome sequence of the probiotic <i>Lactobacillus rhamnosus</i> ATCC 53103. <i>Journal of Bacteriology</i> , 2009 , 191, 7630-1	3.5	66
193	Complete genome sequence and comparative analysis of the fish pathogen <i>Lactococcus garvieae</i> . <i>PLoS ONE</i> , 2011 , 6, e23184	3.7	66
192	Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse. <i>Gene</i> , 1992 , 112, 189-95	3.8	65

191	A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus. <i>Nucleic Acids Research</i> , 1997 , 25, 1802-8	20.1	64
190	Multiple omics uncovers host-gut microbial mutualism during prebiotic fructooligosaccharide supplementation. <i>DNA Research</i> , 2014 , 21, 469-80	4.5	62
189	Gut microorganisms act together to exacerbate inflammation in spinal cords. <i>Nature</i> , 2020 , 585, 102-106	50.4	62
188	Comparative Genomic Insights into Ecophysiology of Neutrophilic, Microaerophilic Iron Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2015 , 6, 1265	5.7	61
187	Chromosome painting in silico in a bacterial species reveals fine population structure. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1454-64	8.3	61
186	Cloning and characterization of the 2-C-methyl-D-erythritol 4-phosphate (MEP) pathway genes of a natural-rubber producing plant, <i>Hevea brasiliensis</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2008 , 72, 2903-17	2.1	59
185	Draft genome sequencing and comparative analysis of <i>Aspergillus sojae</i> NBRC4239. <i>DNA Research</i> , 2011 , 18, 165-76	4.5	57
184	Human chromosome 11 DNA sequence and analysis including novel gene identification. <i>Nature</i> , 2006 , 440, 497-500	50.4	57
183	Microbiome profile of the amniotic fluid as a predictive biomarker of perinatal outcome. <i>Scientific Reports</i> , 2017 , 7, 12171	4.9	56
182	Comparative genomic analyses of <i>Streptococcus mutans</i> provide insights into chromosomal shuffling and species-specific content. <i>BMC Genomics</i> , 2009 , 10, 358	4.5	56
181	Qualitative rather than quantitative changes are hallmarks of fibroblasts in bleomycin-induced pulmonary fibrosis. <i>American Journal of Pathology</i> , 2013 , 183, 758-73	5.8	55
180	Comparative genome analysis of the mouse imprinted gene impact and its nonimprinted human homolog IMPACT: toward the structural basis for species-specific imprinting. <i>Genome Research</i> , 2000 , 10, 1878-89	9.7	55
179	RNA polymerase III dependence of the human L1 promoter and possible participation of the RNA polymerase II factor YY1 in the RNA polymerase III transcription system. <i>Nucleic Acids Research</i> , 1995 , 23, 3704-9	20.1	55
178	A unique dermal dendritic cell subset that skews the immune response toward Th2. <i>PLoS ONE</i> , 2013 , 8, e73270	3.7	54
177	Birth and death of genes linked to chromosomal inversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 1501-6	11.5	54
176	Circadian oscillations of microbial and functional composition in the human salivary microbiome. <i>DNA Research</i> , 2017 , 24, 261-270	4.5	52
175	Intestinal Dysbiosis and Biotin Deprivation Induce Alopecia through Overgrowth of <i>Lactobacillus murinus</i> in Mice. <i>Cell Reports</i> , 2017 , 20, 1513-1524	10.6	50
174	The genomic structure and expression of MJD, the Machado-Joseph disease gene. <i>Journal of Human Genetics</i> , 2001 , 46, 413-22	4.3	50

173	Gut microbiota-derived D-serine protects against acute kidney injury. <i>JCI Insight</i> , 2018 , 3,	9.9	50
172	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	11.5	49
171	Comparative genome analysis of three eukaryotic parasites with differing abilities to transform leukocytes reveals key mediators of Theileria-induced leukocyte transformation. <i>MBio</i> , 2012 , 3, e00204-12	7.8	48
170	Nucleotide sequence database policies. <i>Science</i> , 2002 , 298, 1333	33.3	48
169	Novel bile acid biosynthetic pathways are enriched in the microbiome of centenarians. <i>Nature</i> , 2021 , 599, 458-464	50.4	48
168	CTRP3 plays an important role in the development of collagen-induced arthritis in mice. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 443, 42-8	3.4	47
167	Complete genome sequence of the bacterium Porphyromonas gingivalis TDC60, which causes periodontal disease. <i>Journal of Bacteriology</i> , 2011 , 193, 4259-60	3.5	47
166	High-sensitive fluorescent DNA sequencing and its application for detection and mass-screening of point mutations. <i>Electrophoresis</i> , 1992 , 13, 560-5	3.6	47
165	Ecophysiological consequences of alcoholism on human gut microbiota: implications for ethanol-related pathogenesis of colon cancer. <i>Scientific Reports</i> , 2016 , 6, 27923	4.9	47
164	Individual <i>Apostichopus japonicus</i> fecal microbiome reveals a link with polyhydroxybutyrate producers in host growth gaps. <i>Scientific Reports</i> , 2016 , 6, 21631	4.9	46
163	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	7.8	46
162	<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	2.2	46
161	Complete genome sequence of <i>Bradyrhizobium</i> sp. S23321: insights into symbiosis evolution in soil oligotrophs. <i>Microbes and Environments</i> , 2012 , 27, 306-15	2.6	46
160	Complete genome sequences of <i>Arcobacter butzleri</i> ED-1 and <i>Arcobacter</i> sp. strain L, both isolated from a microbial fuel cell. <i>Journal of Bacteriology</i> , 2011 , 193, 6411-2	3.5	46
159	Uremic Toxin-Producing Gut Microbiota in Rats with Chronic Kidney Disease. <i>Nephron</i> , 2017 , 135, 51-60	3.3	45
158	Complete genome sequence of the wild-type commensal <i>Escherichia coli</i> strain SE15, belonging to phylogenetic group B2. <i>Journal of Bacteriology</i> , 2010 , 192, 1165-6	3.5	45
157	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005 , 437, 551-5	50.4	45
156	Commensal <i>Lactobacillus</i> Controls Immune Tolerance during Acute Liver Injury in Mice. <i>Cell Reports</i> , 2017 , 21, 1215-1226	10.6	44

155	Computer-guided design of optimal microbial consortia for immune system modulation. <i>ELife</i> , 2018 , 7,	8.9	44
154	Polymicrobial Amniotic Fluid Infection with Mycoplasma/Ureaplasma 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, 112-25	3.8	44
153	Nucleotide substitutions in Staphylococcus aureus strains, Mu50, Mu3, and N315. <i>DNA Research</i> , 2004 , 11, 51-6	4.5	43
152	Complete nucleotide sequence of TOL plasmid pDK1 provides evidence for evolutionary history of IncP-7 catabolic plasmids. <i>Journal of Bacteriology</i> , 2010 , 192, 4337-47	3.5	41
151	Structural and functional analysis of a 0.5-Mb chicken region orthologous to the imprinted mammalian Ascl2/Mash2-Igf2-H19 region. <i>Genome Research</i> , 2005 , 15, 154-65	9.7	41
150	Mutual reinforcement of inflammation and carcinogenesis by the Helicobacter pylori CagA oncoprotein. <i>Scientific Reports</i> , 2015 , 5, 10024	4.9	40
149	CTRP6 is an endogenous complement regulator that can effectively treat induced arthritis. <i>Nature Communications</i> , 2015 , 6, 8483	17.4	40
148	Complete genome sequence of Lactococcus lactis IO-1, a lactic acid bacterium that utilizes xylose and produces high levels of L-lactic acid. <i>Journal of Bacteriology</i> , 2012 , 194, 2102-3	3.5	40
147	Effects of bowel preparation on the human gut microbiome and metabolome. <i>Scientific Reports</i> , 2019 , 9, 4042	4.9	38
146	Deciphering the relationship among phosphate dynamics, electron-dense body and lipid accumulation in the green alga Parachlorella kessleri. <i>Scientific Reports</i> , 2016 , 6, 25731	4.9	38
145	Genomic analysis by deep sequencing of the probiotic Lactobacillus brevis KB290 harboring nine plasmids reveals genomic stability. <i>PLoS ONE</i> , 2013 , 8, e60521	3.7	37
144	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	3.5	36
143	Genome analysis suggests that the soil oligotrophic bacterium Agromonas oligotrophica (Bradyrhizobium oligotrophicum) is a nitrogen-fixing symbiont of Aeschynomene indica. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 2542-51	4.8	36
142	Distribution and evolution of nitrogen fixation genes in the phylum Bacteroidetes. <i>Microbes and Environments</i> , 2015 , 30, 44-50	2.6	36
141	Comparative genomic sequence analysis of the human chromosome 21 Down syndrome critical region. <i>Genome Research</i> , 2002 , 12, 1323-32	9.7	36
140	Seasonal transition of active bacterial and archaeal communities in relation to water management in paddy soils. <i>Microbes and Environments</i> , 2013 , 28, 370-80	2.6	35
139	Coordinated changes in DNA methylation in antigen-specific memory CD4 T cells. <i>Journal of Immunology</i> , 2013 , 190, 4076-91	5.3	35
138	Horizontal gene acquisition of Liberibacter plant pathogens from a bacteriome-confined endosymbiont of their psyllid vector. <i>PLoS ONE</i> , 2013 , 8, e82612	3.7	35

137	Identification of a novel <i>Staphylococcus pseudintermedius</i> exfoliative toxin gene and its prevalence in isolates from canines with pyoderma and healthy dogs. <i>FEMS Microbiology Letters</i> , 2010 , 312, 169-75	2.9	35
136	In silico inference of inclusion membrane protein family in obligate intracellular parasites chlamydiae. <i>DNA Research</i> , 2003 , 10, 9-17	4.5	34
135	Complete genome sequence of <i>Finnegoldia magna</i> , an anaerobic opportunistic pathogen. <i>DNA Research</i> , 2008 , 15, 39-47	4.5	33
134	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	7.8	33
133	Analysis of early bacterial communities on volcanic deposits on the island of Miyake (Miyake-jima), Japan: a 6-year study at a fixed site. <i>Microbes and Environments</i> , 2012 , 27, 19-29	2.6	32
132	Complete genomic sequence of the equol-producing bacterium <i>Eggerthella</i> sp. strain YY7918, isolated from adult human intestine. <i>Journal of Bacteriology</i> , 2011 , 193, 5570-1	3.5	32
131	Optimization of Data-Independent Acquisition Mass Spectrometry for Deep and Highly Sensitive Proteomic Analysis. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	32
130	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	3	31
129	Complete genome sequence of <i>Leptospirillum ferrooxidans</i> strain C2-3, isolated from a fresh volcanic ash deposit on the island of Miyake, Japan. <i>Journal of Bacteriology</i> , 2012 , 194, 4122-3	3.5	31
128	Mucin O-glycans facilitate symbiosynthesis to maintain gut immune homeostasis. <i>EBioMedicine</i> , 2019 , 48, 513-525	8.8	30
127	Genome analysis of a novel <i>Bradyrhizobium</i> sp. DOA9 carrying a symbiotic plasmid. <i>PLoS ONE</i> , 2015 , 10, e0117392	3.7	30
126	Draft Genome Sequence of the Betaproteobacterial Endosymbiont Associated with the Fungus <i>Mortierella elongata</i> FMR23-6. <i>Genome Announcements</i> , 2014 , 2,		30
125	Construction and analysis of EST libraries of the trans-polyisoprene producing plant, <i>Eucommia ulmoides</i> Oliver. <i>Planta</i> , 2012 , 236, 1405-17	4.7	30
124	<i>Bifidobacterium kashiwanohense</i> sp. nov., isolated from healthy infant faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011 , 61, 2610-2615	2.2	30
123	Genome-wide survey of mutual homologous recombination in a highly sexual bacterial species. <i>Genome Biology and Evolution</i> , 2012 , 4, 628-40	3.9	30
122	Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. <i>Microbiome</i> , 2019 , 7, 119	16.6	29
121	Dysbiosis of the salivary microbiota in pediatric-onset primary sclerosing cholangitis and its potential as a biomarker. <i>Scientific Reports</i> , 2018 , 8, 5480	4.9	29
120	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, 1356-9	5.9	28

119	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	11.5	26
118	Structures of genes encoding TATA box-binding proteins from <i>Trimeresurus gramineus</i> and <i>T. flavoviridis</i> snakes. <i>Gene</i> , 1995 , 152, 209-13	3.8	26
117	Orphan peak analysis: a novel method for detection of point mutations using an automated fluorescence DNA sequencer. <i>Genomics</i> , 1993 , 15, 415-7	4.3	26
116	<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	2.2	25
115	A case for a <i>Glossina</i> genome project. <i>Trends in Parasitology</i> , 2005 , 21, 107-11	6.4	25
114	Expression of rat alpha 2-macroglobulin gene during pregnancy. <i>Journal of Biochemistry</i> , 1986 , 100, 989-93	3.3	25
113	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	3.7	24
112	Time-series metagenomic analysis reveals robustness of soil microbiome against chemical disturbance. <i>DNA Research</i> , 2015 , 22, 413-24	4.5	24
111	Production of inbred and hybrid transgenic mice carrying large (> 200 kb) foreign DNA fragments by intracytoplasmic sperm injection. <i>Molecular Reproduction and Development</i> , 2005 , 72, 329-35	2.6	24
110	Identification and cloning of a novel cDNA belonging to tetratricopeptide repeat gene family from Down syndrome-critical region 21q22.2. <i>Journal of Biochemistry</i> , 1996 , 120, 820-7	3.1	24
109	Bacterial population dynamics in a laboratory activated sludge reactor monitored by pyrosequencing of 16S rRNA. <i>Microbes and Environments</i> , 2013 , 28, 65-70	2.6	23
108	Systematic identification and sequence analysis of the genomic islands of the enteropathogenic <i>Escherichia coli</i> strain B171-8 by the combined use of whole-genome PCR scanning and fosmid mapping. <i>Journal of Bacteriology</i> , 2008 , 190, 6948-60	3.5	23
107	<i>Sharpea azabuensis</i> gen. nov., sp. nov., a Gram-positive, strictly anaerobic bacterium isolated from the faeces of thoroughbred horses. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 2682-6	2.2	23
106	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	3.6	21
105	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, 68-74	4.1	20
104	Complete genome sequence of the denitrifying and N ₂ O-reducing bacterium <i>Azoarcus</i> sp. strain KH32C. <i>Journal of Bacteriology</i> , 2012 , 194, 1255	3.5	20
103	Rare occurrence of ras and p53 gene mutations in mouse stomach tumors induced by N-methyl-N-nitrosourea. <i>Japanese Journal of Cancer Research</i> , 1997 , 88, 363-8		20
102	Comparison of outer membrane protein genes omp and pmp in the whole genome sequences of <i>Chlamydia pneumoniae</i> isolates from Japan and the United States. <i>Journal of Infectious Diseases</i> , 2000 , 181 Suppl 3, S524-7	7	20

101	Genomic analysis of a NF1-related pseudogene on human chromosome 21. <i>Gene</i> , 1994 , 147, 277-80	3.8	20
100	Proteome analysis of shell matrix proteins in the brachiopod <i>Laqueus rubellus</i> . <i>Proteome Science</i> , 2015 , 13, 21	2.6	19
99	Complete Genome Sequence of the Equol-Producing Bacterium <i>Adlercreutzia equolifaciens</i> DSM 19450T. <i>Genome Announcements</i> , 2013 , 1,		19
98	Complete genome sequence of <i>Bacillus cereus</i> NC7401, which produces high levels of the emetic toxin cereulide. <i>Journal of Bacteriology</i> , 2012 , 194, 4767-8	3.5	19
97	Molecular cloning of a cDNA encoding rat NADH-cytochrome b5 reductase and the corresponding gene. <i>Journal of Biochemistry</i> , 1990 , 107, 810-6	3.1	19
96	Influence of <i>Porphyromonas gingivalis</i> in gut microbiota of streptozotocin-induced diabetic mice. <i>Oral Diseases</i> , 2019 , 25, 868-880	3.5	18
95	Interferon- α constrains cytokine production of group 2 innate lymphoid cells. <i>Immunology</i> , 2016 , 147, 21-9	7.8	18
94	Our second genome-human metagenome: how next-generation sequencer changes our life through microbiology. <i>Advances in Microbial Physiology</i> , 2013 , 62, 119-44	4.4	18
93	Complete genome sequence of the serotype k <i>Streptococcus mutans</i> strain LJ23. <i>Journal of Bacteriology</i> , 2012 , 194, 2754-5	3.5	18
92	Gastric acid inhibitor aggravates indomethacin-induced small intestinal injury via reducing <i>Lactobacillus johnsonii</i> . <i>Scientific Reports</i> , 2019 , 9, 17490	4.9	18
91	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	2.6	17
90	Genomic structure and evolution of the mating type locus in the green seaweed <i>Ulva partita</i> . <i>Scientific Reports</i> , 2017 , 7, 11679	4.9	17
89	Mode of activation of the GC box/Sp1-dependent promoter of the human NADH-cytochrome b5 reductase-encoding gene. <i>Gene</i> , 1995 , 164, 351-5	3.8	17
88	DNA hypermethylation and silencing of correlated with advanced stage and poor postoperative prognosis of esophageal squamous cell carcinoma. <i>Oncotarget</i> , 2017 , 8, 84434-84448	3.3	17
87	A Histone Methyltransferase ESET Is Critical for T Cell Development. <i>Journal of Immunology</i> , 2016 , 197, 2269-79	5.3	17
86	Comprehensive single-cell transcriptome analysis reveals heterogeneity in endometrioid adenocarcinoma tissues. <i>Scientific Reports</i> , 2017 , 7, 14225	4.9	16
85	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,	1.3	16
84	Global gene expression analysis of gill tissues from normal and thermally selected strains of rainbow trout. <i>Fisheries Science</i> , 2012 , 78, 1041-1049	1.9	16

83	Criteria for gene identification and features of genome organization: analysis of 6.5 Mb of DNA sequence from human chromosome 21. <i>Gene</i> , 2000 , 247, 215-32	3.8	16
82	Identification of cis-acting elements involved in an alternative splicing of the amyloid precursor protein (APP) gene. <i>Gene</i> , 1996 , 175, 203-8	3.8	16
81	Emergence of <i>Staphylococcus aureus</i> carrying multiple drug resistance genes on a plasmid encoding exfoliative toxin B. <i>Antimicrobial Agents and Chemotherapy</i> , 2013 , 57, 6131-40	5.9	15
80	Familial 14-Mb deletion at 21q11.2-q21.3 and variable phenotypic expression. <i>Journal of Human Genetics</i> , 2002 , 47, 511-6	4.3	15
79	Identification of two novel primate-specific genes in DSCR. <i>DNA Research</i> , 2002 , 9, 89-97	4.5	15
78	Two types of coagulogen mRNAs found in horseshoe crab (<i>Tachypleus tridentatus</i>) hemocytes: molecular cloning and nucleotide sequences. <i>Journal of Biochemistry</i> , 1986 , 100, 213-20	3.1	15
77	TH1 cell-inducing strain identified from the small intestinal mucosa of patients with Crohn's disease. <i>Gut Microbes</i> , 2020 , 12, 1788898	8.8	15
76	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	7.8	15
75	Unique pioneer microbial communities exposed to volcanic sulfur dioxide. <i>Scientific Reports</i> , 2016 , 6, 19687	4.9	15
74	The L1 family (KpnI family) sequence near the 3' end of human beta-globin gene may have been derived from an active L1 sequence. <i>Nucleic Acids Research</i> , 1987 , 15, 4007-20	20.1	14
73	<i>Lactobacillus kosoi</i> sp. nov., a fructophilic species isolated from kombu, a Japanese sugar-vegetable fermented beverage. <i>Antonie Van Leeuwenhoek</i> , 2018 , 111, 1149-1156	2.1	13
72	The identification and functional implications of human-specific "fixed" amino acid substitutions in the glutamate receptor family. <i>BMC Evolutionary Biology</i> , 2009 , 9, 224	3	13
71	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	6.3	12
70	Ancient DNA analysis of food remains in human dental calculus from the Edo period, Japan. <i>PLoS ONE</i> , 2020 , 15, e0226654	3.7	12
69	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, 246-52	3.3	12
68	Revealing microbial community structures in large- and small-scale activated sludge systems by barcoded pyrosequencing of 16S rRNA gene. <i>Water Science and Technology</i> , 2012 , 66, 2155-61	2.2	12
67	<i>Lactobacillus equicursoris</i> sp. nov., isolated from the faeces of a thoroughbred racehorse. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010 , 60, 109-112	2.2	11
66	Complete genome sequence of the denitrifying and N(2)O-reducing bacterium <i>Pseudogulbenkiania</i> sp. strain NH8B. <i>Journal of Bacteriology</i> , 2011 , 193, 6395-6	3.5	11

65	Complete genomic sequence of the O-desmethylangolensin-producing bacterium <i>Clostridium</i> rRNA cluster XIVa strain SY8519, isolated from adult human intestine. <i>Journal of Bacteriology</i> , 2011 , 193, 5568-5579	3.5	11
64	A 210-kb segment of tandem repeats and retroelements located between imprinted subdomains of mouse distal chromosome 7. <i>DNA Research</i> , 2004 , 11, 325-34	4.5	11
63	<i>Trimeresurus flavoviridis</i> venom gland phospholipase A2 isozymes genes have evolved via accelerated substitutions. <i>Journal of Molecular Recognition</i> , 1995 , 8, 40-6	2.6	10
62	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	4.1	10
61	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	3.9	10
60	Draft Genome Sequencing of the Highly Halotolerant and Allopolyploid Yeast NBRC 1876. <i>Genome Announcements</i> , 2017 , 5,		9
59	<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	2.2	8
58	Revealing the microbial assemblage structure in the human gut microbiome using latent Dirichlet allocation. <i>Microbiome</i> , 2020 , 8, 95	16.6	8
57	Genomic features of <i>Lactococcus lactis</i> IO-1, a lactic acid bacterium that utilizes xylose and produces high levels of L-lactic acid. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013 , 77, 1804-8	2.1	7
56	Complete genomic DNA sequence of the East Asian spotted fever disease agent <i>Rickettsia japonica</i> . <i>PLoS ONE</i> , 2013 , 8, e71861	3.7	7
55	Isolation of a novel human gene from the Down syndrome critical region of chromosome 21q22.2. <i>Journal of Biochemistry</i> , 1997 , 122, 872-7	3.1	7
54	Sequence-tagged NotI sites of human chromosome 21: sequence analysis and mapping. <i>Genomics</i> , 1993 , 17, 39-44	4.3	7
53	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	5.4	7
52	<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, 330-5	4.2	7
51	Genome Sequence of " <i>Serratia symbiotica</i> " Strain IS, a Facultative Bacterial Symbiont of the Pea Aphid. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	6
50	Complete genome sequence of <i>Bifidobacterium pseudocatenulatum</i> JCM 1200(T) isolated from infant feces. <i>Journal of Biotechnology</i> , 2015 , 210, 68-9	3.7	6
49	Repeated selective enrichment process of sediment microbiota occurred in sea cucumber guts. <i>Environmental Microbiology Reports</i> , 2019 , 11, 797-807	3.7	6
48	Large-scale microfabricated channel plates for high-throughput, fully automated DNA sequencing. <i>Electrophoresis</i> , 2008 , 29, 4723-32	3.6	6

47	Identification of the homozygously deleted region at chromosome 1p36.2 in human neuroblastoma. <i>Medical and Pediatric Oncology</i> , 2000 , 35, 516-21		6
46	The influences of low protein diet on the intestinal microbiota of mice. <i>Scientific Reports</i> , 2020 , 10, 17077	4.9	6
45	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, 362-5	7.4	6
44	Pancreatic glycoprotein 2 is a first line of defense for mucosal protection in intestinal inflammation. <i>Nature Communications</i> , 2021 , 12, 1067	17.4	6
43	Complete genome sequence of <i>Bifidobacterium catenulatum</i> JCM 1194(T) isolated from human feces. <i>Journal of Biotechnology</i> , 2015 , 210, 25-6	3.7	5
42	Complete Genome Sequence of a Phenanthrene Degradator, <i>Mycobacterium</i> sp. Strain EPa45 (NBRC 110737), Isolated from a Phenanthrene-Degrading Consortium. <i>Genome Announcements</i> , 2015 , 3,		5
41	<i>Vibrio aphrogenes</i> sp. nov., in the Rumoiensis clade isolated from a seaweed. <i>PLoS ONE</i> , 2017 , 12, e0180953	9.7	5
40	Fecal microbiota transplantation for recurrent infection in a patient with ulcerative colitis. <i>Intestinal Research</i> , 2018 , 16, 142-146	4.1	5
39	Changes in the bacterial community in the fermentation process of kōji, a Japanese sugar-vegetable fermented beverage. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017 , 81, 403-410	2.1	5
38	Complete nucleotide sequence of pLD-TEX-KL, a 66-kb plasmid of <i>Legionella dumoffii</i> TEX-KL strain. <i>Plasmid</i> , 2007 , 58, 261-8	3.3	5
37	Molecular cloning and characterization of a gene expressed in mouse developing tongue, mDscr5 gene, a homolog of human DSCR5 (Down syndrome Critical Region gene 5). <i>Mammalian Genome</i> , 2001 , 12, 347-51	3.2	5
36	Sixty new STSs (sequence-tagged sites) of human chromosome 21. <i>DNA Research</i> , 1994 , 1, 85-9	4.5	5
35	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	1.1	5
34	Complete genome sequence of <i>Bifidobacterium angulatum</i> JCM 7096(T) isolated from human feces. <i>Journal of Biotechnology</i> , 2015 , 211, 10-1	3.7	4
33	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	5	4
32	Draft Genome Sequence of <i>Cytophaga fermentans</i> JCM 21142T, a Facultative Anaerobe Isolated from Marine Mud. <i>Genome Announcements</i> , 2014 , 2,		4
31	Assessment and Improvement of Methods for Microbial DNA Preparation from Fecal Samples 2011 , 191-198		4
30	BAC library construction and BAC end sequencing of five <i>Drosophila</i> species: the comparative map with the <i>D. melanogaster</i> genome. <i>Genes and Genetic Systems</i> , 2008 , 83, 245-56	1.4	4

29	An exon-trapping system with a newly constructed trapping vector pEXT2; its application to the proximal region of the human chromosome 21 long arm. <i>FEBS Letters</i> , 1993 , 325, 303-8	3.8	4
28	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	3.7	4
27	sp. nov., sp. nov. and subsp. subsp. nov., isolated from human faeces, and creation of subsp. subsp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 473-480	2.2	4
26	<i>Staphylococcus cohnii</i> is a potentially biotherapeutic skin commensal alleviating skin inflammation. <i>Cell Reports</i> , 2021 , 35, 109052	10.6	4
25	Complete Genome Sequence of <i>Bifidobacterium scardovii</i> Strain JCM 12489T, Isolated from Human Blood. <i>Genome Announcements</i> , 2015 , 3,		3
24	Complete genome sequence of <i>Bifidobacterium bifidum</i> JCM 1255(T) isolated from feces of a breast-fed infant. <i>Journal of Biotechnology</i> , 2015 , 210, 66-7	3.7	3
23	Complete genome sequence of <i>Bifidobacterium breve</i> JCM 1192(T) isolated from infant feces. <i>Journal of Biotechnology</i> , 2015 , 210, 81-2	3.7	3
22	Complete Genome Sequence of <i>Bifidobacterium kashiwanohense</i> JCM 15439T, Isolated from Feces from a Healthy Japanese Infant. <i>Genome Announcements</i> , 2015 , 3,		3
21	Identification of large ancient duplications associated with human gene deserts. <i>Nature Genetics</i> , 2005 , 37, 1041-3	36.3	3
20	Polymorphisms of <i>Trimeresurus flavoviridis</i> venom gland phospholipase A2 isozyme genes. <i>Bioscience, Biotechnology and Biochemistry</i> , 1994 , 58, 1510-1	2.1	3
19	Draft Genome Sequence of <i>Lactobacillus farciminis</i> NBRC 111452, Isolated from Kōbo, a Japanese Sugar-Vegetable Fermented Beverage. <i>Genome Announcements</i> , 2016 , 4,		2
18	Draft Genome Sequence of <i>Bacteroides reticulotermitis</i> Strain JCM 10512T, Isolated from the Gut of a Termite. <i>Genome Announcements</i> , 2014 , 2,		2
17	The <i>Parachlorella</i> Genome and Transcriptome Endorse Active RWP-RK, Meiosis and Flagellar Genes in Trebouxiophyceyan Algae. <i>Cytologia</i> , 2019 , 84, 323-330	0.9	2
16	Altered microbiota composition reflects enhanced communication in 15q11-13 CNV mice. <i>Neuroscience Research</i> , 2020 , 161, 59-67	2.9	2
15	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	3.7	2
14	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	3.7	2
13	Complete Genome Sequence of <i>Winogradskyella</i> sp. Strain PG-2, a Proteorhodopsin-Containing Marine Flavobacterium. <i>Genome Announcements</i> , 2014 , 2,		1
12	Typing of X chromosomes bearing Tabby allele in mouse preimplantation embryos by detection of a microsatellite marker. <i>Experimental Animals</i> , 1996 , 45, 395-8	1.8	1

11	Cloning and Nucleotide Sequencing of Two Insecticidal-Endotoxin Genes from <i>Bacillus thuringiensis</i> var. <i>kurstaki</i> HD-1 DNA. <i>Agricultural and Biological Chemistry</i> , 1987 , 51, 455-463		1
10	Pyrosequencing Analysis of Bacterial Species Affected by Ethanol-Extract from Activated Sludge. <i>Journal of Water and Environment Technology</i> , 2019 , 17, 9-17	1.1	1
9	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	3.7	1
8	Revealing microbial assemblage structure in the human gut microbiome using latent Dirichlet allocation		1
7	Gut microbiota composition in obese and non-obese adult relatives from the highlands of Papua New Guinea. <i>FEMS Microbiology Letters</i> , 2020 , 367,	2.9	1
6	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 , 155520	10.2	1
5	Multiple nutritional and gut microbial factors associated with allergic rhinitis: the Hitachi Health Study. <i>Scientific Reports</i> , 2022 , 12, 3359	4.9	0
4	3. Microbial community analysis of aquaculture habitat using next generation sequencer. <i>Nippon Suisan Gakkaishi</i> , 2014 , 80, 1005-1005	0.2	
3	Monitoring of ribosomal RNA in the supernatant of activated sludge. <i>Journal of Japan Society of Civil Engineers Ser G (Environmental Research)</i> , 2013 , 69, III_231-III_239	0.1	
2	Dysregulation of the Intestinal Microbiome in Patients With Haploinsufficiency of A20. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 787667	5.9	
1	Mapping the Environmental Microbiome 2019 , 17-28		