

Natalia N Ivanova

List of Publications by Year in descending order

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466
papers

35,584
citations

7568

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167
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482
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482
docs citations

482
times ranked

29306
citing authors

#	ARTICLE	IF	CITATIONS
1	DeepPlasmid: deep learning accurately separates plasmids from bacterial chromosomes. <i>Nucleic Acids Research</i> , 2022, 50, e17-e17.	14.5	18
2	The Genome of the Acid Soil-Adapted Strain <i>Rhizobium favelukesii</i> OR191 Encodes Determinants for Effective Symbiotic Interaction With Both an Inverted Repeat Lacking Clade and a Phaseoloid Legume Host. <i>Frontiers in Microbiology</i> , 2022, 13, 735911.	3.5	2
3	<i>Sodalis ligni</i> Strain 159R Isolated from an Anaerobic Lignin-Degrading Consortium. <i>Microbiology Spectrum</i> , 2022, 10, e0234621.	3.0	1
4	The role of zinc in the adaptive evolution of polar phytoplankton. <i>Nature Ecology and Evolution</i> , 2022, 6, 965-978.	7.8	14
5	A centimeter-long bacterium with DNA contained in metabolically active, membrane-bound organelles. <i>Science</i> , 2022, 376, 1453-1458.	12.6	45
6	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
7	The IMG/M data management and analysis system v.6.0: new tools and advanced capabilities. <i>Nucleic Acids Research</i> , 2021, 49, D751-D763.	14.5	332
8	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. <i>Nucleic Acids Research</i> , 2021, 49, D764-D775.	14.5	240
9	VPF-Class: taxonomic assignment and host prediction of uncultivated viruses based on viral protein families. <i>Bioinformatics</i> , 2021, 37, 1805-1813.	4.1	53
10	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of <i>Thermoflexus hugenholtzii</i> and Three Candidate Species From China and Japan. <i>Frontiers in Microbiology</i> , 2021, 12, 632731.	3.5	8
11	High-Quality Draft Genome Sequence of the Siderophilic and Thermophilic <i>Leptolyngbyaceae</i> Cyanobacterium JSC-12. <i>Microbiology Resource Announcements</i> , 2021, 10, e0049521.	0.6	2
12	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , 2021, 6, 960-970.	13.3	248
13	DOE JGI Metagenome Workflow. <i>MSystems</i> , 2021, 6, .	3.8	56
14	Genome Analysis of a Verrucomicrobial Endosymbiont With a Tiny Genome Discovered in an Antarctic Lake. <i>Frontiers in Microbiology</i> , 2021, 12, 674758.	3.5	18
15	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , 2021, 12, 5483.	12.8	29
16	IMG-ABC v.5.0: an update to the IMG/Atlas of Biosynthetic Gene Clusters Knowledgebase. <i>Nucleic Acids Research</i> , 2020, 48, D422-D430.	14.5	64
17	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020, 14, 659-675.	9.8	69
18	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. <i>ISME Journal</i> , 2020, 14, 2527-2541.	9.8	42

