

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	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
2	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	27.8	5,800
3	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, 4569-4574.	7.1	3,325
4	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
5	Bifidobacteria can protect from enteropathogenic infection through production of acetate. <i>Nature</i> , 2011, 469, 543-547.	27.8	1,836
6	Whole genome sequencing of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Lancet, The</i> , 2001, 357, 1225-1240.	13.7	1,835
7	Obesity-induced gut microbial metabolite promotes liver cancer through senescence secretome. <i>Nature</i> , 2013, 499, 97-101.	27.8	1,774
8	Dideoxy sequencing method using denatured plasmid templates. <i>Analytical Biochemistry</i> , 1986, 152, 232-238.	2.4	1,641
9	Genome sequence of the endocellular bacterial symbiont of aphids <i>Buchnera</i> sp. <i>APS. Nature</i> , 2000, 407, 81-86.	27.8	1,194
10	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.	3.4	1,190
11	The DNA sequence of human chromosome 21. <i>Nature</i> , 2000, 405, 311-319.	27.8	1,144
12	Complete genome sequence and comparative analysis of the industrial microorganism <i>Streptomyces avermitilis</i> . <i>Nature Biotechnology</i> , 2003, 21, 526-531.	17.5	1,108
13	Genome sequence of <i>Vibrio parahaemolyticus</i> : a pathogenic mechanism distinct from that of <i>V. cholerae</i> . <i>Lancet, The</i> , 2003, 361, 743-749.	13.7	928
14	A physical map of the human genome. <i>Nature</i> , 2001, 409, 934-941.	27.8	865
15	Th17 Cell Induction by Adhesion of Microbes to Intestinal Epithelial Cells. <i>Cell</i> , 2015, 163, 367-380.	28.9	846
16	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, 12215-12220.	7.1	784
17	Comparative Metagenomics Revealed Commonly Enriched Gene Sets in Human Gut Microbiomes. <i>DNA Research</i> , 2007, 14, 169-181.	3.4	760
18	A defined commensal consortium elicits CD8 T cells and anti-cancer immunity. <i>Nature</i> , 2019, 565, 600-605.	27.8	741

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19	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	13.3	717
20	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.	7.1	651
21	Two FOXP3+CD4+ T cell subpopulations distinctly control the prognosis of colorectal cancers. <i>Nature Medicine</i> , 2016, 22, 679-684.	30.7	641
22	Ectopic colonization of oral bacteria in the intestine drives T _H 1 cell induction and inflammation. <i>Science</i> , 2017, 358, 359-365.	12.6	612
23	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
24	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	17.5	581
25	Genome sequence of the endocellular obligate symbiont of tsetse flies, <i>Wigglesworthia glossinidia</i> . <i>Nature Genetics</i> , 2002, 32, 402-407.	21.4	573
26	Genome Sequence of the Streptomycin-Producing Microorganism <i>Streptomyces griseus</i> IFO 13350. <i>Journal of Bacteriology</i> , 2008, 190, 4050-4060.	2.2	534
27	The 160-Kilobase Genome of the Bacterial Endosymbiont <i>Carsonella</i> . <i>Science</i> , 2006, 314, 267-267.	12.6	501
28	A Novel Superoxide-producing NAD(P)H Oxidase in Kidney. <i>Journal of Biological Chemistry</i> , 2001, 276, 1417-1423.	3.4	456
29	Continuum of overlapping clones spanning the entire human chromosome 21q. <i>Nature</i> , 1992, 359, 380-387.	27.8	436
30	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
31	The gut microbiome of healthy Japanese and its microbial and functional uniqueness. <i>DNA Research</i> , 2016, 23, 125-133.	3.4	387
32	Evolutionary origin of insect <i>Wolbachia</i> nutritional mutualism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10257-10262.	7.1	327
33	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, 17939-17944.	7.1	325
34	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> , 2005, 16, 149-156.	5.5	324
35	Defensive Bacteriome Symbiont with a Drastically Reduced Genome. <i>Current Biology</i> , 2013, 23, 1478-1484.	3.9	314
36	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

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37	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, 3204-3223.	14.5	303
38	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
39	Robustness of Gut Microbiota of Healthy Adults in Response to Probiotic Intervention Revealed by High-Throughput Pyrosequencing. <i>DNA Research</i> , 2013, 20, 241-253.	3.4	272
40	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
41	Genome Sequence of the Lager Brewing Yeast, an Interspecies Hybrid. <i>DNA Research</i> , 2009, 16, 115-129.	3.4	269
42	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, 14925-14930.	7.1	266
43	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.	2.3	266
44	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, 151-161.	3.4	255
45	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	12.6	254
46	Novel bile acid biosynthetic pathways are enriched in the microbiome of centenarians. <i>Nature</i> , 2021, 599, 458-464.	27.8	251
47	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, 1042-1055.	5.5	248
48	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, 215-225.	3.4	243
49	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, 14919-14924.	7.1	241
50	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, 625-628.	27.8	229
51	Construction and Analysis of a Human-Chimpanzee Comparative Clone Map. <i>Science</i> , 2002, 295, 131-134.	12.6	228
52	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, 13272-13277.	7.1	227
53	The Human Intestinal Microbiome: A New Frontier of Human Biology. <i>DNA Research</i> , 2009, 16, 1-12.	3.4	227
54	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, 5555-5560.	7.1	220

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55	Genome of an Endosymbiont Coupling N ₂ Fixation to Cellulolysis Within Protist Cells in Termite Gut. <i>Science</i> , 2008, 322, 1108-1109.	12.6	217
56	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, 183-197.	11.0	215
57	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, 17846-17851.	7.1	213
58	DNA sequence and comparative analysis of chimpanzee chromosome 22. <i>Nature</i> , 2004, 429, 382-388.	27.8	212
59	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, 5605-5609.	7.1	200
60	Characterization of the 17 strains of regulatory T cell-inducing human-derived Clostridia. <i>Gut Microbes</i> , 2014, 5, 333-339.	9.8	182
61	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
62	The complete genomic sequence of <i>Mycoplasma penetrans</i> , an intracellular bacterial pathogen in humans. <i>Nucleic Acids Research</i> , 2002, 30, 5293-5300.	14.5	178
63	Acetate-producing bifidobacteria protect the host from enteropathogenic infection via carbohydrate transporters. <i>Gut Microbes</i> , 2012, 3, 449-454.	9.8	174
64	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.	9.6	172
65	The Whole-genome Sequencing of the Obligate Intracellular Bacterium <i>Orientia tsutsugamushi</i> Revealed Massive Gene Amplification During Reductive Genome Evolution. <i>DNA Research</i> , 2008, 15, 185-199.	3.4	166
66	Accelerated evolution of <i>Trimeresurus flavoviridis</i> venom gland phospholipase A2 isozymes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 5964-5968.	7.1	165
67	A Deeply Branching Thermophilic Bacterium with an Ancient Acetyl-CoA Pathway Dominates a Subsurface Ecosystem. <i>PLoS ONE</i> , 2012, 7, e30559.	2.5	161
68	Comparison of whole genome sequences of <i>Chlamydia pneumoniae</i> J138 from Japan and CWL029 from USA. <i>Nucleic Acids Research</i> , 2000, 28, 2311-2314.	14.5	160
69	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
70	Gut microorganisms act together to exacerbate inflammation in spinal cords. <i>Nature</i> , 2020, 585, 102-106.	27.8	153
71	A proliferative probiotic Bifidobacterium 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
72	Sequence analysis of a KpnI family member near the 3' end of human β -globin gene. <i>Nucleic Acids Research</i> , 1985, 13, 7813-7827.	14.5	148

