

Velvet: Algorithms for de novo short read assembly using

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Citation Report

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1359	Genome Sequence of <i>Burkholderia pseudomallei</i> NCTC 13392. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
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1370	The Draft Genome Sequence of <i>Nocardioides</i> sp. Strain CF8 Reveals the Scope of Its Metabolic Capabilities. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
1371	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
1372	Draft Genome Sequence of <i>Frankia</i> sp. Strain BMG5.12, a Nitrogen-Fixing Actinobacterium Isolated from Tunisian Soils. <i>Genome Announcements</i> , 2013, 1, .	0.8	39
1373	Draft Genome Sequences of <i>Porphyromonas crevioricanis</i> JCM 15906 T and <i>Porphyromonas cansulci</i> JCM 13913 T Isolated from a Canine Oral Cavity. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
1374	Draft Genome Sequences of Three O157 Enteropathogenic <i>Escherichia coli</i> Isolates. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
1375	Draft Genome Sequence of an Oscillatorian Cyanobacterium, Strain ESFC-1. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
1376	Genome Sequence of <i>Clostridium diolis</i> Strain DSM 15410, a Promising Natural Producer of 1,3-Propanediol. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
1377	Genome Sequence of <i>Klebsiella pneumoniae</i> Strain ATCC 25955, an Oxygen-Insensitive Producer of 1,3-Propanediol. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
1378	Genome Sequence of the 2,4,5-Trichlorophenoxyacetate-Degrading Bacterium <i>Burkholderia phenoliruptrix</i> Strain AC1100. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
1379	Draft Genome Sequence of <i>Clostridium tyrobutyricum</i> Strain UC7086, Isolated from Grana Padano Cheese with Late-Blowing Defect. <i>Genome Announcements</i> , 2013, 1, .	0.8	18
1380	Genome Sequence of a Novel Polymer-Grade L-Lactate-Producing Alkaliphile, <i>Exiguobacterium</i> sp. Strain 8-11-1. <i>Genome Announcements</i> , 2013, 1, .	0.8	26
1381	Draft Genome Sequences of Five Strains of <i>Lactobacillus acidophilus</i> , Strain CIP 76.13 T, Isolated from Humans, Strains CIRM-BIA 442 and CIRM-BIA 445, Isolated from Dairy Products, and Strains DSM 20242 and DSM 9126 of Unknown Origin. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
1382	Draft Genome Sequence of <i>Lactobacillus hominis</i> Strain CRBIP 24.179 T, Isolated from Human Intestine. <i>Genome Announcements</i> , 2013, 1, .	0.8	1
1383	Genome Sequences of Six Wheat-Infecting <i>Fusarium</i> Species Isolates. <i>Genome Announcements</i> , 2013, 1, .	0.8	38
1384	High-Quality Draft Genome Sequences of Two <i>Xanthomonas citri</i> pv. <i>malvacearum</i> Strains. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
1385	Draft Genome Sequence of the <i>Xanthomonas cassavae</i> Type Strain CFBP 4642. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
1386	Whole-Genome Sequence of <i>Mycobacterium abscessus</i> Clinical Strain V06705. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
1387	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

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1388	Genome Sequence of <i>Dehalobacter</i> UNSWDHB, a Chloroform-Dechlorinating Bacterium. <i>Genome Announcements</i> , 2013, 1, .	0.8	20
1389	Draft Genome Sequence of the Earliest <i>Cronobacter sakazakii</i> Sequence Type 4 Strain, NCIMB 8272. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
1390	Draft Genome Sequences of Three Newly Identified Species in the Genus <i>Cronobacter</i> , <i>C. helveticus</i> LMG23732 T, <i>C. pulveris</i> LMG24059, and <i>C. zurichensis</i> LMG23730 T. <i>Genome Announcements</i> , 2013, 1, .	0.8	11
1391	Draft Genome Sequence of a Meningitic Isolate of <i>Cronobacter sakazakii</i> Clonal Complex 4, Strain 8399. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
1392	Draft Genome Sequences of <i>Bordetella hinzii</i> and <i>Bordetella trematum</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	7
1393	Draft Genome Sequences of Multidrug-Resistant <i>Acinetobacter</i> sp. Strains from Colombian Hospitals. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
1394	Draft Genome Sequence of the Hydrogen- and Ethanol-Producing Bacterium <i>Clostridium intestinale</i> Strain URNW. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
1395	Draft Genome Sequence of the Biosurfactant-Producing Bacterium <i>Gordonia amicalis</i> Strain CCMA-559, Isolated from Petroleum-Impacted Sediment. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
1396	Draft Genome Sequence of <i>Pseudozyma brasiliensis</i> sp. nov. Strain GHG001, a High Producer of Endo-1,4-Xylanase Isolated from an Insect Pest of Sugarcane. <i>Genome Announcements</i> , 2013, 1, .	0.8	17
1397	Genome Sequence of <i>Dyella ginsengisoli</i> Strain LA-4, an Efficient Degrader of Aromatic Compounds. <i>Genome Announcements</i> , 2013, 1, .	0.8	14
1398	Complete Genome Sequence of <i>Streptococcus pneumoniae</i> Strain A026, a Clinical Multidrug-Resistant Isolate Carrying Tn 2010. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
1399	High-Quality Draft Genome Sequence of <i>Xanthomonas alfalfae</i> subsp. <i>alfalfae</i> Strain CFBP 3836. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
1400	Genome Sequence of Strain MOLA814, a Proteorhodopsin-Containing Representative of the <i>Betaproteobacteria</i> Common in the Ocean. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
1401	Draft Genome Sequence of NDM-1-Producing <i>Klebsiella pneumoniae</i> Clinical Isolate 303K. <i>Genome Announcements</i> , 2013, 1, .	0.8	1
1402	Genome Sequences of 28 <i>Bordetella pertussis</i> U.S. Outbreak Strains Dating from 2010 to 2012. <i>Genome Announcements</i> , 2013, 1, .	0.8	13
1403	Small, Smaller, Smallest: The Origins and Evolution of Ancient Dual Symbioses in a Phloem-Feeding Insect. <i>Genome Biology and Evolution</i> , 2013, 5, 1675-1688.	1.1	276
1404	Draft Genome Sequence of <i>Shewanella decolorationis</i> S12, a Dye-Degrading Bacterium Isolated from a Wastewater Treatment Plant. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
1405	Genome Sequence of Growth-Improving <i>Paenibacillus mucilaginosus</i> Strain KNP414. <i>Genome Announcements</i> , 2013, 1, .	0.8	3

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1406	Livestock Origin for a Human Pandemic Clone of Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2013, 4, .	1.8	177
1407	Genome Sequencing of <i>Ralstonia solanacearum</i> FQY_4, Isolated from a Bacterial Wilt Nursery Used for Breeding Crop Resistance. <i>Genome Announcements</i> , 2013, 1, .	0.8	26
1408	Proteomic and Genetic Analyses Demonstrate that <i>Plasmodium berghei</i> Blood Stages Export a Large and Diverse Repertoire of Proteins. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 426-448.	2.5	65
1409	A Sensitive and Accurate protein domain Classification Tool (SALT) for short reads. <i>Bioinformatics</i> , 2013, 29, 2103-2111.	1.8	10
1410	Piliation of Invasive <i>Streptococcus pneumoniae</i> Isolates in the Era before Pneumococcal Conjugate Vaccine Introduction in Malawi. <i>Vaccine Journal</i> , 2013, 20, 1729-1735.	3.2	12
1411	Genome Sequences and Photosynthesis Gene Cluster Composition of a Freshwater Aerobic Anoxygenic Phototroph, <i>Sandarakinorhabdus</i> sp. Strain AAP62, Isolated from the Shahu Lake in Ningxia, China. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
1412	Draft Genome Sequence of <i>Escherichia coli</i> Strain ATCC 23506 (Serovar O10:K5:H4). <i>Genome Announcements</i> , 2013, 1, e0004913.	0.8	11
1413	Genome Sequence of <i>Klebsiella oxytoca</i> M5a1, a Promising Strain for Nitrogen Fixation and Chemical Production. <i>Genome Announcements</i> , 2013, 1, .	0.8	16
1414	Draft Genome Sequence of Dihydroxyacetone-Producing <i>Gluconobacter thailandicus</i> Strain NBRC 3255. <i>Genome Announcements</i> , 2013, 1, e0011813.	0.8	8
1415	Draft Genome Sequence of <i>Rhodococcus qingshengii</i> Strain BKS 20-40. <i>Genome Announcements</i> , 2013, 1, e0012813.	0.8	2
1416	Draft Genome Sequence of <i>Rhodococcus triatomae</i> Strain BKS 15-14. <i>Genome Announcements</i> , 2013, 1, e0012913.	0.8	3
1417	Draft Genome Sequence of <i>Acinetobacter baumannii</i> Strain MSP4-16. <i>Genome Announcements</i> , 2013, 1, e0013713.	0.8	3
1418	Draft Genome Sequence of <i>Herpotrichiellaceae</i> sp. UM 238 Isolated from Human Skin Scraping. <i>Genome Announcements</i> , 2013, 1, .	0.8	1
1419	Draft Genome Sequence of Medium-Chain-Length Polyhydroxyalkanoate-Producing <i>Pseudomonas putida</i> Strain LS46. <i>Genome Announcements</i> , 2013, 1, e0015113.	0.8	6
1420	Genome Sequence of a Novel Archaeal Fusellovirus Assembled from the Metagenome of a Mexican Hot Spring. <i>Genome Announcements</i> , 2013, 1, e0016413.	0.8	11
1421	Draft Genome Sequence of <i>Meiothermus ruber</i> H328, Which Degrades Chicken Feathers, and Identification of Proteases and Peptidases Responsible for Degradation. <i>Genome Announcements</i> , 2013, 1, .	0.8	15
1422	Draft Genome Sequence of a Thermophilic Member of the Bacillaceae, <i>Anoxybacillus flavithermus</i> Strain Kn10, Isolated from the Kan-nawa Hot Spring in Japan. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
1423	Draft Genome Sequence of <i>Methylobacterium mesophilicum</i> Strain SR1.6/6, Isolated from Citrus sinensis. <i>Genome Announcements</i> , 2013, 1, .	0.8	7

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1424	Genome Sequence of the Multiple-β-Lactam-Antibiotic-Resistant Bacterium <i>Acidovorax</i> sp. Strain MR-S7. <i>Genome Announcements</i> , 2013, 1, .	0.8	13
1425	Genome Sequence of <i>Streptococcus agalactiae</i> Strain O9mas018883, Isolated from a Swedish Cow. <i>Genome Announcements</i> , 2013, 1, .	0.8	10
1426	Genome Sequence of <i>Thermus thermophilus</i> ATCC 33923, a Thermostable Trehalose-Producing Strain. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
1427	Draft Genome Sequence of the Brazilian Toxic Bloom-Forming Cyanobacterium <i>Microcystis aeruginosa</i> Strain SPC777. <i>Genome Announcements</i> , 2013, 1, .	0.8	11
1428	Complete Genome Sequence of <i>Clostridium</i> sp. Strain DL-VIII, a Novel Solventogenic <i>Clostridium</i> Species Isolated from Anaerobic Sludge. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
1429	Genome Sequence of an Epidemic Isolate of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> from Rio de Janeiro, Brazil. <i>Genome Announcements</i> , 2013, 1, .	0.8	9
1430	Complete Genome Sequence of the Encephalomyelitic <i>Burkholderia pseudomallei</i> Strain MSHR305. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
1431	Draft Genome Sequence of <i>Bacillus pumilus</i> CCMA-560, Isolated from an Oil-Contaminated Mangrove Swamp. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
1432	Draft Genome Sequence of <i>Cryptococcus flavescens</i> Strain OH182.9_3C, a Biocontrol Agent against Fusarium Head Blight of Wheat. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
1433	Draft Genome Sequence of <i>Pseudomonas azotifigens</i> Strain DSM 17556 T (6H33b T), a Nitrogen Fixer Strain Isolated from a Compost Pile. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
1434	Complete Genome Sequence of <i>Bacillus thuringiensis</i> Serovar <i>Israelensis</i> Strain HD-789. <i>Genome Announcements</i> , 2013, 1, .	0.8	30
1435	Pan-Genome and Comparative Genome Analyses of <i>Propionibacterium acnes</i> Reveal Its Genomic Diversity in the Healthy and Diseased Human Skin Microbiome. <i>MBio</i> , 2013, 4, e00003-13.	1.8	159
1436	Within-Host Evolution of <i>Burkholderia pseudomallei</i> over a Twelve-Year Chronic Carriage Infection. <i>MBio</i> , 2013, 4, .	1.8	121
1437	Genomic Insights to Control the Emergence of Vancomycin-Resistant Enterococci. <i>MBio</i> , 2013, 4, .	1.8	136
1438	Genome Sequence of <i>Klebsiella oxytoca</i> SA2, an Endophytic Nitrogen-Fixing Bacterium Isolated from the Pioneer Grass <i>Psammochloa villosa</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	20
1439	Draft Genome Sequence of <i>Pseudomonas veronii</i> Strain 1YdBTEX2. <i>Genome Announcements</i> , 2013, 1, .	0.8	14
1440	Complete Genome of <i>Serratia</i> sp. Strain FGI 94, a Strain Associated with Leaf-Cutter Ant Fungus Gardens. <i>Genome Announcements</i> , 2013, 1, e0023912.	0.8	15
1441	Draft Genome Sequence of <i>Frankia</i> sp. Strain BCU110501, a Nitrogen-Fixing Actinobacterium Isolated from Nodules of <i>Discaria trinevis</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	40

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1442	Draft Genome Sequence of Vancomycin-Heteroresistant <i>Staphylococcus epidermidis</i> Strain UC7032, Isolated from Food. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
1443	Draft Genome Sequences of Strains of <i>Pasteurella multocida</i> Isolated from the United Kingdom and the United States. <i>Genome Announcements</i> , 2013, 1, .	0.8	1
1444	A second-generation assembly of the <i>Drosophila simulans</i> genome provides new insights into patterns of lineage-specific divergence. <i>Genome Research</i> , 2013, 23, 89-98.	2.4	157
1445	Full-Genome Deep Sequencing and Phylogenetic Analysis of Novel Human Betacoronavirus. <i>Emerging Infectious Diseases</i> , 2013, 19, 736-42B.	2.0	131
1446	Application of a MAX-CUT Heuristic to the Contig Orientation Problem in Genome Assembly. , 2013, , .		0
1447	Suffix-Tree Based Error Correction of NGS Reads Using Multiple Manifestations of an Error. , 2013, , .		4
1448	Draft Genome Sequence of <i>Frankia</i> sp. Strain CN3, an Atypical, Noninfective (Nod ⁺) Ineffective (Fix ⁻) Isolate from <i>Coriaria nepalensis</i> . <i>Genome Announcements</i> , 2013, 1, e0008513.	0.8	51
1449	The Epidemic of Extended-Spectrum-β-Lactamase-Producing <i>Escherichia coli</i> ST131 Is Driven by a Single Highly Pathogenic Subclone, <i>H</i> 30-Rx. <i>MBio</i> , 2013, 4, e00377-13.	1.8	380
1450	Evolutionary Dynamics of <i>Vibrio cholerae</i> O1 following a Single-Source Introduction to Haiti. <i>MBio</i> , 2013, 4, .	1.8	118
1451	Complete Genome Sequence of the Hyperthermophilic Sulfate-Reducing Bacterium <i>Thermodesulfobacterium geofontis</i> OPF15 ^T . <i>Genome Announcements</i> , 2013, 1, e0016213.	0.8	4
1452	Draft Genome Sequence of Uropathogenic <i>Escherichia coli</i> Strain J96. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
1453	Inbreeding depression in urban environments of the bird's nest fungus <i>Cyathus stercoreus</i> (Nidulariaceae: Basidiomycota). <i>Heredity</i> , 2013, 110, 355-362.	1.2	6
1454	Memory efficient minimum substring partitioning. <i>Proceedings of the VLDB Endowment</i> , 2013, 6, 169-180.	2.1	37
1455	Phylogenomics and taxonomy of <i>Lecomtelleae</i> (Poaceae), an isolated panicoid lineage from Madagascar. <i>Annals of Botany</i> , 2013, 112, 1057-1066.	1.4	51
1456	Sequence Comparative Analysis Using Networks: Software for Evaluating De Novo Transcript Assembly from Next-Generation Sequencing. <i>Molecular Biology and Evolution</i> , 2013, 30, 1975-1986.	3.5	12
1457	Genome Sequence of a Plant-Associated Bacterium, <i>Bacillus amyloliquefaciens</i> Strain UCMB5036. <i>Genome Announcements</i> , 2013, 1, e0011113.	0.8	14
1458	Investigating the beneficial traits of <i>Trichoderma hamatum</i> GD12 for sustainable agriculture—insights from genomics. <i>Frontiers in Plant Science</i> , 2013, 4, 258.	1.7	119
1459	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

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1460	Mutualistic Co-evolution of Type III Effector Genes in <i>Sinorhizobium fredii</i> and <i>Bradyrhizobium japonicum</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003204.	2.1	76
1461	Extensive chromosomal reshuffling drives evolution of virulence in an asexual pathogen. <i>Genome Research</i> , 2013, 23, 1271-1282.	2.4	338
1462	Draft Genome Sequence and Description of <i>Janthinobacterium</i> sp. Strain CG3, a Psychrotolerant Antarctic Supraglacial Stream Bacterium. <i>Genome Announcements</i> , 2013, 1, .	0.8	10
1463	Draft Genome Sequence of <i>Escherichia coli</i> Strain Nissle 1917 (Serovar O6:K5:H1). <i>Genome Announcements</i> , 2013, 1, e0004713.	0.8	31
1464	Genome of the pathogen <i>Porphyromonas gingivalis</i> recovered from a biofilm in a hospital sink using a high-throughput single-cell genomics platform. <i>Genome Research</i> , 2013, 23, 867-877.	2.4	58
1465	De Novo Transcriptome Sequencing Reveals Important Molecular Networks and Metabolic Pathways of the Plant, <i>Chlorophytum borivilianum</i> . <i>PLoS ONE</i> , 2013, 8, e83336.	1.1	65
1466	Dominant Role of Nucleotide Substitution in the Diversification of Serotype 3 Pneumococci over Decades and during a Single Infection. <i>PLoS Genetics</i> , 2013, 9, e1003868.	1.5	81
1467	<i>In Vitro</i> Evolution of an Archetypal Enteropathogenic <i>Escherichia coli</i> Strain. <i>Journal of Bacteriology</i> , 2013, 195, 4476-4483.	1.0	12
1468	The fungus-growing termite <i>Macrotermes natalensis</i> harbors bacillaene-producing <i>Bacillus</i> sp. that inhibit potentially antagonistic fungi. <i>Scientific Reports</i> , 2013, 3, 3250.	1.6	117
1469	Transmission of Hypervirulence Traits via Sexual Reproduction within and between Lineages of the Human Fungal Pathogen <i>Cryptococcus gattii</i> . <i>PLoS Genetics</i> , 2013, 9, e1003771.	1.5	45
1470	Whole Genome Sequence of the <i>Treponema</i> Fribourg-Blanc: Unspecified Simian Isolate Is Highly Similar to the Yaws Subspecies. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2172.	1.3	53
1471	Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space. <i>PLoS Computational Biology</i> , 2013, 9, e1003010.	1.5	20
1472	Detection of Mixed Infection from Bacterial Whole Genome Sequence Data Allows Assessment of Its Role in <i>Clostridium difficile</i> Transmission. <i>PLoS Computational Biology</i> , 2013, 9, e1003059.	1.5	75
1473	The Genome and Development-Dependent Transcriptomes of <i>Pyronema confluens</i> : A Window into Fungal Evolution. <i>PLoS Genetics</i> , 2013, 9, e1003820.	1.5	85
1474	Improving Genome Assemblies and Annotations for Nonhuman Primates. <i>ILAR Journal</i> , 2013, 54, 144-153.	1.8	23
1475	Detecting and Comparing Non-Coding RNAs in the High-Throughput Era. <i>International Journal of Molecular Sciences</i> , 2013, 14, 15423-15458.	1.8	22
1476	Genomics of an emerging clone of <i>Salmonella</i> serovar Typhimurium ST313 from Nigeria and the Democratic Republic of Congo. <i>Journal of Infection in Developing Countries</i> , 2013, 7, 696-706.	0.5	30
1477	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	1.5	232

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1478	The Genome Organization of <i>Thermotoga maritima</i> Reflects Its Lifestyle. <i>PLoS Genetics</i> , 2013, 9, e1003485.	1.5	38
1479	Genomic Characterisation of Invasive Non-Typhoidal <i>Salmonella enterica</i> Subspecies <i>enterica</i> Serovar <i>Bovismorbificans</i> Isolates from Malawi. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2557.	1.3	24
1480	Unisexual and Heterosexual Meiotic Reproduction Generate Aneuploidy and Phenotypic Diversity <i>De Novo</i> in the Yeast <i>Cryptococcus neoformans</i> . <i>PLoS Biology</i> , 2013, 11, e1001653.	2.6	145
1481	Next-Generation Sequence Assembly: Four Stages of Data Processing and Computational Challenges. <i>PLoS Computational Biology</i> , 2013, 9, e1003345.	1.5	120
1482	Pneumococcal Capsular Switching: A Historical Perspective. <i>Journal of Infectious Diseases</i> , 2013, 207, 439-449.	1.9	172
1483	Genomes of <i>Ashbya</i> Fungi Isolated from Insects Reveal Four Mating-Type Loci, Numerous Translocations, Lack of Transposons, and Distinct Gene Duplications. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1225-1239.	0.8	35
1484	Nearly finished genomes produced using gel microdroplet culturing reveal substantial intraspecies genomic diversity within the human microbiome. <i>Genome Research</i> , 2013, 23, 878-888.	2.4	53
1485	Functional and Evolutionary Analysis of the Genome of an Obligate Fungal Symbiont. <i>Genome Biology and Evolution</i> , 2013, 5, 891-904.	1.1	54
1486	Horizontal Gene Transfer is a Significant Driver of Gene Innovation in Dinoflagellates. <i>Genome Biology and Evolution</i> , 2013, 5, 2368-2381.	1.1	37
1487	Sequencing Angiosperm Plastid Genomes Made Easy: A Complete Set of Universal Primers and a Case Study on the Phylogeny of Saxifragales. <i>Genome Biology and Evolution</i> , 2013, 5, 989-997.	1.1	195
1488	GSA: An Integrated Analysis System for Gene Sequence. <i>Applied Mechanics and Materials</i> , 2013, 380-384, 2795-2798.	0.2	0
1489	EBARDenovo: highly accurate <i>de novo</i> assembly of RNA-Seq with efficient chimera-detection. <i>Bioinformatics</i> , 2013, 29, 1004-1010.	1.8	33
1490	A Genomic Day in the Life of a Clinical Microbiology Laboratory. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1272-1277.	1.8	60
1491	Whole-Genome Analysis of a Daptomycin-Susceptible <i>Enterococcus faecium</i> Strain and Its Daptomycin-Resistant Variant Arising during Therapy. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 261-268.	1.4	101
1492	New Approaches Indicate Constant Viral Diversity despite Shifts in Assemblage Structure in an Australian Hypersaline Lake. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6755-6764.	1.4	37
1493	SOAPindel: Efficient identification of indels from short paired reads. <i>Genome Research</i> , 2013, 23, 195-200.	2.4	115
1494	Comparative Genomic Analysis of Phylogenetically Closely Related <i>Hydrogenobaculum</i> sp. Isolates from Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2932-2943.	1.4	39
1495	Complete Genome Sequences from Three Genetically Distinct Strains Reveal High Intraspecies Genetic Diversity in the Microsporidian <i>Encephalitozoon cuniculi</i> . <i>Eukaryotic Cell</i> , 2013, 12, 503-511.	3.4	57

#	ARTICLE	IF	CITATIONS
1496	Bioinformatics in High Throughput Sequencing: Application in Evolving Genetic Diseases. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2013, 04, .	0.5	8
1497	Identification of Insertion Deletion Mutations from Deep Targeted Resequencing. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2013, 04, .	0.5	2
1498	Crass: identification and reconstruction of CRISPR from unassembled metagenomic data. <i>Nucleic Acids Research</i> , 2013, 41, e105-e105.	6.5	146
1499	Draft Genome Sequence of <i>Pasteurella multocida</i> A:3 Strain 671/90. <i>Genome Announcements</i> , 2013, 1, .	0.8	12
1500	Genome Sequence of <i>Streptomyces viridosporus</i> Strain T7A ATCC 39115, a Lignin-Degrading Actinomycete. <i>Genome Announcements</i> , 2013, 1, .	0.8	20
1501	Long-Term Diversity and Genome Adaptation of <i>Acinetobacter baylyi</i> in a Minimal-Medium Chemostat. <i>Genome Biology and Evolution</i> , 2013, 5, 87-97.	1.1	10
1502	Genomic Diversity and Fitness of <i>E. coli</i> Strains Recovered from the Intestinal and Urinary Tracts of Women with Recurrent Urinary Tract Infection. <i>Science Translational Medicine</i> , 2013, 5, 184ra60.	5.8	148
1503	Sequencing and Functional Annotation of Avian Pathogenic <i>Escherichia coli</i> Serogroup O78 Strains Reveal the Evolution of <i>E. coli</i> Lineages Pathogenic for Poultry via Distinct Mechanisms. <i>Infection and Immunity</i> , 2013, 81, 838-849.	1.0	82
1504	Molecular characterization and phylogenetic analysis of <i>Murray Valley encephalitis virus</i> and <i>West Nile virus</i> (Kunjin subtype) from an arbovirus disease outbreak in horses in Victoria, Australia, in 2011. <i>Journal of Veterinary Diagnostic Investigation</i> , 2013, 25, 35-44.	0.5	17
1505	SPA: a short peptide assembler for metagenomic data. <i>Nucleic Acids Research</i> , 2013, 41, e91-e91.	6.5	15
1506	Phylogenomics and Analysis of Shared Genes Suggest a Single Transition to Mutualism in <i>Wolbachia</i> of Nematodes. <i>Genome Biology and Evolution</i> , 2013, 5, 1668-1674.	1.1	49
1507	Previously undescribed grass pollen antigens are the major inducers of T helper 2 cytokine-producing T cells in allergic individuals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3459-3464.	3.3	88
1508	Comparison of Metabolic Capacities and Inference of Gene Content Evolution in Mosquito-Associated <i>Spiroplasma diminutum</i> and <i>S. taiwanense</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1512-1523.	1.1	35
1509	QUAST: quality assessment tool for genome assemblies. <i>Bioinformatics</i> , 2013, 29, 1072-1075.	1.8	6,983
1510	Reprever: resolving low-copy duplicated sequences using template driven assembly. <i>Nucleic Acids Research</i> , 2013, 41, e128-e128.	6.5	7
1511	Identification of a Sex-Linked SNP Marker in the Salmon Louse (<i>Lepeophtheirus salmonis</i>) Using RAD Sequencing. <i>PLoS ONE</i> , 2013, 8, e77832.	1.1	63
1512	Transcriptomic Analysis of Cadmium Stress Response in the Heavy Metal Hyperaccumulator <i>Sedum alfredii</i> Hance. <i>PLoS ONE</i> , 2013, 8, e64643.	1.1	100
1513	Complete Genome Sequence of <i>Micromonospora</i> Strain L5, a Potential Plant-Growth-Regulating Actinomycete, Originally Isolated from <i>Casuarina equisetifolia</i> Root Nodules. <i>Genome Announcements</i> , 2013, 1, .	0.8	19

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1515	Genetic characteristics of bla NDM-1-positive plasmid in <i>Citrobacter freundii</i> isolate separated from a clinical infectious patient. <i>Journal of Medical Microbiology</i> , 2013, 62, 1332-1337.	0.7	25
1516	Horizontal Transfer of DNA from the Mitochondrial to the Plastid Genome and Its Subsequent Evolution in Milkweeds (Apocynaceae). <i>Genome Biology and Evolution</i> , 2013, 5, 1872-1885.	1.1	129
1517	Recent Recombination Events in the Core Genome Are Associated with Adaptive Evolution in <i>Enterococcus faecium</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1524-1535.	1.1	87
1518	Identification of the galactosyltransferase of <i>Cryptococcus neoformans</i> involved in the biosynthesis of basidiomycete-type glycosylinositolphosphoceramide. <i>Glycobiology</i> , 2013, 23, 1210-1219.	1.3	7
1519	Expanding the Marine Virosphere Using Metagenomics. <i>PLoS Genetics</i> , 2013, 9, e1003987.	1.5	259
1520	Purification and characterization of oxygen-inducible haem catalase from oxygen-tolerant <i>Bifidobacterium asteroides</i> . <i>Microbiology (United Kingdom)</i> , 2013, 159, 89-95.	0.7	20
1521	Comparative Metagenomic and Metatranscriptomic Analysis of Hindgut Paunch Microbiota in Wood- and Dung-Feeding Higher Termites. <i>PLoS ONE</i> , 2013, 8, e61126.	1.1	149
1522	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , 2013, 14, R11.	13.9	296
1523	The genome and developmental transcriptome of the strongylid nematode <i>Haemonchus contortus</i> . <i>Genome Biology</i> , 2013, 14, R89.	13.9	192
1524	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
1525	Genomic Diversity of "Deep Ecotype" <i>Alteromonas macleodii</i> Isolates: Evidence for Pan-Mediterranean Clonal Frames. <i>Genome Biology and Evolution</i> , 2013, 5, 1220-1232.	1.1	71
1526	A strategy to capture and characterize the synaptic transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7464-7469.	3.3	49
1527	Genome-wide association study identifies vitamin B ₅ biosynthesis as a host specificity factor in <i>Campylobacter</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11923-11927.	3.3	267
1528	Complete Genome Sequences of Elephant Endotheliotropic Herpesviruses 1A and 1B Determined Directly from Fatal Cases. <i>Journal of Virology</i> , 2013, 87, 6700-6712.	1.5	52
1529	Draft Genome Sequence of <i>Agrobacterium</i> sp. Strain UHFBA-218, Isolated from Rhizosphere Soil of Crown Gall-Infected Cherry Rootstock Colt. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
1530	Draft Genome Sequence of <i>Lactobacillus plantarum</i> Strain AY01, Isolated from the Raw Material of Fermented Goat Milk Cheese. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
1531	Transcriptome Analysis of <i>Thapsia laciniata</i> Rouy Provides Insights into Terpenoid Biosynthesis and Diversity in Apiaceae. <i>International Journal of Molecular Sciences</i> , 2013, 14, 9080-9098.	1.8	43

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1533	Self-adaptive containers: Building resource-efficient applications with low programmer overhead. , 2013, , .		4
1534	The Importance of Total Genome Databases in Research on Akoya Pearl Oyster. <i>Zoological Science</i> , 2013, 30, 781-782.	0.3	3
1535	<i>Cecropia peltata</i> Accumulates Starch or Soluble Glycogen by Differentially Regulating Starch Biosynthetic Genes. <i>Plant Cell</i> , 2013, 25, 1400-1415.	3.1	23
1536	An RNA-Seq Transcriptome Analysis of Orthophosphate-Deficient White Lupin Reveals Novel Insights into Phosphorus Acclimation in Plants. <i>Plant Physiology</i> , 2013, 161, 705-724.	2.3	184
1537	High-Throughput Compression of FASTQ Data with SeqDB. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 213-218.	1.9	27
1538	Distinct lipopeptide production systems for <i>WLP</i> (white line-inducing principle) in <i>Pseudomonas fluorescens</i> and <i>Pseudomonas putida</i> . <i>Environmental Microbiology Reports</i> , 2013, 5, 160-169.	1.0	29
1539	Identification and characterization of the genetic changes responsible for the characteristic smooth-to-rough morphotype alterations of clinically persistent <i>Mycobacterium abscessus</i> . <i>Molecular Microbiology</i> , 2013, 90, 612-629.	1.2	142
1540	De Bruijn Graph-Based Whole-Genomic Sequence Assembly Algorithms and Applications. , 2013, , .		0
1541	Transcriptome sequencing as a platform to elucidate molecular components of the diapause response in the Asian tiger mosquito <i>Aedes albopictus</i> . <i>Physiological Entomology</i> , 2013, 38, 173-181.	0.6	26
1542	Nonagricultural reservoirs contribute to emergence and evolution of <i>Pseudomonas syringae</i> crop pathogens. <i>New Phytologist</i> , 2013, 199, 800-811.	3.5	84
1543	A dynamic hashing approach to build the de bruijn graph for genome assembly. , 2013, , .		1
1544	Optimal DNA shotgun sequencing: Noisy reads are as good as noiseless reads. , 2013, , .		22
1545	CloudRS: An error correction algorithm of high-throughput sequencing data based on scalable framework. , 2013, , .		19
1546	A new genome assembly method based on dynamic overlap. , 2013, , .		0
1547	Metagenome Survey of a Multispecies and Alga-Associated Biofilm Revealed Key Elements of Bacterial-Algal Interactions in Photobioreactors. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6196-6206.	1.4	111
1548	Gene Content and Diversity of the Loci Encoding Biosynthesis of Capsular Polysaccharides of the 15 Serovar Reference Strains of <i>Haemophilus parasuis</i> . <i>Journal of Bacteriology</i> , 2013, 195, 4264-4273.	1.0	37
1549	Draft Genome Sequence of <i>Pseudoalteromonas luteoviolacea</i> Strain B (ATCC 29581). <i>Genome Announcements</i> , 2013, 1, e0004813.	0.8	10

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1551	Metagenomics uncovers a new group of low GC and ultra-small marine Actinobacteria. Scientific Reports, 2013, 3, 2471.	1.6	182
1552	The Evolution of Genomic Instability in the Obligate Endosymbionts of Whiteflies. Genome Biology and Evolution, 2013, 5, 783-793.	1.1	60
1553	Plastome Sequences of <i>Lygodium japonicum</i> and <i>Marsilea crenata</i> Reveal the Genome Organization Transformation from Basal Ferns to Core Leptosporangiates. Genome Biology and Evolution, 2013, 5, 1403-1407.	1.1	36
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1556	The Genome of the Anaerobic Fungus <i>Orpinomyces</i> sp. Strain C1A Reveals the Unique Evolutionary History of a Remarkable Plant Biomass Degradator. Applied and Environmental Microbiology, 2013, 79, 4620-4634.	1.4	224
1557	H-NS Plays a Role in Expression of <i>Acinetobacter baumannii</i> Virulence Features. Infection and Immunity, 2013, 81, 2574-2583.	1.0	100
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1561	Horizontal gene transfer converts non-toxicogenic <i>Clostridium difficile</i> strains into toxin producers. Nature Communications, 2013, 4, 2601.	5.8	163
1562	The non-human primate reference transcriptome resource (NHPRTR) for comparative functional genomics. Nucleic Acids Research, 2013, 41, D906-D914.	6.5	67
1563	Integrated whole-genome sequencing and temporospatial analysis of a continuing Group A <i>Streptococcus</i> epidemic. Emerging Microbes and Infections, 2013, 2, 1-8.	3.0	16
1564	Genome Sequence of the Extreme Obligate Alkaliphile <i>Bacillus marmarensis</i> Strain DSM 21297. Genome Announcements, 2013, 1, .	0.8	7
1565	Harnessing virtual machines to simplify next-generation DNA sequencing analysis. Bioinformatics, 2013, 29, 2075-2083.	1.8	25
1566	Transcriptome Analysis to Identify Putative Floral-Specific Genes and Flowering Regulatory-Related Genes of Sweet Potato. Bioscience, Biotechnology and Biochemistry, 2013, 77, 2169-2174.	0.6	33
1567	RNA-Seq reveals early distinctions and late convergence of gene expression between diapause and quiescence in the Asian tiger mosquito, <i>Aedes albopictus</i> . Journal of Experimental Biology, 2013, 216, 4082-90.	0.8	68
1568	Genome Sequencing Identifies Two Nearly Unchanged Strains of Persistent <i>Listeria monocytogenes</i> Isolated at Two Different Fish Processing Plants Sampled 6 Years Apart. Applied and Environmental Microbiology, 2013, 79, 2944-2951.	1.4	110

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1570	Tracking the establishment of local endemic populations of an emergent enteric pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17522-17527.	3.3	124
1571	Genome Sequence of <i>Clostridium butyricum</i> Strain DSM 10702, a Promising Producer of Biofuels and Biochemicals. <i>Genome Announcements</i> , 2013, 1, .	0.8	9
1572	Identification of a New Enamovirus Associated with Citrus Vein Enation Disease by Deep Sequencing of Small RNAs. <i>Phytopathology</i> , 2013, 103, 1077-1086.	1.1	66
1573	Association of a DNA Virus with Grapevines Affected by Red Blotch Disease in California. <i>Phytopathology</i> , 2013, 103, 1069-1076.	1.1	150
1574	De Novo Transcriptome Sequencing in <i>Trigonella foenum-graecum</i> L. to Identify Genes Involved in the Biosynthesis of Diosgenin. <i>Plant Genome</i> , 2013, 6, plantgenome2012.08.0021.	1.6	39
1575	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
1576	Complete genome sequence of <i>Granulicella mallensis</i> type strain MP5ACTX8T, an acidobacterium from tundra soil. <i>Standards in Genomic Sciences</i> , 2013, 9, 71-82.	1.5	20
1577	Genome Sequence of <i>Sphingomonas xenophaga</i> QYY, an Anthraquinone-Degrading Strain. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
1578	Complete Genome Sequence of <i>Simiduia agarivorans</i> SA1 T , a Marine Bacterium Able To Degrade a Variety of Polysaccharides. <i>Genome Announcements</i> , 2013, 1, .	0.8	12
1579	Draft Genome Sequences of Two Bulgarian <i>Bacillus anthracis</i> Strains. <i>Genome Announcements</i> , 2013, 1, e0015213.	0.8	2
1580	Draft Genome Sequences of <i>Helicobacter pylori</i> Strains Isolated from Regions of Low and High Gastric Cancer Risk in Colombia. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
1581	Data compression for sequencing data. <i>Algorithms for Molecular Biology</i> , 2013, 8, 25.	0.3	82
1582	Genome Sequences of Two Morphologically Distinct and Thermophilic <i>Bacillus coagulans</i> Strains, H-1 and XZL9. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
1583	Complete genome sequence of <i>Coriobacterium glomerans</i> type strain (PW2T) from the midgut of <i>Pyrhocoris apterus</i> L. (red soldier bug). <i>Standards in Genomic Sciences</i> , 2013, 8, 15-25.	1.5	8
1584	Complete genome sequence of the bile-resistant pigment-producing anaerobe <i>Alistipes finegoldii</i> type strain (AHN2437T). <i>Standards in Genomic Sciences</i> , 2013, 8, 26-36.	1.5	12
1585	High-quality-draft genome sequence of the yellow-pigmented flavobacterium <i>Joostella marina</i> type strain (En5T). <i>Standards in Genomic Sciences</i> , 2013, 8, 37-46.	1.5	11
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1587	Genome sequence of the free-living aerobic spirochete <i>Turneriella parva</i> type strain (HT), and emendation of the species <i>Turneriella parva</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 228-238.	1.5	11
1588	Genome analysis of <i>Desulfotomaculum kuznetsovii</i> strain 17T reveals a physiological similarity with <i>Pelotomaculum thermopropionicum</i> strain SIT.. <i>Standards in Genomic Sciences</i> , 2013, 8, 69-87.	1.5	42
1589	<i>Thermus oshimai</i> JL-2 and <i>T. thermophilus</i> JL-18 genome analysis illuminates pathways for carbon, nitrogen, and sulfur cycling. <i>Standards in Genomic Sciences</i> , 2013, 7, 449-468.	1.5	31
1590	Complete genome sequence of <i>Streptococcus agalactiae</i> strain SA20-06, a fish pathogen associated to meningoencephalitis outbreaks. <i>Standards in Genomic Sciences</i> , 2013, 8, 188-197.	1.5	33
1591	Complete genome sequence of <i>Dehalobacter restrictus</i> PER-K23T. <i>Standards in Genomic Sciences</i> , 2013, 8, 375-388.	1.5	44
1592	Permanent draft genome sequences of the symbiotic nitrogen fixing <i>Ensifer meliloti</i> strains BO21CC and AK58. <i>Standards in Genomic Sciences</i> , 2013, 9, 352-333.	1.5	7
1593	Genome sequence of the phage-gene rich marine <i>Phaeobacter arcticus</i> type strain DSM 23566T. <i>Standards in Genomic Sciences</i> , 2013, 8, 450-464.	1.5	9
1594	Genome sequence of the <i>Leisingera aquimarina</i> type strain (DSM 24565T), a member of the marine <i>Roseobacter</i> clade rich in extrachromosomal elements. <i>Standards in Genomic Sciences</i> , 2013, 8, 389-402.	1.5	17
1595	Genome sequence of <i>Phaeobacter caeruleus</i> type strain (DSM 24564T), a surface-associated member of the marine <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013, 8, 403-419.	1.5	12
1596	Non-contiguous finished genome sequence of plant-growth promoting <i>Serratia proteamaculans</i> S4. <i>Standards in Genomic Sciences</i> , 2013, 8, 441-449.	1.5	26
1597	Genome sequence of the chemoheterotrophic soil bacterium <i>Saccharomonospora cyanea</i> type strain (NA-134T). <i>Standards in Genomic Sciences</i> , 2013, 9, 28-41.	1.5	4
1598	Genome sequence of the moderately thermophilic sulfur-reducing bacterium <i>Thermanaerovibrio velox</i> type strain (Z-9701T) and emended description of the genus <i>Thermanaerovibrio</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 57-70.	1.5	8
1599	Genome sequence of the <i>Litoreibacter arenae</i> type strain (DSM 19593T), a member of the <i>Roseobacter</i> clade isolated from sea sand. <i>Standards in Genomic Sciences</i> , 2013, 9, 117-127.	1.5	8
1600	Genome sequence of <i>Frateuria aurantia</i> type strain (KondÅ´ 67T), a xanthomonade isolated from <i>Lilium auratum</i> Lindl.. <i>Standards in Genomic Sciences</i> , 2013, 9, 83-92.	1.5	3
1601	Complete genome sequence of <i>Granulicella tundricola</i> type strain MP5ACTX9T, an Acidobacteria from tundra soil. <i>Standards in Genomic Sciences</i> , 2013, 9, 449-461.	1.5	17
1602	3DScapeCS: application of three dimensional, parallel, dynamic network visualization in Cytoscape. <i>BMC Bioinformatics</i> , 2013, 14, 322.	1.2	14
1603	Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H1T), reclassification of <i>Spirochaeta caldaria</i> , <i>Spirochaeta stenostrepta</i> , and <i>Spirochaeta zuelzeri</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzeri</i> comb. nov., and emendation of the genus <i>Treponema</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 88-105.	1.5	44
1604	Complete genome sequence of the halophilic bacterium <i>Spirochaeta africana</i> type strain (Z-7692T) from the alkaline Lake Magadi in the East African Rift. <i>Standards in Genomic Sciences</i> , 2013, 8, 165-176.	1.5	3

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1606	Genome sequence of the reddish-pigmented <i>Rubellimicrobium thermophilum</i> type strain (DSM 16684T), a member of the <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013, 8, 480-490.	1.5	6
1607	Genome sequence of <i>Phaeobacter daeponensis</i> type strain (DSM 23529T), a facultatively anaerobic bacterium isolated from marine sediment, and emendation of <i>Phaeobacter daeponensis</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 142-159.	1.5	12
1608	Complete genome sequence of the marine methyl-halide oxidizing <i>Leisingera methylohalidivorans</i> type strain (DSM 14336T), a representative of the <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013, 9, 128-141.	1.5	15
1609	Complete genome sequence of <i>Enterobacter</i> sp. IIT-BT 08: A potential microbial strain for high rate hydrogen production. <i>Standards in Genomic Sciences</i> , 2013, 9, 359-369.	1.5	16
1610	Genome sequence of <i>Phaeobacter inhibens</i> type strain (T5T), a secondary metabolite producing representative of the marine <i>Roseobacter</i> clade, and emendation of the species description of <i>Phaeobacter inhibens</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 334-350.	1.5	26
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1612	Benchmark datasets for the DNA fragment assembly problem. <i>International Journal of Bio-Inspired Computation</i> , 2013, 5, 384.	0.6	19
1613	Answering biological questions by querying k-mer databases. <i>Concurrency Computation Practice and Experience</i> , 2013, 25, 497-509.	1.4	21
1614	Whole-Genome Sequence of a Freshwater Aerobic Anoxygenic Phototroph, <i>Porphyrobacter</i> sp. Strain AAP82, Isolated from the Huguangyan Maar Lake in Southern China. <i>Genome Announcements</i> , 2013, 1, e0007213.	0.8	5
1615	<i>NEUROSPORA</i> AND THE DEAD-END HYPOTHESIS: GENOMIC CONSEQUENCES OF SELFING IN THE MODEL GENUS. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3600-3616.	1.1	30
1616	Genome Sequence of <i>Sporolactobacillus laevolacticus</i> DSM442, an Efficient Polymer-Grade d-Lactate Producer from Agricultural Waste Cottonseed as a Nitrogen Source. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
1617	High-Quality Draft Genome Sequences of <i>Xanthomonas axonopodis</i> pv. <i>glycines</i> Strains CFBP 2526 and CFBP 7119. <i>Genome Announcements</i> , 2013, 1, .	0.8	26
1618	Draft Genome Sequence of <i>Catelicoccus marimammalium</i> , a Novel Species Commonly Found in Gull Feces. <i>Genome Announcements</i> , 2013, 1, .	0.8	9
1619	Draft Genome Sequence of <i>Lactobacillus pobuzihii</i> E100301 T. <i>Genome Announcements</i> , 2013, 1, .	0.8	1
1620	Complete Genome of <i>Enterobacteriaceae</i> Bacterium Strain FGI 57, a Strain Associated with Leaf-Cutter Ant Fungus Gardens. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
1621	Complete Genome Sequence of <i>Campylobacter fetus</i> subsp. <i>venerealis</i> Biovar Intermedius, Isolated from the Prepuce of a Bull. <i>Genome Announcements</i> , 2013, 1, .	0.8	11
1622	Draft Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> Strain YF11. <i>Genome Announcements</i> , 2013, 1, .	0.8	6

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1623	Genome Sequence of <i>Clostridium tyrobutyricum</i> ATCC 25755, a Butyric Acid-Overproducing Strain. <i>Genome Announcements</i> , 2013, 1, .	0.8	27
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1862	Genome Sequences of <i>Streptococcus thermophilus</i> Strains MTH17CL396 and M17PTZA496 from Fontina, an Italian PDO Cheese. <i>Genome Announcements</i> , 2014, 2, .	0.8	17
1863	Complete Genome Sequence of a <i>Brucella ceti</i> ST26 Strain Isolated from a Striped Dolphin (<i>Stenella</i>) Tj ETQq1 1 0.784314 rgBT /Ov	0.8	10
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1882	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> Strain M30, Isolated from a Chronic Pressure Ulcer in an Elderly Patient. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
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1884	Complete Genome Sequences of Three Iberian <i>Brucella suis</i> Biovar 2 Strains Isolated from Wild Boars. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
1885	Draft Genome Sequence of Beneficial Rice Rhizosphere Isolate <i>Pseudomonas aeruginosa</i> PUPa3. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
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1887	Draft Genome Sequences of Respiratory and Urinary Tract Isolates of <i>Acinetobacter baumannii</i> from the Same Patient. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
1888	Draft Genome Sequences of the Alga-Degrading Bacteria <i>Aeromonas hydrophila</i> Strain AD9 and <i>Pseudomonas pseudoalcaligenes</i> Strain AD6. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
1889	Genome Sequences of <i>Cupriavidus metallidurans</i> Strains NA1, NA4, and NE12, Isolated from Space Equipment. <i>Genome Announcements</i> , 2014, 2, .	0.8	23
1890	Genome Sequence of a Newly Isolated Nicotine-Degrading Bacterium, <i>Ochrobactrum</i> sp. SJY1. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
1891	Draft Genome Sequence of <i>Xanthomonas axonopodis</i> pv. <i>allii</i> Strain CFBP 6369. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
1892	Whole-Genome Sequence of <i>Streptococcus macedonicus</i> Strain 33MO, Isolated from the Curd of Morlacco Cheese in the Veneto Region (Italy). <i>Genome Announcements</i> , 2014, 2, .	0.8	8
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1895	Finished Genome of <i>Zymomonas mobilis</i> subsp. <i>mobilis</i> Strain CP4, an Applied Ethanol Producer. <i>Genome Announcements</i> , 2014, 2, .	0.8	13
1896	Draft Genome Assembly of <i>Bordetella bronchiseptica</i> ATCC 10580, a Historical Canine Clinical Isolate. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
1897	Draft Genome Assembly of <i>Delftia acidovorans</i> Type Strain 2167. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
1898	First Genome Sequence of Potential Mycotoxin-Degrading Bacterium <i>Devosia nanyangense</i> DDB001. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
1899	Whole-Genome Sequences of Nine <i>Francisella</i> Isolates. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
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1902	Draft Genome Sequence of <i>Sphingobacterium</i> sp. Strain PM2-P1-29, a Tetracycline-Degrading TetX-Expressing Aerobic Bacterium Isolated from Agricultural Soil. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
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1905	Complete Genome Assembly of <i>Enterococcus faecalis</i> 29212, a Laboratory Reference Strain. <i>Genome Announcements</i> , 2014, 2, .	0.8	13
1906	Complete Genome Assembly of <i>Escherichia coli</i> ATCC 25922, a Serotype O6 Reference Strain. <i>Genome Announcements</i> , 2014, 2, .	0.8	44
1907	Whole-Genome Sequence of <i>Listeria monocytogenes</i> Type Strain 53 XXIII. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
1908	Complete Genome Sequence of <i>Stenotrophomonas maltophilia</i> Type Strain 810-2 (ATCC 13637). <i>Genome Announcements</i> , 2014, 2, .	0.8	16
1909	Complete Genome Assembly of <i>Streptococcus pyogenes</i> ATCC 19615, a Group A α -Hemolytic Reference Strain. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
1910	Draft Genome Sequence of the Bioelectricity-Generating and Dye-Decolorizing Bacterium <i>Proteus hauseri</i> Strain ZMd44. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
1911	Draft Genome Sequence of <i>Cellulosimicrobium</i> sp. Strain MM, Isolated from Arsenic-Rich Microbial Mats of a Himalayan Hot Spring. <i>Genome Announcements</i> , 2014, 2, .	0.8	20

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1912	Genome Assembly of <i>Shigella flexneri</i> ATCC 12022, a Quality Control Reference Strain. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
1913	Whole-Genome <i>Yersinia</i> sp. Assemblies from 10 Diverse Strains. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
1914	Complete Genome Assembly of <i>Staphylococcus epidermidis</i> AmMS 205. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
1915	Draft Genome Sequence of <i>Syntrophorhabdus aromaticivorans</i> Strain UI, a Mesophilic Aromatic Compound-Degrading Syntroph. <i>Genome Announcements</i> , 2014, 2, .	0.8	23
1916	Complete Genome Assembly of <i>Corynebacterium</i> sp. Strain ATCC 6931. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
1917	Complete Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Enteritidis Strain SEJ. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
1918	Genome Sequence of <i>Escherichia coli</i> O157:H7 Strain 2886-75, Associated with the First Reported Case of Human Infection in the United States. <i>Genome Announcements</i> , 2014, 2, .	0.8	25
1919	Whole-Genome Sequences of <i>Streptococcus thermophilus</i> Strains TH1435 and TH1436, Isolated from Raw Goat Milk. <i>Genome Announcements</i> , 2014, 2, .	0.8	28
1920	Draft Genome Sequences of 11 <i>Staphylococcus epidermidis</i> Strains Isolated from Wild Mouse Species. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
1921	Draft Genome Sequence of the Formaldehyde-Resistant Fungus <i>Byssochlamys spectabilis</i> No. 5 (Anamorph <i>Paecilomyces variotii</i> No. 5) (NBRC109023). <i>Genome Announcements</i> , 2014, 2, .	0.8	19
1922	Revised Genome Sequence of <i>Staphylococcus aureus</i> Bacteriophage K. <i>Genome Announcements</i> , 2014, 2, .	0.8	17
1923	Genome Sequences of <i>Lactobacillus</i> sp. Strains wkB8 and wkB10, Members of the Firm-5 Clade, from Honey Bee Guts. <i>Genome Announcements</i> , 2014, 2, .	0.8	30
1924	Genome Sequence of Gammaproteobacterial <i>Pseudohalaea rubra</i> Type Strain DSM 19751, Isolated from Coastal Seawater of the Mediterranean Sea. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
1925	Complete Genome Sequence of <i>Paenibacillus polymyxa</i> CR1, a Plant Growth-Promoting Bacterium Isolated from the Corn Rhizosphere Exhibiting Potential for Biocontrol, Biomass Degradation, and Biofuel Production. <i>Genome Announcements</i> , 2014, 2, .	0.8	22
1926	Complete Genome Sequence of <i>Mycobacterium tuberculosis</i> Strain MtURU-001, Isolated from a Rapidly Progressing Outbreak in Uruguay. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
1927	Draft Genome Sequence of the Nicotinate-Metabolizing Soil Bacterium <i>Bacillus niacini</i> DSM 2923. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
1928	Draft Genome Sequence of <i>Pseudoalteromonas</i> sp. Strain PLSV, an Ulvan-Degrading Bacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
1929	Seeking the source of <i>Pseudomonas aeruginosa</i> infections in a recently opened hospital: an observational study using whole-genome sequencing. <i>BMJ Open</i> , 2014, 4, e006278.	0.8	104

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1931	BLASTAssemb: An approach to construct genetic elements using BLAST. , 2014, , .		0
1932	Effect of Multi-K Contig Merging in de novo DNA Assembly. , 2014, , .		0
1933	Molecular tracing of the emergence, diversification, and transmission of <i>S. aureus</i> sequence type 8 in a New York community. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6738-6743.	3.3	176
1934	Draft Genome Sequence of the <i>Sulfolobales</i> Archaeon AZ1, Obtained through Metagenomic Analysis of a Mexican Hot Spring. <i>Genome Announcements</i> , 2014, 2, .	0.8	19
1935	High-level Relatedness among <i>Mycobacterium abscessus</i> subsp. <i>massiliense</i> Strains from Widely Separated Outbreaks. <i>Emerging Infectious Diseases</i> , 2014, 20, 364-371.	2.0	108
1937	Recent advances in candidate-gene and whole-genome approaches to the discovery of anthelmintic resistance markers and the description of drug/receptor interactions. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2014, 4, 164-184.	1.4	149
1938	Genomic Epidemiology of <i>Vibrio cholerae</i> O1 Associated with Floods, Pakistan, 2010. <i>Emerging Infectious Diseases</i> , 2014, 20, 13-20.	2.0	31
1939	New Alphacoronavirus in <i>Mystacina tuberculata</i> Bats, New Zealand. <i>Emerging Infectious Diseases</i> , 2014, 20, 697-700.	2.0	19
1940	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014, 5, 3956.	5.8	128
1941	A robust SNP barcode for typing <i>Mycobacterium tuberculosis</i> complex strains. <i>Nature Communications</i> , 2014, 5, 4812.	5.8	531
1942	Transcriptomic changes during regeneration of the central nervous system in an echinoderm. <i>BMC Genomics</i> , 2014, 15, 357.	1.2	74
1943	RNA-seq analysis of the influence of anaerobiosis and FNR on <i>Shigella flexneri</i> . <i>BMC Genomics</i> , 2014, 15, 438.	1.2	27
1944	Geneious! Simplified genome skimming methods for phylogenetic systematic studies: A case study in <i>Oreocarya</i> (Boraginaceae). <i>Applications in Plant Sciences</i> , 2014, 2, 1400062.	0.8	74
1945	The mitochondrial and chloroplast genomes of the haptophyte <i>Chrysochromulina tobin</i> contain unique repeat structures and gene profiles. <i>BMC Genomics</i> , 2014, 15, 604.	1.2	30
1946	Genome sequencing and comparative analysis of three <i>Chlamydia pecorum</i> strains associated with different pathogenic outcomes. <i>BMC Genomics</i> , 2014, 15, 23.	1.2	39
1947	Genome sequencing of four <i>Aureobasidium pullulans</i> varieties: biotechnological potential, stress tolerance, and description of new species. <i>BMC Genomics</i> , 2014, 15, 549.	1.2	262
1948	Characterization, sequencing and comparative genomic analysis of vB_AbaM-IME-AB2, a novel lytic bacteriophage that infects multidrug-resistant <i>Acinetobacter baumannii</i> clinical isolates. <i>BMC Microbiology</i> , 2014, 14, 181.	1.3	58

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1949	A multi-step comparison of short-read full plastome sequence assembly methods in grasses. <i>Taxon</i> , 2014, 63, 899-910.	0.4	28
1950	Genome Sequence of <i>Serratia plymuthica</i> RVH1, Isolated from a Raw Vegetable-Processing Line. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
1951	SHEAR: sample heterogeneity estimation and assembly by reference. <i>BMC Genomics</i> , 2014, 15, 84.	1.2	7
1952	Genome Sequence and Annotation of <i>Acremonium chrysogenum</i> , Producer of the β -Lactam Antibiotic Cephalosporin C. <i>Genome Announcements</i> , 2014, 2, .	0.8	35
1953	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
1954	Genome Sequencing of an Extended Series of NDM-Producing <i>Klebsiella pneumoniae</i> Isolates from Neonatal Infections in a Nepali Hospital Characterizes the Extent of Community- versus Hospital-Associated Transmission in an Endemic Setting. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 7347-7357.	1.4	142
1955	Draft Genome Sequences of the <i>Mycobacterium tuberculosis</i> Clinical Strains A2 and A4, Isolated from a Relapse Patient in Taiwan. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
1956	Draft Genome Sequence of the Dye-Decolorizing and Nanowire-Producing Bacterium <i>Shewanella xiamenensis</i> BC01. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
1957	Draft Genome Sequence of Hexachlorohexane (HCH)-Degrading <i>Sphingobium lucknowense</i> Strain F2, Isolated from an HCH Dumpsite. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
1958	Complete Genome Sequence of Equid Herpesvirus 3. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
1959	De Novo Whole-Genome Sequence and Genome Annotation of <i>Lichtheimia ramosa</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	27
1960	Draft Genome Assembly of <i>Pseudomonas aeruginosa</i> Quality Control Reference Strain Boston 41501. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
1961	Draft Genome Sequence of <i>Candidatus Liberibacter asiaticus</i> from California. <i>Genome Announcements</i> , 2014, 2, .	0.8	15
1962	Draft Genome Sequence of the Biofilm-Producing <i>Bacillus subtilis</i> Strain B-1, Isolated from an Oil Field. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
1963	Whole-Genome Sequence of <i>Candidatus Liberibacter solanacearum</i> Strain R1 from California. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
1964	<i>In Vivo</i> mRNA Profiling of Uropathogenic <i>Escherichia coli</i> from Diverse Phylogroups Reveals Common and Group-Specific Gene Expression Profiles. <i>MBio</i> , 2014, 5, e01075-14.	1.8	63
1965	Metagenome-Wide Association of Microbial Determinants of Host Phenotype in <i>Drosophila melanogaster</i> . <i>MBio</i> , 2014, 5, e01631-14.	1.8	112
1966	Emergence of a New Epidemic <i>Neisseria meningitidis</i> Serogroup A Clone in the African Meningitis Belt: High-Resolution Picture of Genomic Changes That Mediate Immune Evasion. <i>MBio</i> , 2014, 5, e01974-14.	1.8	51

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1967	BEETL-fastq: a searchable compressed archive for DNA reads. <i>Bioinformatics</i> , 2014, 30, 2796-2801.	1.8	37
1968	Draft Genome Sequence of Highly Nematicidal <i>Bacillus thuringiensis</i> DB27. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
1969	Genome Sequence of a Hyperthermophilic Archaeon, <i>Thermococcus nautili</i> 30-1, That Produces Viral Vesicles. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
1970	Draft Genome Sequence of <i>Enterobacter cloacae</i> Strain JD6301. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
1971	Comparative Genomic Analysis of Two Multidrug-Resistant Clinical Isolates of ST395 Epidemic Strain of <i>Pseudomonas aeruginosa</i> Obtained 12 Years Apart. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
1972	Draft Genome Sequence of <i>Colletotrichum sublineola</i> , a Destructive Pathogen of Cultivated Sorghum. <i>Genome Announcements</i> , 2014, 2, .	0.8	45
1973	Draft Genome Sequence of Entomopathogenic <i>Serratia liquefaciens</i> Strain FK01. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
1974	Genome Sequence of Thermophilic <i>Bacillus licheniformis</i> Strain 3F-3, an Efficient Pentose-Utilizing Producer of 2,3-Butanediol. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
1975	Complete Genome Sequences of <i>Bacillus subtilis</i> subsp. <i>subtilis</i> Laboratory Strains JH642 (AG174) and AG1839. <i>Genome Announcements</i> , 2014, 2, .	0.8	45
1976	Draft Genome Sequence of the Gammaproteobacterial Strain MOLA455, a Representative of a Ubiquitous Proteorhodopsin-Producing Group in the Ocean. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
1977	Complete Genome Sequence of <i>Methanoregula formicica</i> SMSPT, a Mesophilic Hydrogenotrophic Methanogen Isolated from a Methanogenic Upflow Anaerobic Sludge Blanket Reactor. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
1978	Genome Sequence of <i>Sporolactobacillus terrae</i> DSM 11697, the Type Strain of the Species. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
1979	A Shared Population of Epidemic Methicillin-Resistant <i>Staphylococcus aureus</i> 15 Circulates in Humans and Companion Animals. <i>MBio</i> , 2014, 5, e00985-13.	1.8	95
1980	Draft Genome Sequence of <i>Clostridium scatologenes</i> ATCC 25775, a Chemolithoautotrophic Acetogenic Bacterium Producing 3-Methylindole and 4-Methylphenol. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
1981	Using geometric structures to improve the error correction algorithm of high-throughput sequencing data on MapReduce framework. , 2014, , .		3
1982	Draft Genome Sequences of Two Ulvan-Degrading Isolates, Strains LTR and LOR, That Belong to the <i>Alteromonas</i> Genus. <i>Genome Announcements</i> , 2014, 2, .	0.8	11
1983	Single Clinical Isolates from Acute Uncomplicated Urinary Tract Infections Are Representative of Dominant <i>In Situ</i> Populations. <i>MBio</i> , 2014, 5, e01064-13.	1.8	45
1984	Whole Genome Sequencing of a Methicillin-Resistant <i>Staphylococcus aureus</i> Pseudo-Outbreak in a Professional Football Team. <i>Open Forum Infectious Diseases</i> , 2014, 1, ofu096.	0.4	6

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1985	Draft Genome Sequence of the <i>Gluconobacter oxydans</i> Strain DSM 2003, an Important Biocatalyst for Industrial Use. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
1986	HiPGA: A High Performance Genome Assembler for Short Read Sequence Data. , 2014, , .		2
1987	Draft Genome Assemblies of <i>Proteus mirabilis</i> ATCC 7002 and <i>Proteus vulgaris</i> ATCC 49132. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
1988	Full-Genome Assembly of Reference Strain <i>Providencia stuartii</i> ATCC 33672. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
1989	Draft Genome Sequence of <i>Lactobacillus animalis</i> 381-IL-28. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
1990	Genome Sequence of <i>Marteella</i> sp. Strain AD-3, a Moderately Halophilic Polycyclic Aromatic Hydrocarbon-Degrading Bacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	10
1991	Insights into the Maize Pan-Genome and Pan-Transcriptome. <i>Plant Cell</i> , 2014, 26, 121-135.	3.1	498
1992	Draft Genome Sequences of Eight Enterohepatic <i>Helicobacter</i> Species Isolated from Both Laboratory and Wild Rodents. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
1993	Inter- and Intraspecies Transfer of a <i>Clostridium difficile</i> Conjugative Transposon Conferring Resistance to MLS _B . <i>Microbial Drug Resistance</i> , 2014, 20, 555-560.	0.9	28
1994	The genome of the sparganosis tapeworm <i>Spirometra erinaceieuropaei</i> isolated from the biopsy of a migrating brain lesion. <i>Genome Biology</i> , 2014, 15, 510.	3.8	47
1995	String graph construction using incremental hashing. <i>Bioinformatics</i> , 2014, 30, 3515-3523.	1.8	16
1996	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. <i>Molecular Ecology</i> , 2014, 23, 2442-2451.	2.0	131
1997	Fungal Endopolygalacturonases Are Recognized as Microbe-Associated Molecular Patterns by the Arabidopsis Receptor-Like Protein RESPONSIVENESS TO BOTRYTIS POLYGALACTURONASES1. <i>Plant Physiology</i> , 2014, 164, 352-364.	2.3	249
1998	Genomic insights into the rapid emergence and evolution of MDR in <i>Staphylococcus pseudintermedius</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 997-1007.	1.3	77
1999	Complete mitochondrial genome recovered from the gut metagenome of overwintering monarch butterflies, <i>Danaus plexippus</i> (L.) (Lepidoptera: Nymphalidae, Danainae). <i>Mitochondrial DNA</i> , 2014, 25, 427-428.	0.6	14
2000	Prediction of <i>Staphylococcus aureus</i> Antimicrobial Resistance by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1182-1191.	1.8	303
2001	Genome sequence of the model sulfate reducer <i>Desulfovibrio gigas</i> : a comparative analysis within the <i>Desulfovibrio</i> genus. <i>MicrobiologyOpen</i> , 2014, 3, 513-530.	1.2	37
2002	Comparative single-cell genomics reveals potential ecological niches for the freshwater actinobacteria lineage. <i>ISME Journal</i> , 2014, 8, 2503-2516.	4.4	137

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2003	Identification of a novel type of polyunsaturated fatty acid synthase involved in arachidonic acid biosynthesis. <i>FEBS Letters</i> , 2014, 588, 4032-4036.	1.3	21
2004	Revolutionizing Prokaryotic Systematics Through Next-Generation Sequencing. <i>Methods in Microbiology</i> , 2014, , 75-101.	0.4	7
2005	In vitro selection, via serial passage, of <i>Clostridium difficile</i> mutants with reduced susceptibility to fidaxomicin or vancomycin. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 41-44.	1.3	87
2007	A target enrichment method for gathering phylogenetic information from hundreds of loci: An example from the Compositae. <i>Applications in Plant Sciences</i> , 2014, 2, 1300085.	0.8	178
2008	Multi-Locus Sequence Typing and the Gene-by-Gene Approach to Bacterial Classification and Analysis of Population Variation. <i>Methods in Microbiology</i> , 2014, 41, 201-219.	0.4	2
2009	Detection and mapping of <i>QTL</i> for temperature tolerance and body size in chinook salmon (<i>Oncorhynchus tshawytscha</i>) using genotyping by sequencing. <i>Evolutionary Applications</i> , 2014, 7, 480-492.	1.5	57
2010	Phenotypic and Genotypic Analysis of <i>Clostridium difficile</i> Isolates: a Single-Center Study. <i>Journal of Clinical Microbiology</i> , 2014, 52, 4260-4266.	1.8	35
2011	<i>De novo</i> assembly and characterization of the skeletal muscle and electric organ transcriptomes of the African weakly electric fish <i>Campylomormyrus compressirostris</i> (Mormyridae, Teleostei). <i>Molecular Ecology Resources</i> , 2014, 14, 1222-1230.	2.2	31
2012	High Level Design Approach to Accelerate De Novo Genome Assembly Using FPGAs. , 2014, , .		1
2013	Identification of putative orthologous genes for the phylogenetic reconstruction of temperate woody bamboos (<i>Poaceae</i> : <i>Bambusoideae</i>). <i>Molecular Ecology Resources</i> , 2014, 14, 988-999.	2.2	8
2014	Enabling large-scale next-generation sequence assembly with Blacklight. <i>Concurrency Computation Practice and Experience</i> , 2014, 26, 2157-2166.	1.4	8
2015	Draft genome sequence of <i>Xanthomonas axonopodis</i> pathovar <i>vasculorum</i> NCPPB 900. <i>FEMS Microbiology Letters</i> , 2014, 360, 113-116.	0.7	6
2016	Genome skimming by shotgun sequencing helps resolve the phylogeny of a pantropical tree family. <i>Molecular Ecology Resources</i> , 2014, 14, 966-975.	2.2	102
2017	Inter-viral conflicts that exploit host <i>CRISPR</i> immune systems of <i>Sulfolobus</i> . <i>Molecular Microbiology</i> , 2014, 91, 900-917.	1.2	68
2018	Mapping migration in a songbird using high-resolution genetic markers. <i>Molecular Ecology</i> , 2014, 23, 5726-5739.	2.0	129
2019	Limited genomic consequences of mixed mating in the recently derived sister species pair, <i>Collinsia concolor</i> and <i>Collinsia parryi</i> . <i>Journal of Evolutionary Biology</i> , 2014, 27, 1400-1412.	0.8	9
2020	Comparative Analysis of Two Emerging Rice Seed Bacterial Pathogens. <i>Phytopathology</i> , 2014, 104, 436-444.	1.1	45
2021	Whole plastome sequencing reveals deep plastid divergence and cytonuclear discordance between closely related balsam poplars, <i>Populus balsamifera</i> and <i>Populus atrichocarpa</i> (<i>Salicaceae</i>). <i>New Phytologist</i> , 2014, 204, 693-703.	3.5	105

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2022	Fuelling genetic and metabolic exploration of <i>C₃</i> bioenergy crops through the first reference transcriptome of <i>A. rundo donax</i> . <i>Plant Biotechnology Journal</i> , 2014, 12, 554-567.	4.1	37
2023	Nitrogen as a key regulator of flowering in <i>Fagus crenata</i> : understanding the physiological mechanism of masting by gene expression analysis. <i>Ecology Letters</i> , 2014, 17, 1299-1309.	3.0	86
2025	Detection of Adventitious Agents Using Next-Generation Sequencing. <i>PDA Journal of Pharmaceutical Science and Technology</i> , 2014, 68, 651-660.	0.3	13
2026	Chromera velia, Endosymbioses and the Rhodoplex Hypothesis—Plastid Evolution in Cryptophytes, Alveolates, Stramenopiles, and Haptophytes (CASH Lineages). <i>Genome Biology and Evolution</i> , 2014, 6, 666-684.	1.1	93
2027	Evolutionary genetics and implications of small size and twinning in callitrichine primates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1467-1472.	3.3	66
2028	A type 2 A/C2 plasmid carrying the <i>aacC4</i> apramycin resistance gene and the <i>erm</i> (42) erythromycin resistance gene recovered from two <i>Salmonella enterica</i> serovars. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1021-1025.	1.3	30
2029	Draft genome sequence of <i>Sphingobium</i> sp. strain ba1, resistant to kanamycin and nickel ions. <i>FEMS Microbiology Letters</i> , 2014, 361, 8-9.	0.7	14
2030	Evidence for Soft Selective Sweeps in the Evolution of Pneumococcal Multidrug Resistance and Vaccine Escape. <i>Genome Biology and Evolution</i> , 2014, 6, 1589-1602.	1.1	112
2031	BESST - Efficient scaffolding of large fragmented assemblies. <i>BMC Bioinformatics</i> , 2014, 15, 281.	1.2	157
2032	Comparison of assembly algorithms for improving rate of metatranscriptomic functional annotation. <i>Microbiome</i> , 2014, 2, 39.	4.9	67
2033	Genomes correction and assembling: present methods and tools. <i>Proceedings of SPIE</i> , 2014, , .	0.8	6
2034	Extensive Differences in Gene Expression Between Symbiotic and Aposymbiotic Cnidarians. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 277-295.	0.8	150
2035	Orione, a web-based framework for NGS analysis in microbiology. <i>Bioinformatics</i> , 2014, 30, 1928-1929.	1.8	139
2036	Acetic Acid Bacteria Genomes Reveal Functional Traits for Adaptation to Life in Insect Guts. <i>Genome Biology and Evolution</i> , 2014, 6, 912-920.	1.1	66
2037	A Critical Component of Meiotic Drive in <i>Neurospora</i> Is Located Near a Chromosome Rearrangement. <i>Genetics</i> , 2014, 197, 1165-1174.	1.2	37
2038	Genome Sequence of the Octopine-Type <i>Agrobacterium tumefaciens</i> Strain Ach5. <i>Genome Announcements</i> , 2014, 2, .	0.8	19
2039	Diminishing return for increased Mappability with longer sequencing reads: implications of the k-mer distributions in the human genome. <i>BMC Bioinformatics</i> , 2014, 15, 2.	1.2	39
2040	Detecting epigenetic motifs in low coverage and metagenomics settings. <i>BMC Bioinformatics</i> , 2014, 15, S16.	1.2	7

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2042	Predicting the functional repertoire of an organism from unassembled RNA-seq data. BMC Genomics, 2014, 15, 1003.	1.2	4
2043	Construction of a dairy microbial genome catalog opens new perspectives for the metagenomic analysis of dairy fermented products. BMC Genomics, 2014, 15, 1101.	1.2	64
2044	An improved genome of the model marine alga <i>Ostreococcus tauri</i> unfolds by assessing Illumina de novo assemblies. BMC Genomics, 2014, 15, 1103.	1.2	90
2045	A gene-by-gene population genomics platform: de novo assembly, annotation and genealogical analysis of 108 representative <i>Neisseria meningitidis</i> genomes. BMC Genomics, 2014, 15, 1138.	1.2	164
2046	Core and accessory genome architecture in a group of <i>Pseudomonas aeruginosa</i> Mu-like phages. BMC Genomics, 2014, 15, 1146.	1.2	33
2047	Unusual genome complexity in <i>Lactobacillus salivarius</i> JCM1046. BMC Genomics, 2014, 15, 771.	1.2	44
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2157	Cancer Transcriptome Sequencing and Analysis. , 2014, , 31-47.		1
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2170	Target Capture and Massively Parallel Sequencing of Ultraconserved Elements for Comparative Studies at Shallow Evolutionary Time Scales. <i>Systematic Biology</i> , 2014, 63, 83-95.	2.7	286
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2176	BLESS: Bloom filter-based error correction solution for high-throughput sequencing reads. <i>Bioinformatics</i> , 2014, 30, 1354-1362.	1.8	113
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2571	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015, 3, 62.	4.9	56
2572	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Ai1a-2; a microsymbiont of <i>Andira inermis</i> discovered in Costa Rica. <i>Standards in Genomic Sciences</i> , 2015, 10, 33.	1.5	2
2573	Permanent draft genome sequence of sulfoquinovose-degrading <i>Pseudomonas putida</i> strain SQ1. <i>Standards in Genomic Sciences</i> , 2015, 10, 42.	1.5	6
2574	Genome sequence of the pink-pigmented marine bacterium <i>Loktanella hongkongensis</i> type strain (UST950701-009PT), a representative of the <i>Roseobacter</i> group. <i>Standards in Genomic Sciences</i> , 2015, 10, 51.	1.5	1
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2582	Whole-Genome Sequences of <i>Mycobacterium bovis</i> Strain MbURU-001, Isolated from Fresh Bovine Infected Samples. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
2583	Complete Genome Sequence of <i>Spiroplasma cantharicola</i> CC-1 ^T (DSM 21588), a Bacterium Isolated from Soldier Beetle (<i>Cantharis carolinus</i>). <i>Genome Announcements</i> , 2015, 3, .	0.8	9
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2585	Genome Sequence of <i>Porphyromonas gingivalis</i> Strain AJW4. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
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2588	Genome Sequence of <i>Porphyromonas gingivalis</i> Strain A7436. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
2589	Draft Genome Sequence of <i>Streptomyces ahygroscopicus</i> subsp. <i>wuyiensis</i> CK-15, Isolated from Soil in Fujian Province, China. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
2590	Draft Genome Sequence of <i>Lactobacillus johnsonii</i> Strain 16, Isolated from Mice. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
2591	Draft Genome Sequence of <i>Candidatus Liberibacter asiaticus</i> from <i>Diaphorina citri</i> in Guangdong, China. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
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2596	Complete Genome Sequence of <i>Herbaspirillum hiltneri</i> N3 (DSM 17495), Isolated from Surface-Sterilized Wheat Roots. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
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2598	Next-Generation Whole-Genome Sequencing of Eight Strains of <i>Bacillus cereus</i> , Isolated from Food. <i>Genome Announcements</i> , 2015, 3, .	0.8	13
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2603	Arsenic rich Himalayan hot spring metagenomics reveal genetically novel predator-prey genotypes. <i>Environmental Microbiology Reports</i> , 2015, 7, 812-823.	1.0	47
2604	Characterization of <i>Pseudomonas chlororaphis</i> from <i>Theobroma cacao</i> L. rhizosphere with antagonistic activity against <i>Phytophthora palmivora</i> (Butler). <i>Journal of Applied Microbiology</i> , 2015, 119, 1112-1126.	1.4	29

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2606	Draft Genome Sequence of a Diarrheagenic <i>Morganella morganii</i> Isolate. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
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2743	Genome Sequence of an Efficient Indole-Degrading Bacterium, <i>Cupriavidus</i> sp. Strain IDO, with Potential Polyhydroxyalkanoate Production Applications. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
2744	Draft Genome Sequence of <i>Thauera</i> sp. Strain SWB20, Isolated from a Singapore Wastewater Treatment Facility Using Gel Microdroplets. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
2745	Draft Genome Sequence of <i>Pseudomonas fluorescens</i> SRM1, an Isolate from Spoiled Raw Milk. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
2746	Genome Sequence of <i>Bacillus anthracis</i> Isolated from an Anthrax Burial Site in Pollino National Park, Basilicata Region (Southern Italy). <i>Genome Announcements</i> , 2015, 3, .	0.8	1
2747	Draft Genome Sequences of Three <i>Capnocytophaga canimorsus</i> Strains Isolated from Septic Patients. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
2748	Draft Genome Sequences of Three <i>Capnocytophaga canimorsus</i> Strains Isolated from Healthy Canine Oral Cavities. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
2749	Draft Genome Sequences of Three <i>Capnocytophaga cynodegmi</i> Strains Isolated from the Oral Cavity of Healthy Dogs. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
2750	Draft Genome Sequence of <i>Clostridium tyrobutyricum</i> Strain DIVETGP, Isolated from Cow's Milk for Grana Padano Production. <i>Genome Announcements</i> , 2015, 3, .	0.8	5

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2751	Draft Genome Sequences for Canadian Isolates of <i>Pectobacterium carotovorum</i> subsp. <i>brasiliense</i> with Weak Virulence on Potato. <i>Genome Announcements</i> , 2015, 3, .	0.8	8
2752	Draft Genome Sequence of <i>Clostridium beijerinckii</i> Ne1, Clostridia from an Enrichment Culture Obtained from Australian Subterranean Termite, <i>Nasutitermes exitiosus</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	2
2753	Metagenome Sequencing of a Coastal Marine Microbial Community from Monterey Bay, California. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
2754	High-Quality Draft Genome Sequence of <i>Candida apicola</i> NRRL Y-50540. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
2755	Genome Sequence of <i>Torulaspora delbrueckii</i> NRRL Y-50541, Isolated from Mezcal Fermentation. <i>Genome Announcements</i> , 2015, 3, .	0.8	12
2756	Whole-Genome Sequence of <i>Aquamicrobium</i> sp. Strain SK-2, a Polychlorinated Biphenyl-Utilizing Bacterium Isolated from Sewage Sludge. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
2757	Complete Genome Assemblies for Two Single-Chromosome <i>Vibrio cholerae</i> Isolates, Strains 1154-74 (Serogroup O49) and 10432-62 (Serogroup O27). <i>Genome Announcements</i> , 2015, 3, .	0.8	17
2758	Draft Genomes of Gammaproteobacterial Methanotrophs Isolated from Terrestrial Ecosystems. <i>Genome Announcements</i> , 2015, 3, .	0.8	41
2759	Draft Genome Sequence of Mycoparasite <i>Clonostachys rosea</i> Strain 67-1. <i>Genome Announcements</i> , 2015, 3, .	0.8	34
2760	Genome Sequence of <i>Anoxybacillus geothermalis</i> Strain GSsed3, a Novel Thermophilic Endospore-Forming Species. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
2761	Draft Genome Sequence of <i>Staphylococcus gallinarum</i> DSM 20610 T, Originally Isolated from the Skin of a Chicken. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
2762	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> Strain UV74 Reveals Extensive Variability within Its Genomic Group. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
2763	Complete Genomic Sequence of Issyk-Kul Virus. <i>Genome Announcements</i> , 2015, 3, .	0.8	13
2764	Draft Genome Sequence of a Multidrug-Resistant <i>Acinetobacter baumannii</i> Strain from Chile. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
2765	Genome Sequence of the Soil Bacterium <i>Janthinobacterium</i> sp. KBS0711. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
2766	Draft Genome Sequence of <i>Staphylococcus sciuri</i> subsp. <i>sciuri</i> Strain Z8, Isolated from Human Skin. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
2767	Complete Genome Sequence of <i>Streptococcus pyogenes</i> <i>emm28</i> Clinical Isolate M28PF1, Responsible for a Puerperal Fever. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
2768	Genome Sequence of <i>Klebsiella pneumoniae</i> YZUSK-4, a Bacterium Proposed as a Starter Culture for Fermented Meat Products. <i>Genome Announcements</i> , 2015, 3, .	0.8	0

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2769	Genome Sequence of <i>Geobacillus</i> sp. Strain ZGt-1, an Antibacterial Peptide-Producing Bacterium from Hot Springs in Jordan. <i>Genome Announcements</i> , 2015, 3, .	0.8	8
2770	Draft Genome Sequence of <i>Veillonella tobetsuensis</i> ATCC BAA-2400 T Isolated from Human Tongue Biofilm. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
2771	<i>De Novo</i> Whole-Genome Sequence and Annotation of a <i>Leishmania</i> Strain Isolated from a Case of Post-Kala-Azar Dermal Leishmaniasis. <i>Genome Announcements</i> , 2015, 3, .	0.8	13
2772	Draft Genome Sequence of <i>Saccharomyces cerevisiae</i> Strain NCIM3186 Used in the Production of Bioethanol from Sweet Sorghum. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
2773	Draft Genome Sequences of <i>Ralstonia solanacearum</i> Race 3 Biovar 2 Strains with Different Temperature Adaptations. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
2774	Draft Genome Sequence of <i>Lactobacillus</i> sp. Strain TCF032-E4, Isolated from Fermented Radish. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
2775	Complete Genome Sequence of <i>Enterobacter cloacae</i> UW5, a Rhizobacterium Capable of High Levels of Indole-3-Acetic Acid Production. <i>Genome Announcements</i> , 2015, 3, .	0.8	15
2776	First Complete Genome Sequence of a <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Derby Strain Associated with Pork in France. <i>Genome Announcements</i> , 2015, 3, .	0.8	13
2777	Draft Genome Sequence of <i>Frankia</i> sp. Strain DC12, an Atypical, Noninfective, Ineffective Isolate from <i>Datisca cannabina</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	23
2778	Draft Genome Sequence of <i>Pseudomonas</i> sp. Strain LFM046, a Producer of Medium-Chain-Length Polyhydroxyalkanoate. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
2779	Genome Sequence of <i>Bacillus alveayuensis</i> Strain 24KAM51, a Halotolerant Thermophile Isolated from a Hydrothermal Vent. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
2780	Genome Sequence of <i>Bacillus anthracis</i> Larissa, Associated with a Case of Cutaneous Anthrax in Greece. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
2781	Whole-Genome Sequences of 80 Environmental and Clinical Isolates of <i>Burkholderia pseudomallei</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	38
2782	Complete Genome Sequences of <i>Citrobacter braakii</i> Strains GTA-CB01 and GTA-CB04, Isolated from Ground Beef. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
2783	Whole-Genome Sequence of <i>Mycobacterium bovis</i> BCG-1 (Russia). <i>Genome Announcements</i> , 2015, 3, .	0.8	7
2784	Draft Genome Sequence of <i>Sulfurospirillum</i> sp. Strain MES, Reconstructed from the Metagenome of a Microbial Electrosynthesis System. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
2785	Draft Genome Sequence of High-Temperature-Adapted <i>Protochlamydia</i> sp. HS-T3, an Amoebal Endosymbiotic Bacterium Found in <i>Acanthamoeba</i> Isolated from a Hot Spring in Japan. <i>Genome Announcements</i> , 2015, 3, .	0.8	13
2786	Genome Sequence of <i>Borrelia chilensis</i> VA1, a South American Member of the Lyme Borreliosis Group. <i>Genome Announcements</i> , 2015, 3, .	0.8	6

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2787	Draft Genome Sequence of the <i>Xylella fastidiosa</i> CoDiRO Strain. <i>Genome Announcements</i> , 2015, 3, .	0.8	51
2788	Draft Genome Sequences of Five Spore-Forming Food Isolates of <i>Bacillus pumilus</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	3
2789	Draft Genome Sequence of <i>Methyloferula stellata</i> AR4, an Obligate Methanotroph Possessing Only a Soluble Methane Monooxygenase. <i>Genome Announcements</i> , 2015, 3, .	0.8	28
2790	Genome Sequence and Annotation of a Human Infection Isolate of <i>Escherichia coli</i> O26:H11 Involved in a Raw Milk Cheese Outbreak. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
2791	Draft Genome Sequence of a Cellulase-Producing Psychrotrophic <i>Paenibacillus</i> Strain, IHB B 3415, Isolated from the Cold Environment of the Western Himalayas, India. <i>Genome Announcements</i> , 2015, 3, .	0.8	8
2792	Rapid and Easy <i>In Silico</i> Serotyping of <i>Escherichia coli</i> Isolates by Use of Whole-Genome Sequencing Data. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2410-2426.	1.8	775
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2794	Scribe: Ultra-Accurate Error-Correction of Pooled Sequenced Reads. <i>Lecture Notes in Computer Science</i> , 2015, , 162-174.	1.0	1
2795	Applications of species accumulation curves in large-scale biological data analysis. <i>Quantitative Biology</i> , 2015, 3, 135-144.	0.3	48
2796	Isolation and Characterization of Lytic Phage vB_EcoM_JS09 against Clinically Isolated Antibiotic-Resistant Avian Pathogenic <i>Escherichia coli</i> and Enterotoxigenic <i>Escherichia coli</i> . <i>Intervirology</i> , 2015, 58, 218-231.	1.2	20
2797	Elucidating the role and use of bioinformatics software in life science research. , 2015, , .		8
2798	Draft Genome Sequence of <i>Bacillus amyloliquefaciens</i> XK-4-1, a Plant Growth-Promoting Endophyte with Antifungal Activity. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
2799	Genome Sequence of <i>Bradyrhizobium pachyrhizi</i> Strain PAC48 T , a Nitrogen-Fixing Symbiont of <i>Pachyrhizus erosus</i> (L.) Urb. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
2800	Draft genome sequences of <i>Ceratocystis eucalypticola</i> , <i>Chrysosporthe cubensis</i> , <i>C. deuterocubensis</i> , <i>Davidsoniella virescens</i> , <i>Fusarium temperatum</i> , <i>Graphilbum fragrans</i> , <i>Penicillium nordicum</i> , and <i>Thielaviopsis musarum</i> . <i>IMA Fungus</i> , 2015, 6, 493-506.	1.7	57
2801	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
2802	Genetic and epigenetic variation among inbred mouse littermates: identification of inter-individual differentially methylated regions. <i>Epigenetics and Chromatin</i> , 2015, 8, 54.	1.8	60
2803	Short read error correction using an FM-index. , 2015, , .		5
2804	Partial genome sequence of the haloalkaliphilic soda lake bacterium <i>Thioalkalivibrio thiocyanoxidans</i> ARh 2T. <i>Standards in Genomic Sciences</i> , 2015, 10, 85.	1.5	13

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2809	Utilization of Diverse Sequencing Panels for Future Plant Breeding. , 2015, , 539-561.		0
2810	Next-Generation Sequencing (NGS) Tools and Impact in Plant Breeding. , 2015, , 563-612.		8
2811	Draft Genome Sequence of <i>Bacillus</i> Species from the Rhizosphere of the Desert Plant <i>Rhazya stricta</i> . Genome Announcements, 2015, 3, .	0.8	7
2812	High-quality permanent draft genome sequence of Ensifer meliloti strain 4H41, an effective salt- and drought-tolerant microsymbiont of Phaseolus vulgaris. Standards in Genomic Sciences, 2015, 10, 34.	1.5	4
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2817	A new extant family of primitive moths from <i>Kangaroo Island</i> , <i>Australia</i> , and its significance for understanding early <i>Lepidoptera</i> evolution. Systematic Entomology, 2015, 40, 5-16.	1.7	32
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2819	Genetic Variability of <i>Grapevine Pinot gris virus</i> and Its Association with Grapevine Leaf Mottling and Deformation. Phytopathology, 2015, 105, 555-563.	1.1	79
2820	Resolving phylogenetic relationships of the recently radiated carnivorous plant genus <i>Sarracenia</i> using target enrichment. Molecular Phylogenetics and Evolution, 2015, 85, 76-87.	1.2	108
2821	Dissemination of <i>bla</i> _{OXA-23} in <i>Acinetobacter</i> spp. in China: Main Roles of Conjugative Plasmid pAZJ221 and Transposon Tn ₂₀₀₉ . Antimicrobial Agents and Chemotherapy, 2015, 59, 1998-2005.	1.4	44
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2825	Reference-free detection of isolated SNPs. <i>Nucleic Acids Research</i> , 2015, 43, e11-e11.	6.5	75
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2827	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
2828	Dynamics of MDR <i>Enterobacter cloacae</i> outbreaks in a neonatal unit in Nepal: insights using wider sampling frames and next-generation sequencing. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1008-1015.	1.3	45
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2831	Complete Genome Sequence of <i>Geobacillus</i> strain Y4.1MC1, a Novel CO-Utilizing <i>Geobacillus thermoglucosidasius</i> Strain Isolated from Bath Hot Spring in Yellowstone National Park. <i>Bioenergy Research</i> , 2015, 8, 1039-1045.	2.2	19
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2857	Prevalence of Type VI Secretion System in Spanish <i>Campylobacter jejuni</i> Isolates. <i>Zoonoses and Public Health</i> , 2015, 62, 497-500.	0.9	29
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2876	Implications of Genome-Based Discrimination between <i>Clostridium botulinum</i> Group I and <i>Clostridium sporogenes</i> Strains for Bacterial Taxonomy. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5420-5429.	1.4	57

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2878	Characterization of Hepatitis C Virus Recombination in Cameroon by Use of Nonspecific Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3155-3164.	1.8	28
2879	High-Quality Draft Genome Sequence of the <i>Xanthomonas translucens</i> pv. <i>cerealis</i> Pathotype Strain CFBP 2541. <i>Genome Announcements</i> , 2015, 3, .	0.8	24
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2938	Characterization of Pre-Antibiotic Era <i>Klebsiella pneumoniae</i> Isolates with Respect to Antibiotic/Disinfectant Susceptibility and Virulence in <i>Galleria mellonella</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 3966-3972.	1.4	52
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2941	Genome Sequences of the Lignin-Degrading <i>Pseudomonas</i> sp. Strain YS-1p and <i>Rhizobium</i> sp. Strain YS-1r Isolated from Decaying Wood. <i>Genome Announcements</i> , 2015, 3, .	0.8	20
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3006	Whole-Genome Sequence of <i>Candidatus Liberibacter asiaticus</i> from a Huanglongbing-Affected Citrus Tree in Central Florida. <i>Genome Announcements</i> , 2015, 3, .	0.8	22
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3713	Draft Genome Sequence of <i>Tepidiphilus thermophilus</i> Strain JHK30 ^T (JCM 19170) Tj ETQq1 1 0,784314 rgBT /Over	0,8	4

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3714	Detecting horizontal gene transfer by mapping sequencing reads across species boundaries. <i>Bioinformatics</i> , 2016, 32, i595-i604.	1.8	23
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3717	Draft Genome Sequence of a Multidrug-Resistant <i>Klebsiella pneumoniae</i> Carbapenemase-Producing <i>Acinetobacter baumannii</i> Sequence Type 2 Isolate from Puerto Rico. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
3718	Draft Genome Sequence of Salmonella enterica subsp. enterica Serovar Lille Strain CRJJGF_000101 (Phylum Gammaproteobacteria). <i>Genome Announcements</i> , 2016, 4, .	0.8	4
3719	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Widemarsh Strain CRJJGF_00058 (Phylum <i>Gammaproteobacteria</i>). <i>Genome Announcements</i> , 2016, 4, .	0.8	4
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3726	Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing β -proteobacterium <i>Thioalkalimicrobium cyclicum</i> type strain ALM 1 (DSM 14477T). <i>Standards in Genomic Sciences</i> , 2016, 11, 38.	1.5	6
3727	Comparing polysaccharide decomposition between the type strains <i>Gramella echinicola</i> KMM 6050T (DSM 19838T) and <i>Gramella portivictoriae</i> UST040801-001T (DSM 23547T), and emended description of <i>Gramella echinicola</i> Nedashkovskaya et al. 2005 emend. Shahina et al. 2014 and <i>Gramella portivictoriae</i> Lau et al. 2005. <i>Standards in Genomic Sciences</i> , 2016, 11, 37.	1.5	27
3728	Complete genome sequence of <i>Leuconostoc gelidum</i> subsp. <i>gasicomitatum</i> KG16-1, isolated from vacuum-packaged vegetable sausages. <i>Standards in Genomic Sciences</i> , 2016, 11, 40.	1.5	28
3729	Draft Genome Sequence of <i>Anoxybacillus suryakundensis</i> Strain JS1 ^T (DSM 27374) Tj ETQq1 1_0,784314 rgBT /Qve	0.8	5
3730	Genomic Characterization of a Pattern D <i>Streptococcus pyogenes</i> <i>emm53</i> Isolate Reveals a Genetic Rationale for Invasive Skin Tropicity. <i>Journal of Bacteriology</i> , 2016, 198, 1712-1724.	1.0	22
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3738	Genome Sequence of <i>Salegentibacter salarius</i> KCTC 12974, Isolated from a Marine Solar Saltern of the Yellow Sea in South Korea. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
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3747	The complete chloroplast genome of <i>Gracilariopsis lemaneiformis</i> (Rhodophyta) gives new insight into the evolution of family Gracilariaceae. <i>Journal of Phycology</i> , 2016, 52, 441-450.	1.0	43
3748	First Genome Sequence of a Mexican Multidrug-Resistant <i>Acinetobacter baumannii</i> Isolate. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
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3770	High-quality draft genome sequence of <i>Flavobacterium suncheonense</i> GH29-5T (DSM 17707T) isolated from greenhouse soil in South Korea, and emended description of <i>Flavobacterium suncheonense</i> GH29-5T. <i>Standards in Genomic Sciences</i> , 2016, 11, 42.	1.5	3
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4685	Characterization of the complete chloroplast genome of <i>Allium prattii</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 153-154.	0.2	8
4686	Fitness Tradeoffs of Antibiotic Resistance in Extraintestinal Pathogenic <i>Escherichia coli</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 667-679.	1.1	49
4687	Small RNA-Omics for Virome Reconstruction and Antiviral Defense Characterization in Mixed Infections of Cultivated <i>Solanum</i> Plants. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 707-723.	1.4	23
4688	Whole genome duplication and transposable element proliferation drive genome expansion in <i>Corydoradinae</i> catfishes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20172732.	1.2	32

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4690	Genome Sequence of <i>Serratia marcescens</i> subsp. <i>sakuensis</i> Strain K27, a Marine Bacterium Isolated from Sponge (<i>Haliclona amboinensis</i>). <i>Genome Announcements</i> , 2018, 6, .	0.8	6
4691	Phylogenomic reclassification of the world's most venomous spiders (Mygalomorphae, Atracinae), with implications for venom evolution. <i>Scientific Reports</i> , 2018, 8, 1636.	1.6	53
4692	Comparative Genomics of <i>Tenacibaculum dicentrarchi</i> and <i>Tenacibaculum finnmarkense</i> Highlights Intricate Evolution of Fish-Pathogenic Species. <i>Genome Biology and Evolution</i> , 2018, 10, 452-457.	1.1	36
4693	Genomic and functional characterisation of two <i>Enterococcus</i> strains isolated from Cotija cheese and their potential role in ripening. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2251-2267.	1.7	14
4694	Nuclear, Chloroplast, and Mitochondrial Genome Sequences of the Prospective Microalgal Biofuel Strain <i>Picochlorum soloecismus</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	22
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4696	Bacteriophages of the Urinary Microbiome. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	70
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4698	Distribution and Evolution of Peroxisomes in Alveolates (Apicomplexa, Dinoflagellates, Ciliates). <i>Genome Biology and Evolution</i> , 2018, 10, 1-13.	1.1	21
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4701	Genomic and transcriptomic analysis of the Asian honeybee <i>Apis cerana</i> provides novel insights into honeybee biology. <i>Scientific Reports</i> , 2018, 8, 822.	1.6	68
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4703	Genome sequence and detection of peach rosette mosaic virus. <i>Journal of Virological Methods</i> , 2018, 254, 8-12.	1.0	8
4704	Transcriptome sequence analysis and mining of SSRs in Jhar Ber (<i>Ziziphus nummularia</i> (Burm.f.) Wight) Tj ETQq1 1 0,784314,rgBT /Over 1,6 19	1.6	19
4705	Genomic comparison between members of the Salinibacteraceae family, and description of a new species of <i>Salinibacter</i> (<i>Salinibacter altiplanensis</i> sp. nov.) isolated from high altitude hypersaline environments of the Argentinian Altiplano. <i>Systematic and Applied Microbiology</i> , 2018, 41, 198-212.	1.2	29
4706	Total duplication of the small single copy region in the angiosperm plastome: Rearrangement and inverted repeat instability in <i>Asarum</i> . <i>American Journal of Botany</i> , 2018, 105, 71-84.	0.8	53

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4708	The sea lamprey germline genome provides insights into programmed genome rearrangement and vertebrate evolution. <i>Nature Genetics</i> , 2018, 50, 270-277.	9.4	262
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4710	The complete chloroplast genome sequence of an endangered plant <i>Torreya jackii</i> (Pinales, Taxaceae). <i>Conservation Genetics Resources</i> , 2018, 10, 487-489.	0.4	2
4711	Virome analysis of lily plants reveals a new potyvirus. <i>Archives of Virology</i> , 2018, 163, 1079-1082.	0.9	20
4712	Quantitative species-level ecology of reef fish larvae via metabarcoding. <i>Nature Ecology and Evolution</i> , 2018, 2, 306-316.	3.4	56
4713	Assembly, Annotation, and Comparative Genomics in PATRIC, the All Bacterial Bioinformatics Resource Center. <i>Methods in Molecular Biology</i> , 2018, 1704, 79-101.	0.4	73
4714	Prevalence and persistence of <i>Listeria monocytogenes</i> in premises and products of small food business operators in Northern Ireland. <i>Food Control</i> , 2018, 87, 70-78.	2.8	14
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4721	In vitro and in silico characterisation of <i>Lactobacillus paraplantarum</i> D2-1, a starter culture for soymilk fermentation. <i>International Journal of Food Sciences and Nutrition</i> , 2018, 69, 857-869.	1.3	8
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4724	Analysis of <i>Vibrio</i> seventh pandemic island II and novel genomic islands in relation to attachment sequences among a wide variety of <i>Vibrio cholerae</i> strains. <i>Microbiology and Immunology</i> , 2018, 62, 150-157.	0.7	6

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4742	Draft Genome Sequences of Six Multidrug-Resistant Clinical Strains of <i>Acinetobacter baumannii</i> , Isolated at Two Major Hospitals in Kuwait. <i>Genome Announcements</i> , 2018, 6, .	0.8	5

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4745	Single-cell metagenomics: challenges and applications. <i>Protein and Cell</i> , 2018, 9, 501-510.	4.8	70
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4750	Diversity of Organellar Genomes in Non-photosynthetic Diatoms. <i>Protist</i> , 2018, 169, 351-361.	0.6	36
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4759	A new hybrid approach for MHC genotyping: high-throughput NGS and long read MinION nanopore sequencing, with application to the non-model vertebrate Alpine chamois (<i>Rupicapra rupicapra</i>). <i>Heredity</i> , 2018, 121, 293-303.	1.2	25
4760	Draft Genome Sequence of <i>Marinomonas fungiae</i> Strain AN44 T (JCM 18476 T), Isolated from the Coral <i>Fungia echinata</i> from the Andaman Sea. <i>Genome Announcements</i> , 2018, 6, .	0.8	1

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4762	Draft Genome Sequence of an Isolate of <i>Colletotrichum fructicola</i> , a Causal Agent of Mango Anthracnose. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
4763	Noncontiguous finished genome sequence and description of <i>Bartonella mastomydis</i> sp. nov.. <i>New Microbes and New Infections</i> , 2018, 25, 60-70.	0.8	18
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4765	Genome Sequence of Coxiella-Like Endosymbiont Strain CLE-RmD, a Bacterial Agent in the Cattle Tick (<i>Rhipicephalus microplus</i>) Deutsch Strain. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
4766	Complete chloroplast genome of the tree fern <i>Alsophila podophylla</i> (Cyatheaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 48-49.	0.2	7
4767	Repeat-aware evaluation of scaffolding tools. <i>Bioinformatics</i> , 2018, 34, 2530-2537.	1.8	6
4768	Draft Genome Sequence of <i>Zhihengliuella</i> sp. Strain ISTPL4, a Psychrotolerant and Halotolerant Bacterium Isolated from Pangong Lake, India. <i>Genome Announcements</i> , 2018, 6, .	0.8	11
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4771	A Single-Nucleotide Insertion in a Drug Transporter Gene Induces a Thermotolerance Phenotype in <i>Gluconobacter frateurii</i> by Increasing the NADPH/NADP + Ratio via Metabolic Change. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	15
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4773	Molecular and biological characterization of a novel mild strain of citrus tristeza virus in California. <i>Archives of Virology</i> , 2018, 163, 1795-1804.	0.9	31
4774	The first complete chloroplast genome of a traditional Chinese medicinal herb <i>Odontosoria chinensis</i> (Lindsaeaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 292-293.	0.2	3
4775	Genome variation in nine co-occurring toxic <i>Cylindrospermopsis raciborskii</i> strains. <i>Harmful Algae</i> , 2018, 73, 157-166.	2.2	35
4776	Draft Genome Sequences of 11 <i>Salmonella enterica</i> Serovar Typhimurium Strains Isolated from Human Systemic and Nonsystemic Sites in Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
4777	IDP-denovo: <i>de novo</i> transcriptome assembly and isoform annotation by hybrid sequencing. <i>Bioinformatics</i> , 2018, 34, 2168-2176.	1.8	41
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4780	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	9.4	414
4781	<i>Haemophilus influenzae</i> genome evolution during persistence in the human airways in chronic obstructive pulmonary disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3256-E3265.	3.3	57
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4783	Evolution of the mating types and mating strategies in prominent genera in the Botryosphaeriaceae. <i>Fungal Genetics and Biology</i> , 2018, 114, 24-33.	0.9	17
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4792	Novel Gene Encoding 5-Aminosalicylate 1,2-Dioxygenase from <i>Comamonas</i> sp. Strain QT12 and Catalytic Properties of the Purified Enzyme. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	6
4793	Squeakr: an exact and approximate <i>k</i> -mer counting system. <i>Bioinformatics</i> , 2018, 34, 568-575.	1.8	60
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4795	The Draft Genome Sequence of <i>Clostridium beijerinckii</i> NJP7, a Unique Bacterium Capable of Producing Isopropanol-Butanol from Hemicellulose Through Consolidated Bioprocessing. <i>Current Microbiology</i> , 2018, 75, 305-308.	1.0	13
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4799	Large-scale cultivation of the bumblebee gut microbiota reveals an underestimated bacterial species diversity capable of pathogen inhibition. <i>Environmental Microbiology</i> , 2018, 20, 214-227.	1.8	40
4800	The Microevolution and Epidemiology of <i>Staphylococcus aureus</i> Colonization during Atopic Eczema Disease Flare. <i>Journal of Investigative Dermatology</i> , 2018, 138, 336-343.	0.3	46
4801	<i>Galleria mellonella</i> as an infection model to investigate virulence of <i>Vibrio parahaemolyticus</i> . <i>Virulence</i> , 2018, 9, 197-207.	1.8	43
4802	<i>Coniella lustricola</i> , a new species from submerged detritus. <i>Mycological Progress</i> , 2018, 17, 191-203.	0.5	8
4803	The completed chloroplast genome of <i>Ostrya trichocarpa</i> . <i>Conservation Genetics Resources</i> , 2018, 10, 579-581.	0.4	8
4804	Characterisation of <i>Lactococcus lactis</i> isolates from herbs, fruits and vegetables for use as biopreservatives against <i>Listeria monocytogenes</i> in cheese. <i>Food Control</i> , 2018, 85, 472-483.	2.8	41
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4807	The complete genome of the oil emulsifying strain <i>Thalassolituus oleivorans</i> K-188 from the Barents Sea. <i>Marine Genomics</i> , 2018, 37, 18-20.	0.4	4
4808	ReMILO: reference assisted misassembly detection algorithm using short and long reads. <i>Bioinformatics</i> , 2018, 34, 24-32.	1.8	59
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4816	<i>Grapevine red blotch virus</i>: Absence in Swiss Vineyards and Analysis of Potential Detrimental Effect on Viticultural Performance. <i>Plant Disease</i> , 2018, 102, 651-655.	0.7	27
4817	A Type 3 Prophage of <i>Candidatus</i> <i>Liberibacter asiaticus</i> ™ Carrying a Restriction-Modification System. <i>Phytopathology</i> , 2018, 108, 454-461.	1.1	46
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4820	Development and characterization of 24 microsatellite markers in <i>Primula tosaensis</i> , an endangered primrose, using MiSeq. <i>Plant Species Biology</i> , 2018, 33, 77-80.	0.6	1
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4826	Comparative Genomics of Myxobacterial Chemosensory Systems. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	18
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4831	Draft genome sequence of <i>Chryseobacterium limigenitum</i> SUR2 T (LMG 28734 T) isolated from dehydrated sludge. <i>Brazilian Journal of Microbiology</i> , 2018, 49, 5-6.	0.8	0
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4837	Draft Genome Sequences of the Type Strains of Three <i>Clavibacter</i> Subspecies and Atypical Peach-Colored Strains Isolated from Tomato. Microbiology Resource Announcements, 2018, 7, .	0.3	13
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4856	Performance analysis of parallel de novo genome assembly in shared memory system. <i>IOP Conference Series: Earth and Environmental Science</i> , 2018, 187, 012032.	0.2	0
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4878	Origin and Consequences of Chromosomal Inversions in the <i>virilis</i> Group of <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 3152-3166.	1.1	22
4879	Approaches to variant discovery for conifer transcriptome sequencing. <i>PLoS ONE</i> , 2018, 13, e0205835.	1.1	20
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4881	ImproveAssembly - Tool for identifying new gene products and improving genome assembly. <i>PLoS ONE</i> , 2018, 13, e0206000.	1.1	0
4882	Whole-genome characterization of <i>Shewanella algae</i> strain SYT3 isolated from seawater reveals insight into hemolysis. <i>Future Microbiology</i> , 2018, 13, 1709-1717.	1.0	9
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4884	Whole Genome Characterization of Orthopoxvirus (OPV) Abatino, a Zoonotic Virus Representing a Putative Novel Clade of Old World Orthopoxviruses. <i>Viruses</i> , 2018, 10, 546.	1.5	17
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4900	Which methods are appropriate for the detection of <i>Staphylococcus argenteus</i> and is it worthwhile to distinguish <i>S. argenteus</i> from <i>S. aureus</i> ? <i>Infection and Drug Resistance</i> , 2018, Volume 11, 2335-2344.	1.1	17
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4902	Evolutionary Evidence of Algal Polysaccharide Degradation Acquisition by <i>Pseudoalteromonas carrageenovora</i> 9T to Adapt to Macroalgal Niches. <i>Frontiers in Microbiology</i> , 2018, 9, 2740.	1.5	54
4903	Microsatellite markers for <i>Corybas</i> (Orchidaceae) species in New Zealand. <i>Applications in Plant Sciences</i> , 2018, 6, e01192.	0.8	1
4904	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018, 9, 5094.	5.8	98