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19	Metagenomes from Experimental Hydrologic Manipulation of Restored Coastal Plain Wetland Soils (Tyrell County, North Carolina). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
20	Molecular Dialogues between Early Divergent Fungi and Bacteria in an Antagonism versus a Mutualism. <i>MBio</i> , 2020, 11, .	4.1	19
21	Ecological and genomic analyses of candidate phylum <sc>WPS</sc> bacteria in an unvegetated soil. <i>Environmental Microbiology</i> , 2020, 22, 3143-3157.	3.8	42
22	Novel heavy metal resistance gene clusters are present in the genome of <i>Cupriavidus neocaledonicus</i> STM 6070, a new species of <i>Mimosa pudica</i> microsymbiont isolated from heavy-metal-rich mining site soil. <i>BMC Genomics</i> , 2020, 21, 214.	2.8	18
23	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , 2020, 8, 22.	11.1	91
24	Draft Genome Sequence of <i>Yokenella regensburgei</i> Strain WCD67, Isolated from the Boxelder Bug. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
25	One Complete and Seven Draft Genome Sequences of Subdivision 1 and 3 <i>Acidobacteria</i> Isolated from Soil. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
26	Metagenomes and Metatranscriptomes of a Glucose-Amended Agricultural Soil. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
27	Metatranscriptomic Sequencing of a Cyanobacterial Soil-Surface Consortium with and without a Diverse Underlying Soil Microbiome. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
28	Microbiomes of Velloziaceae from phosphorus-impooverished soils of the campos rupestres, a biodiversity hotspot. <i>Scientific Data</i> , 2019, 6, 140.	5.3	10
29	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019, 4, 1895-1906.	13.3	206
30	Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. <i>Scientific Data</i> , 2019, 6, 129.	5.3	36
31	Metagenomes and metatranscriptomes from boreal potential and actual acid sulfate soil materials. <i>Scientific Data</i> , 2019, 6, 207.	5.3	6
32	Complete Genome Sequence of <i>Serratia quinivorans</i> Strain 124R, a Facultative Anaerobe Isolated on Organosolv Lignin as a Sole Carbon Source. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
33	Draft Genome of <i>Burkholderia cenocepacia</i> TAtI-371, a Strain from the <i>Burkholderia cepacia</i> Complex Retains Antagonism in Different Carbon and Nitrogen Sources. <i>Current Microbiology</i> , 2019, 76, 566-574.	2.2	3
34	A Comparison of Microbial Genome Web Portals. <i>Frontiers in Microbiology</i> , 2019, 10, 208.	3.5	22
35	Complete Genome Sequence for <i>Asinibacterium</i> sp. Strain OR53 and Draft Genome Sequence for <i>Asinibacterium</i> sp. Strain OR43, Two Bacteria Tolerant to Uranium. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	6
36	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	11.1	53

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37	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
38	IMG/VR v.2.0: an integrated data management and analysis system for cultivated and environmental viral genomes. <i>Nucleic Acids Research</i> , 2019, 47, D678-D686.	14.5	174
39	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. <i>Nucleic Acids Research</i> , 2019, 47, D666-D677.	14.5	799
40	High-quality draft genome sequences of <i>Pseudomonas monteilii</i> DSM 14164T, <i>Pseudomonas mosselii</i> DSM 17497T, <i>Pseudomonas plecoglossicida</i> DSM 15088T, <i>Pseudomonas taiwanensis</i> DSM 21245T and <i>Pseudomonas vranovensis</i> DSM 16006T: taxonomic considerations. <i>Access Microbiology</i> , 2019, 1, e000067.	0.5	10
41	Genomes of ubiquitous marine and hypersaline <i>Hydrogenovibrio</i> , <i>Thiomicrobacter</i> and <i>Thiomicrospira</i> spp. encode a diversity of mechanisms to sustain chemolithoautotrophy in heterogeneous environments. <i>Environmental Microbiology</i> , 2018, 20, 2686-2708.	3.8	32
42	Complete Genome Sequence of <i>Thermoanaerobacterium</i> sp. Strain RBIITD, a Butyrate- and Butanol-Producing Thermophile. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
43	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	17.5	414
44	Draft Genome Sequences of New Isolates and the Known Species of the Family Microbacteriaceae Associated with Plants. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	3
45	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. <i>Microbiome</i> , 2018, 6, 161.	11.1	44
46	High-Quality Draft Genome Sequences of Eight Bacteria Isolated from Fungus Gardens Grown by <i>Trachymyrmex septentrionalis</i> Ants. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	3
47	Transfer RNAs with novel cloverleaf structures. <i>Nucleic Acids Research</i> , 2017, 45, gkw898.	14.5	26
48	Complete genome sequence of <i>Jiangella gansuensis</i> strain YIM 002T (DSM 44835T), the type species of the genus <i>Jiangella</i> and source of new antibiotic compounds. <i>Standards in Genomic Sciences</i> , 2017, 12, 21.	1.5	9
49	IMG-ABC: new features for bacterial secondary metabolism analysis and targeted biosynthetic gene cluster discovery in thousands of microbial genomes. <i>Nucleic Acids Research</i> , 2017, 45, D560-D565.	14.5	78
50	Permanent draft genome of <i>Thiobacillus thiooparus</i> DSM 505T, an obligately chemolithoautotrophic member of the Betaproteobacteria. <i>Standards in Genomic Sciences</i> , 2017, 12, 10.	1.5	34
51	RNA-Dependent Cysteine Biosynthesis in Bacteria and Archaea. <i>MBio</i> , 2017, 8, .	4.1	20
52	High quality permanent draft genome sequence of <i>Chryseobacterium bovis</i> DSM 19482T, isolated from raw cow milk. <i>Standards in Genomic Sciences</i> , 2017, 12, 31.	1.5	2
53	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017, 35, 676-683.	17.5	222
54	Permanent Draft Genome Sequence of <i>Desulfurococcus amylolyticus</i> Strain Z-533 ^T , a Peptide and Starch Degradar Isolated from Thermal Springs in the Kamchatka Peninsula and Kunashir Island, Russia. <i>Genome Announcements</i> , 2017, 5, .	0.8	2

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55	Complete Genome Sequence of <i>Nitrosomonas cryotolerans</i> ATCC 49181, a Phylogenetically Distinct Ammonia-Oxidizing Bacterium Isolated from Arctic Waters. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
56	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017, 356, 82-85.	12.6	234
57	Nontargeted virus sequence discovery pipeline and virus clustering for metagenomic data. <i>Nature Protocols</i> , 2017, 12, 1673-1682.	12.0	115
58	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	17.5	1,512
59	High-quality draft genome sequence of <i>Rhizobium mesoamericanum</i> strain STM6155, a <i>Mimosa pudica</i> microsymbiont from New Caledonia. <i>Standards in Genomic Sciences</i> , 2017, 12, 7.	1.5	2
60	High-quality-draft genome sequence of the fermenting bacterium <i>Anaerobium acetethylicum</i> type strain GluBS11T (DSM 29698). <i>Standards in Genomic Sciences</i> , 2017, 12, 24.	1.5	6
61	High-quality permanent draft genome sequence of the <i>Bradyrhizobium elkanii</i> type strain USDA 76T, isolated from <i>Glycine max</i> (L.) Merr. <i>Standards in Genomic Sciences</i> , 2017, 12, 26.	1.5	11
62	IMG/M: integrated genome and metagenome comparative data analysis system. <i>Nucleic Acids Research</i> , 2017, 45, D507-D516.	14.5	451
63	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , 2017, 5, 140.	11.1	102
64	Genome Sequence of <i>Roseovarius</i> sp. Strain MCTG156(2b) Isolated from a Phytoplankton Net Trawl on the Scottish West Coast. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
65	Genomic Analysis of <i>Caldithrix abyssi</i> , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum <i>Calditrichaeota</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 195.	3.5	66
66	Genome Data Provides High Support for Generic Boundaries in <i>Burkholderia</i> Sensu Lato. <i>Frontiers in Microbiology</i> , 2017, 8, 1154.	3.5	122
67	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017, 8, 2264.	3.5	142
68	Draft genome sequence of <i>Actinotignum schaalii</i> DSM 15541T: Genetic insights into the lifestyle, cell fitness and virulence. <i>PLoS ONE</i> , 2017, 12, e0188914.	2.5	5
69	High-quality genome sequence of the radioresistant bacterium <i>Deinococcus ficus</i> KS 0460. <i>Standards in Genomic Sciences</i> , 2017, 12, 46.	1.5	10
70	Draft genome sequence of <i>Dethiobacter alkaliphilus</i> strain AHT1T, a gram-positive sulfidogenic polyextremophile. <i>Standards in Genomic Sciences</i> , 2017, 12, 57.	1.5	16
71	High-quality draft genome sequence of <i>Ensifer meliloti</i> Mlalz-1, a microsymbiont of <i>Medicago laciniata</i> (L.) miller collected in Lanzarote, Canary Islands, Spain. <i>Standards in Genomic Sciences</i> , 2017, 12, 58.	1.5	0
72	Draft genome sequence of <i>Marinobacterium rhizophilum</i> CL-YJ9T (DSM 18822T), isolated from the rhizosphere of the coastal tidal-flat plant <i>Suaeda japonica</i> . <i>Standards in Genomic Sciences</i> , 2017, 12, 65.	1.5	1

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73	Draft genome of <i>Paraburkholderia caballeronis</i> TNe-841T, a free-living, nitrogen-fixing, tomato plant-associated bacterium. <i>Standards in Genomic Sciences</i> , 2017, 12, 80.	1.5	7
74	Genome Sequence of <i>Oceanicola</i> sp. Strain MCTG156(1a), Isolated from a Scottish Coastal Phytoplankton Net Sample. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
75	Draft Genome Sequence of <i>Methylocapsa palsarum</i> NE2 T , an Obligate Methanotroph from Subarctic Soil. <i>Genome Announcements</i> , 2017, 5, .	0.8	13
76	Absence of genome reduction in diverse, facultative endohyphal bacteria. <i>Microbial Genomics</i> , 2017, 3, e000101.	2.0	30
77	Permanent Improved High-Quality Draft Genome Sequence of <i>Nocardia casuarinae</i> Strain BMG51109, an Endophyte of Actinorhizal Root Nodules of <i>Casuarina glauca</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	5
78	Genome Sequence of <i>Arenibacter algicola</i> Strain TG409, a Hydrocarbon-Degrading Bacterium Associated with Marine Eukaryotic Phytoplankton. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
79	Functional Metagenomics of Spacecraft Assembly Cleanrooms: Presence of Virulence Factors Associated with Human Pathogens. <i>Frontiers in Microbiology</i> , 2016, 7, 1321.	3.5	24
80	Genome-Based Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2016, 7, 2003.	3.5	493
81	Draft Genome Sequence of <i>Frankia</i> Strain G2, a Nitrogen-Fixing Actinobacterium Isolated from <i>Casuarina equisetifolia</i> and Able To Nodulate Actinorhizal Plants of the Order <i>Rhamales</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	13
82	Complete genome sequence of <i>Desulfurivibrio alkaliphilus</i> strain AHT2T, a haloalkaliphilic sulfidogen from Egyptian hypersaline alkaline lakes. <i>Standards in Genomic Sciences</i> , 2016, 11, 67.	1.5	26
83	Microbiome Data Science: Understanding Our Microbial Planet. <i>Trends in Microbiology</i> , 2016, 24, 425-427.	7.7	47
84	High-Quality Draft Genomes from <i>Thermus caliditerrae</i> YIM 77777 and <i>T.Âtengchongensis</i> YIM 77401, Isolates from Tengchong, China. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
85	Application of Long Sequence Reads To Improve Genomes for <i>Clostridium thermocellum</i> AD2, <i>Clostridium thermocellum</i> LQRI, and <i>Pelosinus fermentans</i> R7. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
86	Permanent draft genome of <i>Thermithiobacillus tepidarius</i> DSM 3134T, a moderately thermophilic, obligately chemolithoautotrophic member of the Acidithiobacillia. <i>Standards in Genomic Sciences</i> , 2016, 11, 74.	1.5	15
87	Uncovering Earth's virome. <i>Nature</i> , 2016, 536, 425-430.	27.8	880
88	Genome Sequence of <i>Marinobacter</i> sp. Strain MCTG268 Isolated from the Cosmopolitan Marine Diatom <i>Skeletonema costatum</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	1
89	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	14.5	177
90	Permanent Draft Genome Sequence of <i>Nocardia</i> sp. BMG111209, an Actinobacterium Isolated from Nodules of <i>Casuarina glauca</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	3

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91	Complete genome of <i>Nitrospira briensis</i> C-128, an ammonia-oