

De novo assembly of human genomes with massively parallel

Genome Research

20, 265-272

DOI: [10.1101/gr.097261.109](https://doi.org/10.1101/gr.097261.109)

Citation Report

#	ARTICLE	IF	CITATIONS
1	State of the art de novo assembly of human genomes from massively parallel sequencing data. <i>Human Genomics</i> , 2010, 4, 271.	1.4	74
2	De novo assembly of short sequence reads. <i>Briefings in Bioinformatics</i> , 2010, 11, 457-472.	3.2	167
3	Identifying SNPs without a Reference Genome by Comparing Raw Reads. <i>Lecture Notes in Computer Science</i> , 2010, , 147-158.	1.0	35
4	Assembly of large genomes using second-generation sequencing. <i>Genome Research</i> , 2010, 20, 1165-1173.	2.4	390
5	MÃ©tagÃ©nomique du microbiote intestinal : les applications potentielles. <i>Gastroenterologie Clinique Et Biologique</i> , 2010, 34, 24-30.	0.9	0
7	De novo characterization of a whitefly transcriptome and analysis of its gene expression during development. <i>BMC Genomics</i> , 2010, 11, 400.	1.2	344
8	SNP discovery by high-throughput sequencing in soybean. <i>BMC Genomics</i> , 2010, 11, 469.	1.2	94
9	De novo assembly and characterization of root transcriptome using Illumina paired-end sequencing and development of cSSR markers in sweetpotato (<i>Ipomoea batatas</i>). <i>BMC Genomics</i> , 2010, 11, 726.	1.2	386
10	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	13.7	1,058
11	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
12	Building the sequence map of the human pan-genome. <i>Nature Biotechnology</i> , 2010, 28, 57-63.	9.4	237
13	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010, 42, 1027-1030.	9.4	439
14	Whole-genome sequencing and comprehensive variant analysis of a Japanese individual using massively parallel sequencing. <i>Nature Genetics</i> , 2010, 42, 931-936.	9.4	106
15	A Computer Simulator for Assessing Different Challenges and Strategies of de Novo Sequence Assembly. <i>Genes</i> , 2010, 1, 263-282.	1.0	16
16	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. <i>Bioinformatics</i> , 2010, 26, 1277-1283.	1.8	98
17	Challenges of sequencing human genomes. <i>Briefings in Bioinformatics</i> , 2010, 11, 484-498.	3.2	134
18	Correction of sequencing errors in a mixed set of reads. <i>Bioinformatics</i> , 2010, 26, 1284-1290.	1.8	88
19	High-throughput sequencing reveals extensive variation in human-specific L1 content in individual human genomes. <i>Genome Research</i> , 2010, 20, 1262-1270.	2.4	277

#	ARTICLE	IF	CITATIONS
20	Application of second-generation sequencing to cancer genomics. <i>Briefings in Bioinformatics</i> , 2010, 11, 524-534.	3.2	42
21	REAL. , 2010, , .		24
22	TGM6 identified as a novel causative gene of spinocerebellar ataxias using exome sequencing. <i>Brain</i> , 2010, 133, 3510-3518.	3.7	243
23	Next-Generation Sequencing Techniques for Eukaryotic Microorganisms: Sequencing-Based Solutions to Biological Problems. <i>Eukaryotic Cell</i> , 2010, 9, 1300-1310.	3.4	120
24	Using the Velvet <i>de novo</i> Assembler for Short-Read Sequencing Technologies. <i>Current Protocols in Bioinformatics</i> , 2010, 31, Unit 11.5.	25.8	482
25	A window into third-generation sequencing. <i>Human Molecular Genetics</i> , 2010, 19, R227-R240.	1.4	761
26	High throughput DNA sequencing: The new sequencing revolution. <i>Plant Science</i> , 2010, 179, 407-422.	1.7	76
27	Assembly algorithms for next-generation sequencing data. <i>Genomics</i> , 2010, 95, 315-327.	1.3	957
28	A survey of sequence alignment algorithms for next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 473-483.	3.2	765
29	Systems Biology for Ecology. <i>Advances in Ecological Research</i> , 2010, 43, 87-149.	1.4	29
30	Quake: quality-aware detection and correction of sequencing errors. <i>Genome Biology</i> , 2010, 11, R116.	13.9	470
31	Improving draft assemblies by iterative mapping and assembly of short reads to eliminate gaps. <i>Genome Biology</i> , 2010, 11, R41.	13.9	264
32	Genome Sequence of the Tobacco Bacterial Wilt Pathogen <i>Ralstonia solanacearum</i> . <i>Journal of Bacteriology</i> , 2011, 193, 6088-6089.	1.0	57
33	OrchidBase: A Collection of Sequences of the Transcriptome Derived from Orchids. <i>Plant and Cell Physiology</i> , 2011, 52, 238-243.	1.5	78
34	Genome Sequence of the Thermophilic Strain <i>Bacillus coagulans</i> 2-6, an Efficient Producer of High-Optical-Purity L-Lactic Acid. <i>Journal of Bacteriology</i> , 2011, 193, 4563-4564.	1.0	20
35	The Awesome Power of Yeast Evolutionary Genetics: New Genome Sequences and Strain Resources for the <i>Saccharomyces sensu stricto</i> Genus. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 11-25.	0.8	348
36	An improved maximum likelihood formulation for accurate genome assembly. , 2011, , .		4
37	Whole Genome Sequences of Four <i>Brucella</i> Strains. <i>Journal of Bacteriology</i> , 2011, 193, 3674-3675.	1.0	17

#	ARTICLE	IF	CITATIONS
38	Dindel: Accurate indel calls from short-read data. <i>Genome Research</i> , 2011, 21, 961-973.	2.4	383
39	Analysis of Transcriptome Differences between Resistant and Susceptible Strains of the Citrus Red Mite <i>Panonychus citri</i> (Acari: Tetranychidae). <i>PLoS ONE</i> , 2011, 6, e28516.	1.1	81
40	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195.	13.7	1,912
42	A Portrait of the Transcriptome of the Neglected Trematode, <i>Fasciola gigantica</i> —Biological and Biotechnological Implications. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1004.	1.3	84
43	Extensive genomic and transcriptional diversity identified through massively parallel DNA and RNA sequencing of eighteen Korean individuals. <i>Nature Genetics</i> , 2011, 43, 745-752.	9.4	121
44	A Practical Comparison of De Novo Genome Assembly Software Tools for Next-Generation Sequencing Technologies. <i>PLoS ONE</i> , 2011, 6, e17915.	1.1	194
45	Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome de novo assembly. <i>Nature Biotechnology</i> , 2011, 29, 723-730.	9.4	113
46	How to apply de Bruijn graphs to genome assembly. <i>Nature Biotechnology</i> , 2011, 29, 987-991.	9.4	470
47	Evaluation of next-generation sequencing software in mapping and assembly. <i>Journal of Human Genetics</i> , 2011, 56, 406-414.	1.1	116
48	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. <i>Briefings in Functional Genomics</i> , 2011, 10, 322-333.	1.3	41
49	Efficient de novo assembly of single-cell bacterial genomes from short-read data sets. <i>Nature Biotechnology</i> , 2011, 29, 915-921.	9.4	203
50	Evidence of cellulose metabolism by the giant panda gut microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17714-17719.	3.3	455
53	Evaluation of next-generation sequencing software in mapping and assembly. <i>Journal of Human Genetics</i> , 2011, , .	1.1	2
54	The draft genome of the carcinogenic human liver fluke <i>Clonorchis sinensis</i> . <i>Genome Biology</i> , 2011, 12, R107.	13.9	183
55	The draft genome and transcriptome of <i>Cannabis sativa</i> . <i>Genome Biology</i> , 2011, 12, R102.	13.9	479
56	A vertebrate case study of the quality of assemblies derived from next-generation sequences. <i>Genome Biology</i> , 2011, 12, R31.	13.9	32
57	Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. <i>Nature Biotechnology</i> , 2011, 29, 1019-1023.	9.4	284
58	The Monarch Butterfly Genome Yields Insights into Long-Distance Migration. <i>Cell</i> , 2011, 147, 1171-1185.	13.5	509

#	ARTICLE	IF	CITATIONS
59	Transcriptome profiling and digital gene expression by deep-sequencing in normal/regenerative tissues of planarian <i>Dugesia japonica</i> . <i>Genomics</i> , 2011, 97, 364-371.	1.3	56
60	De novo transcriptome sequencing in <i>Salvia miltiorrhiza</i> to identify genes involved in the biosynthesis of active ingredients. <i>Genomics</i> , 2011, 98, 272-279.	1.3	181
61	Targeted Next-Generation Sequencing for the Molecular Genetic Diagnostics of Cardiomyopathies. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 110-122.	5.1	155
62	The impact of next-generation sequencing on genomics. <i>Journal of Genetics and Genomics</i> , 2011, 38, 95-109.	1.7	431
63	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. <i>Nature Biotechnology</i> , 2011, 29, 735-741.	9.4	699
64	Trends and Developments in Bioinformatics in 2010: Prospects and Perspectives. <i>Yearbook of Medical Informatics</i> , 2011, 20, 146-155.	0.8	0
65	Comparing De Novo Genome Assembly: The Long and Short of It. <i>PLoS ONE</i> , 2011, 6, e19175.	1.1	95
66	Genome Assembly Has a Major Impact on Gene Content: A Comparison of Annotation in Two <i>Bos Taurus</i> Assemblies. <i>PLoS ONE</i> , 2011, 6, e21400.	1.1	65
67	High-Throughput Sequencing of Six Bamboo Chloroplast Genomes: Phylogenetic Implications for Temperate Woody Bamboos (Poaceae: Bambusoideae). <i>PLoS ONE</i> , 2011, 6, e20596.	1.1	278
68	The First Insight into the Tissue Specific <i>Taxus</i> Transcriptome via Illumina Second Generation Sequencing. <i>PLoS ONE</i> , 2011, 6, e21220.	1.1	169
69	LOCAS – A Low Coverage Assembly Tool for Resequencing Projects. <i>PLoS ONE</i> , 2011, 6, e23455.	1.1	20
70	Meraculous: De Novo Genome Assembly with Short Paired-End Reads. <i>PLoS ONE</i> , 2011, 6, e23501.	1.1	191
71	Minimal Absent Words in Four Human Genome Assemblies. <i>PLoS ONE</i> , 2011, 6, e29344.	1.1	11
72	Microbial and Plant Cell Synthesis of Secondary Metabolites and Strain Improvement. , 2011, , 121-156.		0
73	A Combined Approach for de novo DNA Sequence Assembly of Very Short Reads. <i>IPSJ Transactions on Bioinformatics</i> , 2011, 4, 21-33.	0.2	2
74	Human genetics and genomics a decade after the release of the draft sequence of the human genome. <i>Human Genomics</i> , 2011, 5, 577.	1.4	86
75	NUCLEAR MONOPLIIDY AND ASEQUAL PROPAGATION OF <i>NANNOCHLOROPSIS OCEANICA</i> (EUSTIGMATOPHYCEAE) AS REVEALED BY ITS GENOME SEQUENCE. <i>Journal of Phycology</i> , 2011, 47, 1425-1432.	1.0	63
76	Limitations of next-generation genome sequence assembly. <i>Nature Methods</i> , 2011, 8, 61-65.	9.0	685

#	ARTICLE	IF	CITATIONS
77	Assemblies: the good, the bad, the ugly. <i>Nature Methods</i> , 2011, 8, 59-60.	9.0	26
78	Genome structural variation discovery and genotyping. <i>Nature Reviews Genetics</i> , 2011, 12, 363-376.	7.7	1,240
79	De novo genome sequencing and comparative genomics of date palm (<i>Phoenix dactylifera</i>). <i>Nature Biotechnology</i> , 2011, 29, 521-527.	9.4	356
80	Next-generation sequencing technologies and applications for human genetic history and forensics. <i>Investigative Genetics</i> , 2011, 2, 23.	3.3	101
81	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
82	Comparative studies of <i>de novo</i> assembly tools for next-generation sequencing technologies. <i>Bioinformatics</i> , 2011, 27, 2031-2037.	1.8	109
83	A scalable, fully automated process for construction of sequence-ready human exome targeted capture libraries. <i>Genome Biology</i> , 2011, 12, R1.	13.9	547
84	RNA-Seq analysis and de novo transcriptome assembly of <i>Hevea brasiliensis</i> . <i>Plant Molecular Biology</i> , 2011, 77, 299-308.	2.0	131
85	Sequencing technologies and genome sequencing. <i>Journal of Applied Genetics</i> , 2011, 52, 413-435.	1.0	591
86	Profiling of the transcriptome of <i>Porphyra yezoensis</i> with Solexa sequencing technology. <i>Science Bulletin</i> , 2011, 56, 2119-2130.	1.7	32
87	An overview to the investigative approach to species testing in wildlife forensic science. <i>Investigative Genetics</i> , 2011, 2, 2.	3.3	116
88	Efficient counting of k-mers in DNA sequences using a bloom filter. <i>BMC Bioinformatics</i> , 2011, 12, 333.	1.2	222
89	Parallelized short read assembly of large genomes using de Bruijn graphs. <i>BMC Bioinformatics</i> , 2011, 12, 354.	1.2	64
90	A new strategy for better genome assembly from very short reads. <i>BMC Bioinformatics</i> , 2011, 12, 493.	1.2	10
91	DecGPU: distributed error correction on massively parallel graphics processing units using CUDA and MPI. <i>BMC Bioinformatics</i> , 2011, 12, 85.	1.2	49
92	Assessing the benefits of using mate-pairs to resolve repeats in de novo short-read prokaryotic assemblies. <i>BMC Bioinformatics</i> , 2011, 12, 95.	1.2	53
93	Deep sequencing of the <i>Camellia sinensis</i> transcriptome revealed candidate genes for major metabolic pathways of tea-specific compounds. <i>BMC Genomics</i> , 2011, 12, 131.	1.2	374
94	An efficient approach to finding <i>Siraitia grosvenorii</i> triterpene biosynthetic genes by RNA-seq and digital gene expression analysis. <i>BMC Genomics</i> , 2011, 12, 343.	1.2	151

#	ARTICLE	IF	CITATIONS
95	WebMGA: a customizable web server for fast metagenomic sequence analysis. BMC Genomics, 2011, 12, 444.	1.2	641
96	Characterization of the sesame (<i>Sesamum indicum</i> L.) global transcriptome using Illumina paired-end sequencing and development of EST-SSR markers. BMC Genomics, 2011, 12, 451.	1.2	354
97	Transcriptome analysis and comparison reveal divergence between two invasive whitefly cryptic species. BMC Genomics, 2011, 12, 458.	1.2	99
98	Sequencing by ligation variation with endonuclease V digestion and deoxyinosine-containing query oligonucleotides. BMC Genomics, 2011, 12, 598.	1.2	13
99	De novo assembly of <i>Euphorbia fischeriana</i> root transcriptome identifies prostratin pathway related genes. BMC Genomics, 2011, 12, 600.	1.2	75
100	Structural variation in the chicken genome identified by paired-end next-generation DNA sequencing of reduced representation libraries. BMC Genomics, 2011, 12, 94.	1.2	25
101	Challenges in studying genomic structural variant formation mechanisms: The short-read dilemma and beyond. BioEssays, 2011, 33, 840-850.	1.2	34
102	Genomics for Key Players in the N Cycle. Methods in Enzymology, 2011, 496, 289-318.	0.4	3
103	Whole-Genome Sequences of Four <i>Mycobacterium bovis</i> BCG Vaccine Strains. Journal of Bacteriology, 2011, 193, 3152-3153.	1.0	28
104	High-quality draft assemblies of mammalian genomes from massively parallel sequence data. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1513-1518.	3.3	1,476
105	Genome Sequence of <i>Paracoccus</i> sp. Strain TRP, a Chlorpyrifos Biodegrader. Journal of Bacteriology, 2011, 193, 1786-1787.	1.0	28
106	PE-Assembler: <i>de novo</i> assembler using short paired-end reads. Bioinformatics, 2011, 27, 167-174.	1.8	98
107	Genome Sequence of <i>Anaerophaga</i> sp. Strain HS1, a Novel, Moderately Thermophilic, Strictly Anaerobic Bacterium Isolated from Hot Spring Sediment. Journal of Bacteriology, 2011, 193, 5572-5572.	1.0	10
108	Meta-IDBA: a <i>de Novo</i> assembler for metagenomic data. Bioinformatics, 2011, 27, i94-i101.	1.8	267
109	Digital gene expression for non-model organisms. Genome Research, 2011, 21, 1905-1915.	2.4	50
110	Complete Genome Sequence of <i>Bacillus amyloliquefaciens</i> XH7, Which Exhibits Production of Purine Nucleosides. Journal of Bacteriology, 2011, 193, 5593-5594.	1.0	17
111	Assemblathon 1: A competitive assessment of <i>de novo</i> short read assembly methods. Genome Research, 2011, 21, 2224-2241.	2.4	443
112	Genome Sequence of <i>Rhodococcus</i> sp. Strain R04, a Polychlorinated-Biphenyl Biodegrader. Journal of Bacteriology, 2011, 193, 5032-5033.	1.0	16

#	ARTICLE	IF	CITATIONS
113	The genome of the leaf-cutting ant<i>Acromyrmex echinator</i> suggests key adaptations to advanced social life and fungus farming. <i>Genome Research</i> , 2011, 21, 1339-1348.	2.4	210
114	Genome Sequence of the Spinosyns-Producing Bacterium <i>Saccharopolyspora spinosa</i> NRRL 18395. <i>Journal of Bacteriology</i> , 2011, 193, 3150-3151.	1.0	21
115	Genome Sequences of <i>Salmonella enterica</i> Serovar Typhimurium, Choleraesuis, Dublin, and Gallinarum Strains of Well- Defined Virulence in Food-Producing Animals. <i>Journal of Bacteriology</i> , 2011, 193, 3162-3163.	1.0	61
116	Genome Sequence of <i>Escherichia coli</i> XH140A, Which Produces <sc> </sc>-Threonine. <i>Journal of Bacteriology</i> , 2011, 193, 6090-6091.	1.0	1
117	FLASH: fast length adjustment of short reads to improve genome assemblies. <i>Bioinformatics</i> , 2011, 27, 2957-2963.	1.8	11,573
118	Draft Genome Sequence of <i>Escherichia coli</i> XH001, a Producer of <sc> </sc>-Threonine in Industry. <i>Journal of Bacteriology</i> , 2011, 193, 6406-6407.	1.0	2
119	Genome-scale transcriptome analysis of the desert poplar, <i>Populus euphratica</i> . <i>Tree Physiology</i> , 2011, 31, 452-461.	1.4	179
120	Genome Sequence of the Rice-Pathogenic Bacterium <i>Acidovorax avenae</i> subsp. <i>avenae</i> RS-1. <i>Journal of Bacteriology</i> , 2011, 193, 5013-5014.	1.0	47
121	Whole-Genome Sequence of a Multidrug-Resistant Clinical Isolate of <i>Acinetobacter lwoffii</i> . <i>Journal of Bacteriology</i> , 2011, 193, 5549-5550.	1.0	31
122	Genome Sequence of <i>Corynebacterium glutamicum</i> S9114, a Strain for Industrial Production of Glutamate. <i>Journal of Bacteriology</i> , 2011, 193, 6096-6097.	1.0	25
123	Complete Genome Sequence of Seawater Bacterium <i>Glaciecola nitratireducens</i> FR1064 T. <i>Journal of Bacteriology</i> , 2011, 193, 7006-7007.	1.0	8
124	Bambus 2: scaffolding metagenomes. <i>Bioinformatics</i> , 2011, 27, 2964-2971.	1.8	124
125	Draft Genome Sequence of <i>Paenibacillus elgii</i> B69, a Strain with Broad Antimicrobial Activity. <i>Journal of Bacteriology</i> , 2011, 193, 4537-4537.	1.0	19
126	Complete Genome Sequence of <i>Bacillus amyloliquefaciens</i> TA208, a Strain for Industrial Production of Guanosine and Ribavirin. <i>Journal of Bacteriology</i> , 2011, 193, 3142-3143.	1.0	16
127	Genome Sequences of Three Tunicamycin-Producing <i>Streptomyces</i> Strains, <i>S. chartreusis</i> NRRL 12338, <i>S. chartreusis</i> NRRL 3882, and <i>S. lysosuperificus</i> ATCC 31396. <i>Journal of Bacteriology</i> , 2011, 193, 7021-7022.	1.0	24
128	De novo assembly and validation of planaria transcriptome by massive parallel sequencing and shotgun proteomics. <i>Genome Research</i> , 2011, 21, 1193-1200.	2.4	100
129	Metagenomic Insights into the Evolution, Function, and Complexity of the Planktonic Microbial Community of Lake Lanier, a Temperate Freshwater Ecosystem. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6000-6011.	1.4	151
130	Multiple reference genomes and transcriptomes for <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2011, 477, 419-423.	13.7	593

#	ARTICLE	IF	CITATIONS
131	Identification of PRRT2 as the causative gene of paroxysmal kinesigenic dyskinesias. <i>Brain</i> , 2011, 134, 3493-3501.	3.7	263
132	Fast scaffolding with small independent mixed integer programs. <i>Bioinformatics</i> , 2011, 27, 3259-3265.	1.8	72
133	Correcting errors in short reads by multiple alignments. <i>Bioinformatics</i> , 2011, 27, 1455-1461.	1.8	145
134	Mugsy: fast multiple alignment of closely related whole genomes. <i>Bioinformatics</i> , 2011, 27, 334-342.	1.8	444
135	Genome Sequence of <i>Enterococcus faecium</i> Clinical Isolate LCT-EF128. <i>Journal of Bacteriology</i> , 2012, 194, 4765-4765.	1.0	4
136	Accurate estimation of short read mapping quality for next-generation genome sequencing. <i>Bioinformatics</i> , 2012, 28, i349-i355.	1.8	29
137	Bioinformatics for the Human Microbiome Project. <i>PLoS Computational Biology</i> , 2012, 8, e1002779.	1.5	73
138	Diverse CRISPRs Evolving in Human Microbiomes. <i>PLoS Genetics</i> , 2012, 8, e1002441.	1.5	125
139	Advances in BAC-Based Physical Mapping and Map Integration Strategies in Plants. <i>Journal of Biomedicine and Biotechnology</i> , 2012, 2012, 1-11.	3.0	37
140	The genome of <i>Prunus mume</i> . <i>Nature Communications</i> , 2012, 3, 1318.	5.8	441
141	Genome Sequences of Type Strains of Seven Species of the Marine Bacterium <i>Pseudoalteromonas</i> . <i>Journal of Bacteriology</i> , 2012, 194, 2746-2747.	1.0	13
142	Draft Genome Sequence of the Novel Agarolytic Bacterium <i>Aquimarina agarilytica</i> ZC1. <i>Journal of Bacteriology</i> , 2012, 194, 2769-2769.	1.0	13
143	Draft Genome Sequence of <i>Rhodococcus</i> sp. Strain P14, a Biodegrader of High-Molecular-Weight Polycyclic Aromatic Hydrocarbons. <i>Journal of Bacteriology</i> , 2012, 194, 3546-3546.	1.0	25
144	Draft Genome Sequence of <i>Gluconobacter oxydans</i> WSH-003, a Strain That Is Extremely Tolerant of Saccharides and Alditols. <i>Journal of Bacteriology</i> , 2012, 194, 4455-4456.	1.0	31
145	Genome Sequences of Three Species in the Family Planctomycetaceae. <i>Journal of Bacteriology</i> , 2012, 194, 3740-3741.	1.0	29
146	Genome Sequence of the Human-Pathogenic Bacterium <i>Vibrio vulnificus</i> Type Strain ATCC 27562. <i>Journal of Bacteriology</i> , 2012, 194, 6954-6955.	1.0	5
147	Genetic Variation in the Acorn Barnacle from Allozymes to Population Genomics. <i>Integrative and Comparative Biology</i> , 2012, 52, 418-429.	0.9	15
148	Draft Genome Sequence of a Novel Bacterial Strain, LSJC7, Belonging to the Family Enterobacteriaceae with Dual Resistance to Arsenic and Tetracycline. <i>Journal of Bacteriology</i> , 2012, 194, 7005-7006.	1.0	7

#	ARTICLE	IF	CITATIONS
149	Draft Genome Sequence of Butanol-Acetone-Producing <i>Clostridium beijerinckii</i> Strain G117. <i>Journal of Bacteriology</i> , 2012, 194, 5470-5471.	1.0	19
150	Draft Genome Sequence of the Sponge-Associated Strain <i>Bacillus atrophaeus</i> C89, a Potential Producer of Marine Drugs. <i>Journal of Bacteriology</i> , 2012, 194, 4454-4454.	1.0	15
151	Genome Sequence of the Protease-Producing Bacterium <i>Rheinheimera nanhaiensis</i> E407-8 T, Isolated from Deep-Sea Sediment of the South China Sea. <i>Journal of Bacteriology</i> , 2012, 194, 7001-7002.	1.0	1
152	Draft Genome Sequence of <i>Aspergillus oryzae</i> Strain 3.042. <i>Eukaryotic Cell</i> , 2012, 11, 1178-1178.	3.4	27
153	Draft Genome Sequence of the Cyanide-Utilizing Bacterium <i>Pseudomonas fluorescens</i> Strain NCIMB 11764. <i>Journal of Bacteriology</i> , 2012, 194, 6618-6619.	1.0	9
154	Draft Genome Sequence of the Yeast <i>Pachysolen tannophilus</i> CBS 4044/NRRL Y-2460. <i>Eukaryotic Cell</i> , 2012, 11, 827-827.	3.4	20
155	Genome Sequence of the Cycloprodigiosin-Producing Bacterial Strain <i>Pseudoalteromonas rubra</i> ATCC 29570. <i>Journal of Bacteriology</i> , 2012, 194, 1637-1638.	1.0	18
156	Draft Genome Sequence of Strain P7-3-5, a New Flavobacteriaceae Bacterium Isolated from Intertidal Sand. <i>Journal of Bacteriology</i> , 2012, 194, 6632-6632.	1.0	1
157	Genome Sequence of <i>Stenotrophomonas maltophilia</i> RR-10, Isolated as an Endophyte from Rice Root. <i>Journal of Bacteriology</i> , 2012, 194, 1280-1281.	1.0	59
158	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain ATCC 27853. <i>Journal of Bacteriology</i> , 2012, 194, 3755-3755.	1.0	14
159	Genome Sequence of <i>Borrelia garinii</i> Strain NMJW1, Isolated from China. <i>Journal of Bacteriology</i> , 2012, 194, 6660-6661.	1.0	16
160	Draft Genome Sequence of <i>Streptomyces</i> sp. Strain SS, Which Produces a Series of Uridyl Peptide Antibiotic Sansanmycins. <i>Journal of Bacteriology</i> , 2012, 194, 6988-6989.	1.0	5
161	Scalable genome scaffolding using integer linear programming. , 2012, , .		6
162	Complete Genome Sequence of <i>Bartonella quintana</i> , a Bacterium Isolated from Rhesus Macaques. <i>Journal of Bacteriology</i> , 2012, 194, 6347-6347.	1.0	7
163	A meta-genome sequencing and assembly preprocessing algorithm inspired by restriction site base composition. , 2012, , .		5
164	Draft Genome Sequence of the Methane-Oxidizing Bacterium <i>Methylococcus capsulatus</i> (Texas). <i>Journal of Bacteriology</i> , 2012, 194, 6626-6626.	1.0	21
165	A <i>de Bruijn</i> Graph Approach to the Quantification of Closely-Related Genomes in a Microbial Community. <i>Journal of Computational Biology</i> , 2012, 19, 814-825.	0.8	18
166	Complete Genome Sequence of <i>Pelagibacterium halotolerans</i> B2T. <i>Journal of Bacteriology</i> , 2012, 194, 197-198.	1.0	20

#	ARTICLE	IF	CITATIONS
167	Theoretical Basis of a New Method for DNA Fragment Assembly in k-mer Graphs. , 2012, , .		3
168	Hypervariable loci in the human gut virome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3962-3966.	3.3	167
169	Intron Gains and Losses in the Evolution of Fusarium and Cryptococcus Fungi. Genome Biology and Evolution, 2012, 4, 1148-1161.	1.1	19
170	Genome Sequence of <i>Corynebacterium glutamicum</i> ATCC 14067, Which Provides Insight into Amino Acid Biosynthesis in Coryneform Bacteria. Journal of Bacteriology, 2012, 194, 742-743.	1.0	25
171	Genome Sequence of the Rice Pathogen <i>Dickeya zeae</i> Strain ZJU1202. Journal of Bacteriology, 2012, 194, 4452-4453.	1.0	20
172	Genome Sequence of the Oleaginous Red Yeast <i>Rhodospiridium toruloides</i> MTCC 457. Eukaryotic Cell, 2012, 11, 1083-1084.	3.4	57
173	Draft Genome Sequence of the Bean-Nodulating <i>Sinorhizobium fredii</i> Strain GR64. Journal of Bacteriology, 2012, 194, 6978-6978.	1.0	2
174	Draft Genome Sequence of the Nitrophenol-Degrading Actinomycete <i>Rhodococcus imtechensis</i> RKJ300. Journal of Bacteriology, 2012, 194, 3543-3543.	1.0	16
175	Draft Genome Sequences of Two <i>Streptococcus pyogenes</i> Strains Involved in Abnormal Sharp Raised Scarlet Fever in China, 2011. Journal of Bacteriology, 2012, 194, 5983-5984.	1.0	3
176	Genome Sequence of <i>Pedobacter arcticus</i> sp. nov., a Sea Ice Bacterium Isolated from Tundra Soil. Journal of Bacteriology, 2012, 194, 6688-6688.	1.0	5
177	Draft Genome Sequence of <i>Bacillus cereus</i> Strain LCT-BC244. Journal of Bacteriology, 2012, 194, 3549-3549.	1.0	4
178	Draft Genome Sequence of <i>Yersinia pestis</i> Strain 2501, an Isolate from the Great Gerbil Plague Focus in Xinjiang, China. Journal of Bacteriology, 2012, 194, 5447-5448.	1.0	4
179	Genome Sequence of <i>Streptomyces</i> sp. Strain TOR3209, a Rhizosphere Microecology Regulator Isolated from Tomato Rhizosphere. Journal of Bacteriology, 2012, 194, 1627-1627.	1.0	13
180	PARALLEL ALGORITHMS FOR MAPPING SHORT DEGENERATE AND WEIGHTED DNA SEQUENCES TO A REFERENCE GENOME. International Journal of Foundations of Computer Science, 2012, 23, 249-259.	0.8	1
181	Transcriptomic Evidence for the Expression of Horizontally Transferred Algal Nuclear Genes in the Photosynthetic Sea Slug, <i>Elysia chlorotica</i> . Molecular Biology and Evolution, 2012, 29, 1545-1556.	3.5	54
182	Draft Genome Sequence of <i>Streptomyces globisporus</i> C-1027, Which Produces an Antitumor Antibiotic Consisting of a Nine-Membered Enediyne with a Chromoprotein. Journal of Bacteriology, 2012, 194, 4144-4144.	1.0	13
183	De Novo Sequencing and Characterization of the Floral Transcriptome of <i>Dendrocalamus latiflorus</i> (Poaceae: Bambusoideae). PLoS ONE, 2012, 7, e42082.	1.1	111
184	Telescope: <i>de novo</i> assembly of highly repetitive regions. Bioinformatics, 2012, 28, i311-i317.	1.8	22

#	ARTICLE	IF	CITATIONS
185	Draft Genome Sequence of <i>Serratia marcescens</i> Strain LCT-SM213. <i>Journal of Bacteriology</i> , 2012, 194, 4477-4478.	1.0	7
186	Genome Sequence of <i>Candidatus Microthrix parvicella</i> -Bio17-1, a Long-Chain-Fatty-Acid-Accumulating Filamentous Actinobacterium from a Biological Wastewater Treatment Plant. <i>Journal of Bacteriology</i> , 2012, 194, 6670-6671.	1.0	27
187	Efficient de novo assembly of large genomes using compressed data structures. <i>Genome Research</i> , 2012, 22, 549-556.	2.4	649
188	Direct Comparisons of Illumina vs. Roche 454 Sequencing Technologies on the Same Microbial Community DNA Sample. <i>PLoS ONE</i> , 2012, 7, e30087.	1.1	360
189	Global Transcriptional Analysis of Olfactory Genes in the Head of Pine Shoot Beetle, <i>Tomicus yunnanensis</i> . <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-10.	2.0	22
190	Genome Sequence of the Aerobic Bacterium <i>Bacillus</i> sp. Strain FJAT-13831. <i>Journal of Bacteriology</i> , 2012, 194, 6633-6633.	1.0	1
191	Complete Genome Sequence of <i>Staphylococcus aureus</i> Bacteriophage GH15. <i>Journal of Virology</i> , 2012, 86, 8914-8915.	1.5	32
192	Complete Genome Sequence of a Thermophilic Methanogen, <i>Methanocella conradii</i> HZ254, Isolated from Chinese Rice Field Soil. <i>Journal of Bacteriology</i> , 2012, 194, 2398-2399.	1.0	24
193	Stitching gene fragments with a network matching algorithm improves gene assembly for metagenomics. <i>Bioinformatics</i> , 2012, 28, i363-i369.	1.8	14
194	<i>Gossamer</i> – a resource-efficient de novo assembler. <i>Bioinformatics</i> , 2012, 28, 1937-1938.	1.8	18
195	Xenome – a tool for classifying reads from xenograft samples. <i>Bioinformatics</i> , 2012, 28, i172-i178.	1.8	211
196	Genome Sequence of <i>Streptomyces auratus</i> Strain AGR0001, a Phoslactomycin-Producing Actinomycete. <i>Journal of Bacteriology</i> , 2012, 194, 5472-5473.	1.0	11
197	Complete Genome Sequence of <i>Paenibacillus mucilaginosus</i> 3016, a Bacterium Functional as Microbial Fertilizer. <i>Journal of Bacteriology</i> , 2012, 194, 2777-2778.	1.0	18
198	Upgraded genomic information of <i>Jatropha curcas</i> L.. <i>Plant Biotechnology</i> , 2012, 29, 123-130.	0.5	74
199	Discovery of Retroviral Homologs in Bats: Implications for the Origin of Mammalian Gammaretroviruses. <i>Journal of Virology</i> , 2012, 86, 4288-4293.	1.5	52
200	Dynamic Nucleotide-Binding Site and Leucine-Rich Repeat-Encoding Genes in the Grass Family <i>Â</i> . <i>Plant Physiology</i> , 2012, 159, 197-210.	2.3	132
201	Transcriptome and Comparative Gene Expression Analysis of <i>Sogatella furcifera</i> (Horváth) in Response to Southern Rice Black-Streaked Dwarf Virus. <i>PLoS ONE</i> , 2012, 7, e36238.	1.1	79
203	Gamma Paleohexaploidy in the Stem Lineage of Core Eudicots: Significance for MADS-Box Gene and Species Diversification. <i>Molecular Biology and Evolution</i> , 2012, 29, 3793-3806.	3.5	127

#	ARTICLE	IF	CITATIONS
204	Oral Spirochetes Implicated in Dental Diseases Are Widespread in Normal Human Subjects and Carry Extremely Diverse Integron Gene Cassettes. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5288-5296.	1.4	20
205	SLIQ: Simple Linear Inequalities for Efficient Contig Scaffolding. <i>Journal of Computational Biology</i> , 2012, 19, 1162-1175.	0.8	8
206	Mitochondrial genome variability within the <i>Candida parapsilosis</i> species complex. <i>Mitochondrion</i> , 2012, 12, 514-519.	1.6	20
207	<i>De novo</i> assembly of the transcriptome of an invasive snail and its multiple ecological applications. <i>Molecular Ecology Resources</i> , 2012, 12, 1133-1144.	2.2	32
208	Genomic dissection of small <i>RNA</i> s in wild rice (<i>Oryza rufipogon</i>): lessons for rice domestication. <i>New Phytologist</i> , 2012, 196, 914-925.	3.5	33
209	Complete Genome Sequence of the Naphthalene-Degrading <i>Pseudomonas putida</i> Strain ND6. <i>Journal of Bacteriology</i> , 2012, 194, 5154-5155.	1.0	33
210	A <i>de novo</i> metagenomic assembly program for shotgun DNA reads. <i>Bioinformatics</i> , 2012, 28, 1455-1462.	1.8	42
211	Computational tools for viral metagenomics and their application in clinical research. <i>Virology</i> , 2012, 434, 162-174.	1.1	59
212	Genome sequences of wild and domestic bactrian camels. <i>Nature Communications</i> , 2012, 3, 1202.	5.8	176
213	COPE: an accurate <i>k</i> -mer-based pair-end reads connection tool to facilitate genome assembly. <i>Bioinformatics</i> , 2012, 28, 2870-2874.	1.8	145
214	Capturing native long-range contiguity by in situ library construction and optical sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18749-18754.	3.3	10
215	Bioinformatics tools and databases for analysis of next-generation sequence data. <i>Briefings in Functional Genomics</i> , 2012, 11, 12-24.	1.3	73
216	A genome triplication associated with early diversification of the core eudicots. <i>Genome Biology</i> , 2012, 13, R3.	13.9	389
217	Current challenges in <i>de novo</i> plant genome sequencing and assembly. <i>Genome Biology</i> , 2012, 13, 243.	13.9	157
218	<i>De novo</i> assembly and characterization of the garlic (<i>Allium sativum</i>) bud transcriptome by Illumina sequencing. <i>Plant Cell Reports</i> , 2012, 31, 1823-1828.	2.8	76
219	Next-generation sequencing of experimental mouse strains. <i>Mammalian Genome</i> , 2012, 23, 490-498.	1.0	53
220	Copy number variation in the cattle genome. <i>Functional and Integrative Genomics</i> , 2012, 12, 609-624.	1.4	60
222	<i>De novo</i> transcriptome sequencing of <i>Momordica cochinchinensis</i> to identify genes involved in the carotenoid biosynthesis. <i>Plant Molecular Biology</i> , 2012, 79, 413-427.	2.0	66

#	ARTICLE	IF	CITATIONS
223	Exploring single-sample SNP and INDEL calling with whole-genome <i>de novo</i> assembly. <i>Bioinformatics</i> , 2012, 28, 1838-1844.	1.8	330
224	A multi-omic map of the lipid-producing yeast <i>Rhodosporidium toruloides</i> . <i>Nature Communications</i> , 2012, 3, 1112.	5.8	324
225	Identification of Representative Genes of the Central Nervous System of the Locust, <i>Locusta migratoria manilensis</i> by Deep Sequencing. <i>Journal of Insect Science</i> , 2012, 12, 1-15.	0.9	9
226	The <i>ARC1</i> E3 Ligase Gene Is Frequently Deleted in Self-Compatible Brassicaceae Species and Has a Conserved Role in <i>Arabidopsis lyrata</i> Self-Pollen Rejection. <i>Plant Cell</i> , 2012, 24, 4607-4620.	3.1	94
227	Transcriptome Characterization and Sequencing-Based Identification of Salt-Responsive Genes in <i>Millettia pinnata</i> , a Semi-Mangrove Plant. <i>DNA Research</i> , 2012, 19, 195-207.	1.5	68
228	Identification of Genes Potentially Related to Biomineralization and Immunity by Transcriptome Analysis of Pearl Sac in Pearl Oyster <i>Pinctada martensii</i> . <i>Marine Biotechnology</i> , 2012, 14, 730-739.	1.1	103
229	Ultrafast clustering algorithms for metagenomic sequence analysis. <i>Briefings in Bioinformatics</i> , 2012, 13, 656-668.	3.2	403
230	A new grapevine virus discovered by deep sequencing of virus- and viroid-derived small RNAs in <i>Cv Pinot gris</i> . <i>Virus Research</i> , 2012, 163, 262-268.	1.1	227
231	The Molecular Basis of Host Specialization in Bean Pathovars of <i>Pseudomonas syringae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 877-888.	1.4	83
232	Mapsembler, targeted and micro assembly of large NGS datasets on a desktop computer. <i>BMC Bioinformatics</i> , 2012, 13, 48.	1.2	31
233	Prediction of the optimum combination of solexa sequencing libraries in genome projects. , 2012, , .		0
234	Adaptive Genetic Variation on the Landscape: Methods and Cases. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2012, 43, 23-43.	3.8	250
235	Paired-end sequencing of Fosmid libraries by Illumina. <i>Genome Research</i> , 2012, 22, 2241-2249.	2.4	52
236	A comparative analysis of the intestinal metagenomes present in guinea pigs (<i>Cavia porcellus</i>) and humans (<i>Homo sapiens</i>). <i>BMC Genomics</i> , 2012, 13, 514.	1.2	43
237	Succinct de Bruijn Graphs. <i>Lecture Notes in Computer Science</i> , 2012, , 225-235.	1.0	116
238	Draft Genome of <i>Omphalotus olearius</i> Provides a Predictive Framework for Sesquiterpenoid Natural Product Biosynthesis in Basidiomycota. <i>Chemistry and Biology</i> , 2012, 19, 772-783.	6.2	150
239	Polar and brown bear genomes reveal ancient admixture and demographic footprints of past climate change. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2382-90.	3.3	310
240	Stepping stones in DNA sequencing. <i>Biotechnology Journal</i> , 2012, 7, 1063-1073.	1.8	59

#	ARTICLE	IF	CITATIONS
241	Optimization of de novo transcriptome assembly from high-throughput short read sequencing data improves functional annotation for non-model organisms. <i>BMC Bioinformatics</i> , 2012, 13, 170.	1.2	31
242	Estimation of sequencing error rates in short reads. <i>BMC Bioinformatics</i> , 2012, 13, 185.	1.2	61
243	Deciphering neo-sex and B chromosome evolution by the draft genome of <i>Drosophila albomicans</i> . <i>BMC Genomics</i> , 2012, 13, 109.	1.2	64
244	De novo sequencing and characterization of <i>Picrorhiza kurroa</i> transcriptome at two temperatures showed major transcriptome adjustments. <i>BMC Genomics</i> , 2012, 13, 126.	1.2	124
245	De novo assembly and characterization of the root transcriptome of <i>Aegilops variabilis</i> during an interaction with the cereal cyst nematode. <i>BMC Genomics</i> , 2012, 13, 133.	1.2	63
246	Transcriptomic analysis of Chinese bayberry (<i>Myrica rubra</i>) fruit development and ripening using RNA-Seq. <i>BMC Genomics</i> , 2012, 13, 19.	1.2	199
247	De novo assembly and characterization of bark transcriptome using Illumina sequencing and development of EST-SSR markers in rubber tree (<i>Hevea brasiliensis</i> Muell. Arg.). <i>BMC Genomics</i> , 2012, 13, 192.	1.2	228
248	Transcriptional profile of <i>Taxus chinensis</i> cells in response to methyl jasmonate. <i>BMC Genomics</i> , 2012, 13, 295.	1.2	87
249	Transcriptome-based exon capture enables highly cost-effective comparative genomic data collection at moderate evolutionary scales. <i>BMC Genomics</i> , 2012, 13, 403.	1.2	253
250	Sequencing and analysis of a South Asian-Indian personal genome. <i>BMC Genomics</i> , 2012, 13, 440.	1.2	29
251	A draft of the genome and four transcriptomes of a medicinal and pesticidal angiosperm <i>Azadirachta indica</i> . <i>BMC Genomics</i> , 2012, 13, 464.	1.2	80
252	A duck RH panel and its potential for assisting NGS genome assembly. <i>BMC Genomics</i> , 2012, 13, 513.	1.2	40
253	Analysis of a native whitefly transcriptome and its sequence divergence with two invasive whitefly species. <i>BMC Genomics</i> , 2012, 13, 529.	1.2	54
254	The genome sequence of <i>Propionibacterium acidipropionici</i> provides insights into its biotechnological and industrial potential. <i>BMC Genomics</i> , 2012, 13, 562.	1.2	74
255	De Novo characterization of the banana root transcriptome and analysis of gene expression under <i>Fusarium oxysporum</i> f. sp. <i>Cubense</i> tropical race 4 infection. <i>BMC Genomics</i> , 2012, 13, 650.	1.2	74
256	De novo assembly and Characterisation of the Transcriptome during seed development, and generation of genic-SSR markers in Peanut (<i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , 2012, 13, 90.	1.2	231
257	Transcriptome analysis of stem development in the tumourous stem mustard <i>Brassica juncea</i> var. <i>tumida</i> Tsen et Lee by RNA sequencing. <i>BMC Plant Biology</i> , 2012, 12, 53.	1.6	49
258	Reference-free SNP calling: improved accuracy by preventing incorrect calls from repetitive genomic regions. <i>Biology Direct</i> , 2012, 7, 17.	1.9	30

#	ARTICLE	IF	CITATIONS
259	Arapan-S: a fast and highly accurate whole-genome assembly software for viruses and small genomes. BMC Research Notes, 2012, 5, 243.	0.6	6
260	A locally funded Puerto Rican parrot (<i>Amazona vittata</i>) genome sequencing project increases avian data and advances young researcher education. GigaScience, 2012, 1, 14.	3.3	40
261	The sequence and analysis of a Chinese pig genome. GigaScience, 2012, 1, 16.	3.3	125
262	SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. GigaScience, 2012, 1, 18.	3.3	4,510
263	Genomics and Genetics of Human and Primate Y Chromosomes. Annual Review of Genomics and Human Genetics, 2012, 13, 83-108.	2.5	90
264	Statistical challenges associated with detecting copy number variations with next-generation sequencing. Bioinformatics, 2012, 28, 2711-2718.	1.8	193
265	The oyster genome reveals stress adaptation and complexity of shell formation. Nature, 2012, 490, 49-54.	13.7	1,966
266	The draft genome of a diploid cotton <i>Gossypium raimondii</i> . Nature Genetics, 2012, 44, 1098-1103.	9.4	935
267	Small World Asynchronous Parallel Model for Genome Assembly. Lecture Notes in Computer Science, 2012, , 145-155.	1.0	10
268	The scope of things to come. , 2012, , 19-34.		1
269	Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. Nature Biotechnology, 2012, 30, 83-89.	9.4	788
270	Microbial Structures, Functions, and Metabolic Pathways in Wastewater Treatment Bioreactors Revealed Using High-Throughput Sequencing. Environmental Science & Technology, 2012, 46, 13244-13252.	4.6	153
271	FinIS: Improved in silico Finishing Using an Exact Quadratic Programming Formulation. Lecture Notes in Computer Science, 2012, , 314-325.	1.0	20
272	Naphthol radical couplings determine structural features and enantiomeric excess of dalesconols in <i>Daldinia eschscholzii</i> . Nature Communications, 2012, 3, 1039.	5.8	50
274	Simplification and Desexualization of Gene Expression in Self-Fertile Nematodes. Current Biology, 2012, 22, 2167-2172.	1.8	68
275	De novo sequencing and comparative analysis of the blueberry transcriptome to discover putative genes related to antioxidants. Gene, 2012, 511, 54-61.	1.0	86
276	A Survey of Copy Number Variation Detection Tools Based on High-Throughput Sequencing Data. Current Protocols in Human Genetics, 2012, 75, Unit7.19.	3.5	18
277	Cloning and characterization of trypsin- and chymotrypsin-like genes in the striped rice stem borer, <i>Chilo suppressalis</i> . Genome, 2012, 55, 281-288.	0.9	15

#	ARTICLE	IF	CITATIONS
278	Next-Generation Sequencing Technologies and Fragment Assembly Algorithms. <i>Methods in Molecular Biology</i> , 2012, 855, 155-174.	0.4	24
279	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2012, 30, 105-111.	9.4	818
280	Library Preparation and Data Analysis Packages for Rapid Genome Sequencing. <i>Methods in Molecular Biology</i> , 2012, 944, 1-22.	0.4	17
281	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	9.4	383
282	MetaVelvet: an extension of Velvet assembler to de novo metagenome assembly from short sequence reads. <i>Nucleic Acids Research</i> , 2012, 40, e155-e155.	6.5	562
283	De Novo Assembly of High-Throughput Sequencing Data with Cloud Computing and New Operations on String Graphs. , 2012, , .		7
284	High throughput sequencing methods for microbiome profiling: application to food animal systems. <i>Animal Health Research Reviews</i> , 2012, 13, 40-53.	1.4	27
285	Space-Efficient and Exact de Bruijn Graph Representation Based on a Bloom Filter. <i>Lecture Notes in Computer Science</i> , 2012, , 236-248.	1.0	51
286	Identification and Characterization of the Echinocandin B Biosynthetic Gene Cluster from <i>Emericella rugulosa</i> NRRL 11440. <i>Journal of the American Chemical Society</i> , 2012, 134, 16781-16790.	6.6	123
287	Next-generation sequencing and large genome assemblies. <i>Pharmacogenomics</i> , 2012, 13, 901-915.	0.6	120
288	Next Generation Sequence Analysis and Computational Genomics Using Graphical Pipeline Workflows. <i>Genes</i> , 2012, 3, 545-575.	1.0	45
289	A Proteomic Survey of Nonribosomal Peptide and Polyketide Biosynthesis in Actinobacteria. <i>Journal of Proteome Research</i> , 2012, 11, 85-94.	1.8	38
290	TIGER: tiled iterative genome assembler. <i>BMC Bioinformatics</i> , 2012, 13, S18.	1.2	8
291	GapFiller: a de novo assembly approach to fill the gap within paired reads. <i>BMC Bioinformatics</i> , 2012, 13, S8.	1.2	324
292	ChopSticks: High-resolution analysis of homozygous deletions by exploiting concordant read pairs. <i>BMC Bioinformatics</i> , 2012, 13, 279.	1.2	2
293	A de novo next generation genomic sequence assembler based on string graph and MapReduce cloud computing framework. <i>BMC Genomics</i> , 2012, 13, S28.	1.2	30
294	Transcriptome analysis of Sacha Inchi (<i>Plukenetia volubilis</i> L.) seeds at two developmental stages. <i>BMC Genomics</i> , 2012, 13, 716.	1.2	62
295	Transcriptome characterization and gene expression of <i>Epinephelus</i> spp in endoplasmic reticulum stress-related pathway during betanodavirus infection in vitro. <i>BMC Genomics</i> , 2012, 13, 651.	1.2	54

#	ARTICLE	IF	CITATIONS
296	De novo characterization of the Chinese fir (<i>Cunninghamia lanceolata</i>) transcriptome and analysis of candidate genes involved in cellulose and lignin biosynthesis. <i>BMC Genomics</i> , 2012, 13, 648.	1.2	72
297	Genome sequence of the necrotrophic fungus <i>Penicillium digitatum</i> , the main postharvest pathogen of citrus. <i>BMC Genomics</i> , 2012, 13, 646.	1.2	205
298	Whole-genome reconstruction and mutational signatures in gastric cancer. <i>Genome Biology</i> , 2012, 13, R115.	13.9	116
299	Feature-by-Feature “Evaluating De Novo Sequence Assembly. <i>PLoS ONE</i> , 2012, 7, e31002.	1.1	50
300	Transcriptome Profiling of Testis during Sexual Maturation Stages in <i>Eriocheir sinensis</i> Using Illumina Sequencing. <i>PLoS ONE</i> , 2012, 7, e33735.	1.1	83
301	De Novo Transcriptomic Analysis of an Oleaginous Microalga: Pathway Description and Gene Discovery for Production of Next-Generation Biofuels. <i>PLoS ONE</i> , 2012, 7, e35142.	1.1	19
302	The Genome of <i>Ganderma lucidum</i> Provide Insights into Triterpense Biosynthesis and Wood Degradation. <i>PLoS ONE</i> , 2012, 7, e36146.	1.1	78
303	Transcriptomic Analysis of the Salivary Glands of an Invasive Whitefly. <i>PLoS ONE</i> , 2012, 7, e39303.	1.1	103
304	An Improvement of Shotgun Proteomics Analysis by Adding Next-Generation Sequencing Transcriptome Data in Orange. <i>PLoS ONE</i> , 2012, 7, e39494.	1.1	15
305	Transcriptome Sequencing and Comparative Analysis of <i>Saccharina japonica</i> (Laminariales). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 TTS</i>	1.1	93
306	IMG/M-HMP: A Metagenome Comparative Analysis System for the Human Microbiome Project. <i>PLoS ONE</i> , 2012, 7, e40151.	1.1	43
307	An Integrated Pipeline for de Novo Assembly of Microbial Genomes. <i>PLoS ONE</i> , 2012, 7, e42304.	1.1	436
308	Transcriptome Analysis of <i>Nicotiana tabacum</i> Infected by Cucumber mosaic virus during Systemic Symptom Development. <i>PLoS ONE</i> , 2012, 7, e43447.	1.1	107
309	De Novo Foliar Transcriptome of <i>Chenopodium amaranticolor</i> and Analysis of Its Gene Expression During Virus-Induced Hypersensitive Response. <i>PLoS ONE</i> , 2012, 7, e45953.	1.1	30
310	Deep Sequencing of the Oral Microbiome Reveals Signatures of Periodontal Disease. <i>PLoS ONE</i> , 2012, 7, e37919.	1.1	329
311	Evaluating Methods for Isolating Total RNA and Predicting the Success of Sequencing Phylogenetically Diverse Plant Transcriptomes. <i>PLoS ONE</i> , 2012, 7, e50226.	1.1	172
312	Correlation Between DNase I Hypersensitive Site Distribution and Gene Expression in HeLa S3 Cells. <i>PLoS ONE</i> , 2012, 7, e42414.	1.1	29
313	MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. <i>PLoS ONE</i> , 2012, 7, e47656.	1.1	208

#	ARTICLE	IF	CITATIONS
314	Transcriptome Sequencing and Annotation for the Jamaican Fruit Bat (<i>Artibeus jamaicensis</i>). PLoS ONE, 2012, 7, e48472.	1.1	77
315	Micro-Scale Genomic DNA Copy Number Aberrations as Another Means of Mutagenesis in Breast Cancer. PLoS ONE, 2012, 7, e51719.	1.1	13
316	FastUniq: A Fast De Novo Duplicates Removal Tool for Paired Short Reads. PLoS ONE, 2012, 7, e52249.	1.1	446
317	Advanced Engineering of Lipid Metabolism in <i>Nicotiana benthamiana</i> Using a Draft Genome and the V2 Viral Silencing-Suppressor Protein. PLoS ONE, 2012, 7, e52717.	1.1	85
318	Sequencing Technologies and Their Use in Plant Biotechnology and Breeding. , 2012, , .		5
319	Modelling DNA Methylation Dynamics. , 0, , .		1
320	Next generation shotgun sequencing and the challenges of de novo genome assembly. South African Journal of Science, 2012, 108, .	0.3	1
321	Test driving genome assemblers. Nature Biotechnology, 2012, 30, 330-331.	9.4	6
322	SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing. Journal of Computational Biology, 2012, 19, 455-477.	0.8	20,193
323	GAGE: A critical evaluation of genome assemblies and assembly algorithms. Genome Research, 2012, 22, 557-567.	2.4	597
324	A beginner's guide to eukaryotic genome annotation. Nature Reviews Genetics, 2012, 13, 329-342.	7.7	553
325	Functional assignment of metagenomic data: challenges and applications. Briefings in Bioinformatics, 2012, 13, 711-727.	3.2	150
326	Sex-Specific Adaptation Drives Early Sex Chromosome Evolution in <i>Drosophila</i> . Science, 2012, 337, 341-345.	6.0	181
327	IDBA-UD: a <i>de novo</i> assembler for single-cell and metagenomic sequencing data with highly uneven depth. Bioinformatics, 2012, 28, 1420-1428.	1.8	2,627
328	Comparative genomics of rhizobia nodulating soybean suggests extensive recruitment of lineage-specific genes in adaptations. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8629-8634.	3.3	234
329	High-Throughput Sequencing Data Analysis Software: Current State and Future Developments. , 2012, , 231-248.		5
330	Applications of High-Throughput Sequencing. , 2012, , 27-53.		1
331	De Novo Short-Read Assembly. , 2012, , 85-105.		0

#	ARTICLE	IF	CITATIONS
332	Genome mapping on nanochannel arrays for structural variation analysis and sequence assembly. <i>Nature Biotechnology</i> , 2012, 30, 771-776.	9.4	586
333	Genome-wide genetic variations are highly correlated with proximal DNA methylation patterns. <i>Genome Research</i> , 2012, 22, 1419-1425.	2.4	41
334	Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biofuel potential. <i>Nature Biotechnology</i> , 2012, 30, 549-554.	9.4	636
335	SEQuel: improving the accuracy of genome assemblies. <i>Bioinformatics</i> , 2012, 28, i188-i196.	1.8	56
336	De novo assembly and genotyping of variants using colored de Bruijn graphs. <i>Nature Genetics</i> , 2012, 44, 226-232.	9.4	564
337	Pathset Graphs: A Novel Approach for Comprehensive Utilization of Paired Reads in Genome Assembly. <i>Lecture Notes in Computer Science</i> , 2012, , 200-212.	1.0	3
338	A hybrid approach for the automated finishing of bacterial genomes. <i>Nature Biotechnology</i> , 2012, 30, 701-707.	9.4	178
339	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012, 30, 693-700.	9.4	946
340	De novo characterization of the antler tip of Chinese Sika deer transcriptome and analysis of gene expression related to rapid growth. <i>Molecular and Cellular Biochemistry</i> , 2012, 364, 93-100.	1.4	41
341	Cranberry microsatellite marker development from assembled next-generation genomic sequence. <i>Molecular Breeding</i> , 2012, 30, 227-237.	1.0	20
342	Genome sequence comparison of two United States live attenuated vaccines of infectious laryngotracheitis virus (ILTV). <i>Virus Genes</i> , 2012, 44, 470-474.	0.7	25
343	Genomics of a phylum distant from flowering plants: conifers. <i>Tree Genetics and Genomes</i> , 2012, 8, 573-582.	0.6	17
344	De novo characterization of the root transcriptome of a traditional Chinese medicinal plant <i>Polygonum cuspidatum</i> . <i>Science China Life Sciences</i> , 2012, 55, 452-466.	2.3	80
345	Asymmetric bioreduction of activated alkenes by a novel isolate of <i>Achromobacter</i> species producing enoate reductase. <i>Applied Microbiology and Biotechnology</i> , 2012, 95, 635-645.	1.7	19
346	Transcriptome analysis of the roots at early and late seedling stages using Illumina paired-end sequencing and development of EST-SSR markers in radish. <i>Plant Cell Reports</i> , 2012, 31, 1437-1447.	2.8	96
347	De novo sequencing and a comprehensive analysis of purple sweet potato (<i>Ipomoea batatas</i> L.) transcriptome. <i>Planta</i> , 2012, 236, 101-113.	1.6	118
348	Sequencing and de novo analysis of the Chinese Sika deer antler-tip transcriptome during the ossification stage using Illumina RNA-Seq technology. <i>Biotechnology Letters</i> , 2012, 34, 813-822.	1.1	40
349	Reference-free transcriptome assembly in non-model animals from next-generation sequencing data. <i>Molecular Ecology Resources</i> , 2012, 12, 834-845.	2.2	142

#	ARTICLE	IF	CITATIONS
350	Bioinformatics Applications in Genomics. <i>Computer</i> , 2012, 45, 57-63.	1.2	6
351	Cape buffalo mitogenomics reveals a Holocene shift in the African human megafauna dynamics. <i>Molecular Ecology</i> , 2012, 21, 3947-3959.	2.0	29
352	Transposon proliferation in an asexual parasitoid. <i>Molecular Ecology</i> , 2012, 21, 3898-3906.	2.0	33
353	Exploiting sparseness in de novo genome assembly. <i>BMC Bioinformatics</i> , 2012, 13, S1.	1.2	279
354	A survey of error-correction methods for next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2013, 14, 56-66.	3.2	205
355	Reference genomes and transcriptomes of <i>Nicotiana sylvestris</i> and <i>Nicotiana tomentosiformis</i> . <i>Genome Biology</i> , 2013, 14, R60.	3.8	192
356	CGAL: computing genome assembly likelihoods. <i>Genome Biology</i> , 2013, 14, R8.	13.9	77
357	Low concordance of multiple variant-calling pipelines: practical implications for exome and genome sequencing. <i>Genome Medicine</i> , 2013, 5, 28.	3.6	381
358	A quantitative reference transcriptome for <i>Nematostella vectensis</i> early embryonic development: a pipeline for de novo assembly in emerging model systems. <i>EvoDevo</i> , 2013, 4, 16.	1.3	57
359	Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. <i>GigaScience</i> , 2013, 2, 4.	3.3	227
360	Comparative analysis of differentially expressed genes in Sika deer antler at different stages. <i>Molecular Biology Reports</i> , 2013, 40, 1665-1676.	1.0	29
361	De Novo Characterization of Leaf Transcriptome Using 454 Sequencing and Development of EST-SSR Markers in Tea (<i>Camellia sinensis</i>). <i>Plant Molecular Biology Reporter</i> , 2013, 31, 524-538.	1.0	57
362	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the <i>Cricetulus griseus</i> draft genome. <i>Nature Biotechnology</i> , 2013, 31, 759-765.	9.4	340
363	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. <i>Nature Genetics</i> , 2013, 45, 891-898.	9.4	350
364	The evolution and pathogenic mechanisms of the rice sheath blight pathogen. <i>Nature Communications</i> , 2013, 4, 1424.	5.8	268
365	GAM-NGS: genomic assemblies merger for next generation sequencing. <i>BMC Bioinformatics</i> , 2013, 14, S6.	1.2	76
366	Evaluating genome architecture of a complex region via generalized bipartite matching. <i>BMC Bioinformatics</i> , 2013, 14, S13.	1.2	2
367	Complete chloroplast genome of the genus <i>Cymbidium</i> : lights into the species identification, phylogenetic implications and population genetic analyses. <i>BMC Evolutionary Biology</i> , 2013, 13, 84.	3.2	262

#	ARTICLE	IF	CITATIONS
368	Analysis and annotation of the hexaploid oat seed transcriptome. <i>BMC Genomics</i> , 2013, 14, 471.	1.2	62
369	Genomics of sablefish (<i>Anoplopoma fimbria</i>): expressed genes, mitochondrial phylogeny, linkage map and identification of a putative sex gene. <i>BMC Genomics</i> , 2013, 14, 452.	1.2	99
370	De novo transcriptome sequencing of axolotl blastema for identification of differentially expressed genes during limb regeneration. <i>BMC Genomics</i> , 2013, 14, 434.	1.2	63
371	Improving mammalian genome scaffolding using large insert mate-pair next-generation sequencing. <i>BMC Genomics</i> , 2013, 14, 257.	1.2	35
372	Comparative genomics of parasitic silkworm microsporidia reveal an association between genome expansion and host adaptation. <i>BMC Genomics</i> , 2013, 14, 186.	1.2	127
373	Draft genome sequence of the rubber tree <i>Hevea brasiliensis</i> . <i>BMC Genomics</i> , 2013, 14, 75.	1.2	222
374	Development of a high density 600K SNP genotyping array for chicken. <i>BMC Genomics</i> , 2013, 14, 59.	1.2	332
375	Transcriptomic profiling of the salt-stress response in the wild recretohalophyte <i>Reaumuria trigyna</i> . <i>BMC Genomics</i> , 2013, 14, 29.	1.2	147
376	GPU-Accelerated Bidirected De Bruijn Graph Construction for Genome Assembly. <i>Lecture Notes in Computer Science</i> , 2013, , 51-62.	1.0	8
377	Genome-wide analysis of <i>Nilaparvata lugens</i> nymphal responses to high density and low quality rice hosts. <i>Insect Science</i> , 2013, 20, 703-716.	1.5	13
378	Whole-genome sequencing reveals untapped genetic potential in Africa's indigenous cereal crop sorghum. <i>Nature Communications</i> , 2013, 4, 2320.	5.8	405
379	The sacred lotus genome provides insights into the evolution of flowering plants. <i>Plant Journal</i> , 2013, 76, 557-567.	2.8	75
380	Critical role of bioinformatics in translating huge amounts of next-generation sequencing data into personalized medicine. <i>Science China Life Sciences</i> , 2013, 56, 110-118.	2.3	31
381	Genome survey uncovers the secrets of sex and lifestyle in caterpillar fungus. <i>Science Bulletin</i> , 2013, 58, 2846-2854.	1.7	126
382	The MaSuRCA genome assembler. <i>Bioinformatics</i> , 2013, 29, 2669-2677.	1.8	1,127
383	Microbial community structure in fermentation process of Shaoxing rice wine by Illumina-based metagenomic sequencing. <i>Journal of the Science of Food and Agriculture</i> , 2013, 93, 3121-3125.	1.7	39
384	Metagenomic analysis of the pinewood nematode microbiome reveals a symbiotic relationship critical for xenobiotics degradation. <i>Scientific Reports</i> , 2013, 3, 1869.	1.6	121
385	Exome sequencing released a case of X-linked adrenoleukodystrophy mimicking recessive hereditary spastic paraplegia. <i>European Journal of Medical Genetics</i> , 2013, 56, 375-378.	0.7	16

#	ARTICLE	IF	CITATIONS
386	Genes encoding FAD-binding proteins in <i>Volvariella volvacea</i> exhibit differential expression in homokaryons and heterokaryons. <i>Microbiological Research</i> , 2013, 168, 533-546.	2.5	13
387	Next-Generation Sequencing (NGS): A Revolutionary Technology in Pharmacogenomics and Personalized Medicine. , 2013, , 39-61.		4
388	GAGE-B: an evaluation of genome assemblers for bacterial organisms. <i>Bioinformatics</i> , 2013, 29, 1718-1725.	1.8	135
389	BRANCH: boosting RNA-Seq assemblies with partial or related genomic sequences. <i>Bioinformatics</i> , 2013, 29, 1250-1259.	1.8	28
390	Polymorphism of the multiple hemoglobins in blood clam <i>Tegillarca granosa</i> and its association with disease resistance to <i>Vibrio parahaemolyticus</i> . <i>Fish and Shellfish Immunology</i> , 2013, 34, 1320-1324.	1.6	14
391	Genome analysis reveals insights into physiology and longevity of the Brandt's bat <i>Myotis brandtii</i> . <i>Nature Communications</i> , 2013, 4, 2212.	5.8	213
392	Tracking the Emergence of High Affinity Aptamers for rhVEGF ₁₆₅ During Capillary Electrophoresis-Systematic Evolution of Ligands by Exponential Enrichment Using High Throughput Sequencing. <i>Analytical Chemistry</i> , 2013, 85, 10761-10770.	3.2	45
393	Oral insecticidal activity of plant-associated pseudomonads. <i>Environmental Microbiology</i> , 2013, 15, 751-763.	1.8	80
394	A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. <i>Nature Genetics</i> , 2013, 45, 1510-1515.	9.4	472
395	RACER: Rapid and accurate correction of errors in reads. <i>Bioinformatics</i> , 2013, 29, 2490-2493.	1.8	64
396	Chromosome-scale scaffolding of de novo genome assemblies based on chromatin interactions. <i>Nature Biotechnology</i> , 2013, 31, 1119-1125.	9.4	1,141
397	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>) Tj ETQq1 1 0.784314 9.4 499 /Over	9.4	499
398	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. <i>Lecture Notes in Computer Science</i> , 2013, , 158-170.	1.0	439
399	Efficient identification of Y chromosome sequences in the human and <i>Drosophila</i> genomes. <i>Genome Research</i> , 2013, 23, 1894-1907.	2.4	98
400	Gigabase-Scale Transcriptome Analysis on Four Species of Pearl Oysters. <i>Marine Biotechnology</i> , 2013, 15, 253-264.	1.1	48
401	Assembler for de novo assembly of large genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3417-24.	3.3	41
402	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. <i>Journal of Computational Biology</i> , 2013, 20, 714-737.	0.8	1,235
403	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20645-20650.	3.3	260

#	ARTICLE	IF	CITATIONS
404	An Introduction to High-Throughput Sequencing Experiments: Design and Bioinformatics Analysis. <i>Methods in Molecular Biology</i> , 2013, 1038, 1-26.	0.4	11
405	The Assembly of Sequencing Data. <i>SpringerBriefs in Systems Biology</i> , 2013, , 41-54.	0.1	0
406	ELOPER: elongation of paired-end reads as a pre-processing tool for improved <i>de novo</i> genome assembly. <i>Bioinformatics</i> , 2013, 29, 1455-1457.	1.8	6
407	Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. <i>Briefings in Bioinformatics</i> , 2013, 14, 213-224.	3.2	54
408	MATE-CLEVER: Mendelian-inheritance-aware discovery and genotyping of midsize and long indels. <i>Bioinformatics</i> , 2013, 29, 3143-3150.	1.8	44
409	De novo assembly and characterization of spotted seal <i>Phoca largha</i> transcriptome using Illumina paired-end sequencing. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2013, 8, 103-110.	0.4	8
410	The okra (<i>Abelmoschus esculentus</i>) transcriptome as a source for gene sequence information and molecular markers for diversity analysis. <i>Gene</i> , 2013, 517, 27-36.	1.0	45
411	Pseudo-Sanger sequencing: massively parallel production of long and near error-free reads using NGS technology. <i>BMC Genomics</i> , 2013, 14, 711.	1.2	12
412	Genome analysis of <i>Pseudoalteromonas flavipulchra</i> JG1 reveals various survival advantages in marine environment. <i>BMC Genomics</i> , 2013, 14, 707.	1.2	23
413	Space-efficient and exact de Bruijn graph representation based on a Bloom filter. <i>Algorithms for Molecular Biology</i> , 2013, 8, 22.	0.3	266
414	Genome and transcriptome sequencing of the halophilic fungus <i>Wallemia ichthyophaga</i> : haloadaptations present and absent. <i>BMC Genomics</i> , 2013, 14, 617.	1.2	107
415	Insights into food preference in hybrid F1 of <i>Siniperca chuatsi</i> (♀) × <i>Siniperca scherzeri</i> (♂), mandarin fish through transcriptome analysis. <i>BMC Genomics</i> , 2013, 14, 601.	1.2	72
416	L_RNA_scaffolder: scaffolding genomes with transcripts. <i>BMC Genomics</i> , 2013, 14, 604.	1.2	129
417	De novo likelihood-based measures for comparing genome assemblies. <i>BMC Research Notes</i> , 2013, 6, 334.	0.6	43
418	De novo characterization of <i>Larix gmelinii</i> (Rupr.) Rupr. transcriptome and analysis of its gene expression induced by jasmonates. <i>BMC Genomics</i> , 2013, 14, 548.	1.2	23
419	Next-generation sequencing-based mRNA and microRNA expression profiling analysis revealed pathways involved in the rapid growth of developing culms in Moso bamboo. <i>BMC Plant Biology</i> , 2013, 13, 119.	1.6	87
420	Transcriptome profiling of peanut gynophores revealed global reprogramming of gene expression during early pod development in darkness. <i>BMC Genomics</i> , 2013, 14, 517.	1.2	62
421	De novo assembly and characterization of fruit transcriptome in <i>Litchi chinensis</i> Sonn and analysis of differentially regulated genes in fruit in response to shading. <i>BMC Genomics</i> , 2013, 14, 552.	1.2	106

#	ARTICLE	IF	CITATIONS
422	Comparative analyses of two Geraniaceae transcriptomes using next-generation sequencing. BMC Plant Biology, 2013, 13, 228.	1.6	38
423	A multi-omic analysis of an Enterococcus faecium mutant reveals specific genetic mutations and dramatic changes in mRNA and protein expression. BMC Microbiology, 2013, 13, 304.	1.3	14
424	OMACC: an Optical-Map-Assisted Contig Connector for improving de novo genome assembly. BMC Systems Biology, 2013, 7, S7.	3.0	4
425	Selection of reference genes for quantitative real-time PCR in six oil-tea camellia based on RNA-seq. Molecular Biology, 2013, 47, 836-851.	0.4	19
426	Comprehensive transcriptomic study on horse gram (Macrotyloma uniflorum): De novo assembly, functional characterization and comparative analysis in relation to drought stress. BMC Genomics, 2013, 14, 647.	1.2	71
427	Transcriptome profiling of fruit development and maturation in Chinese white pear (Pyrus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.2	50
428	A base composition analysis of natural patterns for the preprocessing of metagenome sequences. BMC Bioinformatics, 2013, 14, S5.	1.2	4
429	The regulation of cambial activity in Chinese fir (Cunninghamia) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 69	1.2	69
430	Assessing the Human Gut Microbiota in Metabolic Diseases. Diabetes, 2013, 62, 3341-3349.	0.3	384
431	A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. Methods in Enzymology, 2013, 531, 525-547.	0.4	28
432	Whole-genome sequencing of Oryza brachyantha reveals mechanisms underlying Oryza genome evolution. Nature Communications, 2013, 4, 1595.	5.8	190
433	Whole-Genome Sequences of DA and F344 Rats with Different Susceptibilities to Arthritis, Autoimmunity, Inflammation and Cancer. Genetics, 2013, 194, 1017-1028.	1.2	15
434	GAGM: Genome assembly on GPU using mate pairs. , 2013, , .		5
435	MetaPar: Metagenomic sequence assembly via iterative reclassification. , 2013, , .		0
436	PASQUAL: Parallel Techniques for Next Generation Genome Sequence Assembly. IEEE Transactions on Parallel and Distributed Systems, 2013, 24, 977-986.	4.0	13
437	De novo likelihood-based measures for comparing metagenomic assemblies. , 2013, , .		1
438	A Genomic Distance for Assembly Comparison Based on Compressed Maximal Exact Matches. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 793-798.	1.9	8
439	GGAKE: GPU Based Genome Assembly Using K-Mer Extension. , 2013, , .		3

#	ARTICLE	IF	CITATIONS
440	Large memory high performance computing enables comparison across human gut microbiome of patients with autoimmune diseases and healthy subjects. , 2013, , .		15
441	Genome of the Chinese tree shrew. <i>Nature Communications</i> , 2013, 4, 1426.	5.8	284
442	Structural variation discovery with next-generation sequencing. , 2013, , .		1
443	Accelerating De Bruijn Graph-Based Genome Assembly for High-Throughput Short Read Data. , 2013, , .		1
444	Musket: a multistage <i>k</i> -mer spectrum-based error corrector for Illumina sequence data. <i>Bioinformatics</i> , 2013, 29, 308-315.	1.8	266
445	Complete nucleotide sequence of plasmid pND6-2 from <i>Pseudomonas putida</i> ND6 and characterization of conjugative genes. <i>Gene</i> , 2013, 512, 148-156.	1.0	15
446	ALE: a generic assembly likelihood evaluation framework for assessing the accuracy of genome and metagenome assemblies. <i>Bioinformatics</i> , 2013, 29, 435-443.	1.8	155
447	Current analysis platforms and methods for detecting copy number variation. <i>Physiological Genomics</i> , 2013, 45, 1-16.	1.0	64
448	Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. <i>Science</i> , 2013, 339, 456-460.	6.0	522
449	Next-generation sequencing in the clinic: Promises and challenges. <i>Cancer Letters</i> , 2013, 340, 284-295.	3.2	272
450	The draft genome of watermelon (<i>Citrullus lanatus</i>) and resequencing of 20 diverse accessions. <i>Nature Genetics</i> , 2013, 45, 51-58.	9.4	731
451	Sequence assembly demystified. <i>Nature Reviews Genetics</i> , 2013, 14, 157-167.	7.7	396
452	CalcGen Sequence Assembler Using a Spatio-temporally Efficient DNA Sequence Search Algorithm. <i>Procedia Computer Science</i> , 2013, 23, 122-128.	1.2	0
453	Comparative genomic analysis of <i>Aspergillus oryzae</i> strains 3.042 and RIB40 for soy sauce fermentation. <i>International Journal of Food Microbiology</i> , 2013, 164, 148-154.	2.1	20
454	Genome sequence of the plant growth promoting strain <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> B9601-Y2 and expression of mersacidin and other secondary metabolites. <i>Journal of Biotechnology</i> , 2013, 164, 281-291.	1.9	70
455	Genomic analyses identify distinct patterns of selection in domesticated pigs and Tibetan wild boars. <i>Nature Genetics</i> , 2013, 45, 1431-1438.	9.4	472
456	Building a Genome Analysis Pipeline to Predict Disease Risk and Prevent Disease. <i>Journal of Molecular Biology</i> , 2013, 425, 3993-4005.	2.0	31
457	De-novo characterization of the soft-shelled turtle <i>Pelodiscus sinensis</i> transcriptome using Illumina RNA-Seq technology. <i>Journal of Zhejiang University: Science B</i> , 2013, 14, 58-67.	1.3	18

#	ARTICLE	IF	CITATIONS
458	Differential hippocampal gene expression is associated with climate-related natural variation in memory and the hippocampus in food-caching chickadees. <i>Molecular Ecology</i> , 2013, 22, 397-408.	2.0	29
459	Pathset Graphs: A Novel Approach for Comprehensive Utilization of Paired Reads in Genome Assembly. <i>Journal of Computational Biology</i> , 2013, 20, 359-371.	0.8	14
460	The genomic consequences of adaptive divergence and reproductive isolation between species of manakins. <i>Molecular Ecology</i> , 2013, 22, 3304-3317.	2.0	108
461	The draft genome of sweet orange (<i>Citrus sinensis</i>). <i>Nature Genetics</i> , 2013, 45, 59-66.	9.4	837
462	Draft genome of the wheat A-genome progenitor <i>Triticum urartu</i> . <i>Nature</i> , 2013, 496, 87-90.	13.7	700
463	Peregrine and saker falcon genome sequences provide insights into evolution of a predatory lifestyle. <i>Nature Genetics</i> , 2013, 45, 563-566.	9.4	141
464	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013, 496, 91-95.	13.7	714
465	Global transcriptome analysis and identification of a CONSTANS-like gene family in the orchid <i>Erycina pusilla</i> . <i>Planta</i> , 2013, 237, 1425-1441.	1.6	42
466	Next-generation sequencing reveals genomic features in the Japanese quail. <i>Genomics</i> , 2013, 101, 345-353.	1.3	69
467	Computational solutions for omics data. <i>Nature Reviews Genetics</i> , 2013, 14, 333-346.	7.7	288
468	A new paradigm emerges from the study of de novo mutations in the context of neurodevelopmental disease. <i>Molecular Psychiatry</i> , 2013, 18, 141-153.	4.1	85
469	Human Genome Variation Discovery via Exome and Whole-Genome Sequencing. , 2013, , 94-101.		0
470	The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. <i>Nature Genetics</i> , 2013, 45, 701-706.	9.4	409
471	De novo characterization of <i>Lentinula edodes</i> C91-3 transcriptome by deep Solexa sequencing. <i>Biochemical and Biophysical Research Communications</i> , 2013, 431, 111-115.	1.0	26
472	Comparison of transcriptome under red and blue light culture of <i>Saccharina japonica</i> (Phaeophyceae). <i>Planta</i> , 2013, 237, 1123-1133.	1.6	58
473	Computational meta'omics for microbial community studies. <i>Molecular Systems Biology</i> , 2013, 9, 666.	3.2	253
474	De novo transcriptome sequencing and comparative analysis of differentially expressed genes in <i>Gossypium aridum</i> under salt stress. <i>Gene</i> , 2013, 525, 26-34.	1.0	70
475	Comparative genomic and transcriptomic analyses reveal the hemibiotrophic stage shift of <i>Colletotrichum</i> fungi. <i>New Phytologist</i> , 2013, 197, 1236-1249.	3.5	332

#	ARTICLE	IF	CITATIONS
476	Special features of <i>scp</i> RAD Sequencing data: implications for genotyping. <i>Molecular Ecology</i> , 2013, 22, 3151-3164.	2.0	318
477	New insight into transcription of human endogenous retroviral elements. <i>New Biotechnology</i> , 2013, 30, 314-318.	2.4	15
478	Ground tit genome reveals avian adaptation to living at high altitudes in the Tibetan plateau. <i>Nature Communications</i> , 2013, 4, 2071.	5.8	229
479	Microbial community adaptation to quaternary ammonium biocides as revealed by metagenomics. <i>Environmental Microbiology</i> , 2013, 15, 2850-2864.	1.8	82
480	In-depth proteome analysis of the rubber particle of <i>Hevea brasiliensis</i> (para rubber tree). <i>Plant Molecular Biology</i> , 2013, 82, 155-168.	2.0	70
481	Transcriptomic analysis of rice (<i>Oryza sativa</i>) endosperm using the RNA-Seq technique. <i>Plant Molecular Biology</i> , 2013, 81, 363-378.	2.0	82
482	Genome-wide characterization and expression analysis of genetic variants in sweet orange. <i>Plant Journal</i> , 2013, 75, 954-964.	2.8	22
483	Characterizing developmental and inducible differentiation between juvenile and adult plants of <i>Aechmea fasciata</i> treated with ethylene by transcriptomic analysis. <i>Plant Growth Regulation</i> , 2013, 69, 247-257.	1.8	13
484	The perfect neuroimaging-genetics-computation storm: collision of petabytes of data, millions of hardware devices and thousands of software tools. <i>Brain Imaging and Behavior</i> , 2014, 8, 311-22.	1.1	15
485	Genome analysis and signature discovery for diving and sensory properties of the endangered Chinese alligator. <i>Cell Research</i> , 2013, 23, 1091-1105.	5.7	105
486	High genome heterozygosity and endemic genetic recombination in the wheat stripe rust fungus. <i>Nature Communications</i> , 2013, 4, 2673.	5.8	238
487	PRICE: Software for the Targeted Assembly of Components of (Meta) Genomic Sequence Data. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 865-880.	0.8	250
488	Genome Sequence of <i>Enterobacter cancerogenus</i> YZ1. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
489	Genome Sequence of <i>Xanthomonas campestris</i> pv. <i>campestris</i> Strain Xca5. <i>Genome Announcements</i> , 2013, 1, .	0.8	17
490	Draft Genome Sequence of the <i>Serratia marcescens</i> Strain VGH107, a Taiwanese Clinical Isolate. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
491	Draft Genome Sequence and Annotation of the Entomopathogenic Bacterium <i>Xenorhabdus nematophila</i> Strain F1. <i>Genome Announcements</i> , 2013, 1, .	0.8	10
492	Genome Sequences of Three Atypical <i>Xanthomonas campestris</i> pv. <i>campestris</i> Strains, CN14, CN15, and CN16. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
493	Genome Sequence of <i>Streptomyces violaceusniger</i> Strain SPC6, a Halotolerant Streptomycete That Exhibits Rapid Growth and Development. <i>Genome Announcements</i> , 2013, 1, .	0.8	11

#	ARTICLE	IF	CITATIONS
494	Genome Sequence of the Food Spoilage Yeast <i>Zygosaccharomyces bailii</i> CLIB 213 T. <i>Genome Announcements</i> , 2013, 1, .	0.8	39
495	Genome Sequence of the Bacterium <i>Bifidobacterium longum</i> Strain CMCC P0001, a Probiotic Strain Used for Treating Gastrointestinal Disease. <i>Genome Announcements</i> , 2013, 1, .	0.8	15
496	Genome Sequence of Growth-Improving <i>Paenibacillus mucilaginosus</i> Strain KNP414. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
497	Draft Genome Sequence of the Obligate Halophilic <i>Bacillus</i> sp. Strain NSP22.2, Isolated from a Seasonal Salt Marsh of the Great Rann of Kutch, India. <i>Genome Announcements</i> , 2013, 1, .	0.8	0
498	Draft Genome Sequence of <i>Haemophilus parasuis</i> gx033, a Serotype 4 Strain Isolated from the Swine Lower Respiratory Tract. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
499	Sequencing, Annotation, and Characterization of the Influenza Ferret Infectome. <i>Journal of Virology</i> , 2013, 87, 1957-1966.	1.5	44
500	Draft Genome Sequence of <i>Streptomyces bottropensis</i> ATCC 25435, a Bottromycin-Producing Actinomycete. <i>Genome Announcements</i> , 2013, 1, e0001913.	0.8	6
501	Draft Genome Sequence of <i>Amycolatopsis decaplanina</i> Strain DSM 44594 ^T . <i>Genome Announcements</i> , 2013, 1, e0013813.	0.8	4
502	Draft Genome Sequence of <i>Rhodococcus ruber</i> Strain BKS 20-38. <i>Genome Announcements</i> , 2013, 1, e0013913.	0.8	1
503	Draft Genome Sequences of the <i>Enterococcus faecium</i> Strain LCT-EF258. <i>Genome Announcements</i> , 2013, 1, .	0.8	1
504	Draft Genome Sequence of <i>Streptomyces gancidicus</i> Strain BKS 13-15. <i>Genome Announcements</i> , 2013, 1, e0015013.	0.8	3
505	Genome Sequence of the Polycyclic Aromatic Hydrocarbon-Degrading Bacterium Strain <i>Marinobacter nanhaiticus</i> D15-8W ^T . <i>Genome Announcements</i> , 2013, 1, .	0.8	8
506	Draft Genome Sequence of Biocontrol Bacterium <i>Brevibacillus brevis</i> Strain FJAT-0809-GLX. <i>Genome Announcements</i> , 2013, 1, e0016013.	0.8	7
507	Application of a MAX-CUT Heuristic to the Contig Orientation Problem in Genome Assembly. , 2013, , .		0
508	Draft Genome Sequence of <i>Pseudomonas plecoglossicida</i> Strain NB2011, the Causative Agent of White Nodules in Large Yellow Croaker (<i>Larimichthys crocea</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	38
509	Memory efficient minimum substring partitioning. <i>Proceedings of the VLDB Endowment</i> , 2013, 6, 169-180.	2.1	37
510	DDBJ Read Annotation Pipeline: A Cloud Computing-Based Pipeline for High-Throughput Analysis of Next-Generation Sequencing Data. <i>DNA Research</i> , 2013, 20, 383-390.	1.5	68
511	The <i>Tarenaya hassleriana</i> Genome Provides Insight into Reproductive Trait and Genome Evolution of Crucifers Å. <i>Plant Cell</i> , 2013, 25, 2813-2830.	3.1	95

#	ARTICLE	IF	CITATIONS
512	Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space. <i>PLoS Computational Biology</i> , 2013, 9, e1003010.	1.5	20
513	Neutral Genomic Microevolution of a Recently Emerged Pathogen, <i>Salmonella enterica</i> Serovar Agona. <i>PLoS Genetics</i> , 2013, 9, e1003471.	1.5	94
514	Improving Genome Assemblies and Annotations for Nonhuman Primates. <i>ILAR Journal</i> , 2013, 54, 144-153.	1.8	23
515	The Evolution of the <i>Anopheles</i> 16 Genomes Project. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1191-1194.	0.8	49
516	Next-Generation Sequence Assembly: Four Stages of Data Processing and Computational Challenges. <i>PLoS Computational Biology</i> , 2013, 9, e1003345.	1.5	120
517	Scaffolding low quality genomes using orthologous protein sequences. <i>Bioinformatics</i> , 2013, 29, 160-165.	1.8	13
518	Breakage-fusion-bridge Cycles and Large Insertions Contribute to the Rapid Evolution of Accessory Chromosomes in a Fungal Pathogen. <i>PLoS Genetics</i> , 2013, 9, e1003567.	1.5	166
519	Minimum Core Genome Sequence Typing of Bacterial Pathogens: a Unified Approach for Clinical and Public Health Microbiology. <i>Journal of Clinical Microbiology</i> , 2013, 51, 2582-2591.	1.8	84
520	Dissecting yield-associated loci in super hybrid rice by resequencing recombinant inbred lines and improving parental genome sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14492-14497.	3.3	155
521	SOAPindel: Efficient identification of indels from short paired reads. <i>Genome Research</i> , 2013, 23, 195-200.	2.4	115
522	Transcriptome and Proteome Data Reveal Candidate Genes for Pollinator Attraction in Sexually Deceptive Orchids. <i>PLoS ONE</i> , 2013, 8, e64621.	1.1	46
523	Bioinformatics in High Throughput Sequencing: Application in Evolving Genetic Diseases. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2013, 04, .	0.5	8
524	Complete viral RNA genome sequencing of ultra-low copy samples by sequence-independent amplification. <i>Nucleic Acids Research</i> , 2013, 41, e13-e13.	6.5	75
525	Genome Sequence of the Alkaliphilic Bacterial Strain <i>Bacillus ligninosis</i> L1, a Novel Degradator of Lignin. <i>Genome Announcements</i> , 2013, 1, e0004213.	0.8	5
526	Next Generation Sequencing in Predicting Gene Function in Podophyllotoxin Biosynthesis. <i>Journal of Biological Chemistry</i> , 2013, 288, 466-479.	1.6	102
527	SPA: a short peptide assembler for metagenomic data. <i>Nucleic Acids Research</i> , 2013, 41, e91-e91.	6.5	15
528	QUAST: quality assessment tool for genome assemblies. <i>Bioinformatics</i> , 2013, 29, 1072-1075.	1.8	6,983
529	Bajji genomes reveal low genetic variability and new insights into secondary aquatic adaptations. <i>Nature Communications</i> , 2013, 4, 2708.	5.8	93

#	ARTICLE	IF	CITATIONS
530	Computational Pharmacogenomics. , 2013, , 163-186.		0
531	Complete Genome Sequence of the Probiotic <i>Lactobacillus plantarum</i> Strain ZJ316. <i>Genome Announcements</i> , 2013, 1, e0009413.	0.8	32
532	Analytical Tools and Databases for Metagenomics in the Next-Generation Sequencing Era. <i>Genomics and Informatics</i> , 2013, 11, 102.	0.4	117
533	Genome Sequence of the Pyrene- and Fluoranthene-Degrading Bacterium <i>Cycloclasticus</i> sp. Strain PY97M. <i>Genome Announcements</i> , 2013, 1, .	0.8	14
534	Draft Genome Sequence, and a Sequence-Defined Genetic Linkage Map of the Legume Crop Species <i>Lupinus angustifolius</i> L. <i>PLoS ONE</i> , 2013, 8, e64799.	1.1	99
535	Genome sequence of ground tit <i>Pseudopodoces humilis</i> and its adaptation to high altitude. <i>Genome Biology</i> , 2013, 14, R29.	13.9	81
536	The genome and developmental transcriptome of the strongylid nematode <i>Haemonchus contortus</i> . <i>Genome Biology</i> , 2013, 14, R89.	13.9	192
537	Deep Sequencing of Mixed Total DNA without Barcodes Allows Efficient Assembly of Highly Plastic Ascidian Mitochondrial Genomes. <i>Genome Biology and Evolution</i> , 2013, 5, 1185-1199.	1.1	56
538	Endogenous Gammaretrovirus Acquisition in <i>Mus musculus</i> Subspecies Carrying Functional Variants of the XPR1 Virus Receptor. <i>Journal of Virology</i> , 2013, 87, 9845-9855.	1.5	16
539	ATHLATES: accurate typing of human leukocyte antigen through exome sequencing. <i>Nucleic Acids Research</i> , 2013, 41, e142-e142.	6.5	104
540	The Importance of Total Genome Databases in Research on Akoya Pearl Oyster. <i>Zoological Science</i> , 2013, 30, 781-782.	0.3	3
541	De Bruijn Graph-Based Whole-Genomic Sequence Assembly Algorithms and Applications. , 2013, , .		0
542	Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013, 4, 1858.	5.8	229
543	A dynamic hashing approach to build the de bruijn graph for genome assembly. , 2013, , .		1
544	CloudRS: An error correction algorithm of high-throughput sequencing data based on scalable framework. , 2013, , .		19
545	Using SOAPaligner for Short Reads Alignment. <i>Current Protocols in Bioinformatics</i> , 2013, 44, 11.11.1-17.	25.8	94
546	A new genome assembly method based on dynamic overlap. , 2013, , .		0
547	Reference-assisted chromosome assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1785-1790.	3.3	124

#	ARTICLE	IF	CITATIONS
548	Draft genome of the kiwifruit <i>Actinidia chinensis</i> . <i>Nature Communications</i> , 2013, 4, 2640.	5.8	423
549	DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. <i>Nucleic Acids Research</i> , 2013, 41, e39-e39.	6.5	138
550	Historical variations in mutation rate in an epidemic pathogen, <i>Yersinia pestis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 577-582.	3.3	373
553	Transcriptome Analysis to Identify Putative Floral-Specific Genes and Flowering Regulatory-Related Genes of Sweet Potato. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 2169-2174.	0.6	33
554	Metagenomic sequencing reveals microbiota and its functional potential associated with periodontal disease. <i>Scientific Reports</i> , 2013, 3, 1843.	1.6	207
555	The draft genome of a socially polymorphic halictid bee, <i>Lasioglossum albipes</i> . <i>Genome Biology</i> , 2013, 14, R142.	13.9	72
556	Genome mining reveals the genus <i>Xanthomonas</i> to be a promising reservoir for new bioactive non-ribosomally synthesized peptides. <i>BMC Genomics</i> , 2013, 14, 658.	1.2	21
557	Plastome Sequence Determination and Comparative Analysis for Members of the <i>Lolium</i> - <i>Festuca</i> Grass Species Complex. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 607-616.	0.8	36
558	Draft Genome Sequence of Exopolysaccharide-Producing Thermophilic Bacterium <i>Brevibacillus thermoruber</i> Strain 423. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
559	Draft Genome Sequence of <i>Amphibacillus jilensis</i> Y1T, a Facultatively Anaerobic, Alkaliphilic and Halotolerant Bacterium. <i>Standards in Genomic Sciences</i> , 2013, 8, 491-499.	1.5	1
560	3DScapeCS: application of three dimensional, parallel, dynamic network visualization in Cytoscape. <i>BMC Bioinformatics</i> , 2013, 14, 322.	1.2	14
561	Whole-Genome Sequencing of <i>Lactobacillus shenzhenensis</i> Strain LY-73 T. <i>Genome Announcements</i> , 2013, 1, .	0.8	0
562	Transcriptomic Analysis of <i>Paulownia</i> Infected by <i>Paulownia Witches'-Broom</i> Phytoplasma. <i>PLoS ONE</i> , 2013, 8, e77217.	1.1	65
563	Comparative Chloroplast Genomes of <i>Camellia</i> Species. <i>PLoS ONE</i> , 2013, 8, e73053.	1.1	141
564	De Novo Transcriptome Sequencing and Analysis for <i>Venturia inaequalis</i> , the Devastating Apple Scab Pathogen. <i>PLoS ONE</i> , 2013, 8, e53937.	1.1	32
565	Transcriptomic Immune Response of <i>Tenebrio molitor</i> Pupae to Parasitization by <i>Scleroderma guani</i> . <i>PLoS ONE</i> , 2013, 8, e54411.	1.1	54
566	mRNA-seq Analysis of the <i>Gossypium arboreum</i> transcriptome Reveals Tissue Selective Signaling in Response to Water Stress during Seedling Stage. <i>PLoS ONE</i> , 2013, 8, e54762.	1.1	45
567	Comparative Transcriptional Profiling Provides Insights into the Evolution and Development of the Zygomorphic Flower of <i>Vicia sativa</i> (Papilionoideae). <i>PLoS ONE</i> , 2013, 8, e57338.	1.1	29

#	ARTICLE	IF	CITATIONS
568	Human-to-Bovine Jump of <i>Staphylococcus aureus</i> CC8 Is Associated with the Loss of a $\hat{\rho}^2$ -Hemolysin Converting Prophage and the Acquisition of a New Staphylococcal Cassette Chromosome. <i>PLoS ONE</i> , 2013, 8, e58187.	1.1	63
569	Composition and Expression of Genes Encoding Carbohydrate-Active Enzymes in the Straw-Degrading Mushroom <i>Volvariella volvacea</i> . <i>PLoS ONE</i> , 2013, 8, e58780.	1.1	24
570	RNA-Seq Analysis of <i>Cocos nucifera</i> : Transcriptome Sequencing and De Novo Assembly for Subsequent Functional Genomics Approaches. <i>PLoS ONE</i> , 2013, 8, e59997.	1.1	71
571	CISA: Contig Integrator for Sequence Assembly of Bacterial Genomes. <i>PLoS ONE</i> , 2013, 8, e60843.	1.1	193
572	Comparative Genomic Analysis of the Genus <i>Nocardiopsis</i> Provides New Insights into Its Genetic Mechanisms of Environmental Adaptability. <i>PLoS ONE</i> , 2013, 8, e61528.	1.1	33
573	PeSV-Fisher: Identification of Somatic and Non-Somatic Structural Variants Using Next Generation Sequencing Data. <i>PLoS ONE</i> , 2013, 8, e63377.	1.1	17
574	SOAP3-dp: Fast, Accurate and Sensitive GPU-Based Short Read Aligner. <i>PLoS ONE</i> , 2013, 8, e65632.	1.1	104
575	Transcriptome Analysis and Screening for Potential Target Genes for RNAi-Mediated Pest Control of the Beet Armyworm, <i>Spodoptera exigua</i> . <i>PLoS ONE</i> , 2013, 8, e65931.	1.1	48
576	Rapidly Evolving Genes and Stress Adaptation of Two Desert Poplars, <i>Populus euphratica</i> and <i>P. pruinosa</i> . <i>PLoS ONE</i> , 2013, 8, e66370.	1.1	52
577	Differential Expression Patterns in Chemosensory and Non-Chemosensory Tissues of Putative Chemosensory Genes Identified by Transcriptome Analysis of Insect Pest the Purple Stem Borer <i>Sesamia inferens</i> (Walker). <i>PLoS ONE</i> , 2013, 8, e69715.	1.1	120
578	Genome Annotation of <i>Burkholderia</i> sp. SJ98 with Special Focus on Chemotaxis Genes. <i>PLoS ONE</i> , 2013, 8, e70624.	1.1	9
579	Insights into the Loblolly Pine Genome: Characterization of BAC and Fosmid Sequences. <i>PLoS ONE</i> , 2013, 8, e72439.	1.1	46
580	Optimization of De Novo Short Read Assembly of Seabuckthorn (<i>Hippophae rhamnoides</i> L.) Transcriptome. <i>PLoS ONE</i> , 2013, 8, e72516.	1.1	36
581	SOX9 Duplication Linked to Intersex in Deer. <i>PLoS ONE</i> , 2013, 8, e73734.	1.1	18
582	NeSSM: A Next-Generation Sequencing Simulator for Metagenomics. <i>PLoS ONE</i> , 2013, 8, e75448.	1.1	57
583	Transcriptome Sequencing and Expression Analysis of Terpenoid Biosynthesis Genes in <i>Litsea cubeba</i> . <i>PLoS ONE</i> , 2013, 8, e76890.	1.1	80
584	Floral Transcriptome Sequencing for SSR Marker Development and Linkage Map Construction in the Tea Plant (<i>Camellia sinensis</i>). <i>PLoS ONE</i> , 2013, 8, e81611.	1.1	80
585	Genome-Wide Microsatellite Identification in the Fungus <i>Anisogramma anomala</i> Using Illumina Sequencing and Genome Assembly. <i>PLoS ONE</i> , 2013, 8, e82408.	1.1	37

#	ARTICLE	IF	CITATIONS
586	The Growing Importance of CNVs: New Insights for Detection and Clinical Interpretation. <i>Frontiers in Genetics</i> , 2013, 4, 92.	1.1	49
587	Meta4: a web application for sharing and annotating metagenomic gene predictions using web services. <i>Frontiers in Genetics</i> , 2013, 4, 168.	1.1	8
588	Two Novel Anoxia-Induced Ethylene Response Factors That Interact with Promoters of Deastringency-Related Genes from Persimmon. <i>PLoS ONE</i> , 2014, 9, e97043.	1.1	50
589	Strengths and Limitations of 16S rRNA Gene Amplicon Sequencing in Revealing Temporal Microbial Community Dynamics. <i>PLoS ONE</i> , 2014, 9, e93827.	1.1	508
590	Scanning of Transposable Elements and Analyzing Expression of Transposase Genes of Sweet Potato [<i>Ipomoea batatas</i>]. <i>PLoS ONE</i> , 2014, 9, e90895.	1.1	11
591	Evaluation of a Pooled Strategy for High-Throughput Sequencing of Cosmid Clones from Metagenomic Libraries. <i>PLoS ONE</i> , 2014, 9, e98968.	1.1	18
592	Transcriptome Analysis of <i>Dastarcus helophoroides</i> (Coleoptera: Bothrideridae) Using Illumina HiSeq Sequencing. <i>PLoS ONE</i> , 2014, 9, e100673.	1.1	17
593	6-Hydroxy-3-Succinoylpyridine Hydroxylase Catalyzes a Central Step of Nicotine Degradation in <i>Agrobacterium tumefaciens</i> S33. <i>PLoS ONE</i> , 2014, 9, e103324.	1.1	17
594	Illumina TruSeq Synthetic Long-Reads Empower De Novo Assembly and Resolve Complex, Highly-Repetitive Transposable Elements. <i>PLoS ONE</i> , 2014, 9, e106689.	1.1	180
595	NSIT: Novel Sequence Identification Tool. <i>PLoS ONE</i> , 2014, 9, e108011.	1.1	1
596	Genome Re-Sequencing of Semi-Wild Soybean Reveals a Complex Soja Population Structure and Deep Introgression. <i>PLoS ONE</i> , 2014, 9, e108479.	1.1	26
597	<i>Echinochloa</i> Chloroplast Genomes: Insights into the Evolution and Taxonomic Identification of Two Weedy Species. <i>PLoS ONE</i> , 2014, 9, e113657.	1.1	47
598	PERGA: A Paired-End Read Guided De Novo Assembler for Extending Contigs Using SVM and Look Ahead Approach. <i>PLoS ONE</i> , 2014, 9, e114253.	1.1	18
599	Genetic anchoring of whole-genome shotgun assemblies. <i>Frontiers in Genetics</i> , 2014, 5, 208.	1.1	48
600	Transcriptome Sequencing and Analysis of Leaf Tissue of <i>Avicennia marina</i> Using the Illumina Platform. <i>PLoS ONE</i> , 2014, 9, e108785.	1.1	18
601	The early diverging ascomycetous budding yeast <i>Saitoella complicata</i> has three histone deacetylases belonging to the Clr6, Hos2, and Rpd3 lineages. <i>Journal of General and Applied Microbiology</i> , 2014, 60, 7-12.	0.4	5
602	Generation and Characterization of a Sugarbeet Transcriptome and Transcriptome-Based SSR Markers. <i>Plant Genome</i> , 2014, 7, plantgenome2013.11.0038.	1.6	24
603	Parallel De Bruijn Graph Construction and Traversal for De Novo Genome Assembly. , 2014, , .		58

#	ARTICLE	IF	CITATIONS
604	Crossing-Over in a Hypervariable Species Preferentially Occurs in Regions of High Local Similarity. <i>Molecular Biology and Evolution</i> , 2014, 31, 3016-3025.	3.5	20
605	Whole-Genome Sequencing for Rapid and Accurate Identification of Bacterial Transmission Pathways. <i>Methods in Microbiology</i> , 2014, 41, 123-152.	0.4	4
606	Frequent Expansions of the Bitter Taste Receptor Gene Repertoire during Evolution of Mammals in the Euarchontoglires Clade. <i>Molecular Biology and Evolution</i> , 2014, 31, 2018-2031.	3.5	59
607	Draft Genome Sequence of the Extremophile <i>Acidithiobacillus thiooxidans</i> A01, Isolated from the Wastewater of a Coal Dump. <i>Genome Announcements</i> , 2014, 2, .	0.8	21
608	Genomic Portrait of the Evolution and Epidemic Spread of a Recently Emerged Multidrug-Resistant <i>Shigella flexneri</i> Clone in China. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1119-1126.	1.8	21
609	Assessment of de novo assemblers for draft genomes: a case study with fungal genomes. <i>BMC Genomics</i> , 2014, 15, S10.	1.2	22
610	Genomic signatures of near-extinction and rebirth of the crested ibis and other endangered bird species. <i>Genome Biology</i> , 2014, 15, 557.	3.8	83
611	SAGE: String-overlap Assembly of GENomes. <i>BMC Bioinformatics</i> , 2014, 15, 302.	1.2	23
612	Genome sequencing of <i>Sporisorium scitamineum</i> provides insights into the pathogenic mechanisms of sugarcane smut. <i>BMC Genomics</i> , 2014, 15, 996.	1.2	112
613	Olive fly transcriptomics analysis implicates energy metabolism genes in spinosad resistance. <i>BMC Genomics</i> , 2014, 15, 714.	1.2	27
614	Transcriptome profiling shows gene regulation patterns in a flavonoid pathway in response to exogenous phenylalanine in <i>Boesenbergia rotunda</i> cell culture. <i>BMC Genomics</i> , 2014, 15, 984.	1.2	21
615	Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. <i>Nature Genetics</i> , 2014, 46, 253-260.	9.4	685
616	Next-Generation Sequence Assemblers. <i>SpringerBriefs in Systems Biology</i> , 2014, , 103-116.	0.1	2
617	Tackling soil diversity with the assembly of large, complex metagenomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4904-4909.	3.3	305
618	Genome Sequences of Two <i>Pseudoalteromonas</i> Strains Isolated from the South China Sea. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
619	Metagenomic Data Utilization and Analysis (MEDUSA) and Construction of a Global Gut Microbial Gene Catalogue. <i>PLoS Computational Biology</i> , 2014, 10, e1003706.	1.5	55
620	Genome Sequencing and Comparative Genomics of the Broad Host-Range Pathogen <i>Rhizoctonia solani</i> AG8. <i>PLoS Genetics</i> , 2014, 10, e1004281.	1.5	145
621	Analysis of Deep Sequencing Data. <i>Comprehensive Analytical Chemistry</i> , 2014, , 325-354.	0.7	0

#	ARTICLE	IF	CITATIONS
622	A De Novo Genome Assembly Algorithm for Repeats and Nonrepeats. <i>BioMed Research International</i> , 2014, 2014, 1-16.	0.9	3
623	A consensus approach to vertebrate de novo transcriptome assembly from RNA-seq data: assembly of the duck (<i>Anas platyrhynchos</i>) transcriptome. <i>Frontiers in Genetics</i> , 2014, 5, 190.	1.1	33
624	AlignGraph: algorithm for secondary de novo genome assembly guided by closely related references. <i>Bioinformatics</i> , 2014, 30, i319-i328.	1.8	61
625	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in <i>Lepidoptera</i> . <i>Nature Communications</i> , 2014, 5, 4737.	5.8	196
626	Quo Vadis Venomics? A Roadmap to Neglected Venomous Invertebrates. <i>Toxins</i> , 2014, 6, 3488-3551.	1.5	90
627	Comparative Transcriptome Analysis of Leaves and Roots in Response to Sudden Increase in Salinity in <i>Brassica napus</i> by RNA-seq. <i>BioMed Research International</i> , 2014, 2014, 1-19.	0.9	48
628	Signature Gene Expression Reveals Novel Clues to the Molecular Mechanisms of Dimorphic Transition in <i>Penicillium marneffei</i> . <i>PLoS Genetics</i> , 2014, 10, e1004662.	1.5	38
629	The Draft Genome and Transcriptome of <i>Amaranthus hypochondriacus</i> : A C4 Dicot Producing High-Lysine Edible Pseudo-Cereal. <i>DNA Research</i> , 2014, 21, 585-602.	1.5	52
630	Draft Genome Sequence of <i>Nafulsella turpanensis</i> ZLM-10 T, a Novel Member of the Family <i>Flammeovirgaceae</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	2
631	Draft Genome Sequence of <i>Polaromonas glacialis</i> Strain R3-9, a Psychrotolerant Bacterium Isolated from Arctic Glacial Foreland. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
632	Draft Genome Sequence of a New <i>Shigella flexneri</i> Subserotype, 4S BJ10610. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
633	Complete Genome Sequence of <i>Bacillus anthracis</i> HYU01, Isolated from Soil Samples in the Korean Peninsula. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
634	Draft Genome Sequence of Polychlorinated Biphenyl-Dechlorinating <i>Dehalococcoides mccartyi</i> Strain SG1, Which Carries a Circular Putative Plasmid. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
635	Draft Genome Sequence of the Novel Exopolysaccharide-Producing Bacterium <i>Altibacter lentus</i> Strain JLT2010T, Isolated from Deep Seawater of the South China Sea. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
636	Genome Sequence of a Pandrug-Resistant <i>Pseudomonas aeruginosa</i> Strain, YN-1. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
637	Draft Genome Sequence of a Xylanase-Producing Bacterial Strain, <i>Cellvibrio mixtus</i> J3-8. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
638	BeMADS1 is a key to delivery MADSs into nucleus in reproductive tissues-De novo characterization of <i>Bambusa edulis</i> transcriptome and study of MADS genes in bamboo floral development. <i>BMC Plant Biology</i> , 2014, 14, 179.	1.6	35
639	Computer simulation reveals selection of library is related to read length of solexa sequencing in genome projects. , 2014, , .		0

#	ARTICLE	IF	CITATIONS
640	Effect of Multi-K Contig Merging in de novo DNA Assembly. , 2014, , .		0
641	Whole genome sequencing of the black grouse (<i>Tetrao tetrix</i>): reference guided assembly suggests faster-Z and MHC evolution. <i>BMC Genomics</i> , 2014, 15, 180.	1.2	36
642	A multi-“step comparison of short-read full plastome sequence assembly methods in grasses. <i>Taxon</i> , 2014, 63, 899-910.	0.4	28
643	Thirteen <i>Camellia</i> chloroplast genome sequences determined by high-throughput sequencing: genome structure and phylogenetic relationships. <i>BMC Evolutionary Biology</i> , 2014, 14, 151.	3.2	336
644	Comparative genomic analysis of <i>Klebsiella pneumonia</i> (LCT-KP214) and a mutant strain (LCT-KP289) obtained after spaceflight. <i>BMC Genomics</i> , 2014, 15, 589.	1.2	13
645	SHEAR: sample heterogeneity estimation and assembly by reference. <i>BMC Genomics</i> , 2014, 15, 84.	1.2	7
646	Draft Genome Sequence of <i>Asaia</i> sp. Strain SF2.1, an Important Member of the Microbiome of <i>Anopheles</i> Mosquitoes. <i>Genome Announcements</i> , 2014, 2, .	0.8	10
647	Draft Genome Sequence of Linezolid-Resistant <i>Enterococcus faecalis</i> Clinical Isolate HS0914. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
648	Genome Sequence of the Petroleum Hydrocarbon-Degrading Bacterium <i>Alcanivorax</i> sp. Strain 97CO-5. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
649	BEETL-fastq: a searchable compressed archive for DNA reads. <i>Bioinformatics</i> , 2014, 30, 2796-2801.	1.8	37
650	Draft Genome Sequence of <i>Bacillus subtilis</i> Strain NKYL29, an Antimicrobial-Peptide-Producing Strain from Soil. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
651	Genome Sequence of <i>Bacillus</i> sp. Strain FJAT-14515. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
652	Draft Genome Sequence of a Moderately Halophilic <i>Bacillus megaterium</i> Strain, MSP20.1, Isolated from a Saltern of the Little Rann of Kutch, India. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
653	Draft Genome Sequence of Eggplant (<i>Solanum melongena</i> L.): the Representative <i>Solanum</i> Species Indigenous to the Old World. <i>DNA Research</i> , 2014, 21, 649-660.	1.5	254
654	HiPGA: A High Performance Genome Assembler for Short Read Sequence Data. , 2014, , .		2
655	The locust genome provides insight into swarm formation and long-distance flight. <i>Nature Communications</i> , 2014, 5, 2957.	5.8	437
656	String graph construction using incremental hashing. <i>Bioinformatics</i> , 2014, 30, 3515-3523.	1.8	16
657	Whole-genome sequencing of cultivated and wild peppers provides insights into <i>Capsicum</i> domestication and specialization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5135-5140.	3.3	674

#	ARTICLE	IF	CITATIONS
658	The complex jujube genome provides insights into fruit tree biology. <i>Nature Communications</i> , 2014, 5, 5315.	5.8	251
659	Decelerated genome evolution in modern vertebrates revealed by analysis of multiple lancelet genomes. <i>Nature Communications</i> , 2014, 5, 5896.	5.8	136
660	Draft Genome Sequence of an Extreme Haloarchaeon 3A1-DGR Isolated from a Saltern Crystallizer of the Little Rann of Kutch, India. <i>Indian Journal of Microbiology</i> , 2014, 54, 471-473.	1.5	2
661	Non-referenced genome assembly from epigenomic short-read data. <i>Epigenetics</i> , 2014, 9, 1329-1338.	1.3	3
662	mRNA and Small RNA Transcriptomes Reveal Insights into Dynamic Homoeolog Regulation of Allopolyploid Heterosis in Nascent Hexaploid Wheat. <i>Plant Cell</i> , 2014, 26, 1878-1900.	3.1	308
663	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	6.0	300
664	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	6.0	895
665	RNA-Seq analysis reveals genetic bases of the flowering process in oriental hybrid lily cv. Sorbonne. <i>Russian Journal of Plant Physiology</i> , 2014, 61, 880-892.	0.5	3
666	Adaptations to a Subterranean Environment and Longevity Revealed by the Analysis of Mole Rat Genomes. <i>Cell Reports</i> , 2014, 8, 1354-1364.	2.9	162
667	Genomes correction and assembling: present methods and tools. <i>Proceedings of SPIE</i> , 2014, , .	0.8	6
668	DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. <i>Genome Research</i> , 2014, 24, 2022-2032.	2.4	362
669	Draft Sequences of the Radish (<i>Raphanus sativus</i> L.) Genome. <i>DNA Research</i> , 2014, 21, 481-490.	1.5	165
670	Transcriptome de novo assembly and differentially expressed genes related to cytoplasmic male sterility in kenaf (<i>Hibiscus cannabinus</i> L.). <i>Molecular Breeding</i> , 2014, 34, 1879-1891.	1.0	33
671	ILP-based maximum likelihood genome scaffolding. <i>BMC Bioinformatics</i> , 2014, 15, S9.	1.2	6
672	Transcriptome sequencing of rhizome tissue of <i>Sinopodophyllum hexandrum</i> at two temperatures. <i>BMC Genomics</i> , 2014, 15, 871.	1.2	35
673	Comparative genomic data of the Avian Phylogenomics Project. <i>GigaScience</i> , 2014, 3, 26.	3.3	117
674	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014, 3, 27.	3.3	72
675	ChiloDB: a genomic and transcriptome database for an important rice insect pest <i>Chilo suppressalis</i> . Database: the Journal of Biological Databases and Curation, 2014, 2014, bau065-bau065.	1.4	50

#	ARTICLE	IF	CITATIONS
676	The Draft Assembly of the Radically Organized <i>Stylonychia lemnae</i> Macronuclear Genome. <i>Genome Biology and Evolution</i> , 2014, 6, 1707-1723.	1.1	58
677	Detection of Alternative Splice and Gene Duplication by RNA Sequencing in Japanese Flounder, <i><i>Paralichthys olivaceus</i></i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2419-2424.	0.8	27
678	Insights into novel antimicrobial compounds and antibiotic resistance genes from soil metagenomes. <i>Frontiers in Microbiology</i> , 2014, 5, 489.	1.5	30
679	Comparative Transcriptome Analyses between a Spontaneous Late-Ripening Sweet Orange Mutant and Its Wild Type Suggest the Functions of ABA, Sucrose and JA during Citrus Fruit Ripening. <i>PLoS ONE</i> , 2014, 9, e116056.	1.1	53
680	Genome-wide quantification of homeolog expression ratio revealed nonstochastic gene regulation in synthetic allopolyploid <i><i>Arabidopsis</i></i> . <i>Nucleic Acids Research</i> , 2014, 42, e46-e46.	6.5	108
681	TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. <i>Genome Research</i> , 2014, 24, 310-317.	2.4	81
682	Sequence assembly using next generation sequencing data—challenges and solutions. <i>Science China Life Sciences</i> , 2014, 57, 1140-1148.	2.3	14
683	Complete Genome Sequence of Probiotic <i>Lactobacillus plantarum</i> Strain FMNP01, Isolated from Mango Fruit. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
684	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. <i>Genetics</i> , 2014, 196, 875-890.	1.2	286
685	DNA secondary structures are associated with recombination in major <i>Plasmodium falciparum</i> variable surface antigen gene families. <i>Nucleic Acids Research</i> , 2014, 42, 2270-2281.	6.5	36
686	Characterization of Genetic Diversity in the Nematode <i><i>Pristionchus pacificus</i></i> from Population-Scale Resequencing Data. <i>Genetics</i> , 2014, 196, 1153-1165.	1.2	79
687	ExSPAnDer: a universal repeat resolver for DNA fragment assembly. <i>Bioinformatics</i> , 2014, 30, i293-i301.	1.8	103
688	CarrotDB: a genomic and transcriptomic database for carrot. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau096-bau096.	1.4	87
689	Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis. <i>Genome Biology</i> , 2014, 15, R39.	13.9	245
690	Genome Sequence of a Multidrug-Resistant Strain of <i>Klebsiella pneumoniae</i> , BAMC 07-18, Isolated from a Combat Injury Wound. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
691	Genome sequencing and annotation of <i>Amycolatopsis vancoresmycina</i> strain DSM 44592T. <i>Genomics Data</i> , 2014, 2, 16-17.	1.3	4
692	Exome Sequencing Revealed Novel Germline Mutations in Chinese Peutzâ€“Jeghers Syndrome Patients. <i>Digestive Diseases and Sciences</i> , 2014, 59, 64-71.	1.1	15
693	Comprehensive transcriptional profiling of NaHCO ₃ -stressed <i>Tamarix hispida</i> roots reveals networks of responsive genes. <i>Plant Molecular Biology</i> , 2014, 84, 145-157.	2.0	44

#	ARTICLE	IF	CITATIONS
694	Identification of sturgeon IgD bridges the evolutionary gap between elasmobranchs and teleosts. <i>Developmental and Comparative Immunology</i> , 2014, 42, 138-147.	1.0	39
695	A first Glimpse at the genome of the Baikalian amphipod <i>Eulimnogammarus verrucosus</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2014, 322, 177-189.	0.6	27
696	Transcriptome and proteomic analysis of mango (<i>Mangifera indica</i> Linn) fruits. <i>Journal of Proteomics</i> , 2014, 105, 19-30.	1.2	80
697	Genome sequencing and analysis of the paclitaxel-producing endophytic fungus <i>Penicillium aurantiogriseum</i> NRRL 62431. <i>BMC Genomics</i> , 2014, 15, 69.	1.2	125
698	Transcriptomic analysis of Asiatic lily in the process of vernalization via RNA-seq. <i>Molecular Biology Reports</i> , 2014, 41, 3839-3852.	1.0	26
699	RNA sequencing read depth requirement for optimal transcriptome coverage in <i>Hevea brasiliensis</i> . <i>BMC Research Notes</i> , 2014, 7, 69.	0.6	29
700	Comparative analysis of four essential Gracilariaceae species in China based on whole transcriptomic sequencing. <i>Acta Oceanologica Sinica</i> , 2014, 33, 54-62.	0.4	8
701	De novo sequencing and comparative analysis of three red algal species of Family Solieriaceae to discover putative genes associated with carrageenan biosynthesis. <i>Acta Oceanologica Sinica</i> , 2014, 33, 45-53.	0.4	7
702	Transcriptome sequencing of essential marine brown and red algal species in China and its significance in algal biology and phylogeny. <i>Acta Oceanologica Sinica</i> , 2014, 33, 1-12.	0.4	22
703	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	6.0	254
704	The Genome of the Clonal Raider Ant <i>Cerapachys biroi</i> . <i>Current Biology</i> , 2014, 24, 451-458.	1.8	143
705	Microbiome and Autoimmunity. , 2014, , 329-340.		0
706	De novo finished 2.8 Mbp <i>Staphylococcus aureus</i> genome assembly from 100 bp short and long range paired-end reads. <i>Bioinformatics</i> , 2014, 30, 40-49.	1.8	50
707	The tobacco genome sequence and its comparison with those of tomato and potato. <i>Nature Communications</i> , 2014, 5, 3833.	5.8	503
708	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.	13.5	363
709	Stick Insect Genomes Reveal Natural Selection's Role in Parallel Speciation. <i>Science</i> , 2014, 344, 738-742.	6.0	386
710	Assessing Genetic Diversity among <i>Brettanomyces</i> Yeasts by DNA Fingerprinting and Whole-Genome Sequencing. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4398-4413.	1.4	66
711	Population genomic analyses from low coverage RAD-seq data: a case study on the non-model cucurbit bottle gourd. <i>Plant Journal</i> , 2014, 77, 430-442.	2.8	80

#	ARTICLE	IF	CITATIONS
712	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1777-1786.	1.4	131
713	BLESS: Bloom filter-based error correction solution for high-throughput sequencing reads. <i>Bioinformatics</i> , 2014, 30, 1354-1362.	1.8	113
714	Influenza H7N9 and H9N2 Viruses: Coexistence in Poultry Linked to Human H7N9 Infection and Genome Characteristics. <i>Journal of Virology</i> , 2014, 88, 3423-3431.	1.5	93
715	Genome assembly and annotation for red clover (<i>Trifolium pratense</i> ; Fabaceae). <i>American Journal of Botany</i> , 2014, 101, 327-337.	0.8	69
716	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history. <i>Nature Genetics</i> , 2014, 46, 1303-1310.	9.4	174
717	De Novo Genome Assembly of the Economically Important Weed Horseweed Using Integrated Data from Multiple Sequencing Platforms. <i>Plant Physiology</i> , 2014, 166, 1241-1254.	2.3	101
718	Rapid diversification of five <i>Oryza</i> AA genomes associated with rice adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4954-62.	3.3	145
719	KmerStream: streaming algorithms for <i>k</i> -mer abundance estimation. <i>Bioinformatics</i> , 2014, 30, 3541-3547.	1.8	56
720	Phylotranscriptomic analysis of the origin and early diversification of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4859-68.	3.3	1,123
722	Chloroplast Phylogenomic Analyses Resolve Deep-Level Relationships of an Intractable Bamboo Tribe Arundinarieae (Poaceae). <i>Systematic Biology</i> , 2014, 63, 933-950.	2.7	254
723	RepARK: de novo creation of repeat libraries from whole-genome NGS reads. <i>Nucleic Acids Research</i> , 2014, 42, e80-e80.	6.5	67
724	Identification of gene expression profiles in the actinomycete <i>Gordonia neofelifaecis</i> grown with different steroids. <i>Genome</i> , 2014, 57, 345-353.	0.9	16
725	Characterization of cysteine protease-like genes in the striped rice stem borer, <i>Chilo suppressalis</i> . <i>Genome</i> , 2014, 57, 79-88.	0.9	15
726	The Genome Sequence of the Highly Acetic Acid-Tolerant <i>Zygosaccharomyces bailii</i> -Derived Interspecies Hybrid Strain ISA1307, Isolated From a Sparkling Wine Plant. <i>DNA Research</i> , 2014, 21, 299-313.	1.5	62
727	Characterization of the global transcriptome for cotton (<i>Gossypium hirsutum</i> L.) anther and development of SSR marker. <i>Gene</i> , 2014, 551, 206-213.	1.0	18
728	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184.	6.0	520
729	Mining Tissue-specific Contigs from Peanut (<i>Arachis hypogaea</i> L.) for Promoter Cloning by Deep Transcriptome Sequencing. <i>Plant and Cell Physiology</i> , 2014, 55, 1793-1801.	1.5	22
730	Multiplex sequencing of pooled mitochondrial genomes—a crucial step toward biodiversity analysis using mito-metagenomics. <i>Nucleic Acids Research</i> , 2014, 42, e166-e166.	6.5	230

#	ARTICLE	IF	CITATIONS
731	De novo assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits. <i>Nature Biotechnology</i> , 2014, 32, 1045-1052.	9.4	535
732	Characterization and high cross-species transferability of microsatellite markers from the floral transcriptome of <i>Aspidistra saxicola</i> (Asparagaceae). <i>Molecular Ecology Resources</i> , 2014, 14, 569-577.	2.2	39
733	Comparative Genomics of Flatworms (Platyhelminthes) Reveals Shared Genomic Features of Ecto- and Endoparasitic Neodermata. <i>Genome Biology and Evolution</i> , 2014, 6, 1105-1117.	1.1	73
734	Efficient de novo assembly of highly heterozygous genomes from whole-genome shotgun short reads. <i>Genome Research</i> , 2014, 24, 1384-1395.	2.4	1,000
735	Alterations of the human gut microbiome in liver cirrhosis. <i>Nature</i> , 2014, 513, 59-64.	13.7	1,782
736	Fungal Polyketide Synthase Product Chain-Length Control by Partnering Thiohydrolase. <i>ACS Chemical Biology</i> , 2014, 9, 1576-1586.	1.6	54
737	ChIP-seq reveals a role for CrzA in the Aspergillus fumigatus high-osmolarity glycerol response (HOG) signalling pathway. <i>Molecular Microbiology</i> , 2014, 94, 655-674.	1.2	60
738	Major alterations in transcript profiles between C3 and C4 photosynthesis of an amphibious species <i>Eleocharis baldwinii</i> . <i>Plant Molecular Biology</i> , 2014, 86, 93-110.	2.0	14
739	High-resolution digital profiling of the epigenome. <i>Nature Reviews Genetics</i> , 2014, 15, 814-827.	7.7	112
740	Genome and transcriptome sequencing identifies breeding targets in the orphan crop tef (<i>Eragrostis tef</i>). <i>PLoS ONE</i> , 2014, 9, e101333.	1.2	133
741	Oil accumulation mechanisms of the oleaginous microalga <i>Chlorella protothecoides</i> revealed through its genome, transcriptomes, and proteomes. <i>BMC Genomics</i> , 2014, 15, 582.	1.2	134
742	Comparative genome sequencing reveals chemotype-specific gene clusters in the toxigenic black mold <i>Stachybotrys</i> . <i>BMC Genomics</i> , 2014, 15, 590.	1.2	45
743	The genome of the Tiger Milk mushroom, <i>Lignosus rhinocerotis</i> , provides insights into the genetic basis of its medicinal properties. <i>BMC Genomics</i> , 2014, 15, 635.	1.2	65
744	Performance comparison of second- and third-generation sequencers using a bacterial genome with two chromosomes. <i>BMC Genomics</i> , 2014, 15, 699.	1.2	93
745	A memory-efficient algorithm to obtain splicing graphs and de novo expression estimates from de Bruijn graphs of RNA-Seq data. <i>BMC Genomics</i> , 2014, 15, S6.	1.2	5
746	High-coverage sequencing and annotated assemblies of the budgerigar genome. <i>GigaScience</i> , 2014, 3, 11.	3.3	75
747	De novo assembly of maritime pine transcriptome: implications for forest breeding and biotechnology. <i>Plant Biotechnology Journal</i> , 2014, 12, 286-299.	4.1	115
748	SOAPdenovo-Trans: de novo transcriptome assembly with short RNA-Seq reads. <i>Bioinformatics</i> , 2014, 30, 1660-1666.	1.8	826

#	ARTICLE	IF	CITATIONS
749	The Architecture of a Scrambled Genome Reveals Massive Levels of Genomic Rearrangement during Development. <i>Cell</i> , 2014, 158, 1187-1198.	13.5	152
750	Complementary symbiont contributions to plant decomposition in a fungus-farming termite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14500-14505.	3.3	243
751	Genome sequence and genetic diversity of the common carp, <i>Cyprinus carpio</i> . <i>Nature Genetics</i> , 2014, 46, 1212-1219.	9.4	576
752	A roadmap for natural product discovery based on large-scale genomics and metabolomics. <i>Nature Chemical Biology</i> , 2014, 10, 963-968.	3.9	416
753	Genome sequence of the cultivated cotton <i>Gossypium arboreum</i> . <i>Nature Genetics</i> , 2014, 46, 567-572.	9.4	883
754	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
755	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
756	The Impact of Next-Generation Sequencing Technology on Bacterial Genomics. , 2014, , 31-58.		2
757	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. <i>Nature Communications</i> , 2014, 5, 4340.	5.8	332
758	<i>proovread</i> : large-scale high-accuracy PacBio correction through iterative short read consensus. <i>Bioinformatics</i> , 2014, 30, 3004-3011.	1.8	514
759	The intestinal microbiome of fish under starvation. <i>BMC Genomics</i> , 2014, 15, 266.	1.2	242
760	Reference-free SNP detection: dealing with the data deluge. <i>BMC Genomics</i> , 2014, 15, S10.	1.2	23
761	Integration of bioinformatics to biodegradation. <i>Biological Procedures Online</i> , 2014, 16, 8.	1.4	51
762	Whole-genome sequence variation, population structure and demographic history of the Dutch population. <i>Nature Genetics</i> , 2014, 46, 818-825.	9.4	641
763	Sequencing of the chloroplast genomes of cytoplasmic male-sterile and male-fertile lines of soybean and identification of polymorphic markers. <i>Plant Science</i> , 2014, 229, 208-214.	1.7	12
764	Dissection of the Octoploid Strawberry Genome by Deep Sequencing of the Genomes of <i>Fragaria</i> Species. <i>DNA Research</i> , 2014, 21, 169-181.	1.5	201
765	Rates of genomic divergence in humans, chimpanzees and their lice. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132174.	1.2	29
766	Transcriptome Profiling Identifies Differentially Expressed Genes in Postnatal Developing Pituitary Gland of Miniature Pig. <i>DNA Research</i> , 2014, 21, 207-216.	1.5	36

#	ARTICLE	IF	CITATIONS
767	Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , 2014, 5, 3966.	5.8	124
768	Morphological and molecular studies of <i>Vairimorpha necatrix</i> BM, a new strain of the microsporidium <i>V. necatrix</i> (microsporidia, burenellidae) recorded in the silkworm, <i>Bombyx mori</i> . <i>Experimental Parasitology</i> , 2014, 143, 74-82.	0.5	11
769	Comparative and retrospective molecular analysis of Parapoxvirus (PPV) isolates. <i>Virus Research</i> , 2014, 181, 11-21.	1.1	41
770	Analysis of skin and secretions of Dybowski's frogs (<i>Rana dybowskii</i>) exposed to <i>Staphylococcus aureus</i> or <i>Escherichia coli</i> identifies immune response proteins. <i>Veterinary Journal</i> , 2014, 200, 127-132.	0.6	10
771	Angiosperm Phylogeny Based on 18S/26S rDNA Sequence Data: Constructing a Large Data Set Using Next-Generation Sequence Data. <i>International Journal of Plant Sciences</i> , 2014, 175, 613-650.	0.6	24
772	Blue: correcting sequencing errors using consensus and context. <i>Bioinformatics</i> , 2014, 30, 2723-2732.	1.8	68
773	Draft genome sequence of <i>Microbulbifer elongatus</i> strain HZ11, a brown seaweed-degrading bacterium with potential ability to produce bioethanol from alginate. <i>Marine Genomics</i> , 2014, 18, 83-85.	0.4	18
774	Omega: an Overlap-graph <i>de novo</i> Assembler for Metagenomics. <i>Bioinformatics</i> , 2014, 30, 2717-2722.	1.8	83
775	Transcriptome and gene expression analysis during flower blooming in <i>Rosa chinensis</i> 'Pallida'. <i>Gene</i> , 2014, 540, 96-103.	1.0	31
777	Complete genome sequence of Roseophage vB_DshP-R1, which infects <i>Dinoroseobacter shibae</i> DFL12. <i>Standards in Genomic Sciences</i> , 2014, 9, 31.	1.5	4
778	High quality draft genome sequence of the heavy metal resistant bacterium <i>Halomonas zincidurans</i> type strain B6T. <i>Standards in Genomic Sciences</i> , 2014, 9, 30.	1.5	17
779	What is the difference between the breakpoint graph and the de Bruijn graph?. <i>BMC Genomics</i> , 2014, 15, S6.	1.2	14
780	Draft genome sequence of <i>Bacillus amyloliquefaciens</i> HB-26. <i>Standards in Genomic Sciences</i> , 2014, 9, 775-782.	1.5	4
781	High-quality draft genome sequence of nematocidal <i>Bacillus thuringiensis</i> Sbt003. <i>Standards in Genomic Sciences</i> , 2014, 9, 1-10.	1.5	3
782	MapReduce based parallel suffix tree construction for human genome. , 2014, , .		5
783	SWAP-Assembler: scalable and efficient genome assembly towards thousands of cores. <i>BMC Bioinformatics</i> , 2014, 15, S2.	1.2	35
784	The molecular biology of the olive fly comes of age. <i>BMC Genetics</i> , 2014, 15, S8.	2.7	17
785	HyDA-Vista: towards optimal guided selection of k-mer size for sequence assembly. <i>BMC Genomics</i> , 2014, 15, S9.	1.2	6

#	ARTICLE	IF	CITATIONS
786	Efficient de Bruijn graph construction for genome assembly using a hash table and auxiliary vector data structures. , 2014, , .		1
787	Genome Sequence of Paenibacillus polymyxa Strain CICC 10580, Isolated from the Fruit of Noni () Tj ETQq1 1 0.784314 rgBT ₃ /Overlo	0.8	0
788	Whole Genome Sequence of the Probiotic Strain Lactobacillus paracasei N1115, Isolated from Traditional Chinese Fermented Milk. Genome Announcements, 2014, 2, .	0.8	16
789	Draft genome sequence of Paenibacillus dauci sp. nov., a carrot-associated endophytic actinobacteria. Genomics Data, 2015, 5, 241-253.	1.3	9
790	Sequence-based ultra-dense genetic and physical maps reveal structural variations of allopolyploid cotton genomes. Genome Biology, 2015, 16, 108.	13.9	108
791	Genotypic and phenotypic analyses of a Pseudomonas aeruginosa chronic bronchiectasis isolate reveal differences from cystic fibrosis and laboratory strains. BMC Genomics, 2015, 16, 883.	1.2	30
792	Transcriptome changes in Polygonum multiflorum Thunb. roots induced by methyl jasmonate. Journal of Zhejiang University: Science B, 2015, 16, 1027-1041.	1.3	6
793	Evolutionary history inferred from the de novo assembly of a nonmodel organism, the blue-eyed black lemur. Molecular Ecology, 2015, 24, 4392-4405.	2.0	25
794	High-coverage sequencing and annotated assembly of the genome of the Australian dragon lizard Pogona vitticeps. GigaScience, 2015, 4, 45.	3.3	97
795	Genomes of <i>Candidatus</i> Liberibacter solanacearum TM Haplotype A from New Zealand and the United States Suggest Significant Genome Plasticity in the Species. Phytopathology, 2015, 105, 863-871.	1.1	35
796	Mimosoid legume plastome evolution: IR expansion, tandem repeat expansions and accelerated rate of evolution in clpP. Scientific Reports, 2015, 5, 16958.	1.6	125
797	Evidence for horizontal transfer of mitochondrial DNA to the plastid genome in a bamboo genus. Scientific Reports, 2015, 5, 11608.	1.6	62
798	Functional and structural properties of a novel cellulosome-like multienzyme complex: efficient glycoside hydrolysis of water-insoluble 7-xylosyl-10-deacetylpaclitaxel. Scientific Reports, 2015, 5, 13768.	1.6	23
799	A Memory Efficient Short Read De Novo Assembly Algorithm. IPSJ Transactions on Bioinformatics, 2015, 8, 2-8.	0.2	0
800	Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of Oryza AA genome species. Scientific Reports, 2015, 5, 15655.	1.6	169
801	HipMer. , 2015, , .		57
802	An NGS Workflow Blueprint for DNA Sequencing Data and Its Application in Individualized Molecular Oncology. Cancer Informatics, 2015, 14s5, CIN.S30793.	0.9	10
803	Heuristic pairwise alignment of de Bruijn graphs to facilitate simultaneous transcript discovery in related organisms from RNA-Seq data. BMC Genomics, 2015, 16, S5.	1.2	4

#	ARTICLE	IF	CITATIONS
804	Data in support of the comparative genome analysis of <i>Lysinibacillus</i> B1-CDA, a bacterium that accumulates arsenics. Data in Brief, 2015, 5, 579-585.	0.5	2
805	Application of whole genome re-sequencing data in the development of diagnostic DNA markers tightly linked to a disease-resistance locus for marker-assisted selection in lupin (<i>Lupinus</i>) Tj ETQq1 1 0.784314 rgBT /Overloc 10 Tf 50	1.2	10
806	Genomics and transcriptomics of <i>Xanthomonas campestris</i> species challenge the concept of core type III effectome. BMC Genomics, 2015, 16, 975.	1.2	62
807	Genome analysis of <i>Daldinia eschscholtzii</i> strains UM 1400 and UM 1020, wood-decaying fungi isolated from human hosts. BMC Genomics, 2015, 16, 966.	1.2	16
808	Diversity of nitrogen assimilation pathways among microbial photosynthetic eukaryotes. Journal of Phycology, 2015, 51, 490-506.	1.0	27
809	Genome Sequences of the Race 1 and Race 4 <i>Xanthomonas campestris</i> pv. <i>campestris</i> Strains CFBP 1869 and CFBP 5817. Genome Announcements, 2015, 3, .	0.8	9
810	Genome Sequence of <i>Brevibacillus reuszeri</i> NRRL NRS-1206 ^T , an <i>scpA</i> - <i>N</i> -Carbamoylase-Producing <i>Bacillus</i> -Like Bacterium. Genome Announcements, 2015, 3, .	0.8	3
811	The 474-Kilobase-Pair Complete Genome Sequence of CeV-01B, a Virus Infecting <i>Haptolina</i> () Tj ETQq1 1 0.784314 rgBT /Overloc 0.8 17	0.8	17
812	Heterozygous genome assembly via binary classification of homologous sequence. BMC Bioinformatics, 2015, 16, S5.	1.2	21
813	Inferring the global structure of chromosomes from structural variations. BMC Genomics, 2015, 16, S13.	1.2	2
814	A pipeline for completing bacterial genomes using in silico and wet lab approaches. BMC Genomics, 2015, 16, S7.	1.2	13
815	Complete genome sequence of Roseophage vB_DshP-R1, which infects <i>Dinoroseobacter shibae</i> DFL12. Standards in Genomic Sciences, 2015, 10, 6.	1.5	13
816	misFinder: identify mis-assemblies in an unbiased manner using reference and paired-end reads. BMC Bioinformatics, 2015, 16, 386.	1.2	14
817	Comparative genome analysis identifies two large deletions in the genome of highly-passaged attenuated <i>Streptococcus agalactiae</i> strain YM001 compared to the parental pathogenic strain HN016. BMC Genomics, 2015, 16, 897.	1.2	21
818	Impact of library preparation protocols and template quantity on the metagenomic reconstruction of a mock microbial community. BMC Genomics, 2015, 16, 856.	1.2	79
819	Potential mechanisms of attenuation for rifampicin-passaged strains of <i>Flavobacterium psychrophilum</i> . BMC Microbiology, 2015, 15, 179.	1.3	9
820	LASER: Large genome ASsembly Evaluator. BMC Research Notes, 2015, 8, 709.	0.6	5
821	Draft genome sequence of <i>Halopiger salifodinae</i> KCY07-B2T, an extremely halophilic archaeon isolated from a salt mine. Standards in Genomic Sciences, 2015, 10, 124.	1.5	2

#	ARTICLE	IF	CITATIONS
822	Genome sequence of a dissimilatory Fe(III)-reducing bacterium <i>Geobacter soli</i> type strain GSS01T. <i>Standards in Genomic Sciences</i> , 2015, 10, 118.	1.5	22
823	Genome Sequence of <i>Paenibacillus</i> sp. Strain FJAT-28004 for the Genome Sequencing Project for Genomic Taxonomy and Phylogenomics of <i>Bacillus</i> -Like Bacteria. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
824	Genome Sequence of Type Strain <i>Bacillus decisifrondis</i> E5HC-32 T (DSM 11725 T), Isolated from Soil Underlying the Decaying Leaf Litter of a Slash Pine Forest. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
825	Classification of Metagenomics Data at Lower Taxonomic Level Using a Robust Supervised Classifier. <i>Evolutionary Bioinformatics</i> , 2015, 11, EBO.S20523.	0.6	5
826	Draft Genome Sequence of <i>Sporosarcina globispora</i> W 25 ^T (DSM 4), a Psychrophilic Bacterium Isolated from Soil and River Water. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
827	Genome Sequence of Type Strain <i>Lysinibacillus macroides</i> DSM 54 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
828	Draft Genome Sequence of Type Strain <i>Lysinibacillus xylanilyticus</i> DSM 23493 ^T . <i>Genome Announcements</i> , 2015, 3, .	0.8	1
829	Genome Sequence of <i>Virgibacillus pantothenicus</i> DSM 26 ^T (ATCC 14576), a Mesophilic and Halotolerant Bacterium Isolated from Soil. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
830	Genome Sequence of <i>Bacillus butanolivorans</i> K9 ^T (DSM 18926), an <i>in</i> - <i>Butanol</i> -Consuming Bacterium Isolated from Soil. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
831	Draft Genome Sequence of <i>Bacillus tequilensis</i> Strain FJAT-14262a. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
832	Draft Genome Sequence of <i>Brevibacillus brevis</i> DZQ7, a Plant Growth-Promoting Rhizobacterium with Broad-Spectrum Antimicrobial Activity. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
833	Draft Genome Sequence of <i>Bacillus murimartini</i> LMG 21005 T , an Alkalitolerant Bacterium Isolated from a Church Wall Mural in Germany. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
834	Draft Genome Sequence of <i>Streptomyces mutabilis</i> TRM45540, Isolated from a Hypersaline Soil Sample. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
835	De novo assembly and characterization of skin transcriptome using RNAseq in sheep (<i>Ovis aries</i>). <i>Genetics and Molecular Research</i> , 2015, 14, 1371-1384.	0.3	14
836	Fragmentation and Coverage Variation in Viral Metagenome Assemblies, and Their Effect in Diversity Calculations. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 141.	2.0	33
837	Structural Variation (SV) Markers in the Basidiomycete <i>Volvariella volvacea</i> and Their Application in the Construction of a Genetic Map. <i>International Journal of Molecular Sciences</i> , 2015, 16, 16669-16682.	1.8	4
838	Identification of Genes Putatively Involved in Chitin Metabolism and Insecticide Detoxification in the Rice Leaf Folder (<i>Cnaphalocrocis medinalis</i>) Larvae through Transcriptomic Analysis. <i>International Journal of Molecular Sciences</i> , 2015, 16, 21873-21896.	1.8	16
839	Genome mining and metabolic profiling of the rhizosphere bacterium <i>Pseudomonas</i> sp. SH-C52 for antimicrobial compounds. <i>Frontiers in Microbiology</i> , 2015, 6, 693.	1.5	91

#	ARTICLE	IF	CITATIONS
840	In-Depth Transcriptome Sequencing of Mexican Lime Trees Infected with Candidatus Phytoplasma aurantifolia. PLoS ONE, 2015, 10, e0130425.	1.1	39
841	Complete Taiwanese Macaque (<i>Macaca cyclopis</i>) Mitochondrial Genome: Reference-Assisted de novo Assembly with Multiple k-mer Strategy. PLoS ONE, 2015, 10, e0130673.	1.1	2
842	Genome Sequence Analysis of the Naphthenic Acid Degrading and Metal Resistant Bacterium <i>Cupriavidus gilardii</i> CR3. PLoS ONE, 2015, 10, e0132881.	1.1	44
843	MAFsnip: A Multi-Sample Accurate and Flexible SNP Caller Using Next-Generation Sequencing Data. PLoS ONE, 2015, 10, e0135332.	1.1	4
844	Identification and Expression Profiles of Sex Pheromone Biosynthesis and Transport Related Genes in <i>Spodoptera litura</i> . PLoS ONE, 2015, 10, e0140019.	1.1	46
845	Dynamic transcriptional profiling provides insights into tuberous root development in <i>Rehmannia glutinosa</i> . Frontiers in Plant Science, 2015, 6, 396.	1.7	27
846	Gene Expression Reaction Norms Unravel the Molecular and Cellular Processes Underpinning the Plastic Phenotypes of <i>Alternanthera philoxeroides</i> in Contrasting Hydrological Conditions. Frontiers in Plant Science, 2015, 6, 991.	1.7	9
847	Transcriptomes That Confer to Plant Defense against Powdery Mildew Disease in <i>Lagerstroemia indica</i> . International Journal of Genomics, 2015, 2015, 1-12.	0.8	7
848	Bioinformatics and Omic Approaches for Characterization of Environmental Microorganisms. , 2015, , 483-505.		4
849	Analysis of horse genomes provides insight into the diversification and adaptive evolution of karyotype. Scientific Reports, 2014, 4, 4958.	1.6	108
850	Assembling short reads from jumping libraries with large insert sizes. Bioinformatics, 2015, 31, 3262-3268.	1.8	40
851	Genome-Wide Mapping of Structural Variations Reveals a Copy Number Variant That Determines Reproductive Morphology in Cucumber. Plant Cell, 2015, 27, 1595-1604.	3.1	125
852	Mechanotransduction Mechanisms for Intraventricular Diastolic Vortex Forces and Myocardial Deformations: Part 2. Journal of Cardiovascular Translational Research, 2015, 8, 293-318.	1.1	31
853	Next-generation sequencing approach for connecting secondary metabolites to biosynthetic gene clusters in fungi. Frontiers in Microbiology, 2015, 5, 774.	1.5	80
854	Next-Generation Sequencing and Assembly of Plant Genomes. , 2015, , 53-64.		1
855	Transcriptome sequencing and differential gene expression analysis in <i>Viola yedoensis</i> Makino (Fam.) Tj ETQq1 1 0.784314 rgBT /Over Communications, 2015, 459, 60-65.	1.0	26
856	Draft genome sequence of the novel strain <i>Pseudomonas</i> sp. 10B238 with potential ability to produce antibiotics from deep-sea sediment. Marine Genomics, 2015, 23, 55-57.	0.4	14
857	Complete Genome Sequence of <i>Lactobacillus plantarum</i> Strain B21, a Bacteriocin-Producing Strain Isolated from Vietnamese Fermented Sausage Nem Chua. Genome Announcements, 2015, 3, .	0.8	27

#	ARTICLE	IF	CITATIONS
858	Genome sequence and description of the mosquitocidal and heavy metal tolerant strain <i>Lysinibacillus sphaericus</i> CBAM5. <i>Standards in Genomic Sciences</i> , 2015, 10, 2.	1.5	42
859	De novo assembly and characterization of the skeletal muscle transcriptome of sheep using Illumina paired-end sequencing. <i>Biotechnology Letters</i> , 2015, 37, 1747-1756.	1.1	6
860	Draft Genome Sequence of <i>Vibrio owensii</i> Strain SH-14, Which Causes Shrimp Acute Hepatopancreatic Necrosis Disease. <i>Genome Announcements</i> , 2015, 3, .	0.8	78
861	Removal of redundant contigs from de novo RNA-Seq assemblies via homology search improves accurate detection of differentially expressed genes. <i>BMC Genomics</i> , 2015, 16, 1031.	1.2	30
862	Degeneration of the Nonrecombining Regions in the Mating-Type Chromosomes of the Anther-Smut Fungi. <i>Molecular Biology and Evolution</i> , 2015, 32, 928-943.	3.5	49
863	DNA-Based Storage: Trends and Methods. <i>IEEE Transactions on Molecular, Biological, and Multi-Scale Communications</i> , 2015, 1, 230-248.	1.4	157
864	Chloroplast phylogenomics resolves key relationships in ferns. <i>Journal of Systematics and Evolution</i> , 2015, 53, 448-457.	1.6	64
865	Population-level consequences of complementary sex determination in a solitary parasitoid. <i>BMC Evolutionary Biology</i> , 2015, 15, 98.	3.2	15
866	The complete mitochondrial genome sequence of the green microalga <i>Lobosphaera</i> (<i>Parietochloris</i>) <i>incisa</i> reveals a new type of palindromic repetitive repeat. <i>BMC Genomics</i> , 2015, 16, 580.	1.2	9
867	Reconstructing 16S rRNA genes in metagenomic data. <i>Bioinformatics</i> , 2015, 31, i35-i43.	1.8	139
868	Complete Genome Sequence of an Aldoxime Degradar, <i>Bacillus</i> sp. OxB-1. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
869	Draft Genome Sequence of the Nonmarine Agarolytic Bacterium <i>Cellvibrio</i> sp. OA-2007. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
870	Draft Genome Sequence of Enterohemorrhagic <i>Escherichia coli</i> O157 NCCP15739, Isolated in the Republic of Korea. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
871	A draft genome sequence of an invasive mosquito: an Italian <i>Aedes albopictus</i> . <i>Pathogens and Global Health</i> , 2015, 109, 207-220.	1.0	35
872	Comparative genome analysis of <i>Lysinibacillus</i> B1-CDA, a bacterium that accumulates arsenics. <i>Genomics</i> , 2015, 106, 384-392.	1.3	17
873	Draft Genome Sequence of <i>Bacillus marisflavi</i> TF-11 (JCM 11544), a Carotenoid-Producing Bacterium Isolated from Seawater from a Tidal Flat in the Yellow Sea. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
874	Candidate chemosensory genes identified in <i>Colaphellus bowringi</i> by antennal transcriptome analysis. <i>BMC Genomics</i> , 2015, 16, 1028.	1.2	90
875	Complete genome sequences of bacteriophages P12002L and P12002S, two lytic phages that infect a marine <i>Polaribacter</i> strain. <i>Standards in Genomic Sciences</i> , 2015, 10, 82.	1.5	25

#	ARTICLE	IF	CITATIONS
876	High-Quality Draft Genome Sequence of <i>Aneurinibacillus migulanus</i> ATCC 9999 T (DSM 2895), a Gramicidin S-Producing Bacterium Isolated from Garden Soil. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
877	Draft Genome Sequence of <i>Bacillus</i> sp. FJAT-27238 for Setting up Phylogenomic Analysis of Genomic Taxonomy of <i>Bacillus</i> -Like Bacteria. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
878	Investigation of mercury tolerance in <i>Chromohalobacter israelensis</i> DSM 6768T and <i>Halomonas zincidurans</i> B6T by comparative genomics with <i>Halomonas xinjiangensis</i> TRM 0175T. <i>Marine Genomics</i> , 2015, 19, 15-16.	0.4	12
879	Computational Tools for Taxonomic Microbiome Profiling of Shotgun Metagenomes. , 2015, , 67-80.		5
880	RNA-seq-mediated transcriptome analysis of actively growing and winter dormant shoots identifies non-deciduous habit of evergreen tree tea during winters. <i>Scientific Reports</i> , 2014, 4, 5932.	1.6	52
881	Next-generation sequencing workflow for assembly of nonmodel mitogenomes exemplified with North Pacific albatrosses (<i>Phoebastria</i> spp.). <i>Molecular Ecology Resources</i> , 2015, 15, 893-902.	2.2	18
882	A survey of genome sequence assembly techniques and algorithms using high-performance computing. <i>Journal of Supercomputing</i> , 2015, 71, 293-339.	2.4	4
883	The draft genome, transcriptome, and microbiome of <i>Dermatophagoides farinae</i> reveal a broad spectrum of dust mite allergens. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 539-548.	1.5	172
884	Comparative Genomic Analysis of <i>Pseudomonas chlororaphis</i> PCL1606 Reveals New Insight into Antifungal Compounds Involved in Biocontrol. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 249-260.	1.4	50
885	Identification and characterization of microRNA sequences from bovine mammary epithelial cells. <i>Journal of Dairy Science</i> , 2015, 98, 1696-1705.	1.4	22
886	An $O(m, \log T)$ Time Algorithm for Detecting Superbubbles. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 770-777.	1.9	15
887	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015, 6, 5969.	5.8	164
888	Impacts of the Three Gorges Dam on microbial structure and potential function. <i>Scientific Reports</i> , 2015, 5, 8605.	1.6	129
889	The genome and transcriptome of the zoonotic hookworm <i>Ancylostoma ceylanicum</i> identify infection-specific gene families. <i>Nature Genetics</i> , 2015, 47, 416-422.	9.4	91
890	Comparative genomic sequence analysis of Chinese orf virus strain NA1/11 with other parapoxviruses. <i>Archives of Virology</i> , 2015, 160, 253-266.	0.9	32
891	Insights from 20 years of bacterial genome sequencing. <i>Functional and Integrative Genomics</i> , 2015, 15, 141-161.	1.4	580
892	De novo assembly of bacterial transcriptomes from RNA-seq data. <i>Genome Biology</i> , 2015, 16, 1.	3.8	1,215
893	Genome analysis of <i>Flaviramulus ichthyoenteri</i> Th78T in the family Flavobacteriaceae: insights into its quorum quenching property and potential roles in fish intestine. <i>BMC Genomics</i> , 2015, 16, 38.	1.2	22

#	ARTICLE	IF	CITATIONS
894	The broad-host-range plasmid pSFA231 isolated from petroleum-contaminated sediment represents a new member of the PromA plasmid family. <i>Frontiers in Microbiology</i> , 2014, 5, 777.	1.5	32
895	Draft genome sequence of <i>Paenibacillus algorifonticola</i> sp. nov., an antimicrobial-producing strain. <i>Genomics Data</i> , 2015, 5, 302-308.	1.3	2
896	Addition of acacia gum to a FOS/inulin blend improves its fermentation profile in the Simulator of the Human Intestinal Microbial Ecosystem (SHIMEA®). <i>Journal of Functional Foods</i> , 2015, 16, 211-222.	1.6	21
897	Dramatic improvement in genome assembly achieved using doubled-haploid genomes. <i>Scientific Reports</i> , 2014, 4, 6780.	1.6	21
898	Complete Genome Sequence of <i>Rhodococcus</i> sp. Strain IcdP1 Shows Diverse Catabolic Potential. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
899	Memory efficient assembly of human genome. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550008.	0.3	0
900	Conversion of Uric Acid into Ammonium in Oil-Degrading Marine Microbial Communities: a Possible Role of Halomonads. <i>Microbial Ecology</i> , 2015, 70, 724-740.	1.4	14
901	Draft genome of <i>Bacillus</i> sp. A053 isolated from the Arctic seawater with antimicrobial activity. <i>Marine Genomics</i> , 2015, 22, 19-21.	0.4	2
902	Global Genome and Transcriptome Analyses of <i>Magnaporthe oryzae</i> Epidemic Isolate 98-06 Uncover Novel Effectors and Pathogenicity-Related Genes, Revealing Gene Gain and Lose Dynamics in Genome Evolution. <i>PLoS Pathogens</i> , 2015, 11, e1004801.	2.1	148
903	ConPADE: Genome Assembly Ploidy Estimation from Next-Generation Sequencing Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004229.	1.5	41
904	Genetic architecture of colorectal cancer. <i>Gut</i> , 2015, 64, 1623-1636.	6.1	152
905	Karect: accurate correction of substitution, insertion and deletion errors for next-generation sequencing data. <i>Bioinformatics</i> , 2015, 31, 3421-3428.	1.8	75
906	Capturing prokaryotic dark matter genomes. <i>Research in Microbiology</i> , 2015, 166, 814-830.	1.0	16
907	Newly Emergent Highly Pathogenic H5N9 Subtype Avian Influenza A Virus. <i>Journal of Virology</i> , 2015, 89, 8806-8815.	1.5	14
908	Progressive genomic convergence of two <i>Helicobacter pylori</i> strains during mixed infection of a patient with chronic gastritis. <i>Gut</i> , 2015, 64, 554-561.	6.1	47
909	Genomic sequencing and microsatellite marker development for <i>Boswellia papyrifera</i> , an economically important but threatened tree native to dry tropical forests. <i>AoB PLANTS</i> , 2015, 7, .	1.2	20
910	A naturally occurring prfA truncation in a <i>Listeria monocytogenes</i> field strain contributes to reduced replication and cell-to-cell spread. <i>Veterinary Microbiology</i> , 2015, 179, 91-101.	0.8	37
911	Sequencing of allotetraploid cotton (<i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	9.4	1,560

#	ARTICLE	IF	CITATIONS
912	Whole-Genome Sequencing in Outbreak Analysis. <i>Clinical Microbiology Reviews</i> , 2015, 28, 541-563.	5.7	200
913	Sequencing consolidates molecular markers with plant breeding practice. <i>Theoretical and Applied Genetics</i> , 2015, 128, 779-795.	1.8	96
914	Genome sequence of cultivated Upland cotton (<i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015, 33, 524-530.	9.4	1,064
915	Complete genome sequence of <i>Bacillus</i> sp. YP1, a polyethylene-degrading bacterium from waxworm's gut. <i>Journal of Biotechnology</i> , 2015, 200, 77-78.	1.9	51
916	De novo assembly, gene annotation, and marker development of mulberry (<i>Morus atropurpurea</i>) transcriptome. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	19
917	GASS: genome structural annotation for Eukaryotes based on species similarity. <i>BMC Genomics</i> , 2015, 16, 150.	1.2	7
918	Comparative transcriptome analyses on silk glands of six silkmoths imply the genetic basis of silk structure and coloration. <i>BMC Genomics</i> , 2015, 16, 203.	1.2	24
919	Using the canary genome to decipher the evolution of hormone-sensitive gene regulation in seasonal singing birds. <i>Genome Biology</i> , 2015, 16, 19.	3.8	60
920	The integration of sequencing and bioinformatics in metagenomics. <i>Reviews in Environmental Science and Biotechnology</i> , 2015, 14, 357-383.	3.9	13
921	The Genome of <i>Dendrobium officinale</i> Illuminates the Biology of the Important Traditional Chinese Orchid Herb. <i>Molecular Plant</i> , 2015, 8, 922-934.	3.9	228
922	Complete genome sequence of <i>Pseudomonas fluorescens</i> strain PICF7, an indigenous root endophyte from olive (<i>Olea europaea</i> L.) and effective biocontrol agent against <i>Verticillium dahliae</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 10.	1.5	60
923	Genome Sequence of an Extensively Drug-Resistant Strain of <i>Klebsiella pneumoniae</i> , Strain YN-1, with Carbapenem Resistance. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
924	Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. <i>Molecular Biology and Evolution</i> , 2015, 32, 1880-1889.	3.5	193
925	Draft Genome Sequences of <i>Acinetobacter harbinensis</i> Strain HITLi 7 ^T , Isolated from River Water. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
926	NGS population genetics analyses reveal divergent evolution of a Lyme Borreliosis agent in Europe and Asia. <i>Ticks and Tick-borne Diseases</i> , 2015, 6, 344-351.	1.1	43
927	On the Representation of De Bruijn Graphs. <i>Journal of Computational Biology</i> , 2015, 22, 336-352.	0.8	44
928	Sequencing and characterizing the genome of <i>Estrella lausannensis</i> as an undergraduate project: training students and biological insights. <i>Frontiers in Microbiology</i> , 2015, 6, 101.	1.5	32
929	Complete genome of <i>Bacillus</i> sp. Pc3 isolated from the Antarctic seawater with antimicrobial activity. <i>Marine Genomics</i> , 2015, 20, 1-2.	0.4	5

#	ARTICLE	IF	CITATIONS
930	Harnessing Next Generation Sequencing in Climate Change: RNA-Seq Analysis of Heat Stress-Responsive Genes in <i>Wheat</i> (<i>Triticum aestivum</i> L.). <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 632-647.	1.0	50
931	Genome Sequence of <i>Lactobacillus curieae</i> CCTCC M 2011381 ^T , a Novel Producer of Gamma-aminobutyric Acid. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
932	Draft Genome Sequence of <i>Microbacterium profundum</i> Shh49 ^T , an Actinobacterium Isolated from Deep-Sea Sediment of a Polymetallic Nodule Environment. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
933	Complete genome sequence of <i>Kibdelosporangium phytohabitans</i> KLBMP 1111T, a plant growth promoting endophytic actinomycete isolated from oil-seed plant <i>Jatropha curcas</i> L. <i>Journal of Biotechnology</i> , 2015, 216, 129-130.	1.9	9
934	Draft Genome Sequence of <i>Gluconobacter oxydans</i> NL71, a Strain That Efficiently Biocatalyzes Xylose to Xylonic Acid at a High Concentration. <i>Genome Announcements</i> , 2015, 3, .	0.8	17
935	Molecular characterization of the human microbiome from a reproductive perspective. <i>Fertility and Sterility</i> , 2015, 104, 1344-1350.	0.5	20
936	REFECT., 2015, , .		0
937	Emergence of daptomycin non-susceptibility in colonizing vancomycin-resistant <i>Enterococcus faecium</i> isolates during daptomycin therapy. <i>International Journal of Medical Microbiology</i> , 2015, 305, 902-909.	1.5	40
938	Reference genome of wild goat (<i>capra aegagrus</i>) and sequencing of goat breeds provide insight into genic basis of goat domestication. <i>BMC Genomics</i> , 2015, 16, 431.	1.2	103
939	NoC Architectures as Enablers of Biological Discovery for Personalized and Precision Medicine. , 2015, , .		2
940	Genome sequence of a laccase producing fungus <i>Trametes</i> sp. AH28-2. <i>Journal of Biotechnology</i> , 2015, 216, 167-168.	1.9	5
941	Assembly independent functional annotation of short-read data using SOFA: Short-ORF functional annotation. , 2015, , .		2
942	Second generation physical and linkage maps of yellowtail (<i>Seriola quinqueradiata</i>) and comparison of synteny with four model fish. <i>BMC Genomics</i> , 2015, 16, 406.	1.2	16
943	Complete genome sequence of <i>Rufibacter tibetensis</i> strain 1351, a radiation-resistant bacterium from Tibet plateau. <i>Journal of Biotechnology</i> , 2015, 216, 125-126.	1.9	2
944	Therapeutic effect of the YH6 phage in a murine hemorrhagic pneumonia model. <i>Research in Microbiology</i> , 2015, 166, 633-643.	1.0	31
945	The Endoparasitoid, <i>Cotesia vestalis</i> , Regulates Host Physiology by Reprogramming the Neuropeptide Transcriptional Network. <i>Scientific Reports</i> , 2015, 5, 8173.	1.6	22
946	Survey of genome sequences in a wild sweet potato, <i>Ipomoea trifida</i> (H. B. K.) G. Don. <i>DNA Research</i> , 2015, 22, 171-179.	1.5	107
947	An Overview of Genome Organization and How We Got There: from FISH to Hi-C. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 347-372.	2.9	190

#	ARTICLE	IF	CITATIONS
948	GMcloser: closing gaps in assemblies accurately with a likelihood-based selection of contig or long-read alignments. <i>Bioinformatics</i> , 2015, 31, 3733-3741.	1.8	94
949	Misassembled detection using paired-end sequence reads and optical mapping data. <i>Bioinformatics</i> , 2015, 31, i80-i88.	1.8	41
950	Draft Genome Sequence of Environmental Bacterium <i>Vibrio vulnificus</i> CladeA-yb158. <i>Genome Announcements</i> , 2015, 3, .	0.8	15
951	Exploring the rice dispensable genome using a metagenome-like assembly strategy. <i>Genome Biology</i> , 2015, 16, 187.	3.8	90
952	InteMAP: Integrated metagenomic assembly pipeline for NGS short reads. <i>BMC Bioinformatics</i> , 2015, 16, 244.	1.2	25
953	Evolutionary patchwork of an insecticidal toxin shared between plant-associated pseudomonads and the insect pathogens <i>Photorhabdus</i> and <i>Xenorhabdus</i> . <i>BMC Genomics</i> , 2015, 16, 609.	1.2	46
954	An assembly and alignment-free method of phylogeny reconstruction from next-generation sequencing data. <i>BMC Genomics</i> , 2015, 16, 522.	1.2	143
955	Genome sequencing of adzuki bean (<i>Vigna angularis</i>) provides insight into high starch and low fat accumulation and domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13213-13218.	3.3	104
956	Genome sequence of <i>Cellvibrio pealriver</i> PR1, a xylanolytic and agarolytic bacterium isolated from freshwater. <i>Journal of Biotechnology</i> , 2015, 214, 57-58.	1.9	12
957	Genome Sequence of <i>Schizochytrium</i> sp. CCTCC M209059, an Effective Producer of Docosahexaenoic Acid-Rich Lipids. <i>Genome Announcements</i> , 2015, 3, .	0.8	36
958	Genome Sequence of <i>Brevibacillus formosus</i> F12 ^T for a Genome-Sequencing Project for Genomic Taxonomy and Phylogenomics of <i>Bacillus</i> -Like Bacteria. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
959	High-Quality Genome Sequence of <i>Bacillus vireti</i> DSM 15602 T for Setting Up Phylogenomics for the Genomic Taxonomy of <i>Bacillus</i> -Like Bacteria. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
960	Draft Genome Sequence of <i>Bacillus pseudocaliphilus</i> PN-137 ^T (DSM 8725), an Alkaliphilic Halotolerant Bacterium Isolated from Garden Soils. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
961	Genome Sequence of <i>Anaerobacillus macyae</i> JMM-4 ^T (DSM 16346), the First Genomic Information of the Newly Established Genus <i>Anaerobacillus</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	8
962	Epidemic Clones, Oceanic Gene Pools, and Eco-LD in the Free Living Marine Pathogen <i>Vibrio parahaemolyticus</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 1396-1410.	3.5	98
963	Draft Genome Sequence of Norvancomycin-Producing Strain <i>Amycolatopsis orientalis</i> CICC200066. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
964	A new approach for approximate text search using genomic short-read mapping model. , 2015, , .		1
965	Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies. <i>Nature Communications</i> , 2015, 6, 8212.	5.8	146

#	ARTICLE	IF	CITATIONS
966	Genome Sequence of <i>Paenibacillus wulumuqiensis</i> sp. nov., a Bioflocculant-Producing Species. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
967	ScaffoldScaffolder: solving contig orientation via bidirected to directed graph reduction. <i>Bioinformatics</i> , 2016, 32, 17-24.	1.8	9
968	SWAP-Assembler 2: Scalable Genome Assembler towards Millions of Cores -- Practice and Experience. , 2015, , .		1
969	Mutational bias of Turnip Yellow Mosaic Virus in the context of host anti-viral gene silencing. <i>Virology</i> , 2015, 486, 2-6.	1.1	2
970	Functional overlap of the <i>Arabidopsis</i> leaf and root microbiota. <i>Nature</i> , 2015, 528, 364-369.	13.7	1,062
971	Transcriptome analysis of vertebral bone in the flounder, <i>Paralichthys olivaceus</i> (Teleostei), Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.4	9
972	<i>Gekko japonicus</i> genome reveals evolution of adhesive toe pads and tail regeneration. <i>Nature Communications</i> , 2015, 6, 10033.	5.8	142
973	Genomic Characterization of <i>Dehalococcoides mccartyi</i> Strain JNA That Reductively Dechlorinates Tetrachloroethene and Polychlorinated Biphenyls. <i>Environmental Science & Technology</i> , 2015, 49, 14319-14325.	4.6	32
974	Is the whole greater than the sum of its parts? De novo assembly strategies for bacterial genomes based on paired-end sequencing. <i>BMC Genomics</i> , 2015, 16, 648.	1.2	8
975	Improved Assemblies Using a Source-Agnostic Pipeline for MetaGenomic Assembly by Merging (MeGAMerge) of Contigs. <i>Scientific Reports</i> , 2015, 4, 6480.	1.6	39
976	Transcriptome analysis reveals diversified adaptation of <i>Stipa purpurea</i> along a drought gradient on the Tibetan Plateau. <i>Functional and Integrative Genomics</i> , 2015, 15, 295-307.	1.4	36
977	De novo characterization of the <i>Lycium chinense</i> Mill. leaf transcriptome and analysis of candidate genes involved in carotenoid biosynthesis. <i>Gene</i> , 2015, 555, 458-463.	1.0	21
978	Deciphering the human microbiome using next-generation sequencing data and bioinformatics approaches. <i>Methods</i> , 2015, 79-80, 52-59.	1.9	39
979	Intron evolution in <i>Neurospora</i> : the role of mutational bias and selection. <i>Genome Research</i> , 2015, 25, 100-110.	2.4	9
980	The genome sequence of the orchid <i>Phalaenopsis equestris</i> . <i>Nature Genetics</i> , 2015, 47, 65-72.	9.4	413
981	Linkage analysis and whole-exome sequencing exclude extra mutations responsible for the parkinsonian phenotype of spinocerebellar ataxia-2. <i>Neurobiology of Aging</i> , 2015, 36, 545.e1-545.e7.	1.5	14
982	EPGA: <i>de novo</i> assembly using the distributions of reads and insert size. <i>Bioinformatics</i> , 2015, 31, 825-833.	1.8	25
983	Correcting Illumina data. <i>Briefings in Bioinformatics</i> , 2015, 16, 588-599.	3.2	29

#	ARTICLE	IF	CITATIONS
984	Draft Genome Sequence of <i>Bacillus farraginis</i> R-6540 ^T (DSM 16013), a Spore-Forming Bacterium Isolated at Dairy Farms. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
985	Draft Genome Sequence of Oil-Degrading Bacterium <i>Gallaecimonas pentaromativorans</i> Strain YA_1 from the Southwest Indian Ocean. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
986	Draft Genome Sequences of Type Strains <i>Bacillus drentensis</i> DSM 15600 T and <i>Bacillus novalis</i> DSM 15603 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
987	Nosocomial Co-Transmission of Avian Influenza A(H7N9) and A(H1N1)pdm09 Viruses between 2 Patients with Hematologic Disorders. <i>Emerging Infectious Diseases</i> , 2016, 22, 598-607.	2.0	23
988	Strategies for Sequence Assembly of Plant Genomes. , 2016, , .		3
989	Small GTPases and Stress Responses of <i>wran1</i> in the Straw Mushroom <i>Volvariella volvacea</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 1527.	1.8	7
990	Genome-wide Analysis of Epstein-Barr Virus (EBV) Integration and Strain in C666-1 and Raji Cells. <i>Journal of Cancer</i> , 2016, 7, 214-224.	1.2	70
991	Genome sequencing and systems biology analysis of a lipase-producing bacterial strain. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	0
992	Draft Genome Sequence of <i>Bacillus mesonae</i> FIAT-13985 ^T (=DSM 25968 ^T) for Setting Up Phylogenomics in Genomic Taxonomy of the <i>Bacillus</i> -Like Bacteria. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
993	Complete Genome Sequence of <i>Pontibacter akesuensis</i> Strain AKS 1 T , Which Exhibits Robust Nutrient Metabolism in Harsh Environments. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
994	The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. <i>ELife</i> , 2016, 5, .	2.8	143
995	Comparative Genomics Analysis of Two Different Virulent Bovine <i>Pasteurella multocida</i> Isolates. <i>International Journal of Genomics</i> , 2016, 2016, 1-14.	0.8	27
996	Two Novel Myoviruses from the North of Iraq Reveal Insights into <i>Clostridium difficile</i> Phage Diversity and Biology. <i>Viruses</i> , 2016, 8, 310.	1.5	31
997	Identification of Heat Shock Transcription Factor Genes Involved in Thermotolerance of Octoploid Cultivated Strawberry. <i>International Journal of Molecular Sciences</i> , 2016, 17, 2130.	1.8	16
998	The Complete Plastid Genome Sequence of the Wild Rice <i>Zizania latifolia</i> and Comparative Chloroplast Genomics of the Rice Tribe Oryzaceae, Poaceae. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	1.1	22
999	Comparison of Acceleration Techniques for Selected Low-Level Bioinformatics Operations. <i>Frontiers in Genetics</i> , 2016, 7, 5.	1.1	4
1000	Complete Nucleotide Sequence of pGA45, a 140,698-bp IncFIIY Plasmid Encoding bla _{IMI-3} -Mediated Carbapenem Resistance, from River Sediment. <i>Frontiers in Microbiology</i> , 2016, 7, 188.	1.5	13
1001	A High-resolution Typing Assay for Uropathogenic <i>Escherichia coli</i> Based on Fimbrial Diversity. <i>Frontiers in Microbiology</i> , 2016, 7, 623.	1.5	12

#	ARTICLE	IF	CITATIONS
1002	Genome and Transcriptome Sequences Reveal the Specific Parasitism of the Nematophagous <i>Purpureocillium lilacinum</i> 36-1. <i>Frontiers in Microbiology</i> , 2016, 7, 1084.	1.5	33
1003	The Sequence Characteristics and Expression Models Reveal Superoxide Dismutase Involved in Cold Response and Fruiting Body Development in <i>Volvariella volvacea</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 34.	1.8	26
1004	Screening and Validation of Housekeeping Genes of the Root and Cotyledon of <i>Cunninghamia lanceolata</i> under Abiotic Stresses by Using Quantitative Real-Time PCR. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1198.	1.8	30
1005	Molecular Genetic Characterization of an Anthrabenzoquinone Gene Cluster in <i>Streptomyces</i> Sp. FJS31-2 for the Biosynthesis of BE-24566B and Zunyimycin A. <i>Molecules</i> , 2016, 21, 711.	1.7	10
1006	First insights into the nature and evolution of antisense transcription in nematodes. <i>BMC Evolutionary Biology</i> , 2016, 16, 165.	3.2	12
1007	The Transmission and Antibiotic Resistance Variation in a Multiple Drug Resistance Clade of <i>Vibrio cholerae</i> Circulating in Multiple Countries in Asia. <i>PLoS ONE</i> , 2016, 11, e0149742.	1.1	18
1008	Complete Nucleotide Sequence of IncP-1 β Plasmid pDTC28 Reveals a Non-Functional Variant of the blaGES-Type Gene. <i>PLoS ONE</i> , 2016, 11, e0154975.	1.1	9
1009	Molecular Characterization and Sex Distribution of Chemosensory Receptor Gene Family Based on Transcriptome Analysis of <i>Scaeva pyrastris</i> . <i>PLoS ONE</i> , 2016, 11, e0155323.	1.1	14
1010	A Single Transcriptome of a Green Toad (<i>Bufo viridis</i>) Yields Candidate Genes for Sex Determination and -Differentiation and Non-Anonymous Population Genetic Markers. <i>PLoS ONE</i> , 2016, 11, e0156419.	1.1	18
1011	A Genetic Algorithm for Diploid Genome Reconstruction Using Paired-End Sequencing. <i>PLoS ONE</i> , 2016, 11, e0166721.	1.1	3
1012	The Genome of the Trinidadian Guppy, <i>Poecilia reticulata</i> , and Variation in the Guanapo Population. <i>PLoS ONE</i> , 2016, 11, e0169087.	1.1	79
1013	Comparative genomic and transcriptomic analyses of the Fuzhuan brick tea-fermentation fungus <i>Aspergillus cristatus</i> . <i>BMC Genomics</i> , 2016, 17, 428.	1.2	55
1014	The Complete Chloroplast Genome Sequences of Five <i>Epimedium</i> Species: Lights into Phylogenetic and Taxonomic Analyses. <i>Frontiers in Plant Science</i> , 2016, 7, 306.	1.7	185
1015	Characterization of Genome-Wide Variation in Four-Row Wax, a Waxy Maize Landrace with a Reduced Kernel Row Phenotype. <i>Frontiers in Plant Science</i> , 2016, 7, 667.	1.7	8
1016	The new era of genome sequencing using high-throughput sequencing technology: generation of the first version of the Atlantic cod genome. , 2016, , 1-20.		1
1017	Phage-bacteria interaction network in human oral microbiome. <i>Environmental Microbiology</i> , 2016, 18, 2143-2158.	1.8	87
1018	Genomic analysis of snub-nosed monkeys (<i>Rhinopithecus</i>) identifies genes and processes related to high-altitude adaptation. <i>Nature Genetics</i> , 2016, 48, 947-952.	9.4	109
1019	Systems biology-guided biodesign of consolidated lignin conversion. <i>Green Chemistry</i> , 2016, 18, 5536-5547.	4.6	119

#	ARTICLE	IF	CITATIONS
1020	Complete nucleotide sequence of plasmid pNA6 reveals the high plasticity of IncU family plasmids. <i>Gene</i> , 2016, 591, 74-79.	1.0	6
1021	The complete genome of a viable archaeum isolated from 123-million-year-old rock salt. <i>Environmental Microbiology</i> , 2016, 18, 565-579.	1.8	31
1022	Draft Genome Sequence of <i>Pseudoalteromonas</i> sp. Strain XI10 Isolated from the Brine-Seawater Interface of Erba Deep in the Red Sea. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
1023	Draft Genome Sequence of an Aldoxime Degradar, <i>Rhodococcus</i> sp. Strain YH3-3. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
1024	Draft Genome Sequence of <i>Paramesorhizobium deserti</i> A-3-E T, a Strain Highly Resistant to Diverse β -Lactam Antibiotics. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
1025	Draft Genome Sequence of <i>Bacillus cecembensis</i> PN5 T (DSM 21993), a Psychrotolerant Bacterium Isolated from Soil Samples near the Pindari Glacier. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
1026	Draft Genome Sequence of <i>Brevibacillus choshinensis</i> HPD52 T (DSM 8552), a Bacterial Host for Efficient Expression of Heterologous Proteins. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
1027	Draft Genome Sequence of <i>Bacillus shackletonii</i> LMG 18435 T, Isolated from Volcanic Mossy Soil. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
1028	Draft Genome Sequence of <i>Bacillus muralis</i> LMG 20238 T (DSM 16288), a Spore-Forming Bacterium Isolated from Deteriorated Mural Paintings. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
1029	Unraveling the message: insights into comparative genomics of the naked mole-rat. <i>Mammalian Genome</i> , 2016, 27, 259-278.	1.0	38
1030	High-throughput RNA sequencing reveals structural differences of orthologous brain-expressed genes between western lowland gorillas and humans. <i>Journal of Comparative Neurology</i> , 2016, 524, 288-308.	0.9	2
1031	Metagenomic analysis of anammox communities in three different microbial aggregates. <i>Environmental Microbiology</i> , 2016, 18, 2979-2993.	1.8	133
1032	Anthropogenic effects on bacterial diversity and function along a river-to-estuary gradient in Northwest Greece revealed by metagenomics. <i>Environmental Microbiology</i> , 2016, 18, 4640-4652.	1.8	58
1033	Draft Genome Sequence of <i>Ralstonia solanacearum</i> Strain Rs-T02, Which Represents the Most Prevalent Phylotype in Guangxi, China. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
1034	K-mer Mapping and de Bruijn graphs: The case for velvet fragment assembly. , 2016, , .		4
1035	Draft Genome Sequence of <i>Streptococcus agalactiae</i> Serotype Ia Strain M19, a Multidrug-Resistant Isolate from a Cow with Bovine Mastitis. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
1036	NGS-Based Expression Profiling of HSP Genes During Cold and Freeze Stress in Seabuckthorn (<i>Hippophae rhamnoides</i> L.). <i>Heat Shock Proteins</i> , 2016, , 309-327.	0.2	2
1037	Genetic and Genomic Tools for <i>Cannabis sativa</i> . <i>Critical Reviews in Plant Sciences</i> , 2016, 35, 364-377.	2.7	70

#	ARTICLE	IF	CITATIONS
1038	Draft Genome Sequence of <i>Lactobacillus plantarum</i> XJ25 Isolated from Chinese Red Wine. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
1039	Transcriptome analyses reveal molecular mechanism underlying tapping panel dryness of rubber tree (<i>Hevea brasiliensis</i>). <i>Scientific Reports</i> , 2016, 6, 23540.	1.6	35
1040	CAMIL: Clustering and Assembly with Multiple Instance Learning for phenotype prediction. , 2016, , .		3
1041	Complete Genome Sequence of the Polychlorinated Biphenyl Degradator <i>Rhodococcus</i> sp. WB1. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
1042	An FPGA-based quality filter for de novo sequence assembly pipeline. , 2016, , .		0
1043	GRASPx: efficient homolog-search of short peptide metagenome database through simultaneous alignment and assembly. <i>BMC Bioinformatics</i> , 2016, 17, 283.	1.2	5
1044	SXT/R391 integrative and conjugative elements in <i>Proteus</i> species reveal abundant genetic diversity and multidrug resistance. <i>Scientific Reports</i> , 2016, 6, 37372.	1.6	43
1045	Transcriptome responses in alfalfa associated with tolerance to intensive animal grazing. <i>Scientific Reports</i> , 2016, 6, 19438.	1.6	15
1046	Droplet barcoding for massively parallel single-molecule deep sequencing. <i>Nature Communications</i> , 2016, 7, 11784.	5.8	83
1047	Nested Machine Learning Facilitates Increased Sequence Content for Large-Scale Automated High Resolution Melt Genotyping. <i>Scientific Reports</i> , 2016, 6, 19218.	1.6	34
1048	Draft Genome Sequence of <i>Bacillus simplex</i> DSM 1321 for Setting Up Phylogenomics in Genomic Taxonomy of the <i>Bacillus</i> -Like Bacteria. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
1049	Population structure and minimum core genome typing of <i>Legionella pneumophila</i> . <i>Scientific Reports</i> , 2016, 6, 21356.	1.6	28
1050	Genome-wide profiling of genetic variation in <i>Agrobacterium</i> -transformed rice plants. <i>Journal of Zhejiang University: Science B</i> , 2016, 17, 992-996.	1.3	12
1051	Draft genome sequence of subterranean clover, a reference for genus <i>Trifolium</i> . <i>Scientific Reports</i> , 2016, 6, 30358.	1.6	33
1052	Scalable metagenomics alignment research tool (SMART): a scalable, rapid, and complete search heuristic for the classification of metagenomic sequences from complex sequence populations. <i>BMC Bioinformatics</i> , 2016, 17, 292.	1.2	25
1053	Complete Genome Sequence of <i>Wohlfahrtiimonas chitiniclastica</i> Strain BM-Y, Isolated from the Pancreas of a Zebra in China. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
1054	The complete mitochondrial genome of sponge <i>Tethya</i> sp. (Demospongiae, Tethyida, Tethyidae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 472-474.	0.2	2
1055	Towards hardware-accelerated suffix array construction architecture for the de novo DNA sequence assembly. , 2016, , .		0

#	ARTICLE	IF	CITATIONS
1056	The genome sequence of Sea-Island cotton (<i>Gossypium barbadense</i>) provides insights into the allopolyploidization and development of superior spinnable fibres. <i>Scientific Reports</i> , 2016, 5, 17662.	1.6	294
1057	A Fast Sketch-based Assembler for Genomes. , 2016, , .		3
1058	Effective Utilization of Paired Reads to Improve Length and Accuracy of Contigs in Genome Assembly. , 2016, , .		1
1059	High-performance data structures for de novo assembly of genomes. , 2016, , .		2
1060	Draft Genome Sequence of Toxigenic <i>Corynebacterium ulcerans</i> Strain 03-8664 Isolated from a Human Throat. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
1061	From sequence reads to evolutionary inferences. , 0, , 305-335.		0
1062	De novo transcriptome assembly and comprehensive expression profiling in <i>Crocus sativus</i> to gain insights into apocarotenoid biosynthesis. <i>Scientific Reports</i> , 2016, 6, 22456.	1.6	78
1063	A comparative study of k-spectrum-based error correction methods for next-generation sequencing data analysis. <i>Human Genomics</i> , 2016, 10, 20.	1.4	18
1064	Draft Genome Sequence of <i>Botryosphaeria dothidea</i> , the Pathogen of Apple Ring Rot. <i>Genome Announcements</i> , 2016, 4, .	0.8	19
1065	Therapeutic effect of <i>Pseudomonas aeruginosa</i> phage YH30 on mink hemorrhagic pneumonia. <i>Veterinary Microbiology</i> , 2016, 190, 5-11.	0.8	28
1066	Draft Genome Sequence of <i>Bacillus methylotrophicus</i> FKM10, a Plant Growth-Promoting Rhizobacterium Isolated from Apple Rhizosphere. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
1067	Complete genome sequence of <i>Erysipelothrix rhusiopathiae</i> strain GXBY-1 isolated from acute swine erysipelas outbreaks in south China. <i>Genomics Data</i> , 2016, 8, 70-71.	1.3	18
1068	<i>De novo</i> assembly of transcriptome from next-generation sequencing data. <i>Quantitative Biology</i> , 2016, 4, 94-105.	0.3	5
1069	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. <i>Nature Genetics</i> , 2016, 48, 740-746.	9.4	188
1070	Detection and molecular characterization of a Grapevine Roditis leaf discoloration-associated virus (GRLDaV) variant in an autochthonous grape from Apulia (Italy). <i>Virus Genes</i> , 2016, 52, 428-431.	0.7	9
1071	Complete Genome Sequence of <i>Lysinibacillus sphaericus</i> B1-CDA, a Bacterium That Accumulates Arsenic. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
1072	Hepatitis C virus whole genome sequencing: Current methods/issues and future challenges. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 2016, 53, 341-351.	2.7	12
1073	Draft Genome Sequence of <i>Pseudomonas putida</i> BW11M1, a Banana Rhizosphere Isolate with a Diversified Antimicrobial Armamentarium. <i>Genome Announcements</i> , 2016, 4, .	0.8	10

#	ARTICLE	IF	CITATIONS
1074	Complete genome of <i>Thauera humireducens</i> SgZ-1, a potential bacterium for environmental remediation and wastewater treatment. <i>Journal of Biotechnology</i> , 2016, 225, 59-60.	1.9	12
1075	RNA-seq analysis in forest tree species: bioinformatic problems and solutions. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	25
1076	Genome sequencing and annotation of <i>Kocuria turfanensis</i> HO-9042, to promote exploring high-salt resistance associated gene resources. <i>Journal of Biotechnology</i> , 2016, 224, 51-52.	1.9	1
1077	High-titer lactic acid production by <i>Lactobacillus pentosus</i> FL0421 from corn stover using fed-batch simultaneous saccharification and fermentation. <i>Bioresource Technology</i> , 2016, 214, 74-80.	4.8	80
1078	Complete genome sequence of a novel chlorpyrifos degrading bacterium, <i>Cupriavidus nantongensis</i> X1. <i>Journal of Biotechnology</i> , 2016, 227, 1-2.	1.9	31
1079	Draft Genome Sequence of <i>Mycobacterium tuberculosis</i> KT-0192, Isolated in South Korea. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
1080	Data characterizing the chloroplast genomes of extinct and endangered Hawaiian endemic mints (Lamiaceae) and their close relatives. <i>Data in Brief</i> , 2016, 7, 900-922.	0.5	4
1081	Simple sequence repeat variations expedite phage divergence: Mechanisms of indels and gene mutations. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2016, 789, 48-56.	0.4	3
1082	Characterization of genome-wide microsatellites of <i>Saccharina japonica</i> based on a preliminary assembly of Illumina sequencing reads. <i>Journal of Ocean University of China</i> , 2016, 15, 523-532.	0.6	6
1084	Comparative genomic analysis between newly sequenced <i>Brucella suis</i> Vaccine Strain S2 and the Virulent <i>Brucella suis</i> Strain 1330. <i>BMC Genomics</i> , 2016, 17, 741.	1.2	12
1085	An Improved Genome Assembly of <i>Azadirachta indica</i> A. Juss.. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1835-1840.	0.8	27
1086	De novo assembly and characterization of antennal transcriptome reveal chemosensory system in <i>Nysius ericae</i> . <i>Journal of Asia-Pacific Entomology</i> , 2016, 19, 1077-1087.	0.4	19
1087	SWAP-Assembler 2: Optimization of De Novo Genome Assembler at Extreme Scale. , 2016, , .		13
1088	The complete mitochondrial genome of sponge <i>Halichondria</i> (<i>Halichondria</i>) sp. (Demospongiae), Tj ETQq1 1 0.784314 rgBT /Overlock 1 0.2	0.2	2
1089	Genetic diversity and population structure in cherry (<i>Cerasus pseudocerasus</i> (Lindl). G. Don) along Longmenshan Fault Zones in China with newly developed SSR markers. <i>Scientia Horticulturae</i> , 2016, 212, 11-19.	1.7	15
1090	Identifying wrong assemblies in de novo short read primary sequence assembly contigs. <i>Journal of Biosciences</i> , 2016, 41, 455-474.	0.5	0
1091	Olfactory genes in Tibetan wild boar. <i>Nature Genetics</i> , 2016, 48, 972-973.	9.4	6
1092	Whole genome sequencing as a tool for phylogenetic analysis of clinical strains of <i>Mitis</i> group streptococci. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2016, 35, 1615-1625.	1.3	25

#	ARTICLE	IF	CITATIONS
1093	Draft Genome Sequence of a Tetrabromobisphenol Aâ€“Degrading Strain, <i>Ochrobactrum</i> sp. T, Isolated from an Electronic Waste Recycling Site. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
1094	Genomic characterization of <i>Dehalococcoides mccartyi</i> strain 11a5 reveals a circular extrachromosomal genetic element and a new tetrachloroethene reductive dehalogenase gene. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw235.	1.3	18
1095	The banana salt stress transcriptome: large and small RNA expression in stressed banana. <i>Acta Horticulturae</i> , 2016, , 125-132.	0.1	1
1096	Draft Genome Sequence of Fungus <i>Clonostachys rosea</i> Strain YKD0085. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
1097	An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. <i>Nature Communications</i> , 2016, 7, 13637.	5.8	58
1098	Isolation and characterization of a R2R3-MYB transcription factor gene related to anthocyanin biosynthesis in the spathes of <i>Anthurium andraeanum</i> (Hort.). <i>Plant Cell Reports</i> , 2016, 35, 2151-2165.	2.8	50
1099	A Tetrahydrofolate-Dependent Methyltransferase Catalyzing the Demethylation of Dicamba in <i>Sphingomonas</i> sp. Strain Ndbn-20. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5621-5630.	1.4	16
1100	The present and future of <i>de novo</i> whole-genome assembly. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw096.	3.2	139
1101	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016, 13, 1050-1054.	9.0	1,658
1102	Integrated metabolomics and metagenomics analysis of plasma and urine identified microbial metabolites associated with coronary heart disease. <i>Scientific Reports</i> , 2016, 6, 22525.	1.6	143
1103	Transcriptome Analysis Reveals Candidate Genes Involved in Blister Blight defense in Tea (<i>Camellia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	78
1104	The genome and transcriptome of <i>Trichormus</i> sp. NMC-1: insights into adaptation to extreme environments on the Qinghai-Tibet Plateau. <i>Scientific Reports</i> , 2016, 6, 29404.	1.6	33
1105	Comparative Transcriptome Analysis of Chinary, Assamica and Cambod tea (<i>Camellia sinensis</i>) Types during Development and Seasonal Variation using RNA-seq Technology. <i>Scientific Reports</i> , 2016, 6, 37244.	1.6	15
1106	The genome of the miiuy croaker reveals well-developed innate immune and sensory systems. <i>Scientific Reports</i> , 2016, 6, 21902.	1.6	67
1107	Nitric oxide participates in plant flowering repression by ascorbate. <i>Scientific Reports</i> , 2016, 6, 35246.	1.6	21
1108	Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. <i>Nature Communications</i> , 2016, 7, 12845.	5.8	43
1109	The rubber tree genome reveals new insights into rubber production and species adaptation. <i>Nature Plants</i> , 2016, 2, 16073.	4.7	324
1110	Whole genome analysis of halotolerant and alkalotolerant plant growth-promoting rhizobacterium <i>Klebsiella</i> sp. D5A. <i>Scientific Reports</i> , 2016, 6, 26710.	1.6	90

#	ARTICLE	IF	CITATIONS
1111	Analysis of tigecycline resistance development in clinical <i>Acinetobacter baumannii</i> isolates through a combined genomic and transcriptomic approach. <i>Scientific Reports</i> , 2016, 6, 26930.	1.6	31
1112	Identification of drought-responsive microRNAs and their targets in <i>Ammopiptanthus mongolicus</i> by using high-throughput sequencing. <i>Scientific Reports</i> , 2016, 6, 34601.	1.6	38
1113	Uncovering the composition of microbial community structure and metagenomics among three gut locations in pigs with distinct fatness. <i>Scientific Reports</i> , 2016, 6, 27427.	1.6	168
1114	Long-read sequencing and de novo assembly of a Chinese genome. <i>Nature Communications</i> , 2016, 7, 12065.	5.8	242
1115	Sesterterpene ophiobolin biosynthesis involving multiple gene clusters in <i>Aspergillus ustus</i> . <i>Scientific Reports</i> , 2016, 6, 27181.	1.6	33
1116	Integrative microbial community analysis reveals full-scale enhanced biological phosphorus removal under tropical conditions. <i>Scientific Reports</i> , 2016, 6, 25719.	1.6	61
1117	The Genome of <i>Undifilum oxytropis</i> Provides Insights into Swainsonine Biosynthesis and Locoism. <i>Scientific Reports</i> , 2016, 6, 30760.	1.6	16
1118	Methodologies for probing the metatranscriptome of grassland soil. <i>Journal of Microbiological Methods</i> , 2016, 131, 122-129.	0.7	19
1119	Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. <i>Scientific Data</i> , 2016, 3, 160076.	2.4	34
1120	Reproductive switching analysis of <i>Daphnia similoides</i> between sexual female and parthenogenetic female by transcriptome comparison. <i>Scientific Reports</i> , 2016, 6, 34241.	1.6	31
1121	Draft Genome Sequence of <i>Bacillus</i> sp. GZT, a 2,4,6-Tribromophenol-Degrading Strain Isolated from the River Sludge of an Electronic Waste-Dismantling Region. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
1122	De novo SNP discovery and genetic linkage mapping in poplar using restriction site associated DNA and whole-genome sequencing technologies. <i>BMC Genomics</i> , 2016, 17, 656.	1.2	33
1123	Assembling the <i>Setaria italica</i> L. Beauv. genome into nine chromosomes and insights into regions affecting growth and drought tolerance. <i>Scientific Reports</i> , 2016, 6, 35076.	1.6	10
1124	Metagenomics, Metatranscriptomics, and Metabolomics Approaches for Microbiome Analysis. <i>Evolutionary Bioinformatics</i> , 2016, 12s1, EBO.S36436.	0.6	227
1125	Genome sequence and overview of <i>Oligoflexus tunisiensis</i> Shr3T in the eighth class Oligoflexia of the phylum Proteobacteria. <i>Standards in Genomic Sciences</i> , 2016, 11, 90.	1.5	12
1126	Whole-genome sequencing and comparative genomic analysis of <i>Escherichia coli</i> O91 strains isolated from symptomatic and asymptomatic human carriers. <i>Gut Pathogens</i> , 2016, 8, 57.	1.6	2
1127	Molecular subtyping and erythromycin resistance of <i>Campylobacter</i> in China. <i>Journal of Applied Microbiology</i> , 2016, 121, 287-293.	1.4	40
1128	Draft Genome Sequence of <i>Mycobacterium tuberculosis</i> KT-0204, Isolated in South Korea. <i>Genome Announcements</i> , 2016, 4, .	0.8	1

#	ARTICLE	IF	CITATIONS
1129	Draft Genome Sequence of Mycobacterium tuberculosis KT-0184, Isolated in South Korea. Genome Announcements, 2016, 4, .	0.8	0
1130	Genome Sequence of Enterococcus pernyi , a Pathogenic Bacterium for the Chinese Oak Silkworm, Antheraea pernyi. Genome Announcements, 2016, 4, .	0.8	5
1131	Long read and single molecule DNA sequencing simplifies genome assembly and TAL effector gene analysis of Xanthomonas translucens. BMC Genomics, 2016, 17, 21.	1.2	97
1132	Metagenomic analysis of microbial consortia enriched from compost: new insights into the role of Actinobacteria in lignocellulose decomposition. Biotechnology for Biofuels, 2016, 9, 22.	6.2	237
1133	Complete genome sequence of probiotic Lactobacillus reuteri ZLR003 isolated from healthy weaned pig. Journal of Biotechnology, 2016, 228, 69-70.	1.9	8
1134	Increased small intestinal permeability and RNA expression profiles of mucosa from terminal ileum in patients with diarrhoea-predominant irritable bowel syndrome. Digestive and Liver Disease, 2016, 48, 880-887.	0.4	19
1135	Assembly of the draft genome of buckwheat and its applications in identifying agronomically useful genes. DNA Research, 2016, 23, 215-224.	1.5	122
1136	An acyltransferase gene that putatively functions in anthocyanin modification was horizontally transferred from Fabaceae into the genus Cuscuta. Plant Diversity, 2016, 38, 149-155.	1.8	9
1137	Molecular identification and sex distribution of two chemosensory receptor families in Athetis lepigone by antennal transcriptome analysis. Journal of Asia-Pacific Entomology, 2016, 19, 571-580.	0.4	18
1138	Complete genome sequence of a marine bacterium with two chromosomes, Pseudoalteromonas translucida KMM 520T. Marine Genomics, 2016, 26, 17-20.	0.4	5
1139	Comparative transcriptome analysis of three color variants of the sea cucumber Apostichopus japonicus. Marine Genomics, 2016, 28, 21-24.	0.4	13
1140	Empirical estimation of sequencing error rates using smoothing splines. BMC Bioinformatics, 2016, 17, 177.	1.2	5
1141	OPERA-LG: efficient and exact scaffolding of large, repeat-rich eukaryotic genomes with performance guarantees. Genome Biology, 2016, 17, 102.	3.8	77
1142	Draft genome sequence of non-shiga toxin-producing Escherichia coli O157 NCCP15738. Gut Pathogens, 2016, 8, 13.	1.6	4
1143	OPTIMA: sensitive and accurate whole-genome alignment of error-prone genomic maps by combinatorial indexing and technology-agnostic statistical analysis. GigaScience, 2016, 5, 2.	3.3	12
1144	Mitochondrial metagenomics: letting the genes out of the bottle. GigaScience, 2016, 5, 15.	3.3	103
1145	Draft genome sequence of Sphingomonas paucimobilis strain LCT-SP1 isolated from the Shenzhou X spacecraft of China. Standards in Genomic Sciences, 2016, 11, 18.	1.5	6
1146	A newly isolated and identified vitamin B12 producing strain: Sinorhizobium meliloti 320. Bioprocess and Biosystems Engineering, 2016, 39, 1527-1537.	1.7	17

#	ARTICLE	IF	CITATIONS
1147	Development of genic SSR markers from an assembled <i>Saccharina japonica</i> genome. <i>Journal of Applied Phycology</i> , 2016, 28, 2479-2484.	1.5	4
1148	Comparative Phylogenomics of Pathogenic and Nonpathogenic Species. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 235-244.	0.8	38
1149	Draft Genome Sequence of <i>Escherichia coli</i> Strain SEC470, Isolated from a Piglet Experiencing Diarrhea. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
1150	Draft Genome Sequence of <i>Bacillus plakortidis</i> P203 T (DSM 19153), an Alkali- and Salt-Tolerant Marine Bacterium. <i>Genome Announcements</i> , 2016, 4, .	0.8	12
1151	Draft Genome Sequence of <i>Desulfitobacterium hafniense</i> Strain DH, a Sulfate-Reducing Bacterium Isolated from Paddy Soils. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
1152	Draft Genome Sequence of <i>Mycobacterium tuberculosis</i> KT-0133, Isolated in South Korea. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
1153	An introduction to plant phylogenomics with a focus on palms. <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 234-255.	0.8	42
1154	The complete chloroplast genome sequence of American bird pepper (<i>Capsicum</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50 46 16	0.6	16
1155	Denoising DNA deep sequencing data—high-throughput sequencing errors and their correction. <i>Briefings in Bioinformatics</i> , 2016, 17, 154-179.	3.2	254
1156	Convergent Substitutions in a Sodium Channel Suggest Multiple Origins of Toxin Resistance in Poison Frogs. <i>Molecular Biology and Evolution</i> , 2016, 33, 1068-1080.	3.5	53
1157	Complete genome sequence of <i>Kocuria flava</i> strain HO-9041, a heavy metal removal bacterium from Xinjiang. <i>Journal of Biotechnology</i> , 2016, 220, 21-22.	1.9	4
1158	Insight into the genome sequence of a sediment-adapted marine bacterium <i>Neptunomonas antarctica</i> S3-22T from Antarctica. <i>Marine Genomics</i> , 2016, 25, 29-31.	0.4	5
1159	Synthetic long-read sequencing reveals intraspecies diversity in the human microbiome. <i>Nature Biotechnology</i> , 2016, 34, 64-69.	9.4	93
1160	Phenalenone Polyketide Cyclization Catalyzed by Fungal Polyketide Synthase and Flavin-Dependent Monooxygenase. <i>Journal of the American Chemical Society</i> , 2016, 138, 4249-4259.	6.6	46
1161	Plastid Phylogenomic Analyses Resolve Tofieldiaceae as the Root of the Early Diverging Monocot Order Alismatales. <i>Genome Biology and Evolution</i> , 2016, 8, 932-945.	1.1	34
1162	Draft Genome Sequences of Two <i>Thiomicrospira</i> Strains Isolated from the Brine-Seawater Interface of Kebrtit Deep in the Red Sea. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
1163	Utilizing de Bruijn graph of metagenome assembly for metatranscriptome analysis. <i>Bioinformatics</i> , 2016, 32, 1001-1008.	1.8	59
1164	Towards plant pangenomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1099-1105.	4.1	203

#	ARTICLE	IF	CITATIONS
1165	Draft Genome Sequence of Type Strain <i>Streptococcus gordonii</i> ATCC 10558. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
1166	Bidirectional Variable-Order de Bruijn Graphs. <i>Lecture Notes in Computer Science</i> , 2016, , 164-178.	1.0	11
1167	Draft Genome Sequence of <i>Bacillus humi</i> LMG 22167 ^T (DSM 16318), an Endospore-Forming Bacterium Isolated from Soil. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
1168	Complete genome sequence of <i>Streptomyces globisporus</i> C-1027, the producer of an enediyne antibiotic lidamycin. <i>Journal of Biotechnology</i> , 2016, 222, 9-10.	1.9	19
1169	The genome of <i>Bacillus aryabhatai</i> T61 reveals its adaptation to Tibetan Plateau environment. <i>Genes and Genomics</i> , 2016, 38, 293-301.	0.5	12
1170	Transcriptome analysis of stem wood of <i>Nothapodytes nimmoniana</i> (Graham) Mabb. identifies genes associated with biosynthesis of camptothecin, an anti-carcinogenic molecule. <i>Journal of Biosciences</i> , 2016, 41, 119-131.	0.5	22
1171	Transcriptome analysis reveals that up-regulation of the fatty acid synthase gene promotes the accumulation of docosahexaenoic acid in <i>Schizochytrium</i> sp. S056 when glycerol is used. <i>Algal Research</i> , 2016, 15, 83-92.	2.4	58
1172	Complete genome sequence of a xanthan-degrading <i>Microbacterium</i> sp. strain XT11 with the potential for xantho-oligosaccharides production. <i>Journal of Biotechnology</i> , 2016, 222, 19-20.	1.9	8
1173	Characterization of <i>Enterococcus faecium</i> bacteriophage IME-EFm5 and its endolysin LysEFm5. <i>Virology</i> , 2016, 492, 11-20.	1.1	45
1174	The genome sequences of <i>Arachis duranensis</i> and <i>Arachis ipaensis</i> , the diploid ancestors of cultivated peanut. <i>Nature Genetics</i> , 2016, 48, 438-446.	9.4	761
1175	Large-scale diversification without genetic isolation in nematode symbionts of figs. <i>Science Advances</i> , 2016, 2, e1501031.	4.7	82
1176	Biofilms on Hospital Shower Hoses: Characterization and Implications for Nosocomial Infections. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2872-2883.	1.4	102
1177	RNA-Seq identifies SPGs as a ventral skeletal patterning cue in sea urchins. <i>Development (Cambridge)</i> , 2016, 143, 703-14.	1.2	24
1178	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. <i>Biotechnology Advances</i> , 2016, 34, 663-686.	6.0	30
1179	The <i>Mycobacterium phlei</i> genome: expectations and surprises. <i>Genome Biology and Evolution</i> , 2016, 8, evw049.	1.1	11
1180	The quest to resolve recent radiations: Plastid phylogenomics of extinct and endangered Hawaiian endemic mints (Lamiaceae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 16-33.	1.2	47
1181	Isolation and Complete Genome Sequence of <i>Algibacter alginolytica</i> sp. nov., a Novel Seaweed-Degrading Bacteroidetes Bacterium with Diverse Putative Polysaccharide Utilization Loci. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2975-2987.	1.4	87
1182	<i>Chloroflexi</i> CL500-11 Populations That Predominate Deep-Lake Hypolimnion Bacterioplankton Rely on Nitrogen-Rich Dissolved Organic Matter Metabolism and C ₁ Compound Oxidation. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1423-1432.	1.4	57

#	ARTICLE	IF	CITATIONS
1183	The Amaryllidaceae alkaloids: biosynthesis and methods for enzyme discovery. <i>Phytochemistry Reviews</i> , 2016, 15, 317-337.	3.1	60
1184	The role of the intestinal microbiota in type 1 diabetes mellitus. <i>Nature Reviews Endocrinology</i> , 2016, 12, 154-167.	4.3	335
1185	The complete chloroplast genome sequence of <i>Cucumis sativus</i> var. <i>Hardwickii</i> , the wild progenitor of cultivated cucumber. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4627-4628.	0.7	8
1186	Scalable Cloud-Based Data Analysis Software Systems for Big Data from Next Generation Sequencing. <i>Studies in Big Data</i> , 2016, , 263-283.	0.8	4
1187	The complete mitochondrial genome sequence of <i>Malus hupehensis</i> var. <i>pinyiensis</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2905-2906.	0.7	3
1188	Characterization of complete mitochondrial genome of Dezhou donkey (<i>Equus asinus</i>) and evolutionary analysis. <i>Current Genetics</i> , 2016, 62, 383-390.	0.8	13
1189	The complete chloroplast genome sequence of wild cucumber (<i>Cucumis sativus</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 T 4524-4525.	0.7	3
1190	Deep sequencing reveals transcriptome re-programming of <i>Polygonum multiflorum</i> thunb. roots to the elicitation with methyl jasmonate. <i>Molecular Genetics and Genomics</i> , 2016, 291, 337-348.	1.0	7
1191	Identification and antagonistic activity of endophytic bacterial strain <i>Paenibacillus</i> sp. 5ÅL8 isolated from the seeds of maize (<i>Zea mays</i> L., Jingke 968). <i>Annals of Microbiology</i> , 2016, 66, 653-660.	1.1	20
1192	Deep sequencing reveals the viral adaptation process of environment-derived H10N8 in mice. <i>Infection, Genetics and Evolution</i> , 2016, 37, 8-13.	1.0	13
1193	De novo transcriptome analysis of <i>Inonotus baumii</i> by RNA-seq. <i>Journal of Bioscience and Bioengineering</i> , 2016, 121, 380-384.	1.1	20
1194	Poplins: population-scale detection of novel sequence insertions. <i>Bioinformatics</i> , 2016, 32, 961-967.	1.8	33
1195	Omics Informatics: From Scattered Individual Software Tools to Integrated Workflow Management Systems. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 926-946.	1.9	7
1196	Short Read Mapping: An Algorithmic Tour. <i>Proceedings of the IEEE</i> , 2017, 105, 436-458.	16.4	63
1197	Unsupervised Binning of Metagenomic Assembled Contigs Using Improved Fuzzy C-Means Method. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1459-1467.	1.9	6
1198	Genetic evolution of Gallid herpesvirus 2 isolated in China. <i>Infection, Genetics and Evolution</i> , 2017, 51, 263-274.	1.0	17
1199	The combination of direct and paired link graphs can boost repetitive genome assembly. <i>Nucleic Acids Research</i> , 2017, 45, e43-e43.	6.5	9
1200	Sequence specific sorting of DNA molecules with FACS using 3dPCR. <i>Scientific Reports</i> , 2017, 7, 39385.	1.6	28

#	ARTICLE	IF	CITATIONS
1201	Jasmonic acid causes short- and long-term alterations to the transcriptome and the expression of defense genes in sugarbeet roots. <i>Plant Gene</i> , 2017, 9, 50-63.	1.4	8
1202	A Dimorphic and Virulence-Enhancing Endosymbiont Bacterium Discovered in <i>Rhizoctonia solani</i> . <i>Phytobiomes Journal</i> , 2017, 1, 14-23.	1.4	24
1203	Whole-Genome Sequence of <i>Streptococcus parauberis</i> Strain SP-llh, Isolated from Cows with Mastitis in Western China. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
1204	Whole genome sequencing data and de novo draft assemblies for 66 teleost species. <i>Scientific Data</i> , 2017, 4, 160132.	2.4	67
1205	Hybrid assembly of the large and highly repetitive genome of <i>Aegilops tauschii</i> , a progenitor of bread wheat, with the MaSuRCA mega-reads algorithm. <i>Genome Research</i> , 2017, 27, 787-792.	2.4	382
1206	Building and Improving Reference Genome Assemblies. <i>Proceedings of the IEEE</i> , 2017, , 1-14.	16.4	6
1207	Complete genome sequence of <i>Amycolatopsis orientalis</i> CCCC200066, the producer of norvancomycin. <i>Journal of Biotechnology</i> , 2017, 247, 6-10.	1.9	7
1208	Discovery of genes coding for carbohydrate-active enzyme by metagenomic analysis of lignocellulosic biomasses. <i>Scientific Reports</i> , 2017, 7, 42623.	1.6	63
1209	Development and characterization of novel microsatellite markers for the Common Pheasant (<i>Phasianus colchicus</i>) using RAD-seq. <i>Avian Research</i> , 2017, 8, .	0.5	13
1210	Draft Genome Sequence of <i>Marinobacter hydrocarbonoclasticus</i> Strain STW2, a Polycyclic Aromatic Hydrocarbon-Degrading and Denitrifying Bacterium from the Rhizosphere of Seagrass <i>Enhalus acodoides</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	5
1211	Single-Molecule Sequencing of the <i>Drosophila serrata</i> Genome. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 781-788.	0.8	24
1212	De novo hybrid assembly of the rubber tree genome reveals evidence of paleotetraploidy in <i>Hevea</i> species. <i>Scientific Reports</i> , 2017, 7, 41457.	1.6	95
1214	Shrimp AHPND-causing plasmids encoding the PirAB toxins as mediated by pirAB-Tn903 are prevalent in various <i>Vibrio</i> species. <i>Scientific Reports</i> , 2017, 7, 42177.	1.6	106
1215	<i>mecA</i> -related structure in methicillin-resistant coagulase-negative staphylococci from street food in Taiwan. <i>Scientific Reports</i> , 2017, 7, 42205.	1.6	9
1216	Genome sequence of a high agarase-producing strain <i>Flammeovirga</i> sp. SJP92. <i>Standards in Genomic Sciences</i> , 2017, 12, 13.	1.5	20
1217	Genomic signatures of adaptation to wine biological ageing conditions in biofilm-forming flor yeasts. <i>Molecular Ecology</i> , 2017, 26, 2150-2166.	2.0	68
1218	The Macronuclear Genome of <i>Stentor coeruleus</i> Reveals Tiny Introns in a Giant Cell. <i>Current Biology</i> , 2017, 27, 569-575.	1.8	105
1219	Isolation and characterization of a virulent bacteriophage infecting <i>Acinetobacter johnsonii</i> from activated sludge. <i>Research in Microbiology</i> , 2017, 168, 472-481.	1.0	19

#	ARTICLE	IF	CITATIONS
1220	H-RACER: Hybrid RACER to Correct Substitution, Insertion, and Deletion Errors. Lecture Notes in Computer Science, 2017, , 62-73.	1.0	0
1221	Genome assembly with in vitro proximity ligation data and whole-genome triplication in lettuce. Nature Communications, 2017, 8, 14953.	5.8	330
1222	Patterns of Genome-Wide Diversity and Population Structure in the <i>Drosophila athabasca</i> Species Complex. Molecular Biology and Evolution, 2017, 34, 1912-1923.	3.5	17
1223	Draft Genome Sequence of <i>Exiguobacterium</i> sp. HVEsp1, a Thermophilic Bacterium Isolated from a Deep-Sea Hydrothermal Vent in the Okinawa Trough. Genome Announcements, 2017, 5, .	0.8	1
1224	Recent Sex Chromosome Divergence despite Ancient Dioecy in the Willow <i>Salix viminalis</i> . Molecular Biology and Evolution, 2017, 34, 1991-2001.	3.5	57
1225	PECC: Correcting contigs based on paired-end read distribution. Computational Biology and Chemistry, 2017, 69, 178-184.	1.1	17
1226	An internet-based bioinformatics toolkit for plant biosecurity diagnosis and surveillance of viruses and viroids. BMC Bioinformatics, 2017, 18, 26.	1.2	52
1227	Discovering and sequencing new plant viral genomes by next-generation sequencing: description of a practical pipeline. Annals of Applied Biology, 2017, 170, 301-314.	1.3	73
1228	The genome and transcriptome of Japanese flounder provide insights into flatfish asymmetry. Nature Genetics, 2017, 49, 119-124.	9.4	178
1229	Sequence Assembly. Methods in Molecular Biology, 2017, 1525, 35-45.	0.4	2
1230	Large-scale parallel genome assembler over cloud computing environment. Journal of Bioinformatics and Computational Biology, 2017, 15, 1740003.	0.3	5
1231	Nanopore sequencing data analysis: state of the art, applications and challenges. Briefings in Bioinformatics, 2018, 19, 1256-1272.	3.2	91
1232	Loss of the <i>ssrA</i> genome island led to partial debromination in the PBDE respiring <i>Dehalococcoides mccartyi</i> strain GY50. Environmental Microbiology, 2017, 19, 2906-2915.	1.8	27
1233	Whole genome analysis of a schistosomiasis-transmitting freshwater snail. Nature Communications, 2017, 8, 15451.	5.8	216
1234	A comparative evaluation of genome assembly reconciliation tools. Genome Biology, 2017, 18, 93.	3.8	57
1235	Transcriptome analysis of <i>Cinnamomum longepaniculatum</i> by high-throughput sequencing. Electronic Journal of Biotechnology, 2017, 28, 58-66.	1.2	28
1236	Genome sequence of the highly weak-acid-tolerant <i>Zygosaccharomyces bailii</i> IST302, amenable to genetic manipulations and physiological studies. FEMS Yeast Research, 2017, 17, .	1.1	20
1237	Comparative analysis of the predicted secretomes of Rosaceae scab pathogens <i>Venturia inaequalis</i> and <i>V. pirina</i> reveals expanded effector families and putative determinants of host range. BMC Genomics, 2017, 18, 339.	1.2	68

#	ARTICLE	IF	CITATIONS
1238	The Genome of Medicinal Plant <i>Macleaya cordata</i> Provides New Insights into Benzylisoquinoline Alkaloids Metabolism. <i>Molecular Plant</i> , 2017, 10, 975-989.	3.9	116
1239	Complete Genome Sequence of Lytic Bacteriophage VPUSM 8 against O1 El Tor Inaba <i>Vibrio cholerae</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	2
1240	Mammalian Systems Biotechnology Reveals Global Cellular Adaptations in a Recombinant CHO Cell Line. <i>Cell Systems</i> , 2017, 4, 530-542.e6.	2.9	84
1241	Genome-wide sequencing of longan (<i>Dimocarpus longan</i> Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. <i>GigaScience</i> , 2017, 6, 1-14.	3.3	103
1242	Identification of endophytic bacterial strain RSE1 from seeds of super hybrid rice Shenliangyou 5814 (<i>Oryza sativa</i> L.) and evaluation of its antagonistic activity. <i>Plant Growth Regulation</i> , 2017, 82, 403-408.	1.8	21
1243	Short- and long-term changes in sugarbeet (<i>Beta vulgaris</i> L.) gene expression due to postharvest jasmonic acid treatment - Data. <i>Data in Brief</i> , 2017, 11, 165-168.	0.5	3
1244	Perpendicular axes of differentiation generated by mitochondrial introgression. <i>Molecular Ecology</i> , 2017, 26, 3241-3255.	2.0	28
1245	Unraveling microbial structure and diversity of activated sludge in a full-scale simultaneous nitrogen and phosphorus removal plant using metagenomic sequencing. <i>Enzyme and Microbial Technology</i> , 2017, 102, 16-25.	1.6	100
1246	Genome sequence of a rice pest, the white-backed planthopper (<i>Sogatella furcifera</i>). <i>GigaScience</i> , 2017, 6, 1-9.	3.3	43
1247	Molecular identification of differential expression genes associated with sex pheromone biosynthesis in <i>Spodoptera exigua</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 795-809.	1.0	21
1248	TRA. , 2017, , .		0
1249	Draft Genome Sequence of <i>Rhizobium</i> sp. Strain TBD182, an Antagonist of the Plant-Pathogenic Fungus <i>Fusarium oxysporum</i> , Isolated from a Novel Hydroponics System Using Organic Fertilizer. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
1250	The mitochondrial genome of the lepidopteran host cadaver (<i>Thitarodes</i> sp.) of <i>Ophiocordyceps sinensis</i> and related phylogenetic analysis. <i>Gene</i> , 2017, 598, 32-42.	1.0	8
1251	Analysis of <i>de novo</i> sequencing and transcriptome assembly and lignocellulolytic enzymes gene expression of <i>Coriopsis gallica</i> HTC. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 460-468.	0.6	3
1252	Plant Genome DataBase Japan (PGDBj). <i>Methods in Molecular Biology</i> , 2017, 1533, 45-77.	0.4	10
1253	Transcriptomics and proteomics reveal genetic and biological basis of superior biomass crop <i>Miscanthus</i> . <i>Scientific Reports</i> , 2017, 7, 13777.	1.6	13
1255	Complete Genome Sequence of a Potential Novel <i>Bacillus</i> sp. Strain, FJAT-18017, Isolated from a Potato Field. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
1257	Genome of wild olive and the evolution of oil biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9413-E9422.	3.3	233

#	ARTICLE	IF	CITATIONS
1258	DNA sequencing at 40: past, present and future. <i>Nature</i> , 2017, 550, 345-353.	13.7	729
1259	Genomic adaptation to polyphagy and insecticides in a major East Asian noctuid pest. <i>Nature Ecology and Evolution</i> , 2017, 1, 1747-1756.	3.4	269
1260	The Contig Assembly Problem and Its Algorithmic Solutions. , 2017, , 267-298.		0
1261	Sequencing, Assembly, and Annotation of the Soybean Genome. <i>Compendium of Plant Genomes</i> , 2017, , 73-82.	0.3	5
1262	Physicochemical characterization of high-quality bacterial cellulose produced by <i>Komagataeibacter</i> sp. strain W1 and identification of the associated genes in bacterial cellulose production. <i>RSC Advances</i> , 2017, 7, 45145-45155.	1.7	54
1263	<i>Panax ginseng</i> genome examination for ginsenoside biosynthesis. <i>GigaScience</i> , 2017, 6, 1-15.	3.3	150
1264	Characterization and prevalence of a novel white spot syndrome viral genotype in naturally infected wild crayfish, <i>Procambarus clarkii</i> , in Shanghai, China. <i>VirusDisease</i> , 2017, 28, 250-261.	1.0	21
1265	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	9.4	356
1266	Survey of gene splicing algorithms based on reads. <i>Bioengineered</i> , 2017, 8, 750-758.	1.4	2
1267	Deep sequencing of antennal transcriptome from <i>Callosobruchus chinensis</i> to characterize odorant binding protein and chemosensory protein genes. <i>Journal of Stored Products Research</i> , 2017, 74, 13-21.	1.2	16
1268	Genome Architecture and Evolution of a Unichromosomal Asexual Nematode. <i>Current Biology</i> , 2017, 27, 2928-2939.e6.	1.8	56
1269	Nosocomial transmission of <i>Clostridium difficile</i> Genotype ST81 in a General Teaching Hospital in China traced by whole genome sequencing. <i>Scientific Reports</i> , 2017, 7, 9627.	1.6	26
1270	Ancestral acquisitions, gene flow and multiple evolutionary trajectories of the type three secretion system and effectors in <i>Xanthomonas</i> plant pathogens. <i>Molecular Ecology</i> , 2017, 26, 5939-5952.	2.0	56
1271	Whole-genome sequencing of eukaryotes: From sequencing of DNA fragments to a genome assembly. <i>Russian Journal of Genetics</i> , 2017, 53, 631-639.	0.2	8
1272	Genome Sequencing of Steroid-Producing Bacteria with Illumina Technology. <i>Methods in Molecular Biology</i> , 2017, 1645, 29-44.	0.4	1
1273	Pedigree-based genome re-sequencing reveals genetic variation patterns of elite backbone varieties during modern rice improvement. <i>Scientific Reports</i> , 2017, 7, 292.	1.6	8
1274	Phage-host associations in a full-scale activated sludge plant during sludge bulking. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6495-6504.	1.7	20
1275	Connections between the human gut microbiome and gestational diabetes mellitus. <i>GigaScience</i> , 2017, 6, 1-12.	3.3	204

#	ARTICLE	IF	CITATIONS
1276	Thauera phenolivorans sp. nov., a phenol degrading bacterium isolated from activated sludge. Antonie Van Leeuwenhoek, 2017, 110, 1681-1690.	0.7	21
1277	Development and Characterization of SSR Markers to Study Genetic Diversity and Population Structure of Horsegram Germplasm (Macrotyloma uniflorum). Plant Molecular Biology Reporter, 2017, 35, 550-561.	1.0	19
1278	De novo Assembly of a Genome. , 2017, , 107-125.		0
1279	Comparison of de novo assembly statistics of Cucumis sativus L., 2017, , .		1
1280	Pipelined Multi-FPGA Genomic Data Clustering. Lecture Notes in Computer Science, 2017, , 558-568.	1.0	0
1281	Assembly of cucumber (Cucumis sativus L.) somaclones. , 2017, , .		1
1282	Screening for the ancient polar bear mitochondrial genome reveals low integration of mitochondrial pseudogenes (<i>numts</i>) in bears. Mitochondrial DNA Part B: Resources, 2017, 2, 251-254.	0.2	5
1283	Genome Analysis. Compendium of Plant Genomes, 2017, , 3-19.	0.3	0
1284	Sub genome anchored physical frameworks of the allotetraploid Upland cotton (Gossypium hirsutum) Tj ETQq0 0 0 rgBT /Overlock 10 T 7, 15274.	1.6	23
1285	Identification of Quantitative Trait Loci for Resistance to RSVD in Red Sea Bream (Pagrus major). Marine Biotechnology, 2017, 19, 601-613.	1.1	29
1286	K-Mer Counting Using Bloom Filters with an FPGA-Attached HMC. , 2017, , .		21
1287	Transcriptome differences between 20- and 3,000-year-old Platycladus orientalis reveal that ROS are involved in senescence regulation. Electronic Journal of Biotechnology, 2017, 29, 68-77.	1.2	8
1288	Metagenomic analysis reveals wastewater treatment plants as hotspots of antibiotic resistance genes and mobile genetic elements. Water Research, 2017, 123, 468-478.	5.3	604
1289	A scalable and memory-efficient algorithm for de novo transcriptome assembly of non-model organisms. BMC Genomics, 2017, 18, 387.	1.2	7
1290	The wolf reference genome sequence (Canis lupus lupus) and its implications for Canis spp. population genomics. BMC Genomics, 2017, 18, 495.	1.2	73
1291	Construction of high-resolution recombination maps in Asian seabass. BMC Genomics, 2017, 18, 63.	1.2	26
1292	CNV discovery for milk composition traits in dairy cattle using whole genome resequencing. BMC Genomics, 2017, 18, 265.	1.2	87
1293	Whole genome sequencing of an ExPEC that caused fatal pneumonia at a pig farm in Changchun, China. BMC Veterinary Research, 2017, 13, 169.	0.7	10

#	ARTICLE	IF	CITATIONS
1294	Comparative genomic analysis of Shiga toxin-producing and non-Shiga toxin-producing <i>Escherichia coli</i> O157 isolated from outbreaks in Korea. <i>Gut Pathogens</i> , 2017, 9, 7.	1.6	3
1295	Achieving Mainstream Nitrogen Removal through Coupling Anammox with Denitratation. <i>Environmental Science & Technology</i> , 2017, 51, 8405-8413.	4.6	222
1296	Using metagenomics to investigate human and environmental resistomes. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2690-2703.	1.3	87
1297	Development of EST-SSR markers through de novo RNA sequencing and application for biomass productivity in kenaf (<i>Hibiscus cannabinus</i> L.). <i>Genes and Genomics</i> , 2017, 39, 1139-1156.	0.5	11
1298	From next-generation resequencing reads to a high-quality variant data set. <i>Heredity</i> , 2017, 118, 111-124.	1.2	68
1299	Comprehensive definition of genome features in <i>Spirodela polyrhiza</i> by high-depth physical mapping and short-read DNA sequencing strategies. <i>Plant Journal</i> , 2017, 89, 617-635.	2.8	115
1300	Cautionary Tales of Inapproximability. <i>Journal of Computational Biology</i> , 2017, 24, 213-216.	0.8	2
1301	Genomic study of the Type IVC secretion system in <i>Clostridium difficile</i> : understanding <i>C. difficile</i> evolution via horizontal gene transfer. <i>Genome</i> , 2017, 60, 8-16.	0.9	7
1302	Transcriptome analysis of mud crab (<i>Scylla paramamosain</i>) gills in response to Mud crab reovirus (MCRV). <i>Fish and Shellfish Immunology</i> , 2017, 60, 545-553.	1.6	39
1303	Comprehensive variation discovery and recovery of missing sequence in the pig genome using multiple de novo assemblies. <i>Genome Research</i> , 2017, 27, 865-874.	2.4	116
1304	Exploration of de Bruijn Graph Filtering for de novo Assembly Using GraphLab. , 2017, , .		0
1305	<i>Phytophthora megakarya</i> and <i>Phytophthora palmivora</i> , Closely Related Causal Agents of Cacao Black Pod Rot, Underwent Increases in Genome Sizes and Gene Numbers by Different Mechanisms. <i>Genome Biology and Evolution</i> , 2017, 9, 536-557.	1.1	71
1306	Strategies and Tools for Sequencing and Assembly of Plant Genomes. <i>Compendium of Plant Genomes</i> , 2017, , 81-93.	0.3	4
1307	Draft genome of the reindeer (<i>Rangifer tarandus</i>). <i>GigaScience</i> , 2017, 6, 1-5.	3.3	41
1308	Bioinformatics in Microbiome Analysis. <i>Methods in Microbiology</i> , 2017, 44, 1-18.	0.4	4
1310	Draft Genome Sequence of <i>Glycomyces fuscus</i> TRM 49117, Isolated from a Hypersaline Soil Sample. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
1311	Draft Genome Sequence of <i>Myroides</i> sp. N17-2, a Multidrug-Resistant Bacterium Isolated from Radiation-Polluted Soils. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
1312	The WRKY Transcription Factor Family in Model Plants and Crops. <i>Critical Reviews in Plant Sciences</i> , 2017, 36, 311-335.	2.7	231

#	ARTICLE	IF	CITATIONS
1313	De Novo Assembly of Complete Chloroplast Genomes from Non-model Species Based on a K-mer Frequency-Based Selection of Chloroplast Reads from Total DNA Sequences. <i>Frontiers in Plant Science</i> , 2017, 8, 1271.	1.7	18
1314	<i>Apophysomyces variabilis</i> : draft genome sequence and comparison of predictive virulence determinants with other medically important Mucorales. <i>BMC Genomics</i> , 2017, 18, 736.	1.2	20
1315	Development of novel InDel markers and genetic diversity in <i>Chenopodium quinoa</i> through whole-genome re-sequencing. <i>BMC Genomics</i> , 2017, 18, 685.	1.2	47
1316	HiMMe: using genetic patterns as a proxy for genome assembly reliability assessment. <i>BMC Genomics</i> , 2017, 18, 694.	1.2	3
1317	Transcriptome Sequencing and Comparative Analysis of <i>Piptoporus betulinus</i> in Response to Birch Sawdust Induction. <i>Forests</i> , 2017, 8, 374.	0.9	4
1318	Two Novel Sets of Genes Essential for Nicotine Degradation by <i>Sphingomonas melonis</i> TY. <i>Frontiers in Microbiology</i> , 2016, 7, 2060.	1.5	12
1319	Defining and Evaluating a Core Genome Multilocus Sequence Typing Scheme for Whole-Genome Sequence-Based Typing of <i>Klebsiella pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 371.	1.5	53
1320	Structure and Function of the Fecal Microbiota in Diarrheic Neonatal Piglets. <i>Frontiers in Microbiology</i> , 2017, 8, 502.	1.5	103
1321	Genome Sequencing Reveals the Complex Polysaccharide-Degrading Ability of Novel Deep-Sea Bacterium <i>Flammeovirga pacifica</i> WPAGA1. <i>Frontiers in Microbiology</i> , 2017, 8, 600.	1.5	40
1322	Metagenomic Sequencing of Diamondback Moth Gut Microbiome Unveils Key Holobiont Adaptations for Herbivory. <i>Frontiers in Microbiology</i> , 2017, 8, 663.	1.5	134
1323	Genome-Wide Analyses Reveal Genes Subject to Positive Selection in <i>Pasteurella multocida</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 961.	1.5	36
1324	Metagenomic Analysis of Cecal Microbiome Identified Microbiota and Functional Capacities Associated with Feed Efficiency in Landrace Finishing Pigs. <i>Frontiers in Microbiology</i> , 2017, 8, 1546.	1.5	80
1325	Describing Genomic and Epigenomic Traits Underpinning Emerging Fungal Pathogens. <i>Advances in Genetics</i> , 2017, 100, 73-140.	0.8	17
1326	HaVec: An Efficient de Bruijn Graph Construction Algorithm for Genome Assembly. <i>International Journal of Genomics</i> , 2017, 2017, 1-12.	0.8	3
1327	Scaffolding of long read assemblies using long range contact information. <i>BMC Genomics</i> , 2017, 18, 527.	1.2	194
1328	De novo transcriptome analysis shows differential expression of genes in salivary glands of edible bird's nest producing swiftlets. <i>BMC Genomics</i> , 2017, 18, 504.	1.2	9
1329	Transcriptome sequencing and delimitation of sympatric <i>Oscarella</i> species (<i>O. carmela</i> and <i>O. pearsei</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.1	35
1330	Genome sequencing and comparative genomics reveal a repertoire of putative pathogenicity genes in chilli anthracnose fungus <i>Colletotrichum truncatum</i> . <i>PLoS ONE</i> , 2017, 12, e0183567.	1.1	54

#	ARTICLE	IF	CITATIONS
1331	Bloomfish: A Highly Scalable Distributed K-mer Counting Framework. , 2017, , .		12
1332	Genome Sequence of <i>Staphylococcus aureus</i> PX03, an Acetoin-Producing Strain with a Small-Sized Genome. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
1333	The sea cucumber genome provides insights into morphological evolution and visceral regeneration. <i>PLoS Biology</i> , 2017, 15, e2003790.	2.6	202
1334	Comparing and Evaluating Metagenome Assembly Tools from a Microbiologist's Perspective - Not Only Size Matters!. <i>PLoS ONE</i> , 2017, 12, e0169662.	1.1	186
1335	Draft Genome Sequence of <i>Lactobacillus brevis</i> Strain 3M004, a Probiotic with Potential Quorum-Sensing Regulation. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
1336	Genome-wide identification of conserved and novel microRNAs in one bud and two tender leaves of tea plant (<i>Camellia sinensis</i>) by small RNA sequencing, microarray-based hybridization and genome survey scaffold sequences. <i>BMC Plant Biology</i> , 2017, 17, 212.	1.6	55
1337	Negative correlation between rates of molecular evolution and flowering cycles in temperate woody bamboos revealed by plastid phylogenomics. <i>BMC Plant Biology</i> , 2017, 17, 260.	1.6	27
1338	The whole genomic analysis of orf virus strain HN3/12 isolated from Henan province, central China. <i>BMC Veterinary Research</i> , 2017, 13, 260.	0.7	8
1339	Metagenomic mining pectinolytic microbes and enzymes from an apple pomace-adapted compost microbial community. <i>Biotechnology for Biofuels</i> , 2017, 10, 198.	6.2	27
1340	Genome characterization of a novel binary toxin-positive strain of <i>Clostridium difficile</i> and comparison with the epidemic 027 and 078 strains. <i>Gut Pathogens</i> , 2017, 9, 42.	1.6	15
1341	Comparative genomic analysis and characteristics of NCCP15740, the major type of enterotoxigenic <i>Escherichia coli</i> in Korea. <i>Gut Pathogens</i> , 2017, 9, 55.	1.6	3
1342	Microbial phylogeny determines transcriptional response of resistome to dynamic composting processes. <i>Microbiome</i> , 2017, 5, 103.	4.9	60
1343	Complete Genome Sequence of the Extremely Thermoacidophilic Archaeon <i>Acidianus manzaensis</i> YN-25. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
1344	K-mer clustering algorithm using a MapReduce framework: application to the parallelization of the Inchworm module of Trinity. <i>BMC Bioinformatics</i> , 2017, 18, 467.	1.2	17
1345	Genome sequence of the white-rot fungus <i>Irpex lacteus</i> F17, a type strain of lignin degrader fungus. <i>Standards in Genomic Sciences</i> , 2017, 12, 55.	1.5	15
1346	Complete genome sequence of <i>Thermotoga</i> sp. strain RQ7. <i>Standards in Genomic Sciences</i> , 2017, 12, 62.	1.5	9
1347	High-quality-draft genomic sequence of <i>Paenibacillus ferrarius</i> CY1T with the potential to bioremediate Cd, Cr and Se contamination. <i>Standards in Genomic Sciences</i> , 2017, 12, 60.	1.5	4
1348	Genome sequence of <i>Acuticoccus yangtzensis</i> JL1095T (DSM 28604T) isolated from the Yangtze Estuary. <i>Standards in Genomic Sciences</i> , 2017, 12, 91.	1.5	4

#	ARTICLE	IF	CITATIONS
1349	Scalable Assembly for Massive Genomic Graphs. , 2017, , .		2
1350	Parallelizing Big De Bruijn Graph Construction on Heterogeneous Processors. , 2017, , .		3
1351	Endolysin LysEF-P10 shows potential as an alternative treatment strategy for multidrug-resistant <i>Enterococcus faecalis</i> infections. <i>Scientific Reports</i> , 2017, 7, 10164.	1.6	38
1352	CLOVE: classification of genomic fusions into structural variation events. <i>BMC Bioinformatics</i> , 2017, 18, 346.	1.2	8
1353	Taxonomic and Functional Diversity of a <i>Quercus pyrenaica</i> Willd. Rhizospheric Microbiome in the Mediterranean Mountains. <i>Forests</i> , 2017, 8, 390.	0.9	8
1354	ntCard: a streaming algorithm for cardinality estimation in genomics data. <i>Bioinformatics</i> , 2017, 33, 1324-1330.	1.8	53
1355	Draft Genome Sequence of <i>Pseudomonas stutzeri</i> LH-42, Isolated from Petroleum-Contaminated Soil. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
1356	Approaches for in silico finishing of microbial genome sequences. <i>Genetics and Molecular Biology</i> , 2017, 40, 553-576.	0.6	17
1357	Genome sequence and annotation of <i>Sporolactobacillus pectinivorans</i> GD201205 T, a lactic acid-producing bacterium. <i>Annals of Microbiology</i> , 2018, 68, 159-162.	1.1	1
1358	Use of a draft genome of coffee (<i>Coffea arabica</i>) to identify <i>SNP</i> s associated with caffeine content. <i>Plant Biotechnology Journal</i> , 2018, 16, 1756-1766.	4.1	48
1359	Transcriptome analysis of carotenoid biosynthesis in the <i>Brassica campestris</i> L. subsp. <i>chinensis</i> var. <i>rosularis</i> Tsen. <i>Scientia Horticulturae</i> , 2018, 235, 116-123.	1.7	6
1360	Rhizospheric microbial communities are driven by <i>Panax ginseng</i> at different growth stages and biocontrol bacteria alleviates replanting mortality. <i>Acta Pharmaceutica Sinica B</i> , 2018, 8, 272-282.	5.7	122
1361	Genome Sequence of a Marine Alkane Degrader, <i>Alcanivorax</i> sp. Strain 97CO-6. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
1362	Draft genome of the milu (<i>Elaphurus davidianus</i>). <i>GigaScience</i> , 2018, 7, .	3.3	22
1363	Phylogenetic analyses of the genes involved in carotenoid biosynthesis in algae. <i>Acta Oceanologica Sinica</i> , 2018, 37, 89-101.	0.4	13
1364	Characterization of the complete mitochondrial genome of <i>Metastrongylus salmi</i> (<i>M. salmi</i>) derived from Tibetan pigs in Tibet, China. <i>Acta Parasitologica</i> , 2018, 63, 280-286.	0.4	3
1365	Comparative genome and transcriptome analysis reveal the medicinal basis and environmental adaptation of artificially cultivated <i>Taiwanofungus camphoratus</i> . <i>Mycological Progress</i> , 2018, 17, 871-883.	0.5	9
1366	A new approach for comprehensively describing heterogametic sex chromosomes. <i>DNA Research</i> , 2018, 25, 375-382.	1.5	7

#	ARTICLE	IF	CITATIONS
1367	The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. <i>Cancer Cell</i> , 2018, 33, 607-619.e15.	7.7	88
1368	Knockout of <i>rapC</i> Improves the Bacillomycin D Yield Based on <i>De Novo</i> Genome Sequencing of <i>Bacillus amyloliquefaciens</i> fmbJ. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 4422-4430.	2.4	23
1369	Draft Genome Sequence of <i>Bacillus velezensis</i> B6, a Rhizobacterium That Can Control Plant Diseases. <i>Genome Announcements</i> , 2018, 6, .	0.8	4
1370	Genomic Analyses Yield Markers for Identifying Agronomically Important Genes in Potato. <i>Molecular Plant</i> , 2018, 11, 473-484.	3.9	73
1371	Metagenomics Reveals the Impact of Wastewater Treatment Plants on the Dispersal of Microorganisms and Genes in Aquatic Sediments. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	144
1372	Two reassortant types of highly pathogenic H5N8 avian influenza virus from wild birds in Central China in 2016. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-8.	3.0	12
1373	Genome sequencing and heterologous expression of antiporters reveal alkaline response mechanisms of <i>Halomonas alkalicola</i> . <i>Extremophiles</i> , 2018, 22, 221-231.	0.9	6
1374	Molecular cloning and analysis of the full-length aciniform spidroin gene from <i>Araneus ventricosus</i> . <i>International Journal of Biological Macromolecules</i> , 2018, 117, 1352-1360.	3.6	23
1375	Chloroplast genome sequence of an endangered non-photosynthetic mycoheterotrophic species <i>Monotropastrum sciaphilum</i> (Andres) G. D. Wallace. <i>Conservation Genetics Resources</i> , 2018, 10, 797-799.	0.4	1
1376	Complete Genome Sequence of a Novel T7-Like Bacteriophage from a <i>Pasteurella multocida</i> Capsular Type A Isolate. <i>Current Microbiology</i> , 2018, 75, 574-579.	1.0	39
1377	Activation of an unconventional meroterpenoid gene cluster in <i>Neosartorya glabra</i> leads to the production of new berkeleyacetals. <i>Acta Pharmaceutica Sinica B</i> , 2018, 8, 478-487.	5.7	22
1378	<i>Streptomyces carminius</i> sp. nov., a novel actinomycete isolated from <i>Sophora alopecuroides</i> in Xinjiang, China. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1807-1814.	0.7	7
1379	Pool deconvolution approach for high-throughput gene mining from <i>Bacillus thuringiensis</i> . <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 1467-1482.	1.7	10
1380	The Draft Genome Sequence of a Novel High-Efficient Butanol-Producing Bacterium <i>Clostridium Diolis</i> Strain WST. <i>Current Microbiology</i> , 2018, 75, 1011-1015.	1.0	10
1381	The genomic and functional landscapes of developmental plasticity in the American cockroach. <i>Nature Communications</i> , 2018, 9, 1008.	5.8	113
1382	Advances in Sequencing and Resequencing in Crop Plants. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, 164, 11-35.	0.6	4
1383	Adaptive evolution to a high purine and fat diet of carnivorans revealed by gut microbiomes and host genomes. <i>Environmental Microbiology</i> , 2018, 20, 1711-1722.	1.8	61
1384	Graph algorithms for DNA sequencing – origins, current models and the future. <i>European Journal of Operational Research</i> , 2018, 264, 799-812.	3.5	16

#	ARTICLE	IF	CITATIONS
1385	Characterization of Carbapenem-Resistant <i>Escherichia coli</i> Isolates Through the Whole-Genome Sequencing Analysis. <i>Microbial Drug Resistance</i> , 2018, 24, 175-180.	0.9	17
1386	Genomic analysis of <i>Microbulbifer</i> sp. Q7 exhibiting degradation activity toward seaweed polysaccharides. <i>Marine Genomics</i> , 2018, 39, 7-10.	0.4	7
1387	Genome structure of <i>Rosa multiflora</i> , a wild ancestor of cultivated roses. <i>DNA Research</i> , 2018, 25, 113-121.	1.5	70
1388	Comparative study of activated sludge with different individual nitrogen sources at a low temperature: Effluent dissolved organic nitrogen compositions, metagenomic and microbial community. <i>Bioresource Technology</i> , 2018, 247, 915-923.	4.8	33
1389	Intelligent mining of large-scale bio-data: Bioinformatics applications. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 10-29.	0.5	29
1390	Complete genome sequence of <i>Pseudoalteromonas espejiana</i> DSM9414T, an amino-acid-requiring strain from seawater. <i>Marine Genomics</i> , 2018, 38, 21-23.	0.4	1
1391	Genomic Analysis and Resistance Mechanisms in <i>Shigella flexneri</i> 2a Strain 301. <i>Microbial Drug Resistance</i> , 2018, 24, 323-336.	0.9	4
1392	Diversity and Distribution Characteristics of Viruses in Soils of a Marine-Terrestrial Ecotone in East China. <i>Microbial Ecology</i> , 2018, 75, 375-386.	1.4	14
1393	Functional genomics analysis reveals the biosynthesis pathways of important cellular components (alginate and fucoidan) of <i>Saccharina</i> . <i>Current Genetics</i> , 2018, 64, 259-273.	0.8	38
1394	Regulation of pregnane-X-receptor and microRNAs on detoxification-related genes expressions in <i>Mugilogobius abei</i> under the exposure to diclofenac. <i>Environmental Pollution</i> , 2018, 233, 395-406.	3.7	19
1395	Urban landscape genomics identifies fine-scale gene flow patterns in an avian invasive. <i>Heredity</i> , 2018, 120, 138-153.	1.2	18
1396	3,6-Dichlorosalicylate Catabolism Is Initiated by the DsmABC Cytochrome P450 Monooxygenase System in <i>Rhizorhabdus dicambivorans</i> Ndbn-20. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	13
1397	Genome-based analysis of virulence determinants of a <i>Serratia marcescens</i> strain from soft tissues following a snake bite. <i>Future Microbiology</i> , 2018, 13, 331-343.	1.0	5
1398	The complete mitochondrial genome of the alvinocaridid shrimp <i>Shinkaicaris leurokolos</i> (Decapoda,) Tj ETQq1 1 0.784314 rgBT /Over... shrimp. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 25, 42-52.	0.4	45
1399	Extreme Scale De Novo Metagenome Assembly. , 2018, , .		20
1400	Copy number variation detection using partial alignment information. , 2018, , .		2
1401	High-quality-draft genome sequence of the heavy metal resistant and exopolysaccharides producing bacterium <i>Mucilaginibacter pedocola</i> TBZ30T. <i>Standards in Genomic Sciences</i> , 2018, 13, 34.	1.5	11
1402	SORA: Scalable Overlap-graph Reduction Algorithms for Genome Assembly using Apache Spark in the Cloud. , 2018, , .		2

#	ARTICLE	IF	CITATIONS
1403	Draft Genome Sequence of the Shrimp Pathogen <i>Vibrio parahaemolyticus</i> ST17.P5-S1, Isolated in Peninsular Malaysia. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	3
1404	Comparative shotgun metagenomic data of the silkworm <i>Bombyx mori</i> gut microbiome. <i>Scientific Data</i> , 2018, 5, 180285.	2.4	39
1405	Finding simple sequence repeats (SSRs) within human genome using MapReduce based K-mer algorithm. , 2018, , .		1
1406	A legacy of the "1% program" The "Chinese Chapter" of the human genome reference sequence. <i>Journal of Genetics and Genomics</i> , 2018, 45, 565-568.	1.7	1
1407	Endangered Père David's deer genome provides insights into population recovering. <i>Evolutionary Applications</i> , 2018, 11, 2040-2053.	1.5	19
1408	High-quality-draft genome sequence of the multiple heavy metal resistant bacterium <i>Pseudaminobacter manganicus</i> JH-7T. <i>Standards in Genomic Sciences</i> , 2018, 13, 29.	1.5	8
1409	Combining QTL mapping with transcriptome and metabolome profiling reveals a possible role for ABA signaling in resistance against the cabbage whitefly in cabbage. <i>PLoS ONE</i> , 2018, 13, e0206103.	1.1	13
1410	Draft Genome Sequence of <i>Azospira</i> sp. Strain I13, a Nitrous Oxide-Reducing Bacterium Harboring Clade II Type <i>nosZ</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	6
1411	Draft Genome Sequence of the First South Korean Clinical Isolate of <i>Burkholderia pseudomallei</i> , H0901. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
1412	Assembly of chloroplast genomes with long- and short-read data: a comparison of approaches using <i>Eucalyptus pauciflora</i> as a test case. <i>BMC Genomics</i> , 2018, 19, 977.	1.2	50
1413	Draft Genome Sequence of <i>Aquincola tertiaricarbonis</i> MIMtkpLc11, an Aerobic Anoxygenic Phototrophic Bacterial Strain Isolated from Biological Soil Crusts. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
1414	Complete genome sequence of <i>Arcticibacterium luteifluviistationis</i> SM1504T, a cytophagaceae bacterium isolated from Arctic surface seawater. <i>Standards in Genomic Sciences</i> , 2018, 13, 33.	1.5	3
1415	Pilot Safety Evaluation of a Novel Strain of <i>Bacteroides ovatus</i> . <i>Frontiers in Genetics</i> , 2018, 9, 539.	1.1	21
1416	The complete chloroplast genome of <i>Plagiorhegma dubia</i> Maxim., a traditional Chinese medicinal herb. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 112-114.	0.2	1
1417	Metagenome Assembly and Contig Assignment. <i>Methods in Molecular Biology</i> , 2018, 1849, 179-192.	0.4	0
1418	Progress of analytical tools and techniques for human gut microbiome research. <i>Journal of Microbiology</i> , 2018, 56, 693-705.	1.3	49
1419	Comprehensive inbred variation discovery in Bama pigs using de novo assemblies. <i>Gene</i> , 2018, 679, 81-89.	1.0	9
1420	Genomic approaches for studying crop evolution. <i>Genome Biology</i> , 2018, 19, 140.	3.8	54

#	ARTICLE	IF	CITATIONS
1421	Metagenome sequencing to analyze the impacts of thiamine supplementation on ruminal fungi in dairy cows fed high-concentrate diets. <i>AMB Express</i> , 2018, 8, 159.	1.4	18
1422	Chromosome Level Genome Assembly and Comparative Genomics between Three Falcon Species Reveals an Unusual Pattern of Genome Organisation. <i>Diversity</i> , 2018, 10, 113.	0.7	31
1423	Evolution of olfactory functions on the fire ant social chromosome. <i>Genome Biology and Evolution</i> , 2018, 10, 2947-2960.	1.1	12
1424	Pseudocohnilembus persalinus genome database - the first genome database of facultative scuticociliatosis pathogens. <i>BMC Genomics</i> , 2018, 19, 676.	1.2	3
1425	De novo genome and transcriptome analyses provide insights into the biology of the trematode human parasite <i>Fasciolopsis buski</i> . <i>PLoS ONE</i> , 2018, 13, e0205570.	1.1	4
1426	The pathogenic mechanisms of <i>Tilletia horrida</i> as revealed by comparative and functional genomics. <i>Scientific Reports</i> , 2018, 8, 15413.	1.6	17
1427	KmerEstimate. , 2018, , .		5
1428	Physiological and genomic properties of <i>Thermus tenuipunicus</i> sp. nov., a novel slight reddish color member isolated from a terrestrial geothermal spring. <i>Systematic and Applied Microbiology</i> , 2018, 41, 611-618.	1.2	12
1429	Draft genome sequence, disease-resistance genes, and phenotype of a <i>Paenibacillus terrae</i> strain (NK3-4) with the potential to control plant diseases. <i>Genome</i> , 2018, 61, 725-734.	0.9	7
1430	Genome survey on invasive veined rapa whelk (<i>Rapana venosa</i>) and development of microsatellite loci on large scale. <i>Journal of Genetics</i> , 2018, 97, 79-86.	0.4	8
1431	An endophytic strain of genus <i>Paenibacillus</i> isolated from the fruits of Noni (<i>Morinda citrifolia</i> L.) has antagonistic activity against a Noni's pathogenic strain of genus <i>Aspergillus</i> . <i>Microbial Pathogenesis</i> , 2018, 125, 158-163.	1.3	17
1432	Comparative genomics and transcriptomics of <i>Chrysolophus</i> provide insights into the evolution of complex plumage colouration. <i>GigaScience</i> , 2018, 7, .	3.3	14
1433	Complete genome of <i>Gongronella</i> sp. w5 provides insight into its relationship with plant. <i>Journal of Biotechnology</i> , 2018, 286, 1-4.	1.9	19
1434	Genome sequence of <i>Halomonas hydrothermalis</i> Y2, an efficient ectoine-producer isolated from pulp mill wastewater. <i>Journal of Biotechnology</i> , 2018, 285, 38-41.	1.9	9
1435	Opposite Polarity Monospore Genome De Novo Sequencing and Comparative Analysis Reveal the Possible Heterothallic Life Cycle of <i>Morchella importuna</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2525.	1.8	31
1436	RNA-Seq and UHPLC-Q-TOF/MS Based Lipidomics Study in <i>Lysiphlebia japonica</i> . <i>Scientific Reports</i> , 2018, 8, 7802.	1.6	6
1437	The floral transcriptome of <i>Machilus yunnanensis</i> , a tree in the magnoliid family Lauraceae. <i>Computational Biology and Chemistry</i> , 2018, 77, 456-465.	1.1	1
1438	Identification of candidate chemosensory receptors in the antennal transcriptome of the large black chafer <i>Holotrichia parallela</i> Motschulsky (Coleoptera: Scarabaeidae). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 28, 63-71.	0.4	17

#	ARTICLE	IF	CITATIONS
1439	Evolutionary progression of mitochondrial gene rearrangements and phylogenetic relationships in Strigidae (Strigiformes). <i>Gene</i> , 2018, 674, 8-14.	1.0	20
1440	Transcriptome analysis of hepatic gene expression and DNA methylation in methionine- and betaine-supplemented geese (<i>Anser cygnoides domesticus</i>). <i>Poultry Science</i> , 2018, 97, 3463-3477.	1.5	14
1441	Optimization of Assembly Pipeline may Improve the Sequence of the Chloroplast Genome in <i>Quercus spinosa</i> . <i>Scientific Reports</i> , 2018, 8, 8906.	1.6	4
1442	Whole Genome Sequencing of Greater Amberjack (<i>Seriola dumerili</i>) for SNP Identification on Aligned Scaffolds and Genome Structural Variation Analysis Using Parallel Resequencing. <i>International Journal of Genomics</i> , 2018, 2018, 1-12.	0.8	28
1443	Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours. <i>Nature Ecology and Evolution</i> , 2018, 2, 1479-1491.	3.4	113
1444	Cyclopropane fatty acid biosynthesis in plants: phylogenetic and biochemical analysis of Litchi Kennedy pathway and acyl editing cycle genes. <i>Plant Cell Reports</i> , 2018, 37, 1571-1583.	2.8	5
1445	Identification of Chemosensory Genes Based on the Transcriptomic Analysis of Six Different Chemosensory Organs in <i>Spodoptera exigua</i> . <i>Frontiers in Physiology</i> , 2018, 9, 432.	1.3	18
1446	Optimized Method of Extracting Rice Chloroplast DNA for High-Quality Plastome Resequencing and de Novo Assembly. <i>Frontiers in Plant Science</i> , 2018, 9, 266.	1.7	24
1447	Draft Genome Sequence of a <i>Vibrio parahaemolyticus</i> Strain, KS17.S5-1, with Multiple Antibiotic Resistance Genes, Which Causes Acute Hepatopancreatic Necrosis Disease in <i>Penaeus monodon</i> in the West Coast of Peninsular Malaysia. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	9
1448	DNA sequence-based re-assessment of archived <i>Cronobacter sakazakii</i> strains isolated from dairy products imported into China between 2005 and 2006. <i>BMC Genomics</i> , 2018, 19, 506.	1.2	5
1449	Diversity of Immunoglobulin Light Chain Genes in Non-Teleost Ray-Finned Fish Uncovers IgL Subdivision into Five Ancient Isotypes. <i>Frontiers in Immunology</i> , 2018, 9, 1079.	2.2	5
1450	Identifying Group-Specific Sequences for Microbial Communities Using Long k-mer Sequence Signatures. <i>Frontiers in Microbiology</i> , 2018, 9, 872.	1.5	17
1451	Distribution and Genetic Characteristics of SXT/R391 Integrative Conjugative Elements in <i>Shewanella</i> spp. From China. <i>Frontiers in Microbiology</i> , 2018, 9, 920.	1.5	17
1452	Arginine Catabolic Mobile Elements in Livestock-Associated Methicillin-Resistant Staphylococcal Isolates From Bovine Mastitic Milk in China. <i>Frontiers in Microbiology</i> , 2018, 9, 1031.	1.5	7
1453	Isolation of Low-Abundant Bacteroidales in the Human Intestine and the Analysis of Their Differential Utilization Based on Plant-Derived Polysaccharides. <i>Frontiers in Microbiology</i> , 2018, 9, 1319.	1.5	15
1454	Whole genome and transcriptome analysis reveal adaptive strategies and pathogenesis of <i>Calonectria pseudoreteauidii</i> to <i>Eucalyptus</i> . <i>BMC Genomics</i> , 2018, 19, 358.	1.2	15
1455	Revealing the influence of microbiota on the quality of Pu-erh tea during fermentation process by shotgun metagenomic and metabolomic analysis. <i>Food Microbiology</i> , 2018, 76, 405-415.	2.1	105
1456	Manipulation of microbial community in the rhizosphere alleviates the replanting issues in <i>Panax ginseng</i> . <i>Soil Biology and Biochemistry</i> , 2018, 125, 64-74.	4.2	64

#	ARTICLE	IF	CITATIONS
1457	Seed Transcriptomics Analysis in <i>Camellia oleifera</i> Uncovers Genes Associated with Oil Content and Fatty Acid Composition. <i>International Journal of Molecular Sciences</i> , 2018, 19, 118.	1.8	56
1458	Human Microbiome Acquisition and Bioinformatic Challenges in Metagenomic Studies. <i>International Journal of Molecular Sciences</i> , 2018, 19, 383.	1.8	41
1459	Whole genome sequence revealed the fine transmission map of carbapenem-resistant <i>Klebsiella pneumoniae</i> isolates within a nosocomial outbreak. <i>Antimicrobial Resistance and Infection Control</i> , 2018, 7, 70.	1.5	26
1460	Measuring metagenome diversity and similarity with Hill numbers. <i>Molecular Ecology Resources</i> , 2018, 18, 1339-1355.	2.2	42
1461	Metagenomic insights into the phylogenetic and functional profiles of soil microbiome from a managed mangrove in Malaysia. <i>Agri Gene</i> , 2018, 9, 5-15.	1.9	28
1462	Modular Traits of the Rhizobiales Root Microbiota and Their Evolutionary Relationship with Symbiotic Rhizobia. <i>Cell Host and Microbe</i> , 2018, 24, 155-167.e5.	5.1	244
1463	Three <i>Salmonella enterica</i> serovar Enteritidis bacteriophages from the <i>Siphoviridae</i> family are promising candidates for phage therapy. <i>Canadian Journal of Microbiology</i> , 2018, 64, 865-875.	0.8	30
1464	Bioinformatics Approaches for Genomics and Post Genomics Applications of Anticancer Plants. , 2018, , 283-317.		3
1465	Multidrug-resistant <i>Citrobacter freundii</i> ST139 co-producing NDM-1 and CMY-152 from China. <i>Scientific Reports</i> , 2018, 8, 10653.	1.6	26
1466	A safe and complete algorithm for metagenomic assembly. <i>Algorithms for Molecular Biology</i> , 2018, 13, 3.	0.3	6
1467	Strategies for Taxonomic and Functional Annotation of Metagenomes. , 2018, , 55-79.		11
1468	Identification of <i>Streptococcus mitis</i> 321A vaccine antigens based on reverse vaccinology. <i>Molecular Medicine Reports</i> , 2018, 17, 7477-7486.	1.1	0
1469	Horizontal gene transfer plays a major role in the pathological convergence of <i>Xanthomonas</i> lineages on common bean. <i>BMC Genomics</i> , 2018, 19, 606.	1.2	38
1470	Construction of Red Fox Chromosomal Fragments from the Short-Read Genome Assembly. <i>Genes</i> , 2018, 9, 308.	1.0	14
1471	Genome sequence and population declines in the critically endangered greater bamboo lemur (<i>Prolemur simus</i>) and implications for conservation. <i>BMC Genomics</i> , 2018, 19, 445.	1.2	17
1472	Ansamycins with Antiproliferative and Antineuroinflammatory Activity from Moss-Soil-Derived <i>Streptomyces cacaoi</i> subsp. <i>asoensis</i> H2S5. <i>Journal of Natural Products</i> , 2018, 81, 1984-1991.	1.5	41
1474	Non-coding RNAs in virology: an RNA genomics approach. <i>Biotechnology and Genetic Engineering Reviews</i> , 2018, 34, 90-106.	2.4	2
1475	Copy Number Variation. <i>Methods in Molecular Biology</i> , 2018, 1793, 231-258.	0.4	31

#	ARTICLE	IF	CITATIONS
1476	Potential Mechanism of Detoxification of Cyanide Compounds by Gut Microbiomes of Bamboo-Eating Pandas. <i>MSphere</i> , 2018, 3, .	1.3	59
1477	Comparing fixed sampling with minimizer sampling when using k-mer indexes to find maximal exact matches. <i>PLoS ONE</i> , 2018, 13, e0189960.	1.1	10
1478	Positive selection on sociobiological traits in invasive fire ants. <i>Molecular Ecology</i> , 2018, 27, 3116-3130.	2.0	22
1479	Identification of Enzymes Involved in Sesterterpene Biosynthesis in Marine Fungi. <i>Methods in Enzymology</i> , 2018, 604, 441-498.	0.4	6
1480	Molecular footprints of inshore aquatic adaptation in Indo-Pacific humpback dolphin (<i>Sousa Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 T</i>)	1.3	10
1481	Metagenomic insights into the diversity and functions of microbial assemblages in lakes. , 2019, , 175-223.		3
1482	Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147.	3.8	21
1483	The complete mitochondrial genome of the hybrid of <i>Schizothorax oconnori</i> (â™€) Ã— <i>Schizothorax waltoni</i> (â™€). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1983-1985.	0.2	1
1484	<i>Chachezhanzia antarctica</i> gen. nov., sp. nov., a novel member of the family â€˜Rhodobacteraceaeâ€™ isolated from Antarctic seawater. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1841-1848.	0.7	10
1485	Arsenic-resistance mechanisms in bacterium <i>Leclercia adecarboxylata</i> strain As3-1: Biochemical and genomic analyses. <i>Science of the Total Environment</i> , 2019, 690, 1178-1189.	3.9	23
1486	GAPPadder: a sensitive approach for closing gaps on draft genomes with short sequence reads. <i>BMC Genomics</i> , 2019, 20, 426.	1.2	15
1487	Whole-Genome Sequencing Reveals a Prolonged and Persistent Intrahospital Transmission of <i>Corynebacterium striatum</i> , an Emerging Multidrug-Resistant Pathogen. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	23
1488	Systems-Level Understanding of Single-Cell Omics. , 2019, , 433-456.		0
1489	Quorum Quenching Enzyme APTM01, an Acylhomoserine-Lactone Acylase from Marine Bacterium of <i>Pseudoalteromonas tetradonis</i> Strain MQS005. <i>Current Microbiology</i> , 2019, 76, 1387-1397.	1.0	10
1490	Comparative Phylogenomics, a Stepping Stone for Bird Biodiversity Studies. <i>Diversity</i> , 2019, 11, 115.	0.7	26
1491	Evolution of <i>Oryza</i> chloroplast genomes promoted adaptation to diverse ecological habitats. <i>Communications Biology</i> , 2019, 2, 278.	2.0	62
1492	GAAP: A Genome Assembly + Annotation Pipeline. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	8
1493	Comparative genomic analysis revealed great plasticity and environmental adaptation of the genomes of <i>Enterococcus faecium</i> . <i>BMC Genomics</i> , 2019, 20, 602.	1.2	40

#	ARTICLE	IF	CITATIONS
1494	Viability and Composition Validation of Commercial Probiotic Products by Selective Culturing Combined with Next-Generation Sequencing. <i>Microorganisms</i> , 2019, 7, 188.	1.6	20
1495	Development of simple sequence repeat markers in <i>Pyropia yezoensis</i> (Bangiales, Rhodophyta) by high-throughput sequencing technology. <i>Aquaculture Research</i> , 2019, 50, 2646-2654.	0.9	19
1496	ENTRNA: a framework to predict RNA foldability. <i>BMC Bioinformatics</i> , 2019, 20, 373.	1.2	6
1497	Enhancement of growth and salt tolerance of tomato seedlings by a natural halotolerant actinobacterium <i>Glutamicibacter halophytocola</i> KLBMP 5180 isolated from a coastal halophyte. <i>Plant and Soil</i> , 2019, 445, 307-322.	1.8	51
1498	Exploring novel herbicidin analogues by transcriptional regulator overexpression and MS/MS molecular networking. <i>Microbial Cell Factories</i> , 2019, 18, 175.	1.9	14
1499	A First Insight into a Draft Genome of Silver Sillago (<i>Sillago sihama</i>) via Genome Survey Sequencing. <i>Animals</i> , 2019, 9, 756.	1.0	16
1500	Are the gut microbial systems of giant pandas unstable?. <i>Heliyon</i> , 2019, 5, e02480.	1.4	17
1501	The allotetraploid origin and asymmetrical genome evolution of the common carp <i>Cyprinus carpio</i> . <i>Nature Communications</i> , 2019, 10, 4625.	5.8	156
1502	<i>Pontibacter beigongshangensis</i> sp. nov., Isolated from the Mash of Wine. <i>Current Microbiology</i> , 2019, 76, 1525-1530.	1.0	12
1503	EPGA-SC : A framework for de novo assembly of single-cell sequencing reads. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	1.9	3
1504	Minimization of energy transduction confers resistance to phosphine in the rice weevil, <i>Sitophilus oryzae</i> . <i>Scientific Reports</i> , 2019, 9, 14605.	1.6	12
1505	The complete mitochondrial genomes of two vent squat lobsters, <i>Munidopsis lauensis</i> and <i>M. Averrilli</i> : Novel gene arrangements and phylogenetic implications. <i>Ecology and Evolution</i> , 2019, 9, 12390-12407.	0.8	16
1506	The wild sweetpotato (<i>Ipomoea trifida</i>) genome provides insights into storage root development. <i>BMC Plant Biology</i> , 2019, 19, 119.	1.6	33
1507	Genomic insights into a robust gamma-aminobutyric acid-producer <i>Lactobacillus brevis</i> CD0817. <i>AMB Express</i> , 2019, 9, 72.	1.4	29
1508	The complete chloroplast genome sequence of <i>Vitis yeshanensis</i> strain "SJTU004". <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3490-3491.	0.2	0
1509	Hidden Markov Model Based Graph Construction Process for DNA Sequence Assembly. <i>IOP Conference Series: Materials Science and Engineering</i> , 2019, 490, 042015.	0.3	0
1510	Identification of candidate chemosensory genes of <i>Ophraella communa</i> LeSage (Coleoptera: Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 102	1.6	18
1511	Effects of sialylated lactulose on the mouse intestinal microbiome using Illumina high-throughput sequencing. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 9067-9076.	1.7	6

#	ARTICLE	IF	CITATIONS
1512	Using Apache Spark on genome assembly for scalable overlap-graph reduction. <i>Human Genomics</i> , 2019, 13, 48.	1.4	2
1513	Construction of complete <i>Tupaia belangeri</i> transcriptome database by whole-genome and comprehensive RNA sequencing. <i>Scientific Reports</i> , 2019, 9, 12372.	1.6	16
1514	PROBABILISTIC MODELING AND ANALYSIS OF DNA FRAGMENTATION. <i>Journal of Biological Systems</i> , 2019, 27, 281-307.	0.5	2
1515	k-Core: Hardware Accelerator for k-Mer Generation and Counting used in Computational Genomics. , 2019, , .		4
1516	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	9.4	363
1517	Current status in whole genome sequencing and analysis of <i>Ipomoea</i> spp.. <i>Plant Cell Reports</i> , 2019, 38, 1365-1371.	2.8	16
1518	DNA Sequencing Technologies. <i>ACM Computing Surveys</i> , 2020, 52, 1-30.	16.1	8
1519	Genome sequence of the Chinese white wax scale insect <i>Ericerus pela</i> : the first draft genome for the Coccidae family of scale insects. <i>GigaScience</i> , 2019, 8, .	3.3	15
1520	A draft genome assembly of halophyte <i>Suaeda aralocaspica</i> , a plant that performs C4 photosynthesis within individual cells. <i>GigaScience</i> , 2019, 8, .	3.3	23
1521	Characterization of <i>Streptomyces sporangiiformans</i> sp. nov., a Novel Soil Actinomycete with Antibacterial Activity against <i>Ralstonia solanacearum</i> . <i>Microorganisms</i> , 2019, 7, 360.	1.6	64
1522	Soft sweep development of resistance in <i>Escherichia coli</i> under fluoroquinolone stress. <i>Journal of Microbiology</i> , 2019, 57, 1056-1064.	1.3	0
1523	Assexon: Assembling Exon Using Gene Capture Data. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431987479.	0.6	15
1524	Using Genomics to Adapt Crops to Climate Change. , 2019, , 91-109.		4
1525	Genetic diversity of <i>Curtobacterium flaccumfaciens</i> revealed by multilocus sequence analysis. <i>European Journal of Plant Pathology</i> , 2019, 154, 189-202.	0.8	15
1526	Mycobacterial metabolic characteristics in a water meter biofilm revealed by metagenomics and metatranscriptomics. <i>Water Research</i> , 2019, 153, 315-323.	5.3	19
1527	Genome sequence of <i>Bacillus anthracis</i> typing phage AP631. <i>Archives of Virology</i> , 2019, 164, 917-921.	0.9	3
1528	Response of the Biocontrol Agent <i>Pseudomonas pseudoalcaligenes</i> AVO110 to <i>Rosellinia necatrix</i> Exudate. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	5
1529	Metagenomic insights into effects of thiamine supplementation on ruminal non-methanogen archaea in high-concentrate diets feeding dairy cows. <i>BMC Veterinary Research</i> , 2019, 15, 7.	0.7	10

#	ARTICLE	IF	CITATIONS
1530	Whole-genome sequence of the bovine blood fluke <i>Schistosoma bovis</i> supports interspecific hybridization with <i>S. haematobium</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007513.	2.1	49
1531	Isolation of a T7-Like Lytic <i>Pasteurella</i> Bacteriophage vB_PmuP_PHB01 and Its Potential Use in Therapy against <i>Pasteurella multocida</i> Infections. <i>Viruses</i> , 2019, 11, 86.	1.5	22
1532	Preventive effect of the phage VB-SavM-JYL01 on rabbit necrotizing pneumonia caused by <i>Staphylococcus aureus</i> . <i>Veterinary Microbiology</i> , 2019, 229, 72-80.	0.8	31
1533	Heterozygous diploid structure of <i>Amorphotheca resinae</i> ZN1 contributes efficient biodegradation on solid pretreated corn stover. <i>Biotechnology for Biofuels</i> , 2019, 12, 126.	6.2	24
1534	Genomic characterization of <i>Escherichia coli</i> LCT-EC001, an extremely multidrug-resistant strain with an amazing number of resistance genes. <i>Gut Pathogens</i> , 2019, 11, 25.	1.6	8
1535	<i>Cryobacterium tepidiphilum</i> sp. nov., isolated from rhizosphere soil of lettuce (var. <i>ramosa</i> Hort.). <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1611-1621.	0.7	11
1536	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019, 364, .	6.0	266
1537	Identifying similar transcripts in a related organism from de Bruijn graphs of RNA-Seq data, with applications to the study of salt and waterlogging tolerance in <i>Melilotus</i> . <i>BMC Genomics</i> , 2019, 20, 425.	1.2	0
1538	Rat Genome Assemblies, Annotation, and Variant Repository. <i>Methods in Molecular Biology</i> , 2019, 2018, 43-70.	0.4	7
1539	Identification and Characterization of Resistance-Breaking (RB) Isolates of <i>Citrus tristeza virus</i> . <i>Methods in Molecular Biology</i> , 2019, 2015, 105-126.	0.4	1
1540	Microbial diversity and antibiotic resistome in swine farm environments. <i>Science of the Total Environment</i> , 2019, 685, 197-207.	3.9	74
1541	Misassembly of long reads undermines de novo-assembled ethnicity-specific genomes: validation in a Chinese Han population. <i>Human Genetics</i> , 2019, 138, 757-769.	1.8	6
1542	Comprehensive Integration of Single-Cell Data. <i>Cell</i> , 2019, 177, 1888-1902.e21.	13.5	9,755
1543	Anti-diabetic effect of oligosaccharides from seaweed <i>Sargassum confusum</i> via JNK-IRS1/PI3K signalling pathways and regulation of gut microbiota. <i>Food and Chemical Toxicology</i> , 2019, 131, 110562.	1.8	78
1544	De novo transcriptome assembly of a facultative parasitic nematode <i>Pelodera</i> (syn. <i>Rhabditis</i>) stronglyloides. <i>Gene</i> , 2019, 710, 30-38.	1.0	3
1545	Bioinformatic analyses of a potential <i>Salmonella</i> -virus-FelixO1 biocontrol phage BPS15S6 and the characterisation and anti-Enterobacteriaceae-pathogen activity of its endolysin LyS15S6. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1577-1592.	0.7	6
1546	Current challenges and solutions of <i>de novo</i> assembly. <i>Quantitative Biology</i> , 2019, 7, 90-109.	0.3	46
1547	The Draft Genome of Eggplant. <i>Compendium of Plant Genomes</i> , 2019, , 55-63.	0.3	0

#	ARTICLE	IF	CITATIONS
1548	Advances in Eggplant Genome Sequencing. Compendium of Plant Genomes, 2019, , 65-70.	0.3	1
1549	Spirosoma sordidisoli sp. nov., a propanil-degrading bacterium isolated from a herbicide-contaminated soil. Antonie Van Leeuwenhoek, 2019, 112, 1523-1532.	0.7	16
1550	Vibrio profundus sp. nov., isolated from a deep-sea seamount. Antonie Van Leeuwenhoek, 2019, 112, 1603-1610.	0.7	7
1551	Genome survey and SSR analysis of <i>Apocynum venetum</i> . Bioscience Reports, 2019, 39, .	1.1	32
1552	Hidden genomic evolution in a morphospeciesâ€”The landscape of rapidly evolving genes in Tetrahymena. PLoS Biology, 2019, 17, e3000294.	2.6	31
1553	Draft genome of the big-headed turtle Platysternon megacephalum. Scientific Data, 2019, 6, 60.	2.4	26
1554	Gene expression profiles that shape high and low oil content sesames. BMC Genetics, 2019, 20, 45.	2.7	18
1555	Characteristics of two transferable aminoglycoside resistance plasmids in Escherichia coli isolated from pig and chicken manure. Frontiers of Environmental Science and Engineering, 2019, 13, 1.	3.3	3
1556	The "wildness" of the giant panda gut microbiome and its relevance to effective translocation. Global Ecology and Conservation, 2019, 18, e00644.	1.0	34
1557	Transcriptome analysis identifies novel responses and potential regulatory genes involved in 12-deoxyphorbol-13-phenylacetate biosynthesis of Euphorbia resinifera. Industrial Crops and Products, 2019, 135, 138-145.	2.5	8
1558	Unveiling novel targets of paclitaxel resistance by single molecule long-read RNA sequencing in breast cancer. Scientific Reports, 2019, 9, 6032.	1.6	13
1559	GMASS: a novel measure for genome assembly structural similarity. BMC Bioinformatics, 2019, 20, 147.	1.2	4
1560	Complete genome sequence of Raoultella sp. strain X13, a promising cell factory for the synthesis of CdS quantum dots. 3 Biotech, 2019, 9, 120.	1.1	5
1561	Comparative genomic analysis of enterotoxigenic Escherichia coli O159 strains isolated from diarrheal patients in Korea. Gut Pathogens, 2019, 11, 9.	1.6	3
1562	Combined Genomic, Transcriptomic, Proteomic, and Physiological Characterization of the Growth of Pecoramyces sp. F1 in Monoculture and Co-culture With a Syntrophic Methanogen. Frontiers in Microbiology, 2019, 10, 435.	1.5	25
1563	Distribution and characteristics of SGI1/PGI2 genomic island from Proteus strains in China. Infection, Genetics and Evolution, 2019, 70, 123-130.	1.0	9
1564	The antibiotic resistance and pathogenicity of a multidrug-resistant Elizabethkingia anophelis isolate. MicrobiologyOpen, 2019, 8, e804.	1.2	23
1565	Structure of a green algal photosystem I in complex with a large number of light-harvesting complex I subunits. Nature Plants, 2019, 5, 263-272.	4.7	98

#	ARTICLE	IF	CITATIONS
1566	Genomic characterization of a potentially novel <i>Streptococcus</i> species producing exopolysaccharide. <i>3 Biotech</i> , 2019, 9, 132.	1.1	2
1567	Acoel genome reveals the regulatory landscape of whole-body regeneration. <i>Science</i> , 2019, 363, .	6.0	125
1568	Complete Genome Sequence of an <i>N</i> -Acyl Homoserine Lactone Producer, <i>Breoghania</i> sp. Strain L-A4, Isolated from Rhizosphere of <i>Phragmites australis</i> in a Coastal Wetland. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
1569	On the Close Relatedness of Two Rice-Parasitic Root-Knot Nematode Species and the Recent Expansion of <i>Meloidogyne graminicola</i> in Southeast Asia. <i>Genes</i> , 2019, 10, 175.	1.0	16
1570	Platanus-allee is a de novo haplotype assembler enabling a comprehensive access to divergent heterozygous regions. <i>Nature Communications</i> , 2019, 10, 1702.	5.8	92
1571	Independent Microevolution Mediated by Mobile Genetic Elements of Individual <i>Clostridium difficile</i> Isolates from Clade 4 Revealed by Whole-Genome Sequencing. <i>MSystems</i> , 2019, 4, .	1.7	16
1572	Production Phase Affects the Bioaerosol Microbial Composition and Functional Potential in Swine Confinement Buildings. <i>Animals</i> , 2019, 9, 90.	1.0	27
1573	Microbial synergistic interactions for reductive dechlorination of polychlorinated biphenyls. <i>Science of the Total Environment</i> , 2019, 666, 368-376.	3.9	66
1574	<i>Pseudomonas qingdaonensis</i> sp. nov., an aflatoxin-degrading bacterium, isolated from peanut rhizospheric soil. <i>Archives of Microbiology</i> , 2019, 201, 673-678.	1.0	19
1575	Plastid phylogenomic insights into the evolution of Caryophyllales. <i>Molecular Phylogenetics and Evolution</i> , 2019, 134, 74-86.	1.2	101
1576	Whole metagenome of injected and produced fluids reveal the heterogenetic characteristics of the microbial community in a water-flooded oil reservoir. <i>Journal of Petroleum Science and Engineering</i> , 2019, 176, 1198-1207.	2.1	8
1577	Unraveling the complex genome of <i>Saccharum spontaneum</i> using Polyploid Gene Assembler. <i>DNA Research</i> , 2019, 26, 205-216.	1.5	8
1578	Sequencing of Capsicum Organellar Genomes. <i>Compendium of Plant Genomes</i> , 2019, , 153-172.	0.3	0
1579	Integrative Omic Analysis of Neuroblastoma. , 2019, , 311-326.		2
1580	A New Approach for De Bruijn Graph Construction in De Novo Genome Assembling. , 2019, , .		2
1581	Paragraph: a graph-based structural variant genotyper for short-read sequence data. <i>Genome Biology</i> , 2019, 20, 291.	3.8	104
1582	The genome of a subterrestrial nematode reveals adaptations to heat. <i>Nature Communications</i> , 2019, 10, 5268.	5.8	22
1583	Restructured <i>Lactococcus lactis</i> strains with emergent properties constructed by a novel highly efficient screening system. <i>Microbial Cell Factories</i> , 2019, 18, 198.	1.9	5

#	ARTICLE	IF	CITATIONS
1584	Proteomic and Transcriptomic Changes in Hibernating Grizzly Bears Reveal Metabolic and Signaling Pathways that Protect against Muscle Atrophy. <i>Scientific Reports</i> , 2019, 9, 19976.	1.6	19
1585	Computational Strategies for Scalable Genomics Analysis. <i>Genes</i> , 2019, 10, 1017.	1.0	9
1586	Review, Evaluation, and Directions for Gene-Targeted Assembly for Ecological Analyses of Metagenomes. <i>Frontiers in Genetics</i> , 2019, 10, 957.	1.1	8
1587	The mitochondrial genome of the ornate sheep tick, <i>Dermacentor marginatus</i> . <i>Experimental and Applied Acarology</i> , 2019, 79, 421-432.	0.7	4
1588	Whole Genome Re-sequencing Reveals Natural Variation and Adaptive Evolution of <i>Phytophthora sojae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2792.	1.5	39
1589	Functional Characterization and Genomic Analysis of the Chlorantraniliprole-Degrading Strain <i>Pseudomonas</i> Sp. GW13. <i>Bioengineering</i> , 2019, 6, 106.	1.6	5
1590	PaKman: Scalable Assembly of Large Genomes on Distributed Memory Machines. , 2019, , .		4
1591	Metagenomics of Meat and Poultry. , 2019, , 939-962.		0
1592	CSA: a web service for the complete process of ChIP-Seq analysis. <i>BMC Bioinformatics</i> , 2019, 20, 515.	1.2	2
1593	Re-assessing the diversity of negative strand RNA viruses in insects. <i>PLoS Pathogens</i> , 2019, 15, e1008224.	2.1	101
1594	Genome sequencing of a yeast-like fungal strain P6, a novel species of <i>Aureobasidium</i> spp.: insights into its taxonomy, evolution, and biotechnological potentials. <i>Annals of Microbiology</i> , 2019, 69, 1475-1488.	1.1	8
1595	Characterisation of a newly detected bacteriophage infecting <i>Bordetella bronchiseptica</i> in swine. <i>Archives of Virology</i> , 2019, 164, 33-40.	0.9	19
1596	<i>Rhizobium album</i> sp. nov., isolated from a propanil-contaminated soil. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 319-327.	0.7	9
1597	Draft genome of the cotton aphid <i>Aphis gossypii</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019, 105, 25-32.	1.2	55
1598	gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. <i>Nucleic Acids Research</i> , 2019, 47, D637-D648.	6.5	70
1599	Genomic epidemiological investigation of a <i>Streptococcus suis</i> outbreak in Guangxi, China, 2016. <i>Infection, Genetics and Evolution</i> , 2019, 68, 249-252.	1.0	16
1600	Considerations in using OpenCL on GPUs and FPGAs for throughput-oriented genomics workloads. <i>Future Generation Computer Systems</i> , 2019, 94, 148-159.	4.9	19
1601	Understanding antimicrobial discovery and resistance from a metagenomic and metatranscriptomic perspective: advances and applications. <i>Environmental Microbiology Reports</i> , 2019, 11, 62-86.	1.0	34

#	ARTICLE	IF	CITATIONS
1602	Coexpression of Methyltransferase Gene <i>dmt50</i> and Methylene Tetrahydrofolate Reductase Gene Increases <i>Arabidopsis thaliana</i> Dicamba Resistance. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 1443-1452.	2.4	6
1603	A critical comparison of technologies for a plant genome sequencing project. <i>GigaScience</i> , 2019, 8, .	3.3	41
1604	Characterization of Somatically-Acquired Copy Number Alterations in Chronic Lymphocytic Leukaemia Using Shallow Whole Genome Sequencing. <i>Methods in Molecular Biology</i> , 2019, 1881, 327-353.	0.4	1
1605	An integrated metagenomic/metaproteomic investigation of microbiota in dajiang-meju, a traditional fermented soybean product in Northeast China. <i>Food Research International</i> , 2019, 115, 414-424.	2.9	57
1606	Fall webworm genomes yield insights into rapid adaptation of invasive species. <i>Nature Ecology and Evolution</i> , 2019, 3, 105-115.	3.4	82
1607	Draft genome Sequence of Phosphate-Accumulating Bacterium <i>Acinetobacter tandoii</i> SC36 from a Mangrove Wetland Ecosystem Provides Insights into Elements of Phosphorus Removal. <i>Current Microbiology</i> , 2019, 76, 207-212.	1.0	7
1608	Bioconversion of lignin into bioplastics by <i>Pandora</i> sp. B-6: molecular mechanism. <i>Environmental Science and Pollution Research</i> , 2019, 26, 2761-2770.	2.7	38
1609	FastEch: A Fast Sketch-Based Assembler for Genomes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1091-1106.	1.9	4
1610	Efficient Mining Multi-Mers in a Variety of Biological Sequences. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 949-958.	1.9	5
1611	Phenotype Prediction from Metagenomic Data Using Clustering and Assembly with Multiple Instance Learning (CAMIL). <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 828-840.	1.9	5
1612	Enhanced shortcut nitrogen removal and metagenomic analysis of functional microbial communities in a double sludge system treating ammonium-rich wastewater. <i>Environmental Technology (United Kingdom)</i> , 2020, 41, 1071-1081.	0.2	1
1613	Bioinformatics Tools for Soil Microbiome Analysis. <i>SpringerBriefs in Environmental Science</i> , 2020, , 61-70.	0.3	1
1614	Dates and rates in grapevine plastomes: evolution in slow motion. <i>Current Genetics</i> , 2020, 66, 123-140.	0.8	10
1615	Transcriptome exploration to provide a resource for the study of <i>Auricularia heimuer</i> . <i>Journal of Forestry Research</i> , 2020, 31, 1881-1887.	1.7	4
1616	New approaches for metagenome assembly with short reads. <i>Briefings in Bioinformatics</i> , 2020, 21, 584-594.	3.2	140
1617	<i>Mucilaginibacter hurinus</i> sp. nov., isolated from briquette warehouse soil. <i>Archives of Microbiology</i> , 2020, 202, 127-134.	1.0	2
1618	<i>Pelagivirga dicentrarchi</i> sp. nov., a member of the family Rhodobacteraceae isolated from the gut microflora of sea bass (<i>Dicentrarchus labrax</i> L.). <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 293-301.	0.7	9
1619	BOOTABLE: Bioinformatics benchmark tool suite for applications and hardware. <i>Future Generation Computer Systems</i> , 2020, 102, 1016-1026.	4.9	5

#	ARTICLE	IF	CITATIONS
1620	Lacisediminimonas profundus gen. nov., sp. nov., a member of the family Oxalobacteraceae isolated from freshwater sediment. Antonie Van Leeuwenhoek, 2020, 113, 253-264.	0.7	12
1621	Genome Resource for Barley Leaf Stripe Pathogen <i>Pyrenophora graminea</i> . Plant Disease, 2020, 104, 320-322.	0.7	5
1622	High-throughput sequencing uncover Ficus tikoua Bur. chloroplast genome. Journal of Plant Biochemistry and Biotechnology, 2020, 29, 171-182.	0.9	4
1623	Genome survey and identification of polymorphic microsatellites provide genomic information and molecular markers for the red crab Charybdis feriatus (Linnaeus, 1758) (Decapoda: Brachyura). Tj ETQq1 1 0.7843143BT /Overlock 10	0.7	5
1624	Characterization of an Oxacillin-Susceptible <i>mecA</i> -Positive <i>Staphylococcus aureus</i> Isolate from an Imported Meat Product. Microbial Drug Resistance, 2020, 26, 89-93.	0.9	7
1625	Litorilittus lipolyticus sp. nov., isolated from intertidal sand of the Yellow Sea in China, and emended description of Colwellia asteriadis. Antonie Van Leeuwenhoek, 2020, 113, 449-458.	0.7	9
1626	Preliminary safety assessment of a new Bacteroides fragilis isolate. Food and Chemical Toxicology, 2020, 135, 110934.	1.8	9
1627	Accuracy of <i>de novo</i> assembly of DNA sequences from double-digest libraries varies substantially among software. Molecular Ecology Resources, 2020, 20, 360-370.	2.2	13
1628	Development of simple sequence repeat markers based on whole-genome sequencing to reveal the genetic diversity of Glomerella cingulata in China. Journal of General Plant Pathology, 2020, 86, 2-12.	0.6	5
1629	Phylogenomics – principles, opportunities and pitfalls of big data phylogenetics. Systematic Entomology, 2020, 45, 225-247.	1.7	118
1630	Northern European <i>Salmo trutta</i> (L.) populations are genetically divergent across geographical regions and environmental gradients. Evolutionary Applications, 2020, 13, 400-416.	1.5	26
1631	Actinomadura physcomitrii sp. nov., a novel actinomycete isolated from moss [Physcomitrium sphaericum (Ludw) Fuernr]. Antonie Van Leeuwenhoek, 2020, 113, 677-685.	0.7	22
1632	Draft Genome Sequence of Thermophilic Bacillus sp. TYF-LIM-B05 Directly Producing Ethanol from Various Carbon Sources Including Lignocellulose. Current Microbiology, 2020, 77, 491-499.	1.0	2
1633	Genome Sequences of 72 Bacterial Strains Isolated from Ectocarpus subulatus: A Resource for Algal Microbiology. Genome Biology and Evolution, 2020, 12, 3647-3655.	1.1	30
1634	Genome of Bacillus sp. strain QHF158 provides insights into its parasporal inclusions encoded by the S-layer gene. Brazilian Journal of Microbiology, 2020, 51, 1145-1150.	0.8	2
1635	Corallincola spongiicola sp. nov., isolated from sponge. Antonie Van Leeuwenhoek, 2020, 113, 643-650.	0.7	1
1636	The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis. Molecular Plant, 2020, 13, 336-350.	3.9	73
1637	Early Stage Adaptation of a Mesophilic Green Alga to Antarctica: Systematic Increases in Abundance of Enzymes and LEA Proteins. Molecular Biology and Evolution, 2020, 37, 849-863.	3.5	12

#	ARTICLE	IF	CITATIONS
1638	Edaphocola flava sp. nov., Isolated from Herbicide Bensulfuron-methyl-Contaminated Soil. Current Microbiology, 2020, 77, 300-305.	1.0	3
1639	Long walk to genomics: History and current approaches to genome sequencing and assembly. Computational and Structural Biotechnology Journal, 2020, 18, 9-19.	1.9	171
1640	Complete mitochondrial genomes of two deep-sea pandalid shrimps, Heterocarpus ensifer and Bitias brevis: insights into the phylogenetic position of Pandalidae (Decapoda: Caridea). Journal of Oceanology and Limnology, 2020, 38, 816-825.	0.6	11
1641	<i>Wolbachia</i> supplement biotin and riboflavin to enhance reproduction in planthoppers. ISME Journal, 2020, 14, 676-687.	4.4	108
1642	Genomic landscape and genetic manipulation of the black soldier fly Hermetia illucens, a natural waste recycler. Cell Research, 2020, 30, 50-60.	5.7	136
1643	The genomic architecture of the sex-determining region and sex-related metabolic variation in <i>Ginkgo</i> <i>biloba</i>. Plant Journal, 2020, 104, 1399-1409.	2.8	26
1644	Characterization of a New Transposon, Tn6696, on a blaNDM-1-Carrying Plasmid From Multidrug-Resistant Enterobacter cloacae ssp. dissolvens in China. Frontiers in Microbiology, 2020, 11, 525479.	1.5	9
1645	Haloferax profundus sp. nov. and Haloferax marisrubri sp. nov., Isolated from the Discovery Deep Brine-Seawater Interface in the Red Sea. Microorganisms, 2020, 8, 1475.	1.6	1
1646	Genome-wide analysis revealed the virulence attenuation mechanism of the fish-derived oral attenuated Streptococcus iniae vaccine strain YM011. Fish and Shellfish Immunology, 2020, 106, 546-554.	1.6	4
1647	High conservation combined with high plasticity: genomics and evolution of Borrelia bavariensis. BMC Genomics, 2020, 21, 702.	1.2	14
1648	Temporal dynamics of bacterial communities during seed development and maturation. FEMS Microbiology Ecology, 2020, 96, .	1.3	43
1649	RBUD: A New Functional Potential Analysis Approach for Whole Microbial Genome Shotgun Sequencing. Microorganisms, 2020, 8, 1563.	1.6	1
1650	Resequencing of 145 Landmark Cultivars Reveals Asymmetric Sub-genome Selection and Strong Founder Genotype Effects on Wheat Breeding in China. Molecular Plant, 2020, 13, 1733-1751.	3.9	129
1651	Characterization of Roseibacterium persicum sp. nov., and emended description of the genus Roseibacterium. FEMS Microbiology Letters, 2020, 367, .	0.7	7
1652	First description of antimicrobial resistance in carbapenem-susceptible Klebsiella pneumoniae after imipenem treatment, driven by outer membrane remodeling. BMC Microbiology, 2020, 20, 218.	1.3	14
1653	3-phenyllactic acid production by free whole cells of <i>Lactobacillus crustorum</i> in batch and continuous fermentation systems. Journal of Applied Microbiology, 2020, 129, 335-344.	1.4	9
1654	The social supergene dates back to the speciation time of two Solenopsis fire ant species. Scientific Reports, 2020, 10, 11538.	1.6	6
1655	Clover: a clustering-oriented de novo assembler for Illumina sequences. BMC Bioinformatics, 2020, 21, 528.	1.2	1

#	ARTICLE	IF	CITATIONS
1656	Donkey genomes provide new insights into domestication and selection for coat color. <i>Nature Communications</i> , 2020, 11, 6014.	5.8	63
1657	The First Nonmammalian Pegivirus Demonstrates Efficient In Vitro Replication and High Lymphotropism. <i>Journal of Virology</i> , 2020, 94, .	1.5	9
1658	The chromosome-level wintersweet (<i>Chimonanthus praecox</i>) genome provides insights into floral scent biosynthesis and flowering in winter. <i>Genome Biology</i> , 2020, 21, 200.	3.8	69
1659	PGcloser: Fast Parallel Gap-Closing Tool Using Long-Reads or Contigs to Fill Gaps in Genomes. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432091385.	0.6	5
1660	Phylogenetic Relationships and Potential Functional Attributes of the Genus <i>Parapedobacter</i> : A Member of Family Sphingobacteriaceae. <i>Frontiers in Microbiology</i> , 2020, 11, 1725.	1.5	6
1661	The Most Frequently Used Sequencing Technologies and Assembly Methods in Different Time Segments of the Bacterial Surveillance and RefSeq Genome Databases. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 527102.	1.8	32
1662	The complete mitochondrial genome of <i>Celypha flavipalpana</i> (Lepidoptera: Tortricidae) from Southeast Tibet of China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3547-3548.	0.2	1
1663	<i>Microbispora celluliformans</i> sp. nov., a novel actinomycete with cellulase activity isolated from soil in the cold region. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 2053-2062.	0.7	11
1664	A Review on Sequence Alignment Algorithms for Short Reads Based on Next-Generation Sequencing. <i>IEEE Access</i> , 2020, 8, 189811-189822.	2.6	7
1665	Dynamic PB2-E627K substitution of influenza H7N9 virus indicates the in vivo genetic tuning and rapid host adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23807-23814.	3.3	22
1666	Complete mitochondrial genome analysis of <i>Leptomias</i> sp. (Coleoptera, Curculionidae) from Southeast Tibet of China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3009-3010.	0.2	1
1667	Comparative genomic analysis of a Shiga toxin-producing <i>Escherichia coli</i> (STEC) O145:H25 associated with a severe pediatric case of hemolytic uremic syndrome in Davidson County, Tennessee, US. <i>BMC Genomics</i> , 2020, 21, 564.	1.2	3
1668	Instability of natural selection at candidate barrier loci underlying speciation in wood ants. <i>Molecular Ecology</i> , 2020, 29, 3988-3999.	2.0	13
1669	The complete mitochondrial genome of Antarctic <i>Phaeodactylum tricornutum</i> ICE-H. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2754-2755.	0.2	1
1670	Regional sequence expansion or collapse in heterozygous genome assemblies. <i>PLoS Computational Biology</i> , 2020, 16, e1008104.	1.5	31
1671	The Dynamics, Causes, and Impacts of Mammalian Evolutionary Rates Revealed by the Analyses of <i>Capybara</i> Draft Genome Sequences. <i>Genome Biology and Evolution</i> , 2020, 12, 1444-1458.	1.1	10
1672	Cytokinin regulates the activity of the inflorescence meristem and components of seed yield in oilseed rape. <i>Journal of Experimental Botany</i> , 2020, 71, 7146-7159.	2.4	39
1673	HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. <i>Genome Research</i> , 2020, 30, 1291-1305.	2.4	440

#	ARTICLE	IF	CITATIONS
1674	Systematic Analysis of Escherichia coli Isolates from Sheep and Cattle Suggests Adaption to the Rumen Niche. Applied and Environmental Microbiology, 2020, 86, .	1.4	1
1675	Streptococcus xiaochunlingii sp. nov. E24 Isolated From the Oropharynx of Healthy Chinese Children. Frontiers in Microbiology, 2020, 11, 563213.	1.5	2
1676	Allele-aware chromosome-level genome assembly and efficient transgene-free genome editing for the autotetraploid cultivated alfalfa. Nature Communications, 2020, 11, 2494.	5.8	224
1677	Assessing and Interpreting the Metagenome Heterogeneity With Power Law. Frontiers in Microbiology, 2020, 11, 648.	1.5	5
1678	Balancing selection in Pattern Recognition Receptor signalling pathways is associated with gene function and pleiotropy in a wild rodent. Molecular Ecology, 2020, 29, 1990-2003.	2.0	8
1679	Complete genome sequence of Mycobacterium Mya-zh01, an endophytic bacterium, promotes plant growth and seed germination isolated from flower stalk of Doritaenopsis. Archives of Microbiology, 2020, 202, 1965-1976.	1.0	18
1680	Transcriptome analysis of ovarian maturation in a chondrostei Chinese sturgeon <i>Acipenser sinensis</i>. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2020, 334, 280-293.	0.6	6
1681	Parvibaculum sedimenti sp. nov., A Novel Soil Bacterium Isolated from Sediment. Current Microbiology, 2020, 77, 2056-2063.	1.0	1
1682	Draft genome sequence of the termite, Coptotermes formosanus: Genetic insights into the pyruvate dehydrogenase complex of the termite. Journal of Asia-Pacific Entomology, 2020, 23, 666-674.	0.4	24
1683	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. GigaScience, 2020, 9, .	3.3	35
1684	From asymmetrical to balanced genomic diversification during rediploidization: Subgenomic evolution in allotetraploid fish. Science Advances, 2020, 6, eaaz7677.	4.7	59
1685	<p>Co-Occurrence of the bla<sub>KPC-2</sub> and Mcr-3 Gene in Aeromonas caviae SCAC2001 Isolated from Patients with Diarrheal Disease</p>. Infection and Drug Resistance, 2020, Volume 13, 1527-1536.	1.1	10
1686	Whole-genome sequencing provides insights into the genetic diversity and domestication of bitter melon (Momordica spp.). Horticulture Research, 2020, 7, 85.	2.9	41
1687	Closing Human Reference Genome Gaps: Identifying and Characterizing Gap-Closing Sequences. G3: Genes, Genomes, Genetics, 2020, 10, 2801-2809.	0.8	10
1688	Draft genomes of two outcrossing wild rice, Oryza rufipogon and O. longistaminata , reveal genomic features associated with matingâsystem evolution. Plant Direct, 2020, 4, e00232.	0.8	9
1689	The Battle to Sequence the Bread Wheat Genome: A Tale of the Three Kingdoms. Genomics, Proteomics and Bioinformatics, 2020, 18, 221-229.	3.0	31
1690	Isolation of Clostridium from Yunnan-Tibet hot springs and description of Clostridium thermarum sp. nov. with lignocellulosic ethanol production. Systematic and Applied Microbiology, 2020, 43, 126104.	1.2	23
1691	Psychroflexus maritimus sp. nov., isolated from coastal sediment. Archives of Microbiology, 2020, 202, 2127-2133.	1.0	9

#	ARTICLE	IF	CITATIONS
1692	A New Alignment-Free Whole Metagenome Comparison Tool and Its Application on Gut Microbiomes of Wild Giant Pandas. <i>Frontiers in Microbiology</i> , 2020, 11, 1061.	1.5	11
1693	Powdered activated carbon facilitates methane productivity of anaerobic co-digestion via acidification alleviating: Microbial and metabolic insights. <i>Bioresource Technology</i> , 2020, 313, 123706.	4.8	71
1694	A chromosome-level genome assembly of the parasitoid wasp <i>Pteromalus puparum</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 1384-1402.	2.2	35
1695	Female spider aggression is associated with genetic underpinnings of the nervous system and immune response to pathogens. <i>Molecular Ecology</i> , 2020, 29, 2626-2638.	2.0	5
1696	Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. <i>Nature Communications</i> , 2020, 11, 1427.	5.8	133
1697	Out of Tibet: Genomic Perspectives on the Evolutionary History of Extant Pikas. <i>Molecular Biology and Evolution</i> , 2020, 37, 1577-1592.	3.5	39
1698	Genetic and genomic research for the development of an efficient breeding system in heterostylous self-incompatible common buckwheat (<i>Fagopyrum esculentum</i>). <i>Theoretical and Applied Genetics</i> , 2020, 133, 1641-1653.	1.8	15
1699	Component-Based Design and Assembly of Heuristic Multiple Sequence Alignment Algorithms. <i>Frontiers in Genetics</i> , 2020, 11, 105.	1.1	3
1700	CNVmap: A Method and Software To Detect and Map Copy Number Variants from Segregation Data. <i>Genetics</i> , 2020, 214, 561-576.	1.2	1
1701	Genome Sequence Resource for <i>Elsinoë ampelina</i> , the Causal Organism of Grapevine Anthracnose. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 576-579.	1.4	13
1702	An Integrated Multi-Disciplinary Perspective for Addressing Challenges of the Human Gut Microbiome. <i>Metabolites</i> , 2020, 10, 94.	1.3	13
1703	Sustainable engineering technologies to promote activities of beneficial microbiome. , 2020, , 231-275.		1
1704	Phenotypic and molecular characterisation of a novel species, <i>Mycobacterium hubeiense</i> sp., isolated from the sputum of a patient with secondary tuberculosis in Hubei of China. <i>Epidemiology and Infection</i> , 2020, 148, e49.	1.0	1
1705	Genomic variation between PRSV resistant transgenic SunUp and its progenitor cultivar Sunset. <i>BMC Genomics</i> , 2020, 21, 398.	1.2	3
1706	An integrated Asian human SNV and indel benchmark established using multiple sequencing methods. <i>Scientific Reports</i> , 2020, 10, 9821.	1.6	4
1707	Genomics analysis of the steroid estrogen-degrading bacterium <i>Serratia nematodiphila</i> DH-S01. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 430-440.	0.5	10
1708	Ruminal Methanogenic Responses to the Thiamine Supplementation in High-Concentrate Diets. <i>Animals</i> , 2020, 10, 935.	1.0	2
1709	Genomic Analysis of Putative Virulence Factors Affecting Cytotoxicity of <i>Cronobacter</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3104.	1.5	13

#	ARTICLE	IF	CITATIONS
1710	Comparative genomics and association analysis identifies virulence genes of <i>Cercospora sojina</i> in soybean. <i>BMC Genomics</i> , 2020, 21, 172.	1.2	13
1711	Genomic consequences of population decline in critically endangered pangolins and their demographic histories. <i>National Science Review</i> , 2020, 7, 798-814.	4.6	45
1712	Whole genome sequencing and comparative genomic analysis of oleaginous red yeast <i>Sporobolomyces pararoseus</i> NGR identifies candidate genes for biotechnological potential and ballistospores-shooting. <i>BMC Genomics</i> , 2020, 21, 181.	1.2	9
1713	MAC: Merging Assemblies by Using Adjacency Algebraic Model and Classification. <i>Frontiers in Genetics</i> , 2019, 10, 1396.	1.1	10
1714	Metagenomic Insights into Effects of Thiamine Supplementation on Carbohydrate-Active Enzymes™ Profile in Dairy Cows Fed High-Concentrate Diets. <i>Animals</i> , 2020, 10, 304.	1.0	9
1715	Comparative genomic analysis of <i>Bordetella bronchiseptica</i> isolates from the lungs of pigs with porcine respiratory disease complex (PRDC). <i>Infection, Genetics and Evolution</i> , 2020, 81, 104258.	1.0	6
1716	Repeat-Preserving Decoy Database for False Discovery Rate Estimation in Peptide Identification. <i>Journal of Proteome Research</i> , 2020, 19, 1029-1036.	1.8	24
1717	<i>Extensimonas perlucida</i> sp. nov., a Novel Bacterium Isolated from Sludge. <i>Current Microbiology</i> , 2020, 77, 1316-1320.	1.0	1
1718	<i>Ochrobactrum soli</i> sp. nov., Isolated from a Korean Cattle Farm. <i>Current Microbiology</i> , 2020, 77, 1104-1110.	1.0	5
1719	Genomic Analysis of <i>Wolbachia</i> from <i>Laodelphax striatellus</i> (Delphacidae, Hemiptera) Reveals Insights into Its Æjekyll and Hyde Mode of Infection Pattern. <i>Genome Biology and Evolution</i> , 2020, 12, 3818-3831.	1.1	41
1720	Building near-complete plant genomes. <i>Current Opinion in Plant Biology</i> , 2020, 54, 26-33.	3.5	135
1721	An operon consisting of a P-type ATPase gene and a transcriptional regulator gene responsible for cadmium resistances in <i>Bacillus vietnamensis</i> 151 and <i>Bacillus marisflavi</i> 151. <i>BMC Microbiology</i> , 2020, 20, 18.	1.3	22
1722	Taxonomic Characterization, and Secondary Metabolite Analysis of <i>Streptomyces triticiradicis</i> sp. nov.: A Novel Actinomycete with Antifungal Activity. <i>Microorganisms</i> , 2020, 8, 77.	1.6	20
1723	Shotgun metagenomics approach reveals the bacterial community and metabolic pathways in commercial hongo product, a traditional Korean fermented skate product. <i>Food Research International</i> , 2020, 131, 109030.	2.9	25
1724	Metagenomics methods for the study of plant-associated microbial communities: A review. <i>Journal of Microbiological Methods</i> , 2020, 170, 105860.	0.7	91
1725	Genome Survey and Transcriptome Analysis on Mycelia and Primordia of <i>Agaricus blazei</i> . <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	6
1726	A draft genome assembly of spotted hyena, <i>Crocuta crocuta</i> . <i>Scientific Data</i> , 2020, 7, 126.	2.4	6
1727	Reclassification of <i>Brevibacterium frigoritolerans</i> DSM 8801T as <i>Bacillus frigoritolerans</i> comb. nov. Based on Genome Analysis. <i>Current Microbiology</i> , 2020, 77, 1916-1923.	1.0	20

#	ARTICLE	IF	CITATIONS
1728	Pan-genomics of plants and its applications. , 2020, , 285-306.		2
1729	Strong differentiation within <i>Diplocarpon rosae</i> strains based on microsatellite markers and greenhouse-based inoculation protocol on <i>Rosa</i> . <i>Plant Pathology</i> , 2020, 69, 1093-1107.	1.2	3
1730	First Identification of Human Adenovirus Subtype 21a in China With MinION and Illumina Sequencers. <i>Frontiers in Genetics</i> , 2020, 11, 285.	1.1	3
1731	Molecular Characteristics of <i>Brucella</i> Isolates Collected From Humans in Hainan Province, China. <i>Frontiers in Microbiology</i> , 2020, 11, 452.	1.5	18
1732	Draft Genome Sequence and Annotation of <i>Paracoccus versutus</i> MAL 1HM19, a Nitrate-Reducing, Sulfide-Oxidizing Bacterium. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
1733	<p>Genomic Epidemiology of an Outbreak of Klebsiella pneumoniae ST471 Producing Extended-Spectrum β -Lactamases in a Neonatal Intensive Care Unit</p><p></p>. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1081-1090.	1.1	7
1734	Near-Complete Genomes of Two <i>Trichoderma</i> Species: A Resource for Biological Control of Plant Pathogens. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1036-1039.	1.4	10
1735	Draft Genome Sequences of Multidrug-Resistant <i>Campylobacter jejuni</i> Strains Isolated from Chickens in Central China. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
1736	Biodegradation of phthalate esters by <i>Paracoccus kondratievae</i> BJQ0001 isolated from Jiuqu (Baijiu) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Pollution, 2020, 263, 114506.	3.7	41
1737	Spotlight on a novel bactericidal mechanism and a novel SXT/R391-like integrative and conjugative element, carrying multiple antibiotic resistance genes, in <i>Pseudoalteromonas flavipulchra</i> strain CDM8. <i>Microbiological Research</i> , 2021, 242, 126598.	2.5	7
1738	Tris (1,3-dichloro-2-propyl) phosphate exposure disrupts the gut microbiome and its associated metabolites in mice. <i>Environment International</i> , 2021, 146, 106256.	4.8	11
1739	Genomic epidemiology of <i>Corynebacterium striatum</i> from three regions of China: an emerging national nosocomial epidemic. <i>Journal of Hospital Infection</i> , 2021, 110, 67-75.	1.4	14
1740	Whole-genome assembly and resequencing reveal genomic imprint and key genes of rapid domestication in narrow-leaved lupin. <i>Plant Journal</i> , 2021, 105, 1192-1210.	2.8	12
1741	<i>Halovibrio salipaludis</i> sp. nov., Isolated from Saline-Alkaline Soil. <i>Current Microbiology</i> , 2021, 78, 429-434.	1.0	0
1742	PaKman: A Scalable Algorithm for Generating Genomic Contigs on Distributed Memory Machines. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2021, 32, 1191-1209.	4.0	3
1743	Acetate kinase and peptidases are associated with the proteolytic activity of <i>Lactobacillus helveticus</i> isolated from fermented food. <i>Food Microbiology</i> , 2021, 94, 103651.	2.1	15
1744	Plant herbivorous insect networks: who is eating what revealed by long barcodes using high-throughput sequencing and Trinity assembly. <i>Insect Science</i> , 2021, 28, 127-143.	1.5	7
1745	An Introduction to Whole-Metagenome Shotgun Sequencing Studies. <i>Methods in Molecular Biology</i> , 2021, 2243, 107-122.	0.4	8

#	ARTICLE	IF	CITATIONS
1746	Comparison of Alginate Utilization Pathways in Culturable Bacteria Isolated From Arctic and Antarctic Marine Environments. <i>Frontiers in Microbiology</i> , 2021, 12, 609393.	1.5	11
1747	Two novel venom proteins underlie divergent parasitic strategies between a generalist and a specialist parasite. <i>Nature Communications</i> , 2021, 12, 234.	5.8	25
1748	<i>Puerhibacterium puerhi</i> gen. nov., sp. nov., a novel member of the family Promicromonosporaceae, isolated from Pu-erh tea pile-fermentation. <i>Archives of Microbiology</i> , 2021, 203, 1509-1518.	1.0	7
1749	Genome-wide signatures of mammalian skin covering evolution. <i>Science China Life Sciences</i> , 2021, 64, 1765-1780.	2.3	5
1750	Intestinal transcriptomes in Kazakh sheep with different haplotypes after experimental <i>Echinococcus granulosus</i> infection. <i>Parasite</i> , 2021, 28, 14.	0.8	3
1751	A retrospective survey of <i>Brucella melitensis</i> human infection in Hainan Province, China. <i>Biosafety and Health</i> , 2021, 3, 131-131.	1.2	0
1752	Bioinformatics Approaches for Fungal Biotechnology. , 2021, , 536-554.		0
1753	The Role of Omic Technologies in the Study of the Human Gut Microbiome. , 2021, , 469-481.		0
1754	Phylogeography of subspecies of the sable (<i>Martes zibellina</i> L.) based on mitochondrial genomes: implications for evolutionary history. <i>Mammalian Biology</i> , 2021, 101, 105-120.	0.8	5
1755	Next-generation sequencing for the genetic characterization of Maedi/Visna virus isolated from the northwest of China. <i>Journal of Veterinary Science</i> , 2021, 22, e66.	0.5	2
1756	A Tale of Optimizing the Space Taken by de Bruijn Graphs. <i>Lecture Notes in Computer Science</i> , 2021, , 120-134.	1.0	1
1757	Evolutionary Trajectory of the Replication Mode of Bacterial Replicons. <i>MBio</i> , 2021, 12, .	1.8	10
1758	NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2021, , 47-90.		0
1759	Viromics of extant insect orders unveil the evolution of the flavi-like superfamily. <i>Virus Evolution</i> , 2021, 7, veab030.	2.2	35
1760	Chromosome-scale genome assembly provides insights into the evolution and flavor synthesis of passion fruit (<i>Passiflora edulis</i> Sims). <i>Horticulture Research</i> , 2021, 8, 14.	2.9	62
1761	The characteristic and relationship of <i>Escherichia coli</i> isolated from urine and stones in patients with calcium oxalate stones. <i>Urolithiasis</i> , 2021, 49, 407-414.	1.2	5
1762	The complete chloroplast genome provides insight into the polymorphism and adaptive evolution of <i>Garcinia paucinervis</i> . <i>Biotechnology and Biotechnological Equipment</i> , 2021, 35, 377-391.	0.5	8
1763	Description and genomic characterization of <i>Streptococcus symci</i> sp. nov., isolated from a child's oropharynx. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 113-127.	0.7	8

#	ARTICLE	IF	CITATIONS
1764	Transcriptome profiling and differential expression analysis of the immune-related genes during the acute phase of infection with <i>Mycobacterium marinum</i> in the goldfish (<i>Carassius auratus</i> L.). <i>Aquaculture</i> , 2021, 533, 736198.	1.7	16
1765	Demography, genetic diversity and expansion load in the colonizing species <i>Leontodon longirostris</i> (<i>Asteraceae</i>) throughout its native range. <i>Molecular Ecology</i> , 2021, 30, 1190-1205.	2.0	10
1766	A Chromosome-Level Genome Assembly of the Dark Sleeper <i>Odontobutis potamophila</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
1767	Metagenomics Reveals That Intravenous Injection of Beta-Hydroxybutyric Acid (BHBA) Disturbs the Nasopharynx Microflora and Increases the Risk of Respiratory Diseases. <i>Frontiers in Microbiology</i> , 2020, 11, 630280.	1.5	10
1768	<i>Bacillus salipaludis</i> sp. nov., isolated from saline alkaline soil. <i>Archives of Microbiology</i> , 2021, 203, 2211-2217.	1.0	3
1769	<i>Tenacibaculum pelagium</i> sp. nov., isolated from marine sediment. <i>Archives of Microbiology</i> , 2021, 203, 2229-2236.	1.0	8
1770	Applications of Machine Learning in Human Microbiome Studies: A Review on Feature Selection, Biomarker Identification, Disease Prediction and Treatment. <i>Frontiers in Microbiology</i> , 2021, 12, 634511.	1.5	157
1771	<i>Lentzea alba</i> sp. nov., a novel actinobacterium isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6
1772	<i>Oceanomicrobium pacificus</i> gen. nov., sp. nov., a member of the family Rhodobacteraceae isolated from seawater of tropical western Pacific. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 303-311.	0.7	2
1773	Is Metagenomic Analysis an Effective Way to Analyze Fish Feeding Habits? A Case of the Yellowfin Sea Bream <i>Acanthopagrus latus</i> (Houttuyn) in Daya Bay. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	6
1774	Genomic Comparison of <i>Lactobacillus casei</i> AP and <i>Lactobacillus plantarum</i> DR131 with Emphasis on the Butyric Acid Biosynthetic Pathways. <i>Microorganisms</i> , 2021, 9, 425.	1.6	5
1775	<i>Siccirubicoccus phaeus</i> sp. nov., isolated from oil reservoir water and emended description of the genus <i>Siccirubicoccus</i> . <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 355-364.	0.7	11
1776	A chromosome-level genome of the mud crab (<i>Scylla paramamosain</i> estampador) provides insights into the evolution of chemical and light perception in this crustacean. <i>Molecular Ecology Resources</i> , 2021, 21, 1299-1317.	2.2	17
1777	<i>Herbidospora solisilvae</i> sp. nov., a novel cellulose-degrading actinobacterium isolated from forest soil. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 581-590.	0.7	2
1778	Genomic analysis of <i>Medicago ruthenica</i> provides insights into its tolerance to abiotic stress and demographic history. <i>Molecular Ecology Resources</i> , 2021, 21, 1641-1657.	2.2	17
1779	<i>Tamlana haliotis</i> sp. nov., isolated from the gut of the abalone <i>Haliotis rubra</i> . <i>Archives of Microbiology</i> , 2021, 203, 2357-2364.	1.0	8
1780	Crop pangenomes. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2021, 25, 57-63.	0.4	7
1781	Robust Benchmark Structural Variant Calls of An Asian Using State-of-the-art Long-read Sequencing Technologies. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 192-204.	3.0	6

#	ARTICLE	IF	CITATIONS
1782	Efficiently Merging r-indexes. , 2021, , .		0
1783	Micromonospora rubida sp. nov., a novel actinobacterium isolated from soil of Harbin. Antonie Van Leeuwenhoek, 2021, 114, 697-708.	0.7	2
1784	Climate-driven flyway changes and memory-based long-distance migration. Nature, 2021, 591, 259-264.	13.7	49
1785	Brevibacterium renqingii sp. nov., isolated from the Daqu of Baijiu. Archives of Microbiology, 2021, 203, 2291-2296.	1.0	6
1786	Methods for exploring the faecal microbiome of premature infants: a review. Maternal Health, Neonatology and Perinatology, 2021, 7, 11.	1.0	3
1787	Key metabolism pathways and regulatory mechanisms of high polysaccharide yielding in Hericium erinaceus. BMC Genomics, 2021, 22, 160.	1.2	9
1788	Sulfitobacter algicola sp. nov., isolated from green algae. Archives of Microbiology, 2021, 203, 2351-2356.	1.0	8
1790	RMI-DBG algorithm: A more agile iterative de Bruijn graph algorithm in short read genome assembly. Journal of Bioinformatics and Computational Biology, 2021, 19, 2150005.	0.3	1
1791	Marinisubtilis pacificus gen. nov., sp. nov., a Member of the Family Microbacteriaceae Isolated From a Deep-Sea Seamount. Current Microbiology, 2021, 78, 2136-2142.	1.0	10
1792	Complete and Draft Genome Sequences of the Cruciferous Pathogens Pseudomonas cannabina pv. alisalensis and Pseudomonas syringae pv. maculicola. Microbiology Resource Announcements, 2021, 10, .	0.3	1
1793	ESREEM: Efficient Short Reads Error Estimation Computational Model for Next-generation Genome Sequencing. Current Bioinformatics, 2021, 16, 339-349.	0.7	2
1794	An analysis of the graph processing landscape. Journal of Big Data, 2021, 8, 55.	6.9	11
1795	Draft Genome Sequences of Two Xanthomonas fragariae Strains. Microbiology Resource Announcements, 2021, 10, .	0.3	0
1796	Ruegeria haliotis sp. nov., Isolated from the Gut of the Abalone Haliotis rubra. Current Microbiology, 2021, 78, 2151-2159.	1.0	7
1797	Enabling Genomics Pipelines in Commodity Personal Computers With Flash Storage. Frontiers in Genetics, 2021, 12, 615958.	1.1	0
1798	High-Quality Genome Resource of the Pathogen of <i>Botryosphaeria dothidea</i> Causing Kiwifruit Soft Rot. PhytoFrontiers, 2021, 1, 123-125.	0.8	2
1799	A study of transposable element-associated structural variations (TASVs) using a de novo-assembled Korean genome. Experimental and Molecular Medicine, 2021, 53, 615-630.	3.2	9
1800	The genomic basis of evolutionary differentiation among honey bees. Genome Research, 2021, 31, 1203-1215.	2.4	17

#	ARTICLE	IF	CITATIONS
1801	DNA assembly method for a non-model organism using a more distantly-related reference sequence. , 2021, , .		0
1802	<i>Streptococcus shenyangsis</i> sp. nov., a New Species Isolated from the Oropharynx of a Healthy Child from Shenyang China. <i>Current Microbiology</i> , 2021, 78, 2821-2827.	1.0	4
1803	<i>Pseudomonas quercus</i> sp. nov, associated with leaf spot disease of <i>Quercus mongolica</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	5
1804	Evaluation of the Effects of Different <i>Bacteroides vulgatus</i> Strains against DSS-Induced Colitis. <i>Journal of Immunology Research</i> , 2021, 2021, 1-15.	0.9	18
1805	Whole-Genome Sequence of a Strain of <i>Brucella melitensis</i> Isolated from a Patient with Swelling of the Right Testicle in Inner Mongolia, China. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1806	Genome-wide comparative analyses of GATA transcription factors among 19 <i>Arabidopsis</i> ecotype genomes: Intraspecific characteristics of GATA transcription factors. <i>PLoS ONE</i> , 2021, 16, e0252181.	1.1	25
1807	<i>Stappia albiluteola</i> sp. nov., isolated from marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6
1808	Pan-Genome Analysis of <i>Vibrio cholerae</i> and <i>Vibrio metschnikovii</i> Strains Isolated From Migratory Birds at Dali Nouer Lake in Chifeng, China. <i>Frontiers in Veterinary Science</i> , 2021, 8, 638820.	0.9	10
1809	<i>Salimicrobium humidisoli</i> sp. nov., Isolated from Salineâ€™Alkaline Soil. <i>Current Microbiology</i> , 2021, 78, 3292-3298.	1.0	1
1811	<i>Flavimobilis rhizosphaerae</i> sp. nov., isolated from rhizosphere soil of <i>Spartina alterniflora</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6
1812	<i>Pontibaca salina</i> sp. nov., isolated from marine sediment. <i>Archives of Microbiology</i> , 2021, 203, 4493-4498.	1.0	5
1813	Mitochondrial phylogenomics reveal the origin and adaptive evolution of the deep-sea caridean shrimps (Decapoda: Caridea). <i>Journal of Oceanology and Limnology</i> , 2021, 39, 1948-1960.	0.6	3
1815	Protective effects of different <i>Bacteroides vulgatus</i> strains against lipopolysaccharide-induced acute intestinal injury, and their underlying functional genes. <i>Journal of Advanced Research</i> , 2022, 36, 27-37.	4.4	53
1816	Transcriptome Reveals Roles of Lignin-Modifying Enzymes and Abscisic Acid in the Symbiosis of <i>Mycena</i> and <i>Gastrodia elata</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 6557.	1.8	6
1817	Unraveling the metabolic network of organic acids in solidâ€™state fermentation of Chinese cereal vinegar. <i>Food Science and Nutrition</i> , 2021, 9, 4375-4384.	1.5	14
1818	<i>Streptacidiphilus fuscans</i> sp. nov., a novel actinobacterium isolated from the root of pumpkin (<i>Cucurbita moschata</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	4
1819	Distribution of antibiotic resistance genes and their association with bacteria and viruses in decentralized sewage treatment facilities. <i>Frontiers of Environmental Science and Engineering</i> , 2022, 16, 35.	3.3	18
1821	<i>Pseudoxanthomonas beigongshangi</i> sp. nov., a novel bacteria with predicted nitrite and nitrate reduce ability isolated from pit mud of Baijiu. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1307-1314.	0.7	10

#	ARTICLE	IF	CITATIONS
1822	Surveillance of <i>Borrelia miyamotoi</i> -carrying ticks and genomic analysis of isolates in Inner Mongolia, China. <i>Parasites and Vectors</i> , 2021, 14, 368.	1.0	7
1823	Genome Sequence Resource of <i>Fusarium brachygibbosum</i> Padwick Strain HN-1, a Causal Agent of Maize Stalk Rot Disease. <i>Plant Disease</i> , 2021, . .	0.7	1
1824	<i>Massilia cellulositytica</i> sp. nov., a novel cellulose-degrading bacterium isolated from rhizosphere soil of rice (<i>Oryza sativa</i> L.) and its whole genome analysis. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1529-1540.	0.7	11
1825	<i>Gordonia jinghuaiqii</i> sp. nov. and <i>Gordonia zhaorongruii</i> sp. nov., isolated from Tibetan Plateau wildlife. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	14
1826	<i>Paraliobacillus salinarum</i> sp. nov., isolated from saline soil in Yingkou, China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	4
1827	Gene duplications and phylogenomic conflict underlie major pulses of phenotypic evolution in gymnosperms. <i>Nature Plants</i> , 2021, 7, 1015-1025.	4.7	68
1828	<i>Leucobacter chromiisoli</i> sp. nov., isolated from chromium-containing chemical plant soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
1829	<i>Gulosibacter sediminis</i> sp. nov., isolated from Indian Ocean marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	4
1830	Towards the Well-Tempered Chloroplast DNA Sequences. <i>Plants</i> , 2021, 10, 1360.	1.6	7
1831	Comparative analyses of the <i>Hymenoscyphus fraxineus</i> and <i>Hymenoscyphus albidus</i> genomes reveals potentially adaptive differences in secondary metabolite and transposable element repertoires. <i>BMC Genomics</i> , 2021, 22, 503.	1.2	6
1833	Empirical evaluation of methods for <i>de novo</i> genome assembly. <i>PeerJ Computer Science</i> , 2021, 7, e636.	2.7	15
1835	<i>Gelidibacter pelagius</i> sp. nov., Isolated from Coastal Sediment. <i>Current Microbiology</i> , 2021, 78, 3342-3348.	1.0	5
1837	Genomic Landscape and Phenotypic Assessment of <i>Cronobacter sakazakii</i> Isolated From Raw Material, Environment, and Production Facilities in Powdered Infant Formula Factories in China. <i>Frontiers in Microbiology</i> , 2021, 12, 686189.	1.5	13
1838	Cuttlefish: fast, parallel and low-memory compaction of de Bruijn graphs from large-scale genome collections. <i>Bioinformatics</i> , 2021, 37, i177-i186.	1.8	25
1840	Identification and classification of <i>Croceivirga thetidis</i> sp. nov., a marine Flavobacteriaceae isolated from the hard coral <i>Acropora</i> . <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1407-1416.	0.7	7
1841	Chromosome-level genome of Himalayan yew provides insights into the origin and evolution of the paclitaxel biosynthetic pathway. <i>Molecular Plant</i> , 2021, 14, 1199-1209.	3.9	46
1842	<i>Actinoplanes aureus</i> sp. nov., a novel protease-producing actinobacterium isolated from soil. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1517-1527.	0.7	1
1843	Variations in Microbial Diversity and Metabolite Profiles of Female Landrace Finishing Pigs With Distinct Feed Efficiency. <i>Frontiers in Veterinary Science</i> , 2021, 8, 702931.	0.9	5

#	ARTICLE	IF	CITATIONS
1844	Nitrogeniibacter mangrovi gen. nov., sp. nov., a novel anaerobic and aerobic denitrifying betaproteobacterium and reclassification of Azoarcus pumilus as Aromatoleum pumilum comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	13
1845	Characterization of the chloroplast genome sequence of Bonia amplexicaulis (L.C.Chia, H.L.Fung & Tj ETQq1 1 0.784314 rgBT /Overlo	0.2	1
1847	Isolation and Characterization of Shiga Toxinâ€“Producing <i>Escherichia coli</i> from Retail Beef Samples from Eight Provinces in China. Foodborne Pathogens and Disease, 2021, 18, 616-625.	0.8	4
1848	The whole chloroplast genome in <i>Abelmoschus esculentus</i> L. Moench. New Zealand Journal of Crop and Horticultural Science, 2023, 51, 123-135.	0.7	1
1849	Sediminihaliea albiluteola gen. nov., sp. nov., a new member of the family Halieaceae, isolated from marine sediment. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
1850	Comparative Genome Analysis Provides Molecular Evidence for Reclassification of the Photosynthetic Bacterium Rhodobacter sphaeroides EBL0706 as a Strain of Luteovulum azotoformans. Microorganisms, 2021, 9, 1754.	1.6	3
1851	The complete chloroplast genome sequence of Bromus catharticus Vahl. (Poaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 2825-2827.	0.2	1
1852	Description of Lujinxingia vulgaris sp. nov., isolated from coastal sediment via prey-traps. Antonie Van Leeuwenhoek, 2021, 114, 1805-1818.	0.7	6
1853	Aquimarina algicola sp. nov., isolated from the surface of a marine red alga. Archives of Microbiology, 2021, 203, 5397-5403.	1.0	8
1854	Glycomyces salinus sp. nov., an actinomycete isolated from a hypersaline habitat. Archives of Microbiology, 2021, 203, 5249-5255.	1.0	7
1855	Winogradskyella marina sp. nov., isolated from marine sediment. Archives of Microbiology, 2021, 203, 5381-5386.	1.0	6
1856	Streptomyces luteolifulvus sp. nov., a novel actinomycete isolated from soil in Nanjing, China. Antonie Van Leeuwenhoek, 2021, 114, 1829-1839.	0.7	1
1857	Building a Chinese pan-genome of 486 individuals. Communications Biology, 2021, 4, 1016.	2.0	13
1858	Palleronia sediminis sp. nov. and Flavivirga algicola sp. nov., two marine bacteria isolated from offshore areas near Weihai. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
1859	Aquamicrobium zhengzhouense sp. nov., a Bacterium Isolated from Farmland Soil Applied with Amino Acid Fertilizer. Current Microbiology, 2021, 78, 3798-3803.	1.0	1
1860	The complete chloroplast genome sequence of Arundo formosana Hack. (Poaceae). Mitochondrial DNA Part B: Resources, 2021, 6, 2819-2821.	0.2	0
1861	Massilia puerhi sp. nov., isolated from soil of Pu-erh tea cellar. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	9
1863	Incipient diploidization of the medicinal plant Perilla within 10,000 years. Nature Communications, 2021, 12, 5508.	5.8	35

#	ARTICLE	IF	CITATIONS
1864	<i>Streptomyces botrytidirepellens</i> sp. nov., a novel actinomycete with antifungal activity against <i>Botrytis cinerea</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	5
1865	Genome-Wide Survey Reveals the Microsatellite Characteristics and Phylogenetic Relationships of <i>Harpadon nehereus</i> . <i>Current Issues in Molecular Biology</i> , 2021, 43, 1282-1292.	1.0	6
1866	<i>Massilia rhizosphaerae</i> sp. nov., a rice-associated rhizobacterium with antibacterial activity against <i>Ralstonia solanacearum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	22
1868	<i>Agromyces mariniharenae</i> sp. nov., a novel indole-acetic acid producing actinobacterium isolated from marine sand. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	4
1870	<i>Actinoplanes flavus</i> sp. nov., a novel cellulase-producing actinobacterium isolated from coconut palm rhizosphere soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
1871	Development and preliminary application of novel genomewide SSR markers for genetic diversity analysis of an economically important bio-control agent <i>Platygaster robiniae</i> (Hymenoptera: Tj ETQq1 1 0.784314 0.8 BT /Overlock 10 TF		
1872	Metagenomics Reveals That Proper Placement After Long-Distance Transportation Significantly Affects Calf Nasopharyngeal Microbiota and Is Critical for the Prevention of Respiratory Diseases. <i>Frontiers in Microbiology</i> , 2021, 12, 700704.	1.5	3
1873	Transcriptome-wide identification and characterization of the MYB gene family in sickle seagrass (<i>Thalassia hemprichii</i>). <i>Ecological Genetics and Genomics</i> , 2021, 20, 100093.	0.3	1
1874	Improving the quality of Suancai by inoculating with <i>Lactobacillus plantarum</i> and <i>Pediococcus pentosaceus</i> . <i>Food Research International</i> , 2021, 148, 110581.	2.9	22
1875	The draft genome of the Asian corn borer yields insights into ecological adaptation of a devastating maize pest. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 138, 103638.	1.2	8
1876	Characterization of a <i>Streptococcus</i> species isolated from <i>Siganus guttatus</i> in South China. <i>Aquaculture</i> , 2021, 545, 737163.	1.7	0
1877	Genome sequencing and functional annotation of <i>Bacillus</i> sp. strain BS-Z15 isolated from cotton rhizosphere soil having antagonistic activity against <i>Verticillium dahliae</i> . <i>Archives of Microbiology</i> , 2021, 203, 1565-1575.	1.0	8
1878	<i>Paenibacillus puerhi</i> sp. nov., isolated from the rhizosphere soil of Pu-erh tea plants (<i>Camellia sinensis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 TF	1.0	13
1880	The roles of different <i>Bacteroides fragilis</i> strains in protecting against DSS-induced ulcerative colitis and related functional genes. <i>Food and Function</i> , 2021, 12, 8300-8313.	2.1	21
1883	Specific Protein Database Creation from Transcriptomics Data in Nonmodel Species: Holm Oak (<i>Quercus ilex</i> L.). <i>Methods in Molecular Biology</i> , 2020, 2139, 57-68.	0.4	3
1884	Assessment of Next-Generation Sequence Assembly. <i>SpringerBriefs in Systems Biology</i> , 2014, , 95-101.	0.1	2
1885	Approaches and Challenges of Next-Generation Sequence Assembly Stages. <i>SpringerBriefs in Systems Biology</i> , 2014, , 79-93.	0.1	1
1886	Discovery and Classification of Homeobox Genes in Animal Genomes. <i>Methods in Molecular Biology</i> , 2014, 1196, 3-18.	0.4	4

#	ARTICLE	IF	CITATIONS
1887	Editing the Genome of <i>Wolffia australiana</i> . <i>Compendium of Plant Genomes</i> , 2020, , 165-177.	0.3	1
1888	Meta-Pangenome: At the Crossroad of Pangenomics and Metagenomics. , 2020, , 205-218.		7
1889	The Reyan 7-33-97 Rubber Tree Genome: Insight into Its Structure, Composition and Application. <i>Compendium of Plant Genomes</i> , 2020, , 13-40.	0.3	3
1890	On the Representation of de Bruijn Graphs. <i>Lecture Notes in Computer Science</i> , 2014, , 35-55.	1.0	67
1891	Detection of Copy Number Variations (CNVs) Based on the Coverage Depth from the Next Generation Sequencing Data. , 2017, , 13-22.		2
1892	Mining K-mers of Various Lengths in Biological Sequences. <i>Lecture Notes in Computer Science</i> , 2017, , 186-195.	1.0	6
1893	ReneGENE-Novo: Co-designed Algorithm-Architecture for Accelerated Preprocessing and Assembly of Genomic Short Reads. <i>Lecture Notes in Computer Science</i> , 2018, , 564-577.	1.0	1
1894	Indexing Finite Language Representation of Population Genotypes. <i>Lecture Notes in Computer Science</i> , 2011, , 270-281.	1.0	14
1895	Improved Parallel Processing of Massive De Bruijn Graph for Genome Assembly. <i>Lecture Notes in Computer Science</i> , 2013, , 96-107.	1.0	1
1896	Detecting Superbubbles in Assembly Graphs. <i>Lecture Notes in Computer Science</i> , 2013, , 338-348.	1.0	33
1897	Transcriptome profiling and digital gene expression analysis of the skin of Dybowski's frog (<i>Rana</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5799-5808.	1.7	10
1899	Genome survey sequencing and identification of genomic SSR markers for <i>Rhododendron micranthum</i> . <i>Bioscience Reports</i> , 2020, 40, .	1.1	9
1900	<i>Haloprofundus marisrubri</i> gen. nov., sp. nov., an extremely halophilic archaeon isolated from a brine-seawater interface. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 9-16.	0.8	21
1901	<i>Ponticoccus marisrubri</i> sp. nov., a moderately halophilic marine bacterium of the family Rhodobacteraceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4358-4364.	0.8	7
1902	<i>Ruegeria profundus</i> sp. nov. and <i>Ruegeria marisrubri</i> sp. nov., isolated from the brine-seawater interface at Erba Deep in the Red Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4624-4631.	0.8	17
1903	<i>Bacillus tamaricis</i> sp. nov., an alkaliphilic bacterium isolated from a Tamarix cone soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 558-563.	0.8	9
1904	<i>Acinetobacter piscicola</i> sp. nov., isolated from diseased farmed Murray cod (<i>Maccullochella peelii</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	18
1905	<i>Neptunicoccus sediminis</i> gen. nov., sp. nov., a member of the family Rhodobacteraceae isolated from the Yellow Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1702-1706.	0.8	11

#	ARTICLE	IF	CITATIONS
1906	<i>Xanthomonas prunicola</i> sp. nov., a novel pathogen that affects nectarine (<i>Prunus persica</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 1857-1866.	0.8	19
1907	<i>Amycolatopsis antarctica</i> sp. nov., isolated from the surface of an Antarctic brown macroalga. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2348-2356.	0.8	21
1908	<i>Chitinophaga parva</i> sp. nov., a new member of the family Chitinophagaceae, isolated from soil in a chemical factory. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3452-3457.	0.8	9
1909	<i>Paracoccus salipaludis</i> sp. nov., isolated from saline alkaline soil. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3812-3817.	0.8	11
1910	<i>Paracandidimonas caeni</i> sp. nov., isolated from sludge. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3332-3337.	0.8	10
1911	<i>Vallitalea okinawensis</i> sp. nov., isolated from Okinawa Trough sediment and emended description of the genus <i>Vallitalea</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 404-410.	0.8	17
1912	<i>Coraliomargarita sinensis</i> sp. nov., isolated from a marine solar saltern. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 701-707.	0.8	9
1913	<i>Marinilabilia rubra</i> sp. nov., isolated from a marine solar saltern. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 914-919.	0.8	6
1914	<i>Parabacteroides acidifaciens</i> sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 761-766.	0.8	18
1915	<i>Pseudaminobacter arsenicus</i> sp. nov., an arsenic-resistant bacterium isolated from arsenic-rich aquifers. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 791-797.	0.8	18
1916	<i>Microbulbifer flavimaris</i> sp. nov., a halophilic Gammaproteobacteria isolated from marine sediment of the Yellow Sea, China. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1135-1141.	0.8	8
1917	<i>Bacillus urbisdiaboli</i> sp. nov., isolated from soil sampled in Xinjiang. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1591-1596.	0.8	12
1918	<i>Chitinophaga deserti</i> sp. nov., isolated from desert soil. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1783-1788.	0.8	13
1919	<i>Pedobacter chinensis</i> sp. nov., a cellulose-decomposing bacterium from Arctic tundra soil. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1926-1933.	0.8	13
1920	<i>Jannaschia formosa</i> sp. nov., isolated from marine saltern sediment. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2037-2042.	0.8	12
1921	Genome-based taxonomic classification within the family Thermoactinomycetaceae. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2028-2036.	0.8	33
1922	<i>Muricauda nanhaiensis</i> sp. nov., isolated from seawater of the South China Sea. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2089-2094.	0.8	14
1923	<i>Roseomonas wenyumeiae</i> sp. nov., isolated from faeces of Tibetan antelopes (<i>Pantholops hodgsonii</i>) on the Qinghai Tibet Plateau. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2979-2986.	0.8	10

#	ARTICLE	IF	CITATIONS
1924	<i>Parvularcula marina</i> sp. nov., isolated from surface water of the South China Sea, and emended description of the genus <i>Parvularcula</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2571-2576.	0.8	9
1925	<i>Steroidobacter soli</i> sp. nov., isolated from farmland soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3443-3447.	0.8	14
1926	<i>Kribbella jiaozeuonensis</i> sp. nov., a novel actinomycete isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3500-3507.	0.8	12
1927	<i>Pedobacter helvus</i> sp. nov., isolated from farmland soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3806-3811.	0.8	10
1928	<i>Rhodoferax bucti</i> sp. nov., isolated from fresh water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3903-3909.	0.8	12
1929	<i>Microbispora fusca</i> sp. nov., a novel actinomycete isolated from the ear of wheat (<i>Triticum aestivum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 11	0.8	11
1930	<i>Hyunsoonleella flava</i> sp. nov., isolated from marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 240-245.	0.8	7
1931	<i>Seonamhaeicola maritimus</i> sp. nov., isolated from coastal sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 902-908.	0.8	13
1932	<i>Herbidospora galbida</i> sp. nov., a novel actinobacterium isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1364-1371.	0.8	6
1933	<i>Ornithinimicrobium cerasi</i> sp. nov., isolated from the fruit of <i>Cerasus pseudocerasus</i> and emended description of the genus <i>Ornithinimicrobium</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1691-1697.	0.8	11
1934	<i>Saccharothrix deserti</i> sp. nov., an actinomycete isolated from desert soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1882-1887.	0.8	10
1935	<i>Paracoccus alkanivorans</i> sp. nov., isolated from a deep well with oil reservoir water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2312-2317.	0.8	10
1936	<i>Algibacter pacificus</i> sp. nov., isolated from a deep-sea seamount. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2907-2911.	0.8	9
1937	<i>Streptomyces montanus</i> sp. nov., a novel actinomycete isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3226-3233.	0.8	8
1938	<i>Rhodococcus oryzae</i> sp. nov., a novel actinobacterium isolated from rhizosphere soil of rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.8	10
1939	<i>Denitrobaculum tricleocarpae</i> gen. nov., sp. nov., a marine bacterium from coralline algae <i>Tricleocarpa</i> sp. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3335-3339.	0.8	10
1940	<i>Flavobacterium profundum</i> sp. nov., isolated from a deep-sea seamount. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3633-3638.	0.8	5
1941	<i>Marinicella rhabdoformis</i> sp. nov., isolated from coastal sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3528-3533.	0.8	6

#	ARTICLE	IF	CITATIONS
1942	<i>Caulobacter soli</i> sp. nov., isolated from soil sampled at Jiri Mountain, Republic of Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4158-4164.	0.8	8
1943	<i>Tepidiphilus olei</i> sp. nov., isolated from the production water of a water-flooded oil reservoir in PR China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4364-4371.	0.8	9
1944	<i>Pelagihabitans pacificus</i> gen. nov., sp. nov., a member of the family Flavobacteriaceae isolated from a deep-sea seamount. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4569-4575.	0.8	14
1945	<i>Aeromicrobium piscarium</i> sp. nov., isolated from the intestine of <i>Collichthys lucidus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5280-5286.	0.8	9
1946	<i>Roseomonas bella</i> sp. nov., isolated from lake sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5473-5478.	0.8	7
1947	<i>Seramator thermalis</i> gen. nov., sp. nov., a novel cellulose- and xylan-degrading member of the family Dysgonamonadaceae isolated from a hot spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5717-5724.	0.8	8
1965	Draft Genome Sequence of <i>Dicyma pulvinata</i> Strain 414-3, a Mycoparasite of <i>Cladosporium fulvum</i> , Causal Agent of Tomato Leaf Mold. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
1966	The Draft Whole-Genome Sequence of the Antibiotic Producer <i>Empedobacter haloabium</i> ATCC 31962 Provides Indications for Its Taxonomic Reclassification. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
1967	Applying clinical metagenomics for the detection and characterisation of respiratory infections. , 2019, , 35-49.		3
1968	Current challenges in de novo plant genome sequencing and assembly. <i>Genome Biology</i> , 2012, 13, 243.	13.9	78
1970	LDscaff: LD-based scaffolding of de novo genome assemblies. <i>BMC Bioinformatics</i> , 2020, 21, 570.	1.2	3
1972	Comparative genomics of <i>Cryptococcus neoformans</i> var. <i>grubii</i> associated with meningitis in HIV infected and uninfected patients in Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005628.	1.3	45
1973	De Novo Analysis of Transcriptome Dynamics in the Migratory Locust during the Development of Phase Traits. <i>PLoS ONE</i> , 2010, 5, e15633.	1.1	215
1974	Deep Sequencing of Organ- and Stage-Specific microRNAs in the Evolutionarily Basal Insect <i>Blattella germanica</i> (L.) (Dictyoptera, Blattellidae). <i>PLoS ONE</i> , 2011, 6, e19350.	1.1	94
1975	Targeted Assembly of Short Sequence Reads. <i>PLoS ONE</i> , 2011, 6, e19816.	1.1	41
1976	Evaluating the Fidelity of De Novo Short Read Metagenomic Assembly Using Simulated Data. <i>PLoS ONE</i> , 2011, 6, e19984.	1.1	65
1977	ConDeTri - A Content Dependent Read Trimmer for Illumina Data. <i>PLoS ONE</i> , 2011, 6, e26314.	1.1	216
1978	Transcriptome Analysis of the Oriental Fruit Fly (<i>Bactrocera dorsalis</i>). <i>PLoS ONE</i> , 2011, 6, e29127.	1.1	135

#	ARTICLE	IF	CITATIONS
1979	Rapid Sequencing of the Bamboo Mitochondrial Genome Using Illumina Technology and Parallel Episodic Evolution of Organelle Genomes in Grasses. PLoS ONE, 2012, 7, e30297.	1.1	23
1980	Assessment of Metagenomic Assembly Using Simulated Next Generation Sequencing Data. PLoS ONE, 2012, 7, e31386.	1.1	214
1981	Annotation of the Transcriptome from <i>Taenia pisiformis</i> and Its Comparative Analysis with Three Taeniidae Species. PLoS ONE, 2012, 7, e32283.	1.1	32
1982	Global Transcriptome Profiling of the Pine Shoot Beetle, <i>Tomicus yunnanensis</i> (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 TjE	1.1	47
1983	Transcriptome Analysis of the Chinese White Wax Scale <i>Ericerus pela</i> with Focus on Genes Involved in Wax Biosynthesis. PLoS ONE, 2012, 7, e35719.	1.1	39
1984	Digital Gene Expression Analysis Based on Integrated De Novo Transcriptome Assembly of Sweet Potato [<i>pomoea batatas</i> (L.) Lam.]. PLoS ONE, 2012, 7, e36234.	1.1	156
1985	Basal Jawed Vertebrate Phylogenomics Using Transcriptomic Data from Solexa Sequencing. PLoS ONE, 2012, 7, e36256.	1.1	27
1986	Short Term Evolution of a Highly Transmissible Methicillin-Resistant <i>Staphylococcus aureus</i> Clone (ST228) in a Tertiary Care Hospital. PLoS ONE, 2012, 7, e38969.	1.1	31
1987	ccTSA: A Coverage-Centric Threaded Sequence Assembler. PLoS ONE, 2012, 7, e39232.	1.1	8
1988	Conservation of Gene Cassettes among Diverse Viruses of the Human Gut. PLoS ONE, 2012, 7, e42342.	1.1	33
1989	Deep Insight into the <i>Ganoderma lucidum</i> by Comprehensive Analysis of Its Transcriptome. PLoS ONE, 2012, 7, e44031.	1.1	60
1990	Paired-End Sequencing of Long-Range DNA Fragments for De Novo Assembly of Large, Complex Mammalian Genomes by Direct Intra-Molecule Ligation. PLoS ONE, 2012, 7, e46211.	1.1	7
1991	Transcriptome and Gene Expression Analysis of the Rice Leaf Folder, <i>Cnaphalocrosis medinalis</i> . PLoS ONE, 2012, 7, e47401.	1.1	59
1992	Mind the Gap: Upgrading Genomes with Pacific Biosciences RS Long-Read Sequencing Technology. PLoS ONE, 2012, 7, e47768.	1.1	896
1993	Transcriptome Analysis of Male and Female <i>Sebastiscus marmoratus</i> . PLoS ONE, 2012, 7, e50676.	1.1	16
1994	Transcriptome and Proteome Exploration to Provide a Resource for the Study of <i>Agrocybe aegerita</i> . PLoS ONE, 2013, 8, e56686.	1.1	56
1995	Identification of Optimum Sequencing Depth Especially for De Novo Genome Assembly of Small Genomes Using Next Generation Sequencing Data. PLoS ONE, 2013, 8, e60204.	1.1	73
1996	Complete Plastid Genome Sequencing of Trochodendraceae Reveals a Significant Expansion of the Inverted Repeat and Suggests a Paleogene Divergence between the Two Extant Species. PLoS ONE, 2013, 8, e60429.	1.1	48

#	ARTICLE	IF	CITATIONS
1997	Effects of GC Bias in Next-Generation-Sequencing Data on De Novo Genome Assembly. PLoS ONE, 2013, 8, e62856.	1.1	224
1998	Characterization of Pythium Transcriptome and Gene Expression Analysis at Different Stages of Fermentation. PLoS ONE, 2013, 8, e65552.	1.1	6
1999	Metabolic Engineering of the Phenylpropanoid Pathway Enhances the Antioxidant Capacity of Saussurea involucreta. PLoS ONE, 2013, 8, e70665.	1.1	51
2000	Transcriptome Characteristics and Six Alternative Expressed Genes Positively Correlated with the Phase Transition of Annual Cambial Activities in Chinese Fir (<i>Cunninghamia lanceolata</i> (Lamb.) Hook). PLoS ONE, 2013, 8, e71562.	1.1	26
2001	Plastid Genome Sequence of a Wild Woody Oil Species, <i>Prinsepia utilis</i> , Provides Insights into Evolutionary and Mutational Patterns of Rosaceae Chloroplast Genomes. PLoS ONE, 2013, 8, e73946.	1.1	60
2002	Comparing Memory-Efficient Genome Assemblers on Stand-Alone and Cloud Infrastructures. PLoS ONE, 2013, 8, e75505.	1.1	21
2003	Discovery of Microorganisms and Enzymes Involved in High-Solids Decomposition of Rice Straw Using Metagenomic Analyses. PLoS ONE, 2013, 8, e77985.	1.1	50
2004	Complete Sequencing of Five Araliaceae Chloroplast Genomes and the Phylogenetic Implications. PLoS ONE, 2013, 8, e78568.	1.1	82
2005	Overexpression of Multiple Detoxification Genes in Deltamethrin Resistant <i>Laodelphax striatellus</i> (Hemiptera: Delphacidae) in China. PLoS ONE, 2013, 8, e79443.	1.1	34
2006	Comparative Transcriptome Analysis of Salivary Glands of Two Populations of Rice Brown Planthopper, <i>Nilaparvata lugens</i> , That Differ in Virulence. PLoS ONE, 2013, 8, e79612.	1.1	100
2007	Transcriptome Analysis of Leaf Tissue of <i>Raphanus sativus</i> by RNA Sequencing. PLoS ONE, 2013, 8, e80350.	1.1	26
2008	Transcriptome Analysis of <i>Salicornia europaea</i> under Saline Conditions Revealed the Adaptive Primary Metabolic Pathways as Early Events to Facilitate Salt Adaptation. PLoS ONE, 2013, 8, e80595.	1.1	41
2009	Two-Step Source Tracing Strategy of <i>Yersinia pestis</i> and Its Historical Epidemiology in a Specific Region. PLoS ONE, 2014, 9, e85374.	1.1	9
2010	Characterization of the Miiuy Croaker (<i>Miichthys miiuy</i>) Transcriptome and Development of Immune-Relevant Genes and Molecular Markers. PLoS ONE, 2014, 9, e94046.	1.1	63
2011	Rapid Development of Microsatellite Markers for <i>Callosobruchus chinensis</i> Using Illumina Paired-End Sequencing. PLoS ONE, 2014, 9, e95458.	1.1	22
2012	Identification and Characterization of a New Erythromycin Biosynthetic Gene Cluster in <i>Actinopolyspora erythraea</i> YIM90600, a Novel Erythronolide-Producing Halophilic Actinomycete Isolated from Salt Field. PLoS ONE, 2014, 9, e108129.	1.1	17
2013	Transcriptome Sequencing and Identification of Cold Tolerance Genes in Hardy <i>Corylus</i> Species (C.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	14
2014	Comparison of the Transcriptome between Two Cotton Lines of Different Fiber Color and Quality. PLoS ONE, 2014, 9, e112966.	1.1	26

#	ARTICLE	IF	CITATIONS
2015	Identification of Regulatory Genes Implicated in Continuous Flowering of Longan (<i>Dimocarpus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	1.1	26
2016	Transcriptome Sequence Analysis of an Ornamental Plant, <i>Ananas comosus</i> var. <i>bracteatus</i> , Revealed the Potential Unigenes Involved in Terpenoid and Phenylpropanoid Biosynthesis. <i>PLoS ONE</i> , 2015, 10, e0119153.	1.1	21
2017	Flexible, Fast and Accurate Sequence Alignment Profiling on GPGPU with PaSWAS. <i>PLoS ONE</i> , 2015, 10, e0122524.	1.1	13
2018	Analyses of the Complete Genome and Gene Expression of Chloroplast of Sweet Potato [<i>Ipomoea batata</i>]. <i>PLoS ONE</i> , 2015, 10, e0124083.	1.1	42
2019	Antennal Transcriptome Analysis of Odorant Reception Genes in the Red Turpentine Beetle (RTB), <i>Dendroctonus valens</i> . <i>PLoS ONE</i> , 2015, 10, e0125159.	1.1	81
2020	Regulation of HbPIP2;3, a Latex-Abundant Water Transporter, Is Associated with Latex Dilution and Yield in the Rubber Tree (<i>Hevea brasiliensis</i> Muell. Arg.). <i>PLoS ONE</i> , 2015, 10, e0125595.	1.1	20
2021	RNA-Seq Based De Novo Transcriptome Assembly and Gene Discovery of <i>Cistanche deserticola</i> Fleshy Stem. <i>PLoS ONE</i> , 2015, 10, e0125722.	1.1	14
2022	Hybrid De Novo Genome Assembly Using MiSeq and SOLiD Short Read Data. <i>PLoS ONE</i> , 2015, 10, e0126289.	1.1	6
2023	Transcripts and MicroRNAs Responding to Salt Stress in <i>Musa acuminata</i> Colla (AAA Group) cv. Berangan Roots. <i>PLoS ONE</i> , 2015, 10, e0127526.	1.1	47
2024	From Peer-Reviewed to Peer-Reproduced in Scholarly Publishing: The Complementary Roles of Data Models and Workflows in Bioinformatics. <i>PLoS ONE</i> , 2015, 10, e0127612.	1.1	27
2025	Quorum: An Error Corrector for Illumina Reads. <i>PLoS ONE</i> , 2015, 10, e0130821.	1.1	71
2026	Bioinformatics Analysis of the Complete Genome Sequence of the Mango Tree Pathogen <i>Pseudomonas syringae</i> pv. <i>syringae</i> UMAF0158 Reveals Traits Relevant to Virulence and Epiphytic Lifestyle. <i>PLoS ONE</i> , 2015, 10, e0136101.	1.1	25
2027	Unusually Large Number of Mutations in Asexually Reproducing Clonal Planarian <i>Dugesia japonica</i> . <i>PLoS ONE</i> , 2015, 10, e0143525.	1.1	41
2028	Selecting Superior De Novo Transcriptome Assemblies: Lessons Learned by Leveraging the Best Plant Genome. <i>PLoS ONE</i> , 2016, 11, e0146062.	1.1	93
2029	Tolerant and Susceptible Sesame Genotypes Reveal Waterlogging Stress Response Patterns. <i>PLoS ONE</i> , 2016, 11, e0149912.	1.1	42
2030	Transcriptome Sequencing and Analysis for Culm Elongation of the World's Largest Bamboo (<i>Dendrocalamus sinicus</i>). <i>PLoS ONE</i> , 2016, 11, e0157362.	1.1	20
2031	Draft Genomes of <i>Anopheles cracens</i> and <i>Anopheles maculatus</i> : Comparison of Simian Malaria and Human Malaria Vectors in Peninsular Malaysia. <i>PLoS ONE</i> , 2016, 11, e0157893.	1.1	8
2032	Deciphering the Draft Genome of <i>Toxoplasma gondii</i> RH Strain. <i>PLoS ONE</i> , 2016, 11, e0157901.	1.1	28

#	ARTICLE	IF	CITATIONS
2033	Comprehensive Virus Detection Using Next Generation Sequencing in Grapevine Vascular Tissues of Plants Obtained from the Wine Regions of Bohemia and Moravia (Czech Republic). PLoS ONE, 2016, 11, e0167966.	1.1	59
2034	Identification and expression profile analysis of odorant binding protein and chemosensory protein genes in Bemisia tabaci MED by head transcriptome. PLoS ONE, 2017, 12, e0171739.	1.1	57
2035	Transcriptome using Illumina sequencing reveals the traits of spermatogenesis and developing testes in Eriocheir sinensis. PLoS ONE, 2017, 12, e0172478.	1.1	22
2036	De novo transcriptome analysis and microsatellite marker development for population genetic study of a serious insect pest, Rhopalosiphum padi (L.) (Hemiptera: Aphididae). PLoS ONE, 2017, 12, e0172513.	1.1	41
2037	De novo assembly and analysis of the transcriptome of Rumex patientia L. during cold stress. PLoS ONE, 2017, 12, e0186470.	1.1	8
2038	Characterization of the Lycium barbarum fruit transcriptome and development of EST-SSR markers. PLoS ONE, 2017, 12, e0187738.	1.1	41
2039	The blood DNA virome in 8,000 humans. PLoS Pathogens, 2017, 13, e1006292.	2.1	259
2040	e-RGA: enhanced Reference Guided Assembly of Complex Genomes. EMBnet Journal, 2011, 17, 46.	0.2	17
2042	Combining De Bruijn Graphs, Overlap Graphs and Microassembly for De Novo Genome Assembly. Izvestiya of Saratov University New Series Series: Mathematics Mechanics Informatics, 2013, 13, 51-57.	0.2	3
2043	Transcriptome Profiles of Populus euphratica upon Heat Shock stress. Current Genomics, 2014, 15, 326-340.	0.7	19
2044	The Challenge of Genome Sequence Assembly. Open Bioinformatics Journal, 2018, 11, 231-239.	1.0	4
2045	Identification of common carp innate immune genes with whole-genome sequencing and RNA-Seq data. Journal of Integrative Bioinformatics, 2011, 8, 169.	1.0	12
2046	Dna Sequence Assembly Involving an Acyclic Graph Model. Foundations of Computing and Decision Sciences, 2013, 38, 25-34.	0.5	5
2047	Urbanization and Waterborne Pathogen Emergence in Low-Income Countries: Where and How to Conduct Surveys?. International Journal of Environmental Research and Public Health, 2020, 17, 480.	1.2	14
2048	mBLAST: Keeping up with the Sequencing Explosion for (Meta) Genome Analysis. Journal of Data Mining in Genomics & Proteomics, 2013, 04, .	0.5	16
2049	Memory Optimization for Global Protein Network Alignment Using Pushdown Automata and De Bruijn Graph. Journal of Software, 2014, 9, .	0.6	2
2050	Insights into The Human Gut Microbiome - A Review. SBV Journal of Basic Clinical and Applied Health Science, 2018, 1, 103-110.	0.2	3
2051	Dynamic changes of yak (Bos grunniens) gut microbiota during growth revealed by polymerase chain reaction-denaturing gradient gel electrophoresis and metagenomics. Asian-Australasian Journal of Animal Sciences, 2017, 30, 957-966.	2.4	10

#	ARTICLE	IF	CITATIONS
2052	Deep Sequencing Data Analysis: Challenges and Solutions. , 0, , .		4
2053	Augmenting transcriptome assembly by combining <i>de novo</i> and genome-guided tools. PeerJ, 2013, 1, e133.	0.9	19
2054	An extended genovo metagenomic assembler by incorporating paired-end information. PeerJ, 2013, 1, e196.	0.9	14
2055	Transcriptome analysis of immature xylem in the Chinese fir at different developmental phases. PeerJ, 2016, 4, e2097.	0.9	16
2056	Improving ancient DNA genome assembly. PeerJ, 2017, 5, e3126.	0.9	15
2057	Characterization of the mitochondrial genome of <i>Arge bella</i> Wei & Du sp. nov. (Hymenoptera: Argidae). PeerJ, 2018, 6, e6131.	0.9	7
2058	Low genetic diversity in captive populations of the critically endangered Blue-crowned Laughingthrush (<i>Garrulax courtoisi</i>) revealed by a panel of novel microsatellites. PeerJ, 2019, 7, e6643.	0.9	4
2059	The complete chloroplast genome of <i>Microcycas calocoma</i> (Miq.) A. DC. (Zamiaceae, Cycadales) and evolution in Cycadales. PeerJ, 2020, 8, e8305.	0.9	6
2060	Ultra Efficient Acceleration for De Novo Genome Assembly via Near-Memory Computing. , 2021, , .		5
2061	<i>Agilicoccus flavus</i> gen. nov., sp. nov., a novel member of the family Dermatophilaceae isolated from the Pearl River. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	14
2062	Description and genome analysis of <i>Microvirga antarctica</i> sp. nov., a novel pink-pigmented psychrotolerant bacterium isolated from Antarctic soil. Antonie Van Leeuwenhoek, 2021, 114, 2219-2228.	0.7	3
2063	<i>Umezawaea beigongshangensis</i> sp. nov., Isolated From the Mash of Baijiu. Current Microbiology, 2021, 78, 4127-4131.	1.0	2
2064	Identification of a novel <i>Candida metapsilosis</i> isolate reveals multiple hybridization events. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	6
2065	Music of metagenomics—a review of its applications, analysis pipeline, and associated tools. Functional and Integrative Genomics, 2022, 22, 3-26.	1.4	3
2066	Comparative Genomics Reveals Recent Adaptive Evolution in Himalayan Giant Honeybee <i>Apis laboriosa</i> . Genome Biology and Evolution, 2021, 13, .	1.1	7
2067	<i>Pontibacter flavimaris</i> sp. nov., of the family Hymenobacteraceae, isolated from marine sediment. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	4
2068	The genome of the black cutworm <i>Agrotis ipsilon</i> . Insect Biochemistry and Molecular Biology, 2021, 139, 103665.	1.2	8
2070	Personal Genomes: A New Frontier in Database Research. Lecture Notes in Computer Science, 2011, , 78-88.	1.0	0

#	ARTICLE	IF	CITATIONS
2072	Parallel and Memory-Efficient Reads Indexing for Genome Assembly. Lecture Notes in Computer Science, 2012, , 272-280.	1.0	0
2073	Sequencing of the mink genome: plans and perspectives. , 2012, , 209-215.		1
2074	Recent Advances in Sequencing Technology. Soft and Biological Matter, 2012, , 281-308.	0.3	0
2076	Analysis Pipelines for Next- Generation Sequencing Data. Chapman & Hall/CRC Mathematical and Computational Biology Series, 2012, , .	0.1	0
2077	A De Novo Metagenomic Assembly Program for Shotgun DNA Reads. , 2013, , 1-4.		0
2078	Genome Assembly Algorithms: A Survey. Hans Journal of Computational Biology, 2013, 03, 7-14.	0.0	0
2079	The Ordered Set of Connected Parts of a Polygonal Graph. Izvestiya of Saratov University New Series Series: Mathematics Mechanics Informatics, 2013, 13, 44-51.	0.2	0
2080	De Novo Assembly Algorithms. SpringerBriefs in Systems Biology, 2013, , 55-83.	0.1	0
2081	Modern Techniques for DNA and RNA Assessments. Success in Academic Surgery, 2014, , 107-126.	0.1	0
2082	Advances in the compression of high-throughput DNA sequencing data. Shenzhen Daxue Xuebao (Ligong Ban)/Journal of Shenzhen University Science and Engineering, 2013, 30, 409-415.	0.1	0
2083	Preprocessing and Storing High-Throughput Sequencing Data. Computational Methods in Science and Technology, 0, , 9-20.	0.3	0
2084	On Algorithmic Complexity of Biomolecular Sequence Assembly Problem. Lecture Notes in Computer Science, 2014, , 183-195.	1.0	2
2085	Tapping the Wealth of Microbial Data in High-Throughput Metabolic Model Reconstruction. Methods in Molecular Biology, 2014, 1191, 19-45.	0.4	0
2088	De Bruijn Graph based De novo Genome Assembly. Journal of Software, 2014, 9, .	0.6	0
2090	Annotation Pipelines for Next-Generation Sequencing Projects. Computational Biology, 2015, , 325-367.	0.1	0
2091	Background History of the National and International Brassica rapa Genome Sequencing Initiatives. Compendium of Plant Genomes, 2015, , 17-23.	0.3	0
2092	De Novo Genome Assembly of Next-Generation Sequencing Data. Compendium of Plant Genomes, 2015, , 41-51.	0.3	0
2094	AvaliaÃ§Ã£o de Desempenho Paralelo de Montadores de DNA Velvet e SOAPdenovo2. , 0, , .		1

#	ARTICLE	IF	CITATIONS
2095	Uma abordagem do algoritmo do montador de DNA SOAPdenovo. , 0, , .		0
2097	Fast and Flexible Text Search Using Genomic Short-Read Mapping Model. ETRI Journal, 2016, 38, 518.	1.2	0
2099	Fuzzy-based Spectral Alignment for Correcting DNA Sequence from Next Generation Sequencer. Telkomnika (Telecommunication Computing Electronics and Control), 2016, 14, 707.	0.6	0
2110	SHIVGAMI : Simplifying the titanlc blastx process using aVailable GAthering of coMputational units. Canadian Journal of Biotechnology, 2017, 1, 32-33.	0.3	0
2115	Motiliproteus coralliicola sp. nov., a bacterium isolated from coral. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3292-3295.	0.8	7
2116	Marinobacter bohaiensis sp. nov., a moderate halophile isolated from benthic sediment of the Bohai Sea. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3534-3539.	0.8	11
2117	Creation of a web server for de novo genome assembly on the basis of combining the results obtained by various assemblers. , 0, , .		0
2118	Advancements in Next-Generation Sequencing for Detecting Minimal Residual Disease. , 2019, , 159-192.		0
2121	The Genome of Prunus mume. Compendium of Plant Genomes, 2019, , 31-52.	0.3	0
2123	EML: A Scalable, Transparent Meta-Learning Paradigm for Big Data Applications. Intelligent Systems Reference Library, 2019, , 35-59.	1.0	1
2124	Modern Techniques for DNA, RNA, and Protein Assessment. Success in Academic Surgery, 2019, , 65-104.	0.1	0
2125	Development and Genome Sequence of a Laboratory-Inbred Miniature Pig Facilitate Study of Human Diabetic Disease. SSRN Electronic Journal, 0, , .	0.4	0
2126	Histidinibacterium lentulum gen. nov., sp. nov., a marine bacterium from the culture broth of marine microalga Picochlorum sp. 122. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 578-583.	0.8	8
2128	Proposal of Parashewanella gen. nov. to accommodate Parashewanella curva sp. nov. and Parashewanella spongiae comb. nov. in the Shewanellaceae. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1259-1264.	0.8	16
2129	Microbispora sitophila sp. nov., a novel actinobacterium isolated from rhizosphere soil of wheat (Triticum aestivum L.). International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	4
2130	Actinomadura litoris sp. nov., an actinobacterium isolated from sandy soil in Sanya. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	6
2131	Nocardia bovisstercoris sp. nov., an actinobacterium isolated from cow dung. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	8
2132	Kaistella gelatinilytica sp. nov., a flavobacterium isolated from Antarctic soil. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	0.8	7

#	ARTICLE	IF	CITATIONS
2133	Sequencing and Assembling Genomes and Chromosomes of Cereal Crops. <i>Methods in Molecular Biology</i> , 2020, 2072, 27-37.	0.4	1
2134	Draft Genome Sequence of Teicoplanin-Producing Strain <i>Actinoplanes teichomyceticus</i> CICC 203265. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
2135	<i>Agromyces tardus</i> sp. nov., an actinobacterium isolated from the rhizosphere soil of wheat (<i>Triticum</i>) Tj ETQq0 0 0 ggBT /Overlock 10 Tf	0.8	6
2136	<i>Ferruginivarius sediminum</i> gen. nov., sp. nov., isolated from a marine solar saltern. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3056-3061.	0.8	9
2138	<i>Flavobacterium cerinum</i> sp. nov., isolated from Arctic tundra soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3745-3750.	0.8	11
2140	OBSOLETE: NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2020, , .		0
2142	RNA beyond humans. , 2020, , 117-138.		3
2144	<i>Bacillus aquiflavi</i> sp. nov., isolated from yellow water of strongly flavored Chinese baijiu. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3406-3412.	0.8	9
2145	<i>Oleiliquidispirillum nitrogeniifigens</i> gen. nov., sp. nov., a new member of the family Rhodospirillaceae isolated from oil reservoir water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3468-3474.	0.8	11
2146	<i>Exilibacterium tricleocarpae</i> gen. nov., sp. nov., a marine bacterium from coralline algae <i>Tricleocarpa</i> sp.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3427-3432.	0.8	10
2147	<i>Aequorivita sinensis</i> sp. nov., isolated from sediment of the East China Sea, and reclassification of <i>Vitellibacter todarodis</i> as <i>Aequorivita todarodis</i> comb. nov. and <i>Vitellibacter aquimaris</i> as <i>Aequorivita aquimaris</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3323-3327.	0.8	13
2148	Genome Sequence of the Oleaginous Yeast <i>Rhodotorula paludigena</i> Strain CM33, a Potential Strain for Biofuel Production. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
2149	<i>Glycomyces albidus</i> sp. nov., a novel actinobacterium isolated from rhizosphere soil of wheat (<i>Triticum aestivum</i> L.). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3096-3104.	0.8	7
2151	<i>Maribacter algarum</i> sp. nov., a new member of the family Flavobacteriaceae isolated from the red alga <i>Gelidium amansii</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3679-3685.	0.8	9
2152	<i>Phytoactinopolyspora mesophila</i> sp. nov., isolated from a saline "alkaline soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4179-4185.	0.8	10
2154	The <i>Wolfiporia cocos</i> Genome and Transcriptome Shed Light on the Formation of Its Edible and Medicinal Sclerotium. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 455-467.	3.0	11
2155	Functional metagenomic analysis of quorum sensing signaling in a nitrifying community. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 79.	2.9	8
2156	Analysis of Sex Chromosome Evolution in the Clade Palaeognathae from Phased Genome Assembly. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	2

#	ARTICLE	IF	CITATIONS
2157	Improved method for the extraction of high-quality DNA from lignocellulosic compost samples for metagenomic studies. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 8881-8893.	1.7	9
2159	Complete Genome Sequence of a Quorum-Sensing Bacterium, <i>Oceanicola</i> sp. Strain D3, Isolated from a Microplastic Surface in Coastal Water of Qingdao, China. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
2160	Updates on Legume Genome Sequencing. <i>Methods in Molecular Biology</i> , 2020, 2107, 1-18.	0.4	6
2162	K-mer Mapping and RDBMS Indexes. <i>Lecture Notes in Computer Science</i> , 2020, , 70-82.	1.0	2
2163	<i>Nocardia stercoris</i> sp. nov., a novel actinomycete isolated from the cow dung. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 493-498.	0.8	8
2164	<i>Streptomyces oryziradicis</i> sp. nov., a novel actinomycete isolated from rhizosphere soil of rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 267 T	0.8	9
2167	<i>Formosa maritima</i> sp. nov., isolated from coastal sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 982-988.	0.8	4
2168	<i>Actinomadura harenae</i> sp. nov., a novel actinomycete isolated from sea sand in Sanya. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 766-772.	0.8	6
2170	Bioinformatics services for analyzing massive genomic datasets. <i>Genomics and Informatics</i> , 2020, 18, e8.	0.4	6
2171	<i>Dokdonia sinensis</i> sp. nov., a flavobacterium isolated from surface seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1617-1622.	0.8	4
2172	Identification and characterization of the glycoside hydrolase family 18 genes from the entomopathogenic fungus <i>Isaria cicadae</i> genome. <i>Canadian Journal of Microbiology</i> , 2020, 66, 274-287.	0.8	3
2173	<i>Dyadobacter bucti</i> sp. nov., isolated from subsurface sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2281-2287.	0.8	9
2174	<i>Mumia zhuanghuii</i> sp. nov., isolated from the intestinal contents of plateau pika (<i>Ochotona</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 T	0.8	8
2176	<i>Chryseobacterium panacisoli</i> sp. nov., isolated from ginseng-cultivation soil with ginsenoside-converting activity. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6
2178	<i>Halomonas salipaludis</i> sp. nov., isolated from a saline-alkali wetland soil. <i>Archives of Microbiology</i> , 2021, 203, 6033-6039.	1.0	2
2179	<i>Frigidibacter oleivorans</i> sp. nov., isolated from a deep well with oil reservoir water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4339-4344.	0.8	5
2180	<i>Nitriicola iocasae</i> sp. nov., a bacterium isolated from sediment collected at a cold seep field in the South China Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4897-4902.	0.8	7
2181	<i>Salinimicrobium nanhaiense</i> sp. nov. and <i>Salinimicrobium oceani</i> sp. nov., two novel species of the family Flavobacteriaceae isolated from the South China Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5263-5270.	0.8	10

#	ARTICLE	IF	CITATIONS
2182	<i>Planctomonas psychrotolerans</i> sp. nov., isolated from rhizosphere soil of <i>Suaeda salsa</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5271-5279.	0.8	4
2183	<i>Poritiphilus flavus</i> gen. nov., sp. nov., a member of the family Flavobacteriaceae isolated from coral <i>Porites lutea</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5620-5626.	0.8	8
2184	<i>Aliikangiella coralliicola</i> sp. nov., a bacterium isolated from coral <i>Porites lutea</i> , and proposal of Pleioneaceae fam. nov. to accommodate <i>Pleionea</i> and <i>Aliikangiella</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5880-5887.	0.8	13
2185	<i>Brucella</i> outer membrane protein Omp25 induces microglial cells in vitro to secrete inflammatory cytokines and inhibit apoptosis. International Journal of Clinical and Experimental Medicine, 2015, 8, 17530-5.	1.3	18
2186	Genome assembly and annotation. , 2022, , 49-66.		0
2187	Genomic survey to evaluate the genomic differences between <i>Larimichthys polyactis</i> , <i>L. crocea</i> and their hybrids. Aquaculture Research, 0, , .	0.9	0
2188	<i>Lactobacillus</i> strains inhibit biogenic amine formation in salted mackerel (<i>Scomberomorus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 Td	2.5	11
2189	Efficient iterative Hi-C scaffolder based on N-best neighbors. BMC Bioinformatics, 2021, 22, 569.	1.2	12
2190	The chromosome-level genome provides insight into the molecular mechanism underlying the tortuous branch phenotype of <i>Prunus mume</i> . New Phytologist, 2022, 235, 141-156.	3.5	15
2191	A review of computational tools for generating metagenome-assembled genomes from metagenomic sequencing data. Computational and Structural Biotechnology Journal, 2021, 19, 6301-6314.	1.9	80
2192	A phage cocktail in controlling phage resistance development in multidrug resistant <i>Aeromonas hydrophila</i> with great therapeutic potential. Microbial Pathogenesis, 2022, 162, 105374.	1.3	11
2193	Allele-aware chromosome-scale assembly of the allopolyploid genome of hexaploid Ma bamboo (<i>Dendrocalamus latiflorus</i> Munro). Journal of Integrative Plant Biology, 2022, 64, 649-670.	4.1	24
2194	Using transcriptome Shannon entropy to evaluate the off-target effects and safety of insecticidal siRNAs. Journal of Integrative Agriculture, 2022, 21, 170-177.	1.7	2
2195	Coexistence of virulence and β -lactamase genes in avian pathogenic <i>Escherichia coli</i> . Microbial Pathogenesis, 2022, 163, 105389.	1.3	2
2196	Nematode genome announcement: The draft genome sequence of entomopathogenic nematode <i>Heterorhabditis indica</i> . Journal of Nematology, 2021, 53, 1-3.	0.4	7
2197	Specialised digestive adaptations within the hindgut of a colobine monkey. Innovation(China), 2022, 3, 100207.	5.2	6
2198	Transcriptome Analysis for Identification of Genes Related to Growth and Development, Digestion and Detoxification, Olfaction in the Litchi Stink Bug <i>Tessaratoma papillosa</i> . Frontiers in Physiology, 2021, 12, 774218.	1.3	1
2199	MONI: A Pangenomic Index for Finding Maximal Exact Matches. Journal of Computational Biology, 2022, 29, 169-187.	0.8	23

#	ARTICLE	IF	CITATIONS
2200	<i>Ornithinimicrobium laminariae</i> sp. nov., isolated from the kelp <i>Laminaria japonica</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
2201	Graph Theoretical Strategies in De Novo Assembly. <i>IEEE Access</i> , 2022, 10, 9328-9339.	2.6	1
2202	Characteristics of Gut Microbiota in Patients with GH-Secreting Pituitary Adenoma. <i>Microbiology Spectrum</i> , 2022, 10, e0042521.	1.2	12
2203	Genome survey sequencing of wild cotton (<i>Gossypium robinsonii</i>) reveals insights into proteomic responses of pollen to extreme heat. <i>Plant, Cell and Environment</i> , 2022, 45, 1242-1256.	2.8	4
2204	The Diesel Tree <i>Sindora glabra</i> Genome Provides Insights Into the Evolution of Oleoresin Biosynthesis. <i>Frontiers in Plant Science</i> , 2021, 12, 794830.	1.7	0
2205	<i>Microbacterium sulfonylureivorans</i> sp. nov., isolated from sulfonylurea herbicides degrading consortium. <i>Archives of Microbiology</i> , 2022, 204, 136.	1.0	6
2206	Genome survey sequence of black carp provides insights into development-related gene duplications. <i>Journal of the World Aquaculture Society</i> , 2022, 53, 1197-1214.	1.2	0
2207	Unveiling lignocellulolytic trait of a goat omasum inhabitant <i>Klebsiella variicola</i> strain HSTU-AAM51 in light of biochemical and genome analyses. <i>Brazilian Journal of Microbiology</i> , 2022, 53, 99-130.	0.8	6
2208	<i>Psychrobacter halodurans</i> sp. nov. and <i>Psychrobacter coccoides</i> sp. nov., two new slightly halophilic bacteria isolated from marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	8
2209	RNA-seq-based transcriptomic analysis of AHL-induced biofilm and pyocyanin inhibition in <i>Pseudomonas aeruginosa</i> by <i>Lactobacillus brevis</i> . <i>International Microbiology</i> , 2022, 25, 447-456.	1.1	5
2210	A quinoprotein dehydrogenase from <i>Pelagibacterium halotolerans</i> ANSP101 oxidizes deoxynivalenol to 3-keto-deoxynivalenol. <i>Food Control</i> , 2022, 136, 108834.	2.8	15
2211	<i>Histidinibacterium aquaticum</i> sp. nov., Isolated from Salt-Field Sea Water. <i>Current Microbiology</i> , 2022, 79, 67.	1.0	0
2212	<i>Spongiibacter pelagi</i> sp. nov., a marine gammaproteobacterium isolated from coastal seawater. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 487.	0.7	6
2213	A tRNA t6A modification system contributes to the sensitivity towards the toxin Î²-N-methylamino-L-alanine (BMAA) in the cyanobacterium <i>Anabaena</i> sp. PCC 7120. <i>Aquatic Toxicology</i> , 2022, 245, 106121.	1.9	2
2214	Marker-Free CRISPR-Cas9 Based Genetic Engineering of the Phytopathogenic Fungus, <i>Penicillium expansum</i> . <i>SSRN Electronic Journal</i> , 0, .	0.4	0
2215	<i>Lysobacter antarcticus</i> sp. nov., an SUF-system-containing bacterium from Antarctic coastal sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
2216	Genome Analysis of the Broad Host Range Necrotroph <i>Nalanthamala psidii</i> Highlights Genes Associated With Virulence. <i>Frontiers in Plant Science</i> , 2022, 13, 811152.	1.7	1
2217	<i>Thermus brevis</i> sp. nov., a moderately thermophilic bacterium isolated from a hot spring microbial mat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	7

#	ARTICLE	IF	CITATIONS
2218	<i>Caldalkalibacillus salinus</i> sp. nov., isolated from a salt lake in Xinjiang, northwest China. <i>Archives of Microbiology</i> , 2022, 204, 179.	1.0	0
2219	De Novo Assembly of 20 Chicken Genomes Reveals the Undetectable Phenomenon for Thousands of Core Genes on Microchromosomes and Subtelomeric Regions. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	40
2220	The Genomics and Population Genomics of the Light Brown Apple Moth, <i>Epiphyas postvittana</i> , an Invasive Tortricid Pest of Horticulture. <i>Insects</i> , 2022, 13, 264.	1.0	5
2221	Genome Resource of American Ginseng Black Spot Pathogen <i>Alternaria panax</i> . <i>Plant Disease</i> , 2022, 106, 1020-1022.	0.7	2
2223	Comparative Metagenomic Study of Rhizospheric and Bulk Mercury-Contaminated Soils in the Mining District of Almad�n. <i>Frontiers in Microbiology</i> , 2022, 13, 797444.	1.5	8
2224	<i>Fulvivirga marina</i> sp. nov. and <i>Fulvivirga sediminis</i> sp. nov., two novel Bacteroidetes isolated from the marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	9
2225	Whole genome sequence of pan drug-resistant clinical isolate of <i>Acinetobacter baumannii</i> ST1890. <i>PLoS ONE</i> , 2022, 17, e0264374.	1.1	4
2226	Genomic signatures of high-altitude adaptation and chromosomal polymorphism in geladas. <i>Nature Ecology and Evolution</i> , 2022, 6, 630-643.	3.4	13
2228	<i>Rhizobium cremeum</i> sp. nov., isolated from sewage and capable of acquisition of heavy metal and aromatic compounds resistance genes. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126322.	1.2	6
2229	Harnessing phosphonate antibiotics argolaphos biosynthesis enables a synthetic biology-based green synthesis of glyphosate. <i>Nature Communications</i> , 2022, 13, 1736.	5.8	10
2230	Description and genome analysis of <i>Luteimonas viscosa</i> sp. nov., a novel bacterium isolated from soil of a sunflower field. <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 749-760.	0.7	2
2231	Chromosome-scale genome assembly provides insights into speciation of allotetraploid and massive biomass accumulation of elephant grass (<i>Pennisetum purpureum</i> Schum.). <i>Molecular Ecology Resources</i> , 2022, 22, 2363-2378.	2.2	11
2232	De novo genome assembly of <i>Bradysia cellarum</i> (Diptera: Sciaridae), a notorious pest in traditional special vegetables in China. <i>Insect Molecular Biology</i> , 2022, 31, 508-518.	1.0	3
2233	Genomics divergence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> isolated from naturally fermented dairy products. <i>Food Research International</i> , 2022, 155, 111108.	2.9	9
2234	Marker-free CRISPR-Cas9 based genetic engineering of the phytopathogenic fungus, <i>Penicillium expansum</i> . <i>Fungal Genetics and Biology</i> , 2022, 160, 103689.	0.9	7
2235	<i>Halorubrum salipaludis</i> sp. nov., isolated from the saline-alkaline soil. <i>Archives of Microbiology</i> , 2022, 204, 103.	1.0	1
2237	<i>Robertkochia sediminum</i> sp. nov., isolated from coastal sediment. <i>Archives of Microbiology</i> , 2022, 204, 13.	1.0	6
2238	<i>Shewanella nanhaiensis</i> sp. nov., a marine bacterium isolated from sediment of South China Sea, and emended descriptions of <i>Shewanella woodyi</i> , <i>Shewanella hanedai</i> and <i>Shewanella canadensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	14

#	ARTICLE	IF	CITATIONS
2239	Modular control of multiple pathways of <i>Corynebacterium glutamicum</i> for 5-aminolevulinic acid production. <i>AMB Express</i> , 2021, 11, 179.	1.4	11
2240	Antimicrobial resistance of <i>Escherichia coli</i> , <i>Enterobacter</i> spp., <i>Klebsiella pneumoniae</i> and <i>Enterococcus</i> spp. isolated from the feces of giant panda. <i>BMC Microbiology</i> , 2022, 22, 102.	1.3	9
2241	<i>Nocardia albiluteola</i> sp. nov., a novel lignin-degrading actinobacterium isolated from rhizosphere soil of pumpkin. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	4
2242	Reclassification of 11 Members of the Family Rhodobacteraceae at Genus and Species Levels and Proposal of <i>Pseudogemmibacter hezensis</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2022, 13, 849695.	1.5	47
2243	Biodegradation of chlortetracycline by <i>Bacillus cereus</i> LZ01: Performance, degradative pathway and possible genes involved. <i>Journal of Hazardous Materials</i> , 2022, 434, 128941.	6.5	24
2244	Systems biology of cancer progression. , 0, , 1-6.		0
2245	Lessons from cancer genome sequencing. , 0, , 7-19.		0
2317	<i>Psychroserpens luteolus</i> sp. nov., isolated from <i>Gelidium</i> , reclassification of <i>Ichthyenterobacterium magnum</i> as <i>Psychroserpens magnus</i> comb. nov., <i>Flavihalobacter algicola</i> as <i>Psychroserpens algicola</i> comb. nov., <i>Arcticiflavibacter luteus</i> as <i>Psychroserpens luteus</i> comb. nov. <i>Archives of Microbiology</i> , 2022, 204, 279.	1.0	4
2318	Advancing Mitochondrial Metagenomics: A New Assembly Strategy and Validating the Power of Seed-Based Approach. <i>Diversity</i> , 2022, 14, 317.	0.7	1
2319	Towards practical and robust DNA-based data archiving using the yin-yang codec system. <i>Nature Computational Science</i> , 2022, 2, 234-242.	3.8	33
2320	Optimized Metavirome Analysis of Marine DNA Virus Communities for Taxonomic Profiling. <i>Ocean Science Journal</i> , 2022, 57, 259-268.	0.6	3
2321	Complete Genome Sequence of <i>Paenibacillus polymyxa</i> DSM 365, a Soil Bacterium of Agricultural and Industrial Importance. <i>Microbiology Resource Announcements</i> , 2022, 11, e0032922.	0.3	4
2322	The complete chloroplast genome of <i>Persicaria perfoliata</i> and comparative analysis with Four Medicinal Plants of Polygonaceae. <i>Genome</i> , 2022, , .	0.9	0
2323	A deep dive into genome assemblies of non-vertebrate animals. , 0, 2, .		4
2324	<i>Brevibacillus dissolubilis</i> sp. nov., Isolated from Fresh Water. <i>Current Microbiology</i> , 2022, 79, 194.	1.0	7
2325	Description of <i>Prasinibacter corallicola</i> gen. nov., sp. nov., a zeaxanthin-producing bacterium isolated from stony coral <i>Porites lutea</i> . <i>Antonie Van Leeuwenhoek</i> , 0, , .	0.7	0
2326	Exploring the Benefits of Metal Ions in Phage Cocktail for the Treatment of Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Infection. <i>Infection and Drug Resistance</i> , 0, Volume 15, 2689-2702.	1.1	5
2327	Comparative genomic analysis reveals cellulase plays an important role in the pathogenicity of <i>Setosphaeria turcica</i> f. sp. <i>zeae</i> . <i>Fungal Biology</i> , 2022, , .	1.1	0

#	ARTICLE	IF	CITATIONS
2328	Discovery and Activation of the Cryptic Cluster from <i>Aspergillus</i> sp. CCCC 400735 for Asperphenalenone Biosynthesis. <i>ACS Chemical Biology</i> , 2022, 17, 1524-1533.	1.6	2
2329	<i>Sessilibacter corallicola</i> gen. nov., sp. nov., a sessile bacterium isolated from coral <i>Porites lutea</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
2330	Genome and transcriptome analysis of rock-dissolving <i>Pseudomonas</i> sp. NLX-4 strain. <i>Bioresources and Bioprocessing</i> , 2022, 9, .	2.0	5
2331	Whey protein and xylitol complex alleviate type 2 diabetes in C57BL/6 mice by regulating the intestinal microbiota. <i>Food Research International</i> , 2022, 157, 111454.	2.9	9
2332	Antioxidant potential of <i>Pediococcus pentosaceus</i> strains from the sow milk bacterial collection in weaned piglets. <i>Microbiome</i> , 2022, 10, .	4.9	16
2333	<i>Nocardia rosealba</i> sp. nov., a novel ligninase-producing Actinobacterium isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
2334	<i>Lysobacter chinensis</i> sp. nov., a cellulose-degrading strain isolated from cow dung compost. <i>Antonie Van Leeuwenhoek</i> , 0, , .	0.7	0
2335	<i>Nonomuraea aurantiaca</i> sp. nov., a novel cellulase-producing actinobacterium isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
2336	<i>Catellatospora tritici</i> sp. nov., a novel cellulase-producing actinobacterium isolated from rhizosphere soil of wheat (<i>Triticum aestivum</i> L.) and emended description of the genus <i>Catellatospora</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	5
2337	Genomic Analysis of an Excellent Wine-Making Strain <i>Oenococcus oeni</i> SD-2a. <i>Polish Journal of Microbiology</i> , 2022, 71, 279-292.	0.6	1
2338	Isolation of Three Coliphages and the Evaluation of Their Phage Cocktail for Biocontrol of Shiga Toxin-Producing <i>Escherichia coli</i> O157 in Milk. <i>Current Microbiology</i> , 2022, 79, .	1.0	1
2339	<i>Agriterribacter soli</i> sp. nov., isolated from herbicide-contaminated soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	4
2340	Development and validation of a low-density SNP panel for paternity and kinship analysis and evaluation of genetic variability and structure of commercial Pacific white shrimp (<i>Litopenaeus</i>) Tj ETQq0 0 0 rgBT /Overlock 30 Tf 50 25		
2341	Genomic insights to facilitate the construction of a high-xylose-utilization <i>Enterococcus faecalis</i> OPS2 for 2,3-BDO production. <i>Chemical Engineering Journal</i> , 2022, 448, 137617.	6.6	5
2342	Genome sequence and pathogenicity of <i>Vibrio vulnificus</i> strain MCCC 1A08743 isolated from contaminated prawns. <i>Biology Open</i> , 2022, 11, .	0.6	2
2343	<i>Halomonas salinarum</i> sp. nov., a moderately halophilic bacterium isolated from saline soil in Yingkou, China. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	3
2344	Bile acid metabolism and signaling, the microbiota, and metabolic disease. , 2022, 237, 108238.		62
2346	<i>De novo</i> assembly of human genome at single-cell levels. <i>Nucleic Acids Research</i> , 2022, 50, 7479-7492.	6.5	13

#	ARTICLE	IF	CITATIONS
2347	Cellulomonas triticagri sp. nov., isolated from the rhizosphere soil of wheat (Triticum aestivum L.). Archives of Microbiology, 2022, 204, .	1.0	1
2348	Protocol: rhPCR and SNaPshot assays to distinguish Plasmodiophora brassicae pathotype clusters. Plant Methods, 2022, 18, .	1.9	4
2349	Benchmarking and Assessment of Eight <i>De Novo</i> Genome Assemblers on Viral Next-Generation Sequencing Data, Including the SARS-CoV-2. OMICS A Journal of Integrative Biology, 2022, 26, 372-381.	1.0	5
2350	Simultaneous compression of multiple error-corrected short-read sets for faster data transmission and better <i>de novo</i> assemblies. Briefings in Functional Genomics, 0, , .	1.3	0
2351	Rhodohalobacter sulfatireducens sp. nov., isolated from a marine solar saltern. Archives of Microbiology, 2022, 204, .	1.0	1
2352	Comparative genome anatomy reveals evolutionary insights into a unique amphitriploid fish. Nature Ecology and Evolution, 2022, 6, 1354-1366.	3.4	29
2353	Comparative genomic analysis reveals cellulase plays an important role in the pathogenicity of Setosphaeria turcica f. sp. zeae. Frontiers in Microbiology, 0, 13, .	1.5	1
2354	Analysis of Growth Phases of Enterotoxigenic Escherichia coli Reveals a Distinct Transition Phase before Entry into Early Stationary Phase with Shifts in Tryptophan, Fucose, and Putrescine Metabolism and Degradation of Neurotransmitter Precursors. Microbiology Spectrum, 2022, 10, .	1.2	5
2355	Quill: A Memory Efficient k-mer Counting and k-mer Querying Tool for Commodity Clusters. , 2022, , .		0
2356	Analysis of the Diversity of Xylophilus ampelinus Strains Held in CIRM-CFBP Reveals a Strongly Homogenous Species. Microorganisms, 2022, 10, 1531.	1.6	2
2357	Genomic and Transcriptional Characteristics of Strain Rum-meliibacillus sp. TYF-LIM-RU47 with an Aptitude of Directly Producing Acetoin from Lignocellulose. Fermentation, 2022, 8, 414.	1.4	1
2358	Development of a genome-wide marker design workflow for onions and its application in target amplicon sequencing-based genotyping. DNA Research, 2022, 29, .	1.5	1
2359	Streptomyces plumbidurans sp. nov., a Pb ²⁺ -tolerant actinomycete. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
2360	Post-translational changes in Phialophora verrucosa via lysine lactylation during prolonged presence in a patient with a CARD9-related immune disorder. Frontiers in Immunology, 0, 13, .	2.2	4
2361	A Novel Potent Crystalline Chitin Decomposer: Chitin Deacetylase from Acinetobacter schindleri MCDA01. Molecules, 2022, 27, 5345.	1.7	7
2362	Nucisporomicrobium flavum gen. nov., sp. nov., a new member of the family Micromonosporaceae isolated from saline-alkali soil. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	9
2363	Metagenomic Approaches for Studying Plant-Microbe Interactions. , 2022, , 243-254.		1
2364	High prevalence and pathogenic potential of Shiga toxin-producing Escherichia coli strains in raw mutton and beef in Shandong, China. Current Research in Food Science, 2022, 5, 1596-1602.	2.7	3

#	ARTICLE	IF	CITATIONS
2365	Cut symbiotic bacteria are involved in nitrogen recycling in the tephritid fruit fly <i>Bactrocera dorsalis</i> . <i>BMC Biology</i> , 2022, 20, .	1.7	11
2366	Chloroplast Genome Annotation Tools: Prolegomena to the Identification of Inverted Repeats. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10804.	1.8	7
2367	<i>Rhizobium quercicola</i> sp. nov., isolated from the leaf of <i>Quercus variabilis</i> in China. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	3
2368	Draft Genome Sequences of the <i>Kocuria subflava</i> Type Strain KCTC 39547 and <i>Kocuria</i> sp. Strain JC486, a Newly Isolated Strain from a Wild Ass Sanctuary in Gujarat, India. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
2369	Antibiotic and metal resistance of <i>Stenotrophomonas maltophilia</i> isolates from Eboling permafrost of the Tibetan Plateau. <i>Environmental Science and Pollution Research</i> , 2023, 30, 11798-11810.	2.7	3
2370	New Multidrug Efflux Systems in a Microcystin-Degrading Bacterium <i>Blastomonas fulva</i> and Its Genomic Feature. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10856.	1.8	1
2371	A Combination of Genome Mining with an OSMAC Approach Facilitates the Discovery of and Contributions to the Biosynthesis of Melleolides from the Basidiomycete <i>Armillaria tabescens</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 12430-12441.	2.4	5
2372	Genomic insight into the nocturnal adaptation of the black-crowned night heron (<i>Nycticorax</i>) Tj ETQq1 1 0.784314 _{1.2} rgBT /Overlock 10 ₂ TT		
2373	Molecular mechanisms through which different carbon sources affect denitrification by <i>Thauera linaloolentis</i> : Electron generation, transfer, and competition. <i>Environment International</i> , 2022, 170, 107598.	4.8	16
2375	Whole genome and transcriptome reveal flavone accumulation in <i>Scutellaria baicalensis</i> roots. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
2376	RFfiller: a robust and fast statistical algorithm for gap filling in draft genomes. <i>PeerJ</i> , 0, 10, e14186.	0.9	1
2377	<i>Kingella pumchi</i> sp. nov., an organism isolated from human vertebral puncture tissue. <i>Antonie Van Leeuwenhoek</i> , 2023, 116, 143-151.	0.7	4
2378	Phylogenomics reveals the evolution, biogeography, and diversification history of voles in the Hengduan Mountains. <i>Communications Biology</i> , 2022, 5, .	2.0	3
2379	<i>Saccharothrix luteola</i> sp. nov., a novel cellulose-degrading actinobacterium isolated from soil and emended description of the genus <i>Saccharothrix</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	0
2380	Chromosome-scale genome assembly provides insights into the molecular mechanisms of tissue development of <i>Populus wilsonii</i> . <i>Communications Biology</i> , 2022, 5, .	2.0	4
2381	<i>Paenibacillus hamazuiensis</i> sp. nov., a bacterium isolated from Hamazui hot spring in Yunnan province, south-west China. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	2
2383	Chromosome-scale genome assembly of the brown anole (<i>Anolis sagrei</i>), an emerging model species. <i>Communications Biology</i> , 2022, 5, .	2.0	15
2384	Population dynamics and demographic history of Eurasian collared lemmings. <i>Bmc Ecology and Evolution</i> , 2022, 22, .	0.7	5

#	ARTICLE	IF	CITATIONS
2385	Discovering dominant ammonia assimilation: Implication for high-strength nitrogen removal in full scale biological treatment of landfill leachate. <i>Chemosphere</i> , 2023, 312, 137256.	4.2	10
2386	Algorithmic and computational comparison of metagenome assemblers. , 2020, 90, 847-854.		0
2387	Biocontrol of methicillin-resistant <i>Staphylococcus aureus</i> using a virulent bacteriophage derived from a temperate one. <i>Microbiological Research</i> , 2023, 267, 127258.	2.5	3
2388	Phased Genome Assemblies. <i>Methods in Molecular Biology</i> , 2023, , 273-286.	0.4	1
2389	An External Memory Approach for Large Genome De Novo Assembly. <i>Lecture Notes in Computer Science</i> , 2022, , 79-90.	1.0	0
2390	Description of a new strain of <i>Streptomonospora nanhaiensis</i> and reclassification of <i>Streptomonospora halotolerans</i> as a later heterotypic synonym of <i>Streptomonospora nanhaiensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	0
2391	<i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Probio-M8 undergoes host adaptive evolution by <i>glcU</i> mutation and translocates to the infant's gut via oral-/entero-mammary routes through lactation. <i>Microbiome</i> , 2022, 10, .	4.9	4
2392	Mining and characterization of the PKS-NRPS hybrid for epicoccamide A: a mannosylated tetramate derivative from <i>Epicoccum</i> sp. CCCC 400996. <i>Microbial Cell Factories</i> , 2022, 21, .	1.9	1
2393	Foodborne Bacterial Pathogen Big Data Genomic Analysis. , 2023, , 23-45.		1
2394	Fecal Microbiota Transplantation Could Improve Chronic Diarrhea in Cynomolgus Monkey by Alleviating Inflammation and Modulating Gut Microbiota. <i>Biomedicine</i> , 2022, 10, 3016.	1.4	1
2395	<i>Fulvirigga sedimenti</i> sp.nov, isolated from the sediment of oceanic tidal zone. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	0
2396	Chromosome-Level Genome Assembly of the Speckled Blue Grouper (<i>Epinephelus cyanopodus</i>) Provides Insight into Its Adaptive Evolution. <i>Biology</i> , 2022, 11, 1810.	1.3	1
2397	Characterizing corn-straw-degrading actinomycetes and evaluating application efficiency in straw-returning experiments. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
2398	Multi-genome metabolic modeling predicts functional inter-dependencies in the <i>Arabidopsis</i> root microbiome. <i>Microbiome</i> , 2022, 10, .	4.9	12
2399	Genome-based taxonomic rearrangement of <i>Oceanobacter</i> -related bacteria including the description of <i>Thalassolituus hydrocarbonoclasticus</i> sp. nov. and <i>Thalassolituus pacificus</i> sp. nov. and emended description of the genus <i>Thalassolituus</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
2400	Microbial and phage communities as well as their interaction in PO saponification wastewater treatment systems. <i>Water Science and Technology</i> , 2023, 87, 354-365.	1.2	1
2401	Description of <i>Jidongwangia harbinensis</i> gen. nov. sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	1
2402	<i>Bacillus subtilis</i> phage phi18: genomic analysis and receptor identification. <i>Archives of Virology</i> , 2023, 168, .	0.9	1

#	ARTICLE	IF	CITATIONS
2403	Transcriptomic and enzymatic analysis reveals the roles of glutamate dehydrogenase in <i>Corynebacterium glutamicum</i> . <i>AMB Express</i> , 2022, 12, .	1.4	1
2404	Genome Sequence Resource of <i>Fusarium proliferatum</i> f. sp. <i>malus domestica</i> MR5, the Causative Agent of Apple Replant Disease. <i>Plant Disease</i> , 0, , .	0.7	0
2405	Diversity and Distribution Characteristics of Viruses from Soda Lakes. <i>Genes</i> , 2023, 14, 323.	1.0	7
2406	The <i>Gynandropsis gynandra</i> genome provides insights into whole-genome duplications and the evolution of C4 photosynthesis in Cleomaceae. <i>Plant Cell</i> , 2023, 35, 1334-1359.	3.1	8
2407	Assembly of a Draft Genome for the Mouse Ectoparasite <i>Myocoptes musculus</i> . <i>Journal of the American Association for Laboratory Animal Science</i> , 2023, 62, 55-63.	0.6	0
2408	Description of novel capsule biosynthesis loci of <i>Campylobacter jejuni</i> clinical isolates from South and South-East Asia. <i>PLoS ONE</i> , 2023, 18, e0280583.	1.1	0
2409	Methods to improve the accuracy of next-generation sequencing. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 11, .	2.0	15
2410	Inhibitory effects of <i>Clostridium butyricum</i> culture and supernatant on inflammatory colorectal cancer in mice. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	4
2411	Structural variation (SV)-based pan-genome and GWAS reveal the impacts of SVs on the speciation and diversification of allotetraploid cottons. <i>Molecular Plant</i> , 2023, 16, 678-693.	3.9	14
2412	The genome sequence and demographic history of <i>Przewalskia tangutica</i> (Solanaceae), an endangered alpine plant on the Qinghai-Tibet Plateau. <i>DNA Research</i> , 2023, 30, .	1.5	1
2413	Distribution and co-occurrence of antibiotic resistance genes and bacterial pathogens in the effluent of decentralized sewage treatment systems in China. <i>International Biodeterioration and Biodegradation</i> , 2023, 180, 105596.	1.9	1
2414	<i>Ectobacillus ponti</i> sp. nov., a novel bacterium isolated from Pearl River Estuary. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
2415	K-mer applied in <i>Mycobacterium tuberculosis</i> genome cluster analysis. <i>Brazilian Journal of Biology</i> , 0, 84, .	0.4	0
2416	The genome of <i>Lignosus tigris</i> : Uncovering its hidden nutraceutical potential. <i>South African Journal of Botany</i> , 2023, 154, 108-119.	1.2	2
2417	De Novo Assembly of an Allotetraploid <i>Artemisia argyi</i> Genome. <i>Agronomy</i> , 2023, 13, 436.	1.3	1
2418	Comparative Transcriptomic Analysis of Key Genes Involved in Citrinin Biosynthesis in <i>Monascus purpureus</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 200.	1.5	3
2419	Chromosome-scale genome assembly and insights into the metabolome and gene regulation of leaf color transition in an important oak species, <i>Quercus dentata</i> . <i>New Phytologist</i> , 2023, 238, 2016-2032.	3.5	13
2421	Whole-Genome Sequence of <i>Lactiplantibacillus plantarum</i> Mut-3, Isolated from Indonesian Fermented Soybean (Tempeh). <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.3	1

#	ARTICLE	IF	CITATIONS
2422	Epidemiological characteristics, virulence potential, antimicrobial resistance profiles, and phylogenetic analysis of <i>Aeromonas caviae</i> isolated from extra-intestinal infections. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 13, .	1.8	3
2423	Dual domestications and origin of traits in grapevine evolution. <i>Science</i> , 2023, 379, 892-901.	6.0	60
2424	<i>Aequorivita vitellina</i> sp. nov. and <i>Aequorivita xiaoshiensis</i> sp. nov., isolated from marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	1
2425	ASLncR: a novel computational tool for prediction of abiotic stress-responsive long non-coding RNAs in plants. <i>Functional and Integrative Genomics</i> , 2023, 23, .	1.4	3
2426	<i>Parvularcula maris</i> sp. nov., an algicidal bacterium isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
2427	Genome-based classification of <i>Pedobacter polysaccharus</i> sp. nov., isolated from Antarctic soil producing exopolysaccharide. <i>FEMS Microbiology Letters</i> , 0, , .	0.7	2
2428	<i>Sphaerisporangium perillae</i> sp. nov., isolated from the root of <i>Perilla frutescens</i> (Linn.) Britt. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
2429	<i>Mumia quercus</i> sp. nov., isolated from the root of <i>Quercus variabilis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	0
2430	Chromosome-level genome assembly of <i>Salvia miltiorrhiza</i> with orange roots uncovers the role of Sm2OGD3 in catalyzing 15,16-dehydrogenation of tanshinones. <i>Horticulture Research</i> , 2023, 10, .	2.9	4
2431	A chromosome-scale genome assembly of <i>Malus domestica</i> , a multi-stress resistant apple variety. <i>Genomics</i> , 2023, 115, 110627.	1.3	6
2432	Genomic and Transcriptomic Approaches Provide a Predictive Framework for Sesquiterpenes Biosynthesis in <i>Desarmillaria tabescens</i> CPCC 401429. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 481.	1.5	0
2433	<i>Sphingomonas beigongshangi</i> sp. nov., Isolated from Pit Mud of Baijiu. <i>Microbiology</i> , 2023, 92, 146-152.	0.5	0
2443	Technological advancement in tool and technique used for biodegradation analysis. , 2023, , 89-102.		0
2461	Caveats for Watermelon Whole Genome Sequencing. <i>Compendium of Plant Genomes</i> , 2023, , 17-21.	0.3	0
2470	Space-Time Trade-Offs for the LCP Array of Wheeler DFAs. <i>Lecture Notes in Computer Science</i> , 2023, , 143-156.	1.0	0
2472	Computational Genomics Approaches for Livestock Improvement and Management. <i>Livestock Diseases and Management</i> , 2023, , 351-376.	0.5	0
2478	<i>Winogradskyella immobilis</i> sp. nov., an Alginate-Hydrolyzing Bacterium Isolated from the Brown Algae <i>Saccharina japonica</i> . <i>Current Microbiology</i> , 2023, 80, .	1.0	0
2489	Prospects of Bioinformatics and Data Acquisition Tools in Boosting the Application of Phytochemicals in Food Sciences. , 2024, , 281-302.		0

#	ARTICLE	IF	CITATIONS
2503	Parendoicoomonas callyspongiae sp. nov. Isolated from a Marine Sponge, Callyspongia elongate, and Reclassification of Sansalvadorimonas verongulae as Parendoicoomonas verongulae comb. nov.. Current Microbiology, 2024, 81, .	1.0	0
2513	The de Bruijn Graph of Sequential Repetition of Patterns in DNA Strings. Trends in Mathematics, 2024, , 825-834.	0.1	0