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4907	DNA Sequence Assembly and Annotation of Genes. <i>Learning Materials in Biosciences</i> , 2018, , 9-24.	0.2	0
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4914	Intergeneric Relationships within the Early-Diverging Angiosperm Family Nymphaeaceae Based on Chloroplast Phylogenomics. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3780.	1.8	11
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4916	Draft Genome Sequence and Brief History of <i>Rhodovulum</i> sp. Strain BSW8. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
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4918	Transcriptomic analysis of crustacean neuropeptide signaling during the moult cycle in the green shore crab, <i>Carcinus maenas</i> . <i>BMC Genomics</i> , 2018, 19, 711.	1.2	58
4919	SKESA: strategic k-mer extension for scrupulous assemblies. <i>Genome Biology</i> , 2018, 19, 153.	3.8	375
4920	Metagenome Assembly and Contig Assignment. <i>Methods in Molecular Biology</i> , 2018, 1849, 179-192.	0.4	0
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4922	De Novo Transcriptome Assembly of <i>Cucurbita Pepo</i> L. Leaf Tissue Infested by <i>Aphis Gossypii</i> . <i>Data</i> , 2018, 3, 36.	1.2	8

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4925	Cross-correlation based detection of contigs overlaps. , 2018, , .		1
4926	Draft Genome Sequence of <i>Prochlorococcus marinus</i> Strain XMU1401, Isolated from the Western Tropical North Pacific Ocean. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
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4933	Draft Genome Sequences of Isolates from Sediments of the River Elbe That Are Highly Tolerant to Diclofenac. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
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4936	Subsampled Assemblies and Hybrid Nucleotide Composition/Differential Coverage Binning for Genome-Resolved Metagenomics. <i>Methods in Molecular Biology</i> , 2018, 1849, 215-225.	0.4	2
4937	The linear mitochondrial genome of the quarantine chytrid <i>Synchytrium endobioticum</i> ; insights into the evolution and recent history of an obligate biotrophic plant pathogen. <i>BMC Evolutionary Biology</i> , 2018, 18, 136.	3.2	30
4938	Genomic characterization reveals significant divergence within <i>Chlorella sorokiniana</i> (Chlorellales,) Tj ETQq1 1 0.784314 rgBT ₂₇ /Overlook	2.4	27
4939	Identification of putative flowering genes and transcription factors from flower de novo transcriptome dataset of tuberose (<i>Polianthes tuberosa</i> L.). <i>Data in Brief</i> , 2018, 20, 2027-2035.	0.5	1
4940	Whole-genome analysis and description of an outbreak due to carbapenem-resistant <i>Ochrobactrum anthropi</i> causing pseudo-bacteraemias. <i>New Microbes and New Infections</i> , 2018, 26, 100-106.	0.8	3

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4943	Species recognition in social amoebae. <i>Journal of Biosciences</i> , 2018, 43, 1025-1036.	0.5	2
4944	An improved approach for reconstructing consensus repeats from short sequence reads. <i>BMC Genomics</i> , 2018, 19, 566.	1.2	1
4945	A Negative-Stranded RNA Virus Infecting Citrus Trees: The Second Member of a New Genus Within the Order Bunyavirales. <i>Frontiers in Microbiology</i> , 2018, 9, 2340.	1.5	53
4946	Characterization of the complete chloroplast genome of <i>Lonicera macranthoides</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1000-1001.	0.2	7
4947	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 2018, 3, 33.	0.9	42
4948	Phylogenomic evidence for ancient recombination between plastid genomes of the <i>Cupressus-Juniperus-Xanthocyparis</i> complex (Cupressaceae). <i>BMC Evolutionary Biology</i> , 2018, 18, 137.	3.2	17
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4950	Comparative Genomics of <i>Wolbachia</i> Cardinium Dual Endosymbiosis in a Plant-Parasitic Nematode. <i>Frontiers in Microbiology</i> , 2018, 9, 2482.	1.5	36
4951	A benchmark study of k-mer counting methods for high-throughput sequencing. <i>GigaScience</i> , 2018, 7, .	3.3	53
4952	The complete chloroplast genome of monotypic fern, <i>Mesopteris tonkinensis</i> (Thelypteridaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 868-869.	0.2	0
4953	Draft genome sequences of <i>Cylindrospermopsis raciborskii</i> strains CS-508 and MVCC14, isolated from freshwater bloom events in Australia and Uruguay. <i>Standards in Genomic Sciences</i> , 2018, 13, 26.	1.5	4
4954	Characterization and Phylogenetic Analysis of Chloroplast and Mitochondria Genomes from the Antarctic Polytrichaceae Species <i>Polytrichum juniperinum</i> and <i>Polytrichum strictum</i> . <i>Diversity</i> , 2018, 10, 89.	0.7	2
4955	Terrestrial species adapted to sea dispersal: Differences in propagule dispersal of two Caribbean mangroves. <i>Molecular Ecology</i> , 2018, 27, 4612-4626.	2.0	25
4956	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
4957	Genome sequencing and assessment of plant growth-promoting properties of a <i>Serratia marcescens</i> strain isolated from vermicompost. <i>BMC Genomics</i> , 2018, 19, 750.	1.2	58
4958	The complete chloroplast genome sequence of <i>Histiopteris incisa</i> (Dennstaedtiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 772-773.	0.2	1

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4960	The complete chloroplast genome sequence of medicinal fern <i>Polypodiodes niponica</i> (Polypodiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 770-771.	0.2	1
4961	Global genetic diversity of var2csa in <i>Plasmodium falciparum</i> with implications for malaria in pregnancy and vaccine development. <i>Scientific Reports</i> , 2018, 8, 15429.	1.6	35
4962	Chromosome assembly of large and complex genomes using multiple references. <i>Genome Research</i> , 2018, 28, 1720-1732.	2.4	94
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4966	Phylogeny of the spider mite sub-family Tetranychinae (Acari: Tetranychidae) inferred from RNA-Seq data. <i>PLoS ONE</i> , 2018, 13, e0203136.	1.1	15
4967	Genomic and phenotypic description of the newly isolated human species <i>Collinsella bouchesdurhonensis</i> sp. nov.. <i>MicrobiologyOpen</i> , 2018, 7, e00580.	1.2	2
4968	De novo transcriptome assembly of the coral <i>Agaricia lamarcki</i> (Lamarck's sheet coral) from mesophotic depth in southwest Puerto Rico. <i>Marine Genomics</i> , 2018, 41, 6-11.	0.4	22
4969	Venom gland transcriptomics and microRNA profiling of juvenile and adult yellow-bellied sea snake, <i>Hydrophis platurus</i> , from Playa del Coco (Guanacaste, Costa Rica). <i>Toxicon</i> , 2018, 153, 96-105.	0.8	14
4970	Barley RNA viromes in six different geographical regions in Korea. <i>Scientific Reports</i> , 2018, 8, 13237.	1.6	21
4971	Identifying genetic diversity of O antigens in <i>Aeromonas hydrophila</i> for molecular serotype detection. <i>PLoS ONE</i> , 2018, 13, e0203445.	1.1	8
4972	Whole genome sequencing reveals the emergence of a <i>Pseudomonas aeruginosa</i> shared strain sub-lineage among patients treated within a single cystic fibrosis centre. <i>BMC Genomics</i> , 2018, 19, 644.	1.2	16
4973	Lignocellulose degradation at the holobiont level: teamwork in a keystone soil invertebrate. <i>Microbiome</i> , 2018, 6, 162.	4.9	70
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4975	Comparative Analysis of de Bruijn Graph Parallel Genome Assemblers. , 2018, , .		2
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4978	Draft Genome Sequence of <i>Mycobacterium setense</i> CSUR47. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
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4980	Reconfiguration of the plastid genome in <i>Lamprocapnos spectabilis</i> : IR boundary shifting, inversion, and intraspecific variation. <i>Scientific Reports</i> , 2018, 8, 13568.	1.6	43
4981	The draft genome sequence of <i>Clostridium</i> sp. strain LJ4 with high furan and phenolic derivatives™ tolerances occurring from lignocellulosic hydrolysates. <i>3 Biotech</i> , 2018, 8, 406.	1.1	2
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4987	Tracing HIV-1 strains that imprint broadly neutralizing antibody responses. <i>Nature</i> , 2018, 561, 406-410.	13.7	47
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4990	Comparative Genomic Analysis of <i>Vibrio diabolicus</i> and Six Taxonomic Synonyms: A First Look at the Distribution and Diversity of the Expanded Species. <i>Frontiers in Microbiology</i> , 2018, 9, 1893.	1.5	24
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4993	Analysis of genome sequence and symbiotic ability of rhizobial strains isolated from seeds of common bean (<i>Phaseolus vulgaris</i>). <i>BMC Genomics</i> , 2018, 19, 645.	1.2	10
4994	GRASShopPER™ An algorithm for de novo assembly based on GPU alignments. <i>PLoS ONE</i> , 2018, 13, e0202355.	1.1	3

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4996	Integrating embryonic development and evolutionary history to characterize tentacle-specific cell types in a ctenophore. <i>Molecular Biology and Evolution</i> , 2018, 35, 2940-2956.	3.5	29
4997	Genomic repeats, misassembly and reannotation: a case study with long-read resequencing of <i>Porphyromonas gingivalis</i> reference strains. <i>BMC Genomics</i> , 2018, 19, 54.	1.2	28
4998	Repeated translocation of a gene cassette drives sex-chromosome turnover in strawberries. <i>PLoS Biology</i> , 2018, 16, e2006062.	2.6	85
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5001	The genome of the biting midge <i>Culicoides sonorensis</i> and gene expression analyses of vector competence for bluetongue virus. <i>BMC Genomics</i> , 2018, 19, 624.	1.2	19
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5004	Draft Genome Sequence of a Trimethylamine-Producing <i>Staphylococcus</i> Isolate from Blood of a Coronary Atherosclerotic Heart Disease Patient. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
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5006	A Comprehensive Study of De Novo Genome Assemblers: Current Challenges and Future Prospective. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431875865.	0.6	37
5007	NGSPanPipe: A Pipeline for Pan-genome Identification in Microbial Strains from Experimental Reads. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1052, 39-49.	0.8	4
5008	The complete plastome sequence of <i>Rubus takesimensis</i> endemic to Ulleung Island, Korea: Insights into molecular evolution of anagenetically derived species in <i>Rubus</i> (Rosaceae). <i>Gene</i> , 2018, 668, 221-228.	1.0	18
5009	Antibodies to Intercellular Adhesion Molecule 1-Binding Plasmodium falciparum Erythrocyte Membrane Protein 1-DBL α Are Biomarkers of Protective Immunity to Malaria in a Cohort of Young Children from Papua New Guinea. <i>Infection and Immunity</i> , 2018, 86, .	1.0	23
5010	Analysis of the complete genome sequence of a potyvirus from passion fruit suggests its taxonomic classification as a member of a new species. <i>Archives of Virology</i> , 2018, 163, 2583-2586.	0.9	18
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5012	The complete chloroplast genome of <i>Sisymbrium irio</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 488-489.	0.2	2

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5014	Network-guided genomic and metagenomic analysis of the faecal microbiota of the critically endangered kakapo. <i>Scientific Reports</i> , 2018, 8, 8128.	1.6	11
5015	Improving amphibian genomic resources: a multitissue reference transcriptome of an iconic invader. <i>GigaScience</i> , 2018, 7, 1-7.	3.3	23
5016	In vivo growth and genomic characterization of rickettsia-like organisms isolated from farmed Chinook salmon (<i>Oncorhynchus tshawytscha</i>) in New Zealand. <i>Journal of Fish Diseases</i> , 2018, 41, 1235-1245.	0.9	4
5017	Complete Genome Sequence of EtG, the First Phage Sequenced from <i>Erwinia tracheiphila</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	5
5018	Diverse <i>Streptococcus pneumoniae</i> Strains Drive a Mucosal-Associated Invariant T-Cell Response Through Major Histocompatibility Complex class II-Related Molecule-Dependent and Cytokine-Driven Pathways. <i>Journal of Infectious Diseases</i> , 2018, 217, 988-999.	1.9	59
5019	Genome Sequence of <i>Azospirillum brasilense</i> REC3, Isolated from Strawberry Plants. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
5020	Complete genomic sequence of a novel macluravirus, alpinia oxyphylla mosaic virus (AloMV), identified in <i>Alpinia oxyphylla</i> . <i>Archives of Virology</i> , 2018, 163, 2579-2582.	0.9	6
5021	First Report of <i>Ligustrum Virus A</i> on <i>Syringa reticulata</i> var. <i>mandshurica</i> (<i>Oleaceae</i>) with a New Yellow Vein and Malformed Needle-Shaped Leaf Disease in China. <i>Plant Disease</i> , 2018, 102, 2053.	0.7	3
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5025	Hospital Epidemiology of Methicillin-Resistant <i>Staphylococcus aureus</i> in a Tertiary Care Hospital in Moshi, Tanzania, as Determined by Whole Genome Sequencing. <i>BioMed Research International</i> , 2018, 2018, 1-12.	0.9	14
5026	Noncontiguous finished genome sequences and descriptions of <i>Actinomyces ihuae</i> , <i>Actinomyces bouchesdurhonensis</i> , <i>Actinomyces urinae</i> , <i>Actinomyces marseillensis</i> , <i>Actinomyces mediterranea</i> and <i>Actinomyces oralis</i> sp. nov. identified by culturomics. <i>New Microbes and New Infections</i> , 2018, 25, 30-44.	0.8	1
5027	Genome analysis and description of <i>Xanthomonas massiliensis</i> sp. nov., a new species isolated from human faeces. <i>New Microbes and New Infections</i> , 2018, 26, 63-72.	0.8	7
5028	Genomic evidence that the live <i>Chlamydia abortus</i> vaccine strain 1B is not attenuated and has the potential to cause disease. <i>Vaccine</i> , 2018, 36, 3593-3598.	1.7	25
5029	The chloroplast genome sequence of bittersweet (<i>Solanum dulcamara</i>): Plastid genome structure evolution in <i>Solanaceae</i> . <i>PLoS ONE</i> , 2018, 13, e0196069.	1.1	84
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5032	Transcriptomic and Network Analyses Reveal Mechanistic-Based Biomarkers of Endocrine Disruption in the Marine Mussel, <i>Mytilus edulis</i> . Environmental Science & Technology, 2018, 52, 9419-9430.	4.6	42
5033	Optimization of Assembly Pipeline may Improve the Sequence of the Chloroplast Genome in <i>Quercus spinosa</i> . Scientific Reports, 2018, 8, 8906.	1.6	4
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5038	Guidelines for RNA-seq projects: applications and opportunities in non-model decapod crustacean species. Hydrobiologia, 2018, 825, 5-27.	1.0	13
5039	Draft Genome Resource for the Potato Powdery Scab Pathogen <i>Spongospora subterranea</i> . Molecular Plant-Microbe Interactions, 2018, 31, 1227-1229.	1.4	17
5040	Draft Genome Sequence of the Novel Enterobacter cloacae Strain amazonensis, a Highly Heavy Metal-Resistant Bacterium from a Contaminated Stream in Amazonas, Brazil. Genome Announcements, 2018, 6, .	0.8	2
5041	Draft Genome Sequences of Six Skin Isolates of <i>Streptococcus pyogenes</i> . Genome Announcements, 2018, 6, .	0.8	1
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5044	Practical dynamic de Bruijn graphs. Bioinformatics, 2018, 34, 4189-4195.	1.8	18
5045	Genomics reveals abundant speciation in the coral reef building alga <i>Porolithon onkodes</i> (Corallinales, Rhodophyta). Journal of Phycology, 2018, 54, 429-434.	1.0	87
5046	Insights into the Genome Sequence of <i>Chromobacterium amazonense</i> Isolated from a Tropical Freshwater Lake. International Journal of Genomics, 2018, 2018, 1-10.	0.8	5
5047	Resolving the rapid plant radiation of early diverging lineages in the tropical Zingiberales: Pushing the limits of genomic data. Molecular Phylogenetics and Evolution, 2018, 128, 55-68.	1.2	53
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5050	Draft genome sequence of <i>Annulohyphomyces stygium</i> , <i>Aspergillus mulundensis</i> , <i>Berkeleyomyces basicola</i> (syn. <i>Thielaviopsis basicola</i>), <i>Ceratocystis smalleyi</i> , two <i>Cercospora beticola</i> strains, <i>Coleophoma cylindrospora</i> , <i>Fusarium fracticaudum</i> , <i>Phialophora</i> cf. <i>hyalina</i> , and <i>Morchella septimelata</i> . <i>IMA Fungus</i> . 2018. 9. 199-223.	1.7	37
5051	Draft Genome Sequences of Three <i>Salmonella enterica</i> Serovar 4,[5],12:i:~ Strains and One <i>S. enterica</i> Serovar Typhimurium Strain, Isolated in Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
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5054	Genome Analysis of Multidrug-Resistant <i>Shewanella</i> algae Isolated From Human Soft Tissue Sample. <i>Frontiers in Pharmacology</i> , 2018, 9, 419.	1.6	20
5055	The Complete Plastome Sequences of Seven Species in <i>Gentiana</i> sect. <i>Kudoa</i> (Gentianaceae): Insights Into Plastid Gene Loss and Molecular Evolution. <i>Frontiers in Plant Science</i> , 2018, 9, 493.	1.7	45
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5057	Gene exchange drives the ecological success of a multi-host bacterial pathogen. <i>Nature Ecology and Evolution</i> , 2018, 2, 1468-1478.	3.4	156
5058	The Genome of a Thermo Tolerant, Pathogenic Albino <i>Aspergillus fumigatus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1827.	1.5	12
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5060	Detecting Small Inversions Using SRinversion. <i>Methods in Molecular Biology</i> , 2018, 1833, 107-114.	0.4	0
5061	The complete chloroplast genome of <i>Leptochilus hemionitideus</i> , a traditional Chinese medical fern. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 784-785.	0.2	3
5062	A Sporadic Four-Year Hospital Outbreak of a ST97-IVa MRSA With Half of the Patients First Identified in the Community. <i>Frontiers in Microbiology</i> , 2018, 9, 1494.	1.5	12
5063	Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. <i>Nature Communications</i> , 2018, 9, 2945.	5.8	56
5064	Full-length transcriptome of <i>Misgurnus anguillicaudatus</i> provides insights into evolution of genus <i>Misgurnus</i> . <i>Scientific Reports</i> , 2018, 8, 11699.	1.6	44
5065	A GWAS on <i>Helicobacter pylori</i> strains points to genetic variants associated with gastric cancer risk. <i>BMC Biology</i> , 2018, 16, 84.	1.7	55
5066	Deep sequencing analysis of a strain of pecan mosaic-associated virus infecting <i>Atractylodes macrocephala</i> Koidz. <i>Journal of Plant Pathology</i> , 2018, 100, 249-255.	0.6	4