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73	Ageing-related changes in the diversity of women's skin microbiomes associated with oral bacteria. <i>Scientific Reports</i> , 2017, 7, 10567.	3.3	148
74	Reductive Evolution of Bacterial Genome in Insect Gut Environment. <i>Genome Biology and Evolution</i> , 2011, 3, 702-714.	2.5	147
75	Cd1d-dependent regulation of bacterial colonization in the intestine of mice. <i>Journal of Clinical Investigation</i> , 2009, 119, 1241-1250.	8.2	146
76	Genome sequence of <i>Symbiobacterium thermophilum</i> , an uncultivable bacterium that depends on microbial commensalism. <i>Nucleic Acids Research</i> , 2004, 32, 4937-4944.	14.5	144
77	Efficient and Stable Transformation of <i>Lactuca sativa</i> L. cv. Cisco (lettuce) Plastids. <i>Transgenic Research</i> , 2006, 15, 205-217.	2.4	140
78	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
79	The genome sequence of <i>Clostridium botulinum</i> 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, 17472-17477.	7.1	135
80	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
81	Evolution in an oncogenic bacterial species with extreme genome plasticity: <i>Helicobacter pylori</i> East Asian genomes. <i>BMC Microbiology</i> , 2011, 11, 104.	3.3	132
82	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
83	A Simplified Method for the Preparation of Transcriptionally Active Liver Nuclear Extracts. <i>DNA and Cell Biology</i> , 1990, 9, 777-781.	1.9	129
84	The Human and Mouse <i>Period1</i> Genes: Five Well-Conserved E-Boxes Additively Contribute to the Enhancement of <i>mPer1</i> Transcription. <i>Genomics</i> , 2000, 65, 224-233.	2.9	129
85	Anammox organism <i>KSU-1</i> expresses a Nir-type copper-containing nitrite reductase instead of a NirS-type with cytochrome <i>cd₁</i> . <i>FEBS Letters</i> , 2012, 586, 1658-1663.	2.8	127
86	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
87	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, 273-284.	11.0	125
88	Architecture and anatomy of the genomic locus encoding the human leukemia-associated transcription factor <i>RUNX1/AML1</i> . <i>Gene</i> , 2001, 262, 23-33.	2.2	123
89	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.	2.9	119
90	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, 2049-2060.	1.3	115

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91	Identification of an internal cis-element essential for the human Li transcription and a nuclear factor(s) binding to the element. <i>Nucleic Acids Research</i> , 1992, 20, 3139-3145.	14.5	112
92	Comparative analysis of chimpanzee and human Y chromosomes unveils complex evolutionary pathway. <i>Nature Genetics</i> , 2006, 38, 158-167.	21.4	110
93	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, 139-146.	2.9	108
94	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
95	Insight into the Transmission Biology and Species-Specific Functional Capabilities of Tsetse (Diptera: Tj ETQq1 1 0.784314 rgBT /Overlo	4.1	105
96	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
97	Multiple Omics Uncovers Host-Gut Microbial Mutualism During Prebiotic Fructooligosaccharide Supplementation. <i>DNA Research</i> , 2014, 21, 469-480.	3.4	101
98	Gut microbiota-derived D-serine protects against acute kidney injury. <i>JCI Insight</i> , 2018, 3, .	5.0	99
99	Tonoplast- and Plasma Membrane-Localized Aquaporin-Family Transporters in Blue Hydrangea Sepals of Aluminum Hyperaccumulating Plant. <i>PLoS ONE</i> , 2012, 7, e43189.	2.5	97
100	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.	1.6	95
101	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, 7070-7078.	3.1	94
102	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, 127-139.	2.2	93
103	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.	3.4	93
104	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
105	Unusually high conservation of untranslated sequences in cDNAs for <i>Trimeresurus flavoviridis</i> phospholipase A2 isozymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 8557-8561.	7.1	91
106	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, 2439-2447.	5.5	90
107	Genome Sequence of the Cat Pathogen, <i>Chlamydophila felis</i> . <i>DNA Research</i> , 2006, 13, 15-23.	3.4	89
108	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, 375-386.	3.4	88

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109	Chromosome Painting In Silico in a Bacterial Species Reveals Fine Population Structure. <i>Molecular Biology and Evolution</i> , 2013, 30, 1454-1464.	8.9	87
110	Microbiome profile of the amniotic fluid as a predictive biomarker of perinatal outcome. <i>Scientific Reports</i> , 2017, 7, 12171.	3.3	86
111	Complete Genome Sequence of the Probiotic <i>Lactobacillus rhamnosus</i> ATCC 53103. <i>Journal of Bacteriology</i> , 2009, 191, 7630-7631.	2.2	85
112	Circadian oscillations of microbial and functional composition in the human salivary microbiome. <i>DNA Research</i> , 2017, 24, 261-270.	3.4	85
113	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, 4302-4307.	5.9	82
114	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
115	Genomic Adaptation of the <i>Lactobacillus casei</i> Group. <i>PLoS ONE</i> , 2013, 8, e75073.	2.5	81
116	Complete Genome Sequence and Comparative Analysis of the Fish Pathogen <i>Lactococcus garvieae</i> . <i>PLoS ONE</i> , 2011, 6, e23184.	2.5	80
117	Comparative Genomic Insights into Ecophysiology of Neutrophilic, Microaerophilic Iron Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2015, 6, 1265.	3.5	78
118	Effects of bowel preparation on the human gut microbiome and metabolome. <i>Scientific Reports</i> , 2019, 9, 4042.	3.3	78
119	Complete Genome Sequence of <i>Bradyrhizobium</i> sp. S23321: Insights into Symbiosis Evolution in Soil Oligotrophs. <i>Microbes and Environments</i> , 2012, 27, 306-315.	1.6	76
120	Draft Genome Sequencing and Comparative Analysis of <i>Aspergillus sojae</i> NBRC4239. <i>DNA Research</i> , 2011, 18, 165-176.	3.4	75
121	Human chromosome 11 DNA sequence and analysis including novel gene identification. <i>Nature</i> , 2006, 440, 497-500.	27.8	74
122	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
123	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
124	Comparative genomic analyses of <i>Streptococcus mutans</i> provide insights into chromosomal shuffling and species-specific content. <i>BMC Genomics</i> , 2009, 10, 358.	2.8	72
125	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, 1802-1808.	14.5	71
126	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, 2903-2917.	1.3	71

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127	Uremic Toxin-Producing Gut Microbiota in Rats with Chronic Kidney Disease. <i>Nephron</i> , 2017, 135, 51-60.	1.8	71
128	A Unique Dermal Dendritic Cell Subset That Skews the Immune Response toward Th2. <i>PLoS ONE</i> , 2013, 8, e73270.	2.5	70
129	Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse. <i>Gene</i> , 1992, 112, 189-195.	2.2	69
130	Distribution and Evolution of Nitrogen Fixation Genes in the Phylum <i>Bacteroidetes</i> . <i>Microbes and Environments</i> , 2015, 30, 44-50.	1.6	67
131	Commensal <i>Lactobacillus</i> Controls Immune Tolerance during Acute Liver Injury in Mice. <i>Cell Reports</i> , 2017, 21, 1215-1226.	6.4	67
132	Comparative Genome Analysis of the Mouse Imprinted Gene <i>Impact</i> and Its Nonimprinted Human Homolog <i>IMPACT</i> : Toward the Structural Basis for Species-Specific Imprinting. <i>Genome Research</i> , 2000, 10, 1878-1889.	5.5	66
133	The genomic structure and expression of MJD, the Machado-Joseph disease gene. <i>Journal of Human Genetics</i> , 2001, 46, 413-422.	2.3	66
134	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
135	Mucin O-glycans facilitate symbiosynthesis to maintain gut immune homeostasis. <i>EBioMedicine</i> , 2019, 48, 513-525.	6.1	66
136	Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. <i>Microbiome</i> , 2019, 7, 119.	11.1	65
137	Computer-guided design of optimal microbial consortia for immune system modulation. <i>ELife</i> , 2018, 7, .	6.0	65
138	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, 3704-3709.	14.5	64
139	Comparative Genome Analysis of Three Eukaryotic Parasites with Differing Abilities To Transform Leukocytes Reveals Key Mediators of <i>Theileria</i> -Induced Leukocyte Transformation. <i>MBio</i> , 2012, 3, e00204-12.	4.1	64
140	<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
141	Nucleotide Sequence Database Policies. <i>Science</i> , 2002, 298, 1333b-1333.	12.6	62
142	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, 1165-1166.	2.2	62
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