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5068	The Novel Phages phiCD5763 and phiCD2955 Represent Two Groups of Big Plasmidial Siphoviridae Phages of <i>Clostridium difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 26.	1.5	18
5069	NGS of Virus-Derived Small RNAs as a Diagnostic Method Used to Determine Viromes of Hungarian Vineyards. <i>Frontiers in Microbiology</i> , 2015, 9, 122.	1.5	95
5070	Genomic Diversity and Evolution of the Fish Pathogen <i>Flavobacterium psychrophilum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 138.	1.5	54
5071	Clinically Relevant ESBL-Producing <i>K. pneumoniae</i> ST307 and <i>E. coli</i> ST38 in an Urban West African Rat Population. <i>Frontiers in Microbiology</i> , 2018, 9, 150.	1.5	40
5072	Genome-Wide Analysis of <i>Corynespora cassicola</i> Leaf Fall Disease Putative Effectors. <i>Frontiers in Microbiology</i> , 2018, 9, 276.	1.5	58
5073	Indigenous <i>Pseudomonas</i> spp. Strains from the Olive (<i>Olea europaea</i> L.) Rhizosphere as Effective Biocontrol Agents against <i>Verticillium dahliae</i> : From the Host Roots to the Bacterial Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 277.	1.5	79
5074	A Retrospective Review of Microbiological Methods Applied in Studies Following the Deepwater Horizon Oil Spill. <i>Frontiers in Microbiology</i> , 2018, 9, 520.	1.5	8
5075	A Comparative Genomic Analysis Provides Novel Insights Into the Ecological Success of the Monophasic <i>Salmonella</i> Serovar 4,[5],12:i:-. <i>Frontiers in Microbiology</i> , 2018, 9, 715.	1.5	65
5076	Overview of Virus Metagenomic Classification Methods and Their Biological Applications. <i>Frontiers in Microbiology</i> , 2018, 9, 749.	1.5	99
5077	Discovery of Phloeophagus Beetles as a Source of <i>Pseudomonas</i> Strains That Produce Potentially New Bioactive Substances and Description of <i>Pseudomonas bohémica</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2018, 9, 913.	1.5	35
5078	Sensitivity of Small RNA-Based Detection of Plant Viruses. <i>Frontiers in Microbiology</i> , 2018, 9, 939.	1.5	50
5079	CowPI: A Rumen Microbiome Focussed Version of the PICRUSt Functional Inference Software. <i>Frontiers in Microbiology</i> , 2018, 9, 1095.	1.5	132
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5164	Harnessing the power of phylogenomics to disentangle the directionality and signatures of interkingdom host jumping in the parasitic fungal genus <i>Tolyposcladium</i> . <i>Mycologia</i> , 2018, 110, 104-117.	0.8	12
5165	Draft Genome Sequence of <i>n</i> -Alkane-Utilizing <i>Acinetobacter</i> sp. Strain BS1, Isolated from Ethane Oxidation Culture. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
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5179	Graph Theory and Definitions. , 2019, , 922-927.		1
5180	Description of three new <i>Peptoniphilus</i> species cultured in the vaginal fluid of a woman diagnosed with bacterial vaginosis: <i>Peptoniphilus pacaensis</i> sp. nov., <i>Peptoniphilus raoultii</i> sp. nov., and <i>Peptoniphilus vaginalis</i> sp. nov.. <i>MicrobiologyOpen</i> , 2019, 8, e00661.	1.2	20
5181	Metagenomic Analysis and its Applications. , 2019, , 184-193.		24
5182	Network Properties. , 2019, , 928-932.		1
5183	Sequence Analysis. , 2019, , 292-322.		8
5184	Whole Genome Sequencing Analysis. , 2019, , 176-183.		6
5185	Next Generation Sequence Analysis. , 2019, , 352-363.		1
5186	Genome Informatics. , 2019, , 178-194.		0
5187	Profiling the Gut Microbiome: Practice and Potential. , 2019, , 200-217.		0
5188	A High-Quality Draft Genome Sequence of <i>Colletotrichum gloeosporioides</i> sensu stricto SMCG1#C, a Causal Agent of Anthracnose on <i>Cunninghamia lanceolata</i> in China. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 139-141.	1.4	21
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5191	The second complete chloroplast genome sequence of <i>Pseudostellaria palibiniana</i> (Takeda) Ohwi (Caryophyllaceae): intraspecies variations based on geographical distribution. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1310-1311.	0.2	22
5192	The complete mitochondrial genome of <i>Aiolocaria hexaspilota</i> (Hope, 1831) (Coleoptera:Coccinellidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1472-1474.	0.2	8
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5194	The complete mitochondrial genome of <i>Nilaparvata lugens</i> (Stål, 1854) captured in China (Hemiptera: Delphacidae): investigation of intraspecies variations between countries. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1677-1678.	0.2	16

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5197	The complete chloroplast genome of horned holly, <i>Ilex cornuta</i> Lindl. & Paxton (Aquifoliaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 1275-1276.	0.2	11
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5199	The complete chloroplast genome of Nepal Holly, <i>Ilex integra</i> Thunb. (Aquifoliaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 1257-1258.	0.2	4
5200	Characterization of the complete chloroplast genome of black poplar (<i>Populus nigra</i> L.). Mitochondrial DNA Part B: Resources, 2019, 4, 1261-1262.	0.2	1
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5202	The second complete chloroplast genome of <i>Dysphania pumilio</i> (R.Br.) mosyakin & clemants (Amaranthaceae): intraspecies variation of invasive weeds. Mitochondrial DNA Part B: Resources, 2019, 4, 1428-1429.	0.2	14
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5217	Adaptation of host transmission cycle during Clostridium difficile speciation. Nature Genetics, 2019, 51, 1315-1320.	9.4	41
5218	The complete mitochondrial genome of Micromus angulatus (Stephens, 1836) (Neuroptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.2	6
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5234	The complete mitochondrial genome of <i>Neocaridina heteropoda koreana</i> Kubo, 1938 (Decapoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Kubo, 1938 (Decapoda: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.2	3
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5359	A whole-cell, high-throughput hydrogenase assay to identify factors that modulate [NiFe]-hydrogenase activity. <i>Journal of Biological Chemistry</i> , 2019, 294, 15373-15385.	1.6	11
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5492	Draft Genome Sequences of Two <i>Staphylococcus warneri</i> Clinical Isolates, Strains SMA0023-04 (UGA3) and SMA0670-05 (UGA28), from Siaya County Referral Hospital, Siaya, Kenya. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
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5494	deGSM: Memory Scalable Construction Of Large Scale de Bruijn Graph. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2157-2166.	1.9	12
5495	Detection of <i>Robinsoniella peoriensis</i> in multiple bone samples of a trauma patient. <i>Anaerobe</i> , 2019, 59, 14-18.	1.0	6
5496	Multiple-Strain Infections of Human Cytomegalovirus With High Genomic Diversity Are Common in Breast Milk From Human Immunodeficiency Virusâ€”Infected Women in Zambia. <i>Journal of Infectious Diseases</i> , 2019, 220, 792-801.	1.9	37
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5498	Draft Genome Sequence of Cold-Tolerant <i>Kurthia gibsonii</i> B83, Isolated from Spinach Leaf. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	8
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5500	The first draft genomes of the ant <i>Formica exsecta</i> , and its <i>Wolbachia</i> endosymbiont reveal extensive gene transfer from endosymbiont to host. <i>BMC Genomics</i> , 2019, 20, 301.	1.2	18
5501	Comparison of mitochondrial DNA enrichment and sequencing methods from fish tissue. <i>Food Chemistry</i> , 2019, 294, 333-338.	4.2	14

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5505	Breaking Free: The Genomics of Allopolyploidy-Facilitated Niche Expansion in White Clover. <i>Plant Cell</i> , 2019, 31, 1466-1487.	3.1	89
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5514	The complete mitochondrial genome of Siberian odorous ant, <i>Dolichoderus sibiricus</i> Emery, 1889 (Hymenoptera: Formicidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 525-526.	0.2	7
5515	The complete mitochondrial genome of tulip tree, <i>Liriodendron tulipifera</i> L. (Magnoliaceae): intra-species variations on mitochondrial genome. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1308-1309.	0.2	14
5516	Diversification of Colonization Factors in a Multidrug-Resistant <i>Escherichia coli</i> Lineage Evolving under Negative Frequency-Dependent Selection. <i>MBio</i> , 2019, 10, .	1.8	106
5517	Whole-Genome Sequence of the Novel <i>Rubrobacter taiwanensis</i> Strain Yellowstone, Isolated from Yellowstone National Park. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
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5521	Non-contiguous finished genome sequencing and description of <i>Enterococcus timonensis</i> sp. nov. isolated from human sputum. <i>New Microbes and New Infections</i> , 2019, 29, 100532.	0.8	2
5522	Computational Biology Approach in Management of Big Data of Healthcare Sector. , 2019, , 247-267.		4
5523	Draft Genome Sequences of 38 <i>Serratia marcescens</i> Isolates Associated with Acroporid Serratiosis. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
5524	Genome- and MS-based mining of antibacterial chlorinated chromones and xanthenes from the phytopathogenic fungus <i>Bipolaris sorokiniana</i> strain 11134. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 5167-5181.	1.7	18
5525	The complete chloroplast genome sequence of <i>Hibiscus syriacus</i> L. "Mamonde"™ (Malvaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 558-559.	0.2	10
5526	The complete mitochondrial genome of <i>Ectomomyrmex javanus</i> Mayr, 1867 (Hymenoptera: Formicidae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1636-1637.	0.2	5
5527	BHap: a novel approach for bacterial haplotype reconstruction. <i>Bioinformatics</i> , 2019, 35, 4624-4631.	1.8	18
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5532	The complete mitochondrial genome sequence of Chinese minnow in Korea, <i>Rhynchocypris oxycephalus</i> (Sauvage and Dabry de Thiersant, 1874). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 662-663.	0.2	5
5533	The complete chloroplast genome of Korean <i>Marchantia polymorpha</i> subsp. <i>ruderalis</i> Bischl. & Boisselier: low genetic diversity between Korea and Japan. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 959-960.	0.2	20
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5536	Draft Genome Sequences of Three Monokaryotic Isolates of the White-Rot Basidiomycete Fungus <i>Dichomitus squalens</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	22
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5541	Comparative analysis of the root and leaf transcriptomes in <i>Chelidonium majus</i> L.. PLoS ONE, 2019, 14, e0215165.	1.1	13
5542	Genome sequence and description of <i>Traorella massiliensis</i> gen. nov., sp. nov., a new bacterial genus isolated from human left colon. New Microbes and New Infections, 2019, 29, 100520.	0.8	2
5543	Characterization of the complete chloroplast genome of <i>Taxillus nigrans</i> . Mitochondrial DNA Part B: Resources, 2019, 4, 472-473.	0.2	3
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5547	Identification and characterization of water chestnut Soymovirus-1 (WCSV-1), a novel Soymovirus in water chestnuts (<i>Eleocharis dulcis</i>). BMC Plant Biology, 2019, 19, 159.	1.6	2
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5552	Genome Sequences of a <i>Staphylococcus aureus</i> Clinical Isolate, Strain SMA0034-04 (UGA22), from Siaya County Referral Hospital in Siaya, Kenya. Microbiology Resource Announcements, 2019, 8, .	0.3	1
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5559	Sequencing-based methods and resources to study antimicrobial resistance. <i>Nature Reviews Genetics</i> , 2019, 20, 356-370.	7.7	263
5560	Draft genome of the brown alga, <i>Nemacystus decipiens</i> , Onna-1 strain: Fusion of genes involved in the sulfated fucan biosynthesis pathway. <i>Scientific Reports</i> , 2019, 9, 4607.	1.6	33
5561	Genomic and Functional Analysis of Emerging Virulent and Multidrug-Resistant <i>Escherichia coli</i> Lineage Sequence Type 648. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	71
5562	Draft Genome Sequence of <i>Streptomyces</i> sp. Strain NL15-2K, a Degradator of Lignin-Derived Aromatic Compounds, Isolated from Forest Soil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
5563	GMASS: a novel measure for genome assembly structural similarity. <i>BMC Bioinformatics</i> , 2019, 20, 147.	1.2	4
5564	The second complete chloroplast genome sequence of <i>Nymphaea alba</i> L. (Nymphaeaceae) to investigate inner-species variations. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1014-1015.	0.2	9
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5567	The complete chloroplast genome of <i>Tetraena mongolica</i> (Zygophyllaceae), an endangered shrub endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1030-1031.	0.2	5
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5572	Sequencing the Plastid Genome of Giant Ragweed (<i>Ambrosia trifida</i> , Asteraceae) From a Herbarium Specimen. <i>Frontiers in Plant Science</i> , 2019, 10, 218.	1.7	18
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5582	A Role for Tetracycline Selection in Recent Evolution of Agriculture-Associated <i>Clostridium difficile</i> PCR Ribotype 078. <i>MBio</i> , 2019, 10, .	1.8	46
5583	Gen2Epi: an automated whole-genome sequencing pipeline for linking full genomes to antimicrobial susceptibility and molecular epidemiological data in <i>Neisseria gonorrhoeae</i> . <i>BMC Genomics</i> , 2019, 20, 165.	1.2	8
5584	Isolation and partial characterization of a new moderate thermophilic <i>Albidovulum</i> sp. SLM16 with transaminase activity from Deception Island, Antarctica. <i>Biological Research</i> , 2019, 52, 5.	1.5	8
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5586	<i>Mesorhizobium carbonis</i> sp. nov., isolated from coal bed water. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1221-1229.	0.7	11
5587	Bioinformatics applied to biotechnology: A review towards bioenergy research. <i>Biomass and Bioenergy</i> , 2019, 123, 195-224.	2.9	17
5588	Genomic and metagenomic signatures of giant viruses are ubiquitous in water samples from sewage, inland lake, waste water treatment plant, and municipal water supply in Mumbai, India. <i>Scientific Reports</i> , 2019, 9, 3690.	1.6	9
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5590	Multiple Genome Sequences of <i>Lactobacillus pentosus</i> Strains Isolated from Biofilms on the Skin of Fermented Green Table Olives. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
5591	Genome Sequence of a Lethal Vascular Wilt Fungus, <i>Verticillium nonalfalfae</i> , a Biological Control Used Against the Invasive <i>Ailanthus altissima</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7

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5596	Genome sequence of <i>Xanthomonas fuscans</i> subsp. <i>fuscans</i> strain Xff49: a new isolate obtained from common beans in Southern Brazil. <i>Brazilian Journal of Microbiology</i> , 2019, 50, 357-367.	0.8	3
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5598	The First Complete Genome Sequence of a Novel <i>Tetrastichus brontispae</i> RNA Virus-1 (TbRV-1). <i>Viruses</i> , 2019, 11, 257.	1.5	4
5599	Genome Sequencing and Interrogation of Genome Databases: A Guide to <i>Neisseria meningitidis</i> Genomics. <i>Methods in Molecular Biology</i> , 2019, 1969, 51-82.	0.4	1
5600	Genome Sequence of <i>Rhodococcus erythropolis</i> Type Strain JCM 3201. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
5601	Sequencing the Obligate Intracellular <i>Rhabdochlamydia helvetica</i> within Its Tick Host <i>Ixodes ricinus</i> to Investigate Their Symbiotic Relationship. <i>Genome Biology and Evolution</i> , 2019, 11, 1334-1344.	1.1	21
5602	Draft Genome Sequence of Halotolerant Bacterium <i>Chromohalobacter salexigens</i> ANJ207, Isolated from Salt Crystal Deposits in Pipelines. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	10
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5604	Comparative Genomics Between <i>Saccharomyces kudriavzevii</i> and <i>S. cerevisiae</i> Applied to Identify Mechanisms Involved in Adaptation. <i>Frontiers in Genetics</i> , 2019, 10, 187.	1.1	27
5605	Transcriptomic analysis of <i>de novo</i> folate biosynthetic genes in <i>Lactobacillus plantarum</i> strain 4_3 in fermented soybean. <i>Food and Function</i> , 2019, 10, 2426-2438.	2.1	6
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5608	The complete chloroplast genome sequence of traditional medical herb, <i>Plantago depressa</i> Willd. (Plantaginaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 437-438.	0.2	9
5609	Complete mitochondrial genome of Siamese cobra (<i>Naja kaouthia</i>) determined using next-generation sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 577-578.	0.2	5

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5611	The complete chloroplast genome, <i>Duchesnea chrysantha</i> (Zoll. & Moritzi) Miq. (Rosoideae). Mitochondrial DNA Part B: Resources, 2019, 4, 951-952.	0.2	5
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5613	The complete chloroplast genome of aniseed tree, <i>Illicium anisatum</i> L. (Schisandraceae). Mitochondrial DNA Part B: Resources, 2019, 4, 1023-1024.	0.2	13
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5618	The complete chloroplast genome of <i>Biondia insignis</i> Tsiang (Apocynaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 280-281.	0.2	3
5619	The Complete chloroplast genome sequence of the <i>Nymphaea lotus</i> L. (Nymphaeaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 389-390.	0.2	5
5620	The complete chloroplast genome sequence of <i>Dysphania pumilio</i> (R.Br.) Mosyakin & Clemants (Amaranthaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 403-404.	0.2	8
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5983	The complete chloroplast genome of <i>Wiesnerella denudata</i> (Mitt.) Steph. (Wiesnerellaceae, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 T	0.2	2
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5991	The second complete mitochondrial genome of <i>Alphitobius diaperinus</i> Panzer, 1797 (Coleoptera:) Tj ETQq0 0 0 rgBT /Overlock 1.9 DNA Part B: Resources, 2020, 5, 2979-2981.	0.2	5
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6026	The Genome of <i>Peronospora belbahrii</i> Reveals High Heterozygosity, a Low Number of Canonical Effectors, and TC-Rich Promoters. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 742-753.	1.4	15
6027	Plastid Genome Evolution in the Subtribe Calypsoinae (Epidendroideae, Orchidaceae). <i>Genome Biology and Evolution</i> , 2020, 12, 867-870.	1.1	16
6028	The loss of photosynthesis pathway and genomic locations of the lost plastid genes in a holoparasitic plant <i>Aeginetia indica</i> . <i>BMC Plant Biology</i> , 2020, 20, 199.	1.6	16
6029	The complete chloroplast genome of <i>Oxybasis glauca</i> (L.) S. Fuentes, Uotila & Borsch (Amaranthaceae) as the first chloroplast genome in genus <i>Oxybasis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1410-1412.	0.2	1
6030	Accelerated bioremediation of petroleum refinery sludge through biostimulation and bioaugmentation of native microbiome. , 2020, , 23-65.		10
6031	Metagenomic and metatranscriptomic insights into the complex nitrogen metabolic pathways in a single-stage bioreactor coupling partial denitrification with anammox. <i>Chemical Engineering Journal</i> , 2020, 398, 125653.	6.6	66
6032	Integrating whole-genome sequencing within the National Antimicrobial Resistance Surveillance Program in the Philippines. <i>Nature Communications</i> , 2020, 11, 2719.	5.8	62
6033	Unprecedented Intraindividual Structural Heteroplasmy in <i>Eleocharis</i> (Cyperaceae, Poales) Plastomes. <i>Genome Biology and Evolution</i> , 2020, 12, 641-655.	1.1	22
6034	Responses of mature symbiotic nodules to the whole-plant systemic nitrogen signaling. <i>Journal of Experimental Botany</i> , 2020, 71, 5039-5052.	2.4	22
6035	Draft Genome Sequence of <i>Bacillus</i> sp. Strain HY001, a High Producer of Isoprene, Isolated from Natto. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
6036	Draft Genome Sequence of the Microcystin-Degrading Bacterium <i>Novosphingobium</i> sp. Strain MD-1. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5
6037	Chloroplast (Cp) Transcriptome of <i>P. davidiana</i> Dode— <i>P. bolleana</i> Lauch provides insight into the Cp drought response and <i>Populus</i> Cp phylogeny. <i>BMC Evolutionary Biology</i> , 2020, 20, 51.	3.2	5
6038	HiC-Hiker: a probabilistic model to determine contig orientation in chromosome-length scaffolds with Hi-C. <i>Bioinformatics</i> , 2020, 36, 3966-3974.	1.8	11
6039	Exploring the phylogeny of the marattialean ferns. <i>Cladistics</i> , 2020, 36, 569-593.	1.5	20
6040	Fatal <i>Clostridium sordellii</i> -mediated hemorrhagic and necrotizing gastroenteropathy in a dog: case report. <i>BMC Veterinary Research</i> , 2020, 16, 152.	0.7	2
6041	Genome mining of the citrus pathogen <i>Elsinoë fawcettii</i> ; prediction and prioritisation of candidate effectors, cell wall degrading enzymes and secondary metabolite gene clusters. <i>PLoS ONE</i> , 2020, 15, e0227396.	1.1	9
6042	Abiotic-stress tolerance in plants-system biology approach. , 2020, , 577-609.		6

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6044	The Concerted Action of Two B3-Like Prophage Genes Excludes Superinfecting Bacteriophages by Blocking DNA Entry into <i>Pseudomonas aeruginosa</i> . <i>Journal of Virology</i> , 2020, 94, .	1.5	5
6045	Draft Genome Sequence and Biosynthetic Potential of the Newly Described Strain <i>Longimicrobium terrae</i> CB-286315 ^T . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0
6046	Tracking the evolution of the two successful CC59 methicillin-resistant <i>Staphylococcus aureus</i> clones in Taiwan: the divergence time of the two clades is estimated to be the 1980s. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 106047.	1.1	4
6047	Mutations in virus-derived small RNAs. <i>Scientific Reports</i> , 2020, 10, 9540.	1.6	7
6048	Structural and genetic characterization of the colitose-containing O-specific polysaccharide from the lipopolysaccharide of <i>Herbaspirillum frisingense</i> GSF30T. <i>International Journal of Biological Macromolecules</i> , 2020, 161, 891-897.	3.6	6
6049	Identification and Characterization of a Pear Chlorotic Leaf Spot-Associated Virus, a Novel Emaravirus Associated with a Severe Disease of Pear Trees in China. <i>Plant Disease</i> , 2020, 104, 2786-2798.	0.7	35
6050	Genomic insights into the phylogeny of <i>Bacillus</i> strains and elucidation of their secondary metabolic potential. <i>Genomics</i> , 2020, 112, 3191-3200.	1.3	15
6051	Lateral Gene Transfer Shapes Diversity of <i>Gardnerella</i> spp.. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 293.	1.8	18
6052	Comparative Plastomics of <i>Ashwagandha</i> (<i>Withania</i> , Solanaceae) and Identification of Mutational Hotspots for Barcoding Medicinal Plants. <i>Plants</i> , 2020, 9, 752.	1.6	37
6053	Metagenomics and stable isotope probing reveal the complementary contribution of fungal and bacterial communities in the recycling of dead biomass in forest soil. <i>Soil Biology and Biochemistry</i> , 2020, 148, 107875.	4.2	71
6054	Low coverage genomic data resolve the population divergence and gene flow history of an Australian rain forest fig wasp. <i>Molecular Ecology</i> , 2020, 29, 3649-3666.	2.0	4
6055	<i>In Vitro</i> Activity of Omadacycline, a New Tetracycline Analog, and Comparators against <i>Clostridioides difficile</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	14
6056	Complete Sequence, Genome Organization and Molecular Detection of Grapevine Line Pattern Virus, a New Putative Anulavirus Infecting Grapevine. <i>Viruses</i> , 2020, 12, 602.	1.5	4
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6058	The complete chloroplast genome of <i>Euonymus szechuanensis</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1130-1131.	0.2	3
6059	The complete mitochondrial genome of fungal endosymbiont, <i>Ophiocordycipitaceae</i> sp., isolated from <i>Ricania speculum</i> (Hemiptera: Ricaniidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1888-1889.	0.2	7
6060	Origin of OXA-23 Variant OXA-239 from a Recently Emerged Lineage of <i>Acinetobacter baumannii</i> International Clone V. <i>MSphere</i> , 2020, 5, .	1.3	50

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6061	The complete mitochondrial genome of <i>Hipparchia autonoe</i> (Esper, 1783) (Lepidoptera): Part B: Resources, 2020, 5, 1542-1544.	0.2	7
6062	Association between bacterial homoplastic variants and radiological pathology in tuberculosis. <i>Thorax</i> , 2020, 75, 584-591.	2.7	8
6063	Episodic and guanine-cytosine-biased bursts of intragenomic and interspecific synonymous divergence in Ajugoideae (Lamiaceae) mitogenomes. <i>New Phytologist</i> , 2020, 228, 1107-1114.	3.5	13
6064	Trait-based approach to bacterial growth efficiency. <i>Environmental Microbiology</i> , 2020, 22, 3494-3504.	1.8	14
6065	Evolution of <i>Salmonella enterica</i> serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	1.5	48
6066	A Modular Metagenomics Pipeline Allowing for the Inclusion of Prior Knowledge Using the Example of Anaerobic Digestion. <i>Microorganisms</i> , 2020, 8, 669.	1.6	1
6067	Draft Genome Sequence of <i>Streptomyces aureovorticillatus</i> HN6, a Strain Antagonistic against <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Race 4. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
6068	Chromosome Architecture and Gene Content of the Emergent Pathogen <i>Acinetobacter haemolyticus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 926.	1.5	4
6069	Lower Bounds, and Exact Enumeration in Particular Cases, for the Probability of Existence of a Universal Cycle or a Universal Word for a Set of Words. <i>Mathematics</i> , 2020, 8, 778.	1.1	0
6070	Comparison of Chloroplast Genomes among Species of Unisexual and Bisexual Clades of the Monocot Family Araceae. <i>Plants</i> , 2020, 9, 737.	1.6	23
6071	Ultraplexing: increasing the efficiency of long-read sequencing for hybrid assembly with k-mer-based multiplexing. <i>Genome Biology</i> , 2020, 21, 68.	3.8	6
6073	<i>Chryseobacterium lacus</i> sp. nov. Isolated From the Surface Water of Two Lakes With Light-Induced Carotenoid Production. <i>Frontiers in Microbiology</i> , 2020, 11, 251.	1.5	11
6074	Seed transmission of sweet potato pakakuy virus in sweet potato (<i>Ipomoea batatas</i>). <i>Journal of General Plant Pathology</i> , 2020, 86, 205-210.	0.6	2
6075	Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. <i>Nature Communications</i> , 2020, 11, 1427.	5.8	133
6076	First Report of <i>Aleurocanthus spiniferus</i> on <i>Ailanthus altissima</i> : Profiling of the Insect Microbiome and MicroRNAs. <i>Insects</i> , 2020, 11, 161.	1.0	11
6077	Transcriptome-based identification of small RNA in plants: The need for robust prediction algorithms. , 2020, , 65-97.		0
6078	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
6079	Diet influences the functions of the human intestinal microbiome. <i>Scientific Reports</i> , 2020, 10, 4247.	1.6	115

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6080	Differential Contribution of the Parental Genomes to a <i>S. cerevisiae</i> × <i>S. uvarum</i> Hybrid, Inferred by Phenomic, Genomic, and Transcriptomic Analyses, at Different Industrial Stress Conditions. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 129.	2.0	15
6081	<i>Bacillus subtilis</i> EA-CB0575 genome reveals clues for plant growth promotion and potential for sustainable agriculture. <i>Functional and Integrative Genomics</i> , 2020, 20, 575-589.	1.4	38
6082	Characterization of invasive <i>Neisseria meningitidis</i> isolates recovered from children in Turkey during a period of increased serogroup B disease, 2013–2017. <i>Vaccine</i> , 2020, 38, 3545-3552.	1.7	4
6083	Characterization of the complete mitochondrial genome of <i>Diplocheila zealandica</i> Redtenbacher (Insecta: Coleoptera: Carabidae) from Henan province. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1234-1235.	0.2	0
6084	Characterization of the complete mitochondrial genome of the maize weevil, <i>Sitophilus zeamais</i> (Insecta: Coleoptera: Curculionidae) from Guizhou province. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1244-1245.	0.2	1
6085	Toward Biorecycling: Isolation of a Soil Bacterium That Grows on a Polyurethane Oligomer and Monomer. <i>Frontiers in Microbiology</i> , 2020, 11, 404.	1.5	64
6086	<i>Anaerococcus marasmi</i> sp. nov., a new bacterium isolated from human gut microbiota. <i>New Microbes and New Infections</i> , 2020, 35, 100655.	0.8	2
6087	Detection of H3N8 influenza A virus with multiple mammalian-adaptive mutations in a rescued Grey seal (<i>Halichoerus grypus</i>) pup. <i>Virus Evolution</i> , 2020, 6, veaa016.	2.2	13
6088	Metabolic response of prokaryotic microbes to sporadic hypoxia in a eutrophic subtropical estuary. <i>Marine Pollution Bulletin</i> , 2020, 154, 111064.	2.3	6
6089	Genome Sequence and Comparative Analysis of <i>Colletotrichum gloeosporioides</i> Isolated from <i>Liriodendron</i> Leaves. <i>Phytopathology</i> , 2020, 110, 1260-1269.	1.1	13
6090	Comprehensive genome-wide identification of angiosperm upstream ORFs with peptide sequences conserved in various taxonomic ranges using a novel pipeline, ESUCA. <i>BMC Genomics</i> , 2020, 21, 260.	1.2	14
6091	Comparative Genomics of a Paddy Field Bacterial Isolate <i>Ochrobactrum</i> sp. CPD-03: Analysis of Chlorpyrifos Degradation Potential. <i>Indian Journal of Microbiology</i> , 2020, 60, 325-333.	1.5	10
6092	Functional genomics by integrated analysis of transcriptome of sweet potato (<i>Ipomoea batatas</i> (L.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 0.5	0.5	6
6093	Draft Genome Sequences of the Type Strains of <i>Actinobacillus indolicus</i> (46K2C) and <i>Actinobacillus porcinus</i> (NM319), Two NAD-Dependent Bacterial Species Found in the Respiratory Tract of Pigs. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
6094	Polyhydroxyalkanoate (PHA) synthase genes and PHA-associated gene clusters in <i>Pseudomonas</i> spp. and <i>Janthinobacterium</i> spp. isolated from Antarctica. <i>Journal of Biotechnology</i> , 2020, 313, 18-28.	1.9	31
6095	Association of <i>Neisseria gonorrhoeae</i> Plasmids With Distinct Lineages and The Economic Status of Their Country of Origin. <i>Journal of Infectious Diseases</i> , 2020, 222, 1826-1836.	1.9	22
6096	Genomic characterisation of <i>Salmonella enterica</i> serovar Wangata isolates obtained from different sources reveals low genomic diversity. <i>PLoS ONE</i> , 2020, 15, e0229697.	1.1	2
6097	Evaluation of Machine Learning Models for Predicting Antimicrobial Resistance of <i>Actinobacillus pleuropneumoniae</i> From Whole Genome Sequences. <i>Frontiers in Microbiology</i> , 2020, 11, 48.	1.5	43

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6099	<i>Clostridium</i> sp. Strain NJ4: A Promising Solventogenic Strain for Butanol Production from Jerusalem Artichoke through Consolidated Bioprocessing. <i>Energy & Fuels</i> , 2020, 34, 3406-3411.	2.5	7
6100	<i>Enterococcus burkinafasonensis</i> sp. nov. isolated from human gut microbiota. <i>New Microbes and New Infections</i> , 2020, 36, 100702.	0.8	6
6101	A Venomics Approach Coupled to High-Throughput Toxin Production Strategies Identifies the First Venom-Derived Melanocortin Receptor Agonists. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 8250-8264.	2.9	13
6102	YerA41, a <i>Yersinia ruckeri</i> Bacteriophage: Determination of a Non-Sequencable DNA Bacteriophage Genome via RNA-Sequencing. <i>Viruses</i> , 2020, 12, 620.	1.5	7
6103	Microsatellite design for species delimitation and insights into ploidy for the Lake Baikal Cladophoraceae species flock. <i>Phycologia</i> , 2020, 59, 355-364.	0.6	3
6104	The complete chloroplast genome of <i>Catalpa speciosa</i> (Warder) Engelman (Bignoniaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2089-2090.	0.2	1
6105	What Is Metagenomics Teaching Us, and What Is Missed?. <i>Annual Review of Microbiology</i> , 2020, 74, 117-135.	2.9	54
6106	Genome Analysis of <i>Endobacterium cerealis</i> , a Novel Genus and Species Isolated from <i>Zea mays</i> Roots in North Spain. <i>Microorganisms</i> , 2020, 8, 939.	1.6	17
6107	Complete mitochondrial genome of the common silverfish <i>Lepisma saccharina</i> (Insecta: Tj ETQq1 1 0.784314 rgBT / Overlock 10	0.2	8
6108	The first complete mitogenome of <i>Cervus canadensis nannodes</i> (Merriam, 1905). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2294-2296.	0.2	4
6109	Detection of S83V GyrA mutation in quinolone-resistant <i>Shewanella</i> algae using comparative genomics. <i>Journal of Microbiology, Immunology and Infection</i> , 2021, 54, 658-664.	1.5	6
6110	The complete chloroplast genomes of two cold hardness coffee trees, <i>Coffea arabica</i> L. (Rubiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1619-1621.	0.2	5
6111	The complete chloroplast genome sequence of limestone endemic, <i>Zabelia tyaihyoni</i> (Caprifoliaceae), in Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1947-1948.	0.2	2
6112	The complete mitochondrial genome of <i>Alphitobius diaperinus</i> Panzer, 1797 (Coleoptera: Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50	0.2	7
6113	Molecular evolutionary and 3D protein structural analyses of <i>Lactobacillus fermentum</i> elongation factor Tu, a novel brain health promoting factor. <i>Genomics</i> , 2020, 112, 3915-3924.	1.3	1
6114	Stool Samples of Acute Diarrhea Inpatients as a Reservoir of ST11 Hypervirulent KPC-2-Producing <i>Klebsiella pneumoniae</i> . <i>MSystems</i> , 2020, 5, .	1.7	42
6115	Genome Report: Whole Genome Sequence and Annotation of the Parasitoid Jewel Wasp <i>Nasonia giraulti</i> Laboratory Strain RV2X[u]. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2565-2572.	0.8	12

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6116	Robust Virome Profiling and Whole Genome Reconstruction of Viruses and Viroids Enabled by Use of Available mRNA and sRNA-Seq Datasets in Grapevine (<i>Vitis vinifera</i> L.). <i>Frontiers in Microbiology</i> , 2020, 11, 1232.	1.5	23
6117	Description of <i>Prevotella rectalis</i> sp. nov., a new bacterium isolated from human rectum. <i>New Microbes and New Infections</i> , 2020, 36, 100703.	0.8	2
6118	Increasing incidence of group B streptococcus neonatal infections in the Netherlands is associated with clonal expansion of CC17 and CC23. <i>Scientific Reports</i> , 2020, 10, 9539.	1.6	25
6119	Comparative genomics of four strains of the edible brown alga, <i>Cladosiphon okamuranus</i> . <i>BMC Genomics</i> , 2020, 21, 422.	1.2	9
6120	Intra-specific comparison of mitochondrial genomes reveals host gene fragment exchange via intron mobility in <i>Tremella fuciformis</i> . <i>BMC Genomics</i> , 2020, 21, 426.	1.2	7
6121	<i>Bacillus tepidophilus</i> sp. nov., isolated from tepid spring. <i>Archives of Microbiology</i> , 2020, 202, 2367-2371.	1.0	8
6122	Confidence intervals for Markov chain transition probabilities based on next generation sequencing reads data. <i>Quantitative Biology</i> , 2020, 8, 143-154.	0.3	1
6123	The complete mitochondrial genome of <i>Nilaparvata lugens</i> (Stål, 1854) captured in Guangxi province, China (Hemiptera: Delphacidae): identification of the origin of <i>N. lugens</i> migrated to Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1960-1961.	0.2	10
6124	The comparison of the complete chloroplast genome of <i>Suaeda japonica</i> Makino presenting different external morphology (Amaranthaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1616-1618.	0.2	10
6125	The complete mitochondrial genome of <i>Riccia fluitans</i> L. (Ricciaceae, Marchantiophyta): investigation of intraspecific variations on mitochondrial genomes of <i>R. fluitans</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1220-1222.	0.2	9
6126	The complete chloroplast genome of <i>Emex australis</i> (Polygonaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1431-1432.	0.2	0
6127	Emerging bacterial fish pathogen <i>Lactococcus garvieae</i> RTCLI04, isolated from rainbow trout (<i>Oncorhynchus mykiss</i>): Genomic features and comparative genomics. <i>Microbial Pathogenesis</i> , 2020, 147, 104368.	1.3	19
6128	The <i>Seminavis robusta</i> genome provides insights into the evolutionary adaptations of benthic diatoms. <i>Nature Communications</i> , 2020, 11, 3320.	5.8	55
6129	The complete chloroplast genome of <i>Selaginella tamariscina</i> (Beauv.) Spring (Selaginellaceae) isolated in Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1654-1656.	0.2	9
6130	The complete chloroplast genome of <i>Catalpa ovata</i> G. Don. (Bignoniaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1800-1801.	0.2	5
6131	Complete chloroplast genome sequence of <i>Betula microphylla</i> (Betulaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2151-2152.	0.2	0
6132	The complete chloroplast genome of <i>Agrimonia pilosa</i> Ledeb. isolated in Korea (Rosaceae): investigation of intraspecific variations on its chloroplast genomes. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2264-2266.	0.2	13
6133	Unearthing the genetic divergence and gene flow of the earthworm <i>Amyntas_YN2017</i> sp. (Oligochaeta: Megascolecidae) populations based on restriction site-associated DNA sequencing. <i>European Journal of Soil Biology</i> , 2020, 99, 103210.	1.4	3

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6134	Extensive Shifts from <i>Cis</i> - to <i>Trans</i> -splicing of Gymnosperm Mitochondrial Introns. <i>Molecular Biology and Evolution</i> , 2020, 37, 1615-1620.	3.5	32
6135	Whole Genome Sequencing and Comparative Genomics of Two Nematicidal <i>Bacillus</i> Strains Reveals a Wide Range of Possible Virulence Factors. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 881-890.	0.8	12
6136	Computational Approaches for Transcriptome Assembly Based on Sequencing Technologies. <i>Current Bioinformatics</i> , 2020, 15, 2-16.	0.7	9
6137	<i>Gorillibacterium timonense</i> sp. nov., isolated from an obese patient. <i>Archives of Microbiology</i> , 2020, 202, 1223-1229.	1.0	1
6138	Genomic sequencing analysis of <i>Acinetobacter baumannii</i> strain ABIQM1, isolated from a meningitis patient. <i>Gene Reports</i> , 2020, 19, 100631.	0.4	0
6139	De novo transcriptome assembly and sex-biased gene expression in the gonads of Amur catfish (<i>Silurus</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10	1.3	17
6140	Recurrent gene duplication in the angiosperm tribe Delphinieae (Ranunculaceae) inferred from intracellular gene transfer events and heteroplasmic mutations in the plastid <i>matK</i> gene. <i>Scientific Reports</i> , 2020, 10, 2720.	1.6	15
6141	Statistical Mitogenome Assembly with RepeaTs. <i>Journal of Computational Biology</i> , 2020, 27, 1407-1421.	0.8	8
6142	Occurrence, infectivity and molecular characterization of hosta virus X in North-east China. <i>Canadian Journal of Plant Pathology</i> , 2020, 42, 595-603.	0.8	2
6143	Genomic Characterization of Newly Completed Genomes of Botulinum Neurotoxin-Producing Species from Argentina, Australia, and Africa. <i>Genome Biology and Evolution</i> , 2020, 12, 229-242.	1.1	8
6144	Development and characterization of 17 microsatellite markers for <i>Sonchus oleraceus</i> . <i>Applications in Plant Sciences</i> , 2020, 8, e11329.	0.8	0
6145	Comparative genomics of <i>Salmonella enterica</i> serovar Enteritidis ST-11 isolated in Uruguay reveals lineages associated with particular epidemiological traits. <i>Scientific Reports</i> , 2020, 10, 3638.	1.6	2
6146	The complete mitochondrial genome of <i>Ochetellus glaber</i> (Mayr, 1862) (Hymenoptera: Formicidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 147-149.	0.2	8
6147	The complete mitochondrial genome of <i>Aphaenogaster famelica</i> (Smith, 1874) (Hymenoptera:) Tj ETQq1 1 0.784314 rgBT / Overlock 10	0.2	12
6148	The complete mitochondrial genome of <i>Nylanderia flavipes</i> (Smith, 1874) (Hymenoptera: Formicidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 420-421.	0.2	5
6149	The complete mitochondrial genome of <i>Rotunda rotundapex</i> (Miyata & Kishida, 1990) (Lepidoptera:) Tj ETQq1 1 0.784314 rgBT / Overlock 10	0.2	6
6150	Next-generation sequencing yields the first complete mitochondrial genome of the ruby dragonet <i>Synchiropus sycorax</i> (Syngnathiformes, Callionymidae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 346-347.	0.2	0
6151	Characterization of the complete chloroplast genome of <i>Festuca sinensis</i> (Gramineae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 358-359.	0.2	0

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6152	A complete chloroplast genome sequence of <i>Gastrodia elata</i> (Orchidaceae) represents high sequence variation in the species. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 517-519.	0.2	21
6153	The complete chloroplast genome sequence of <i>Prunus sibirica</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 581-582.	0.2	2
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6383	The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , 2021, 12, 1749.	5.8	47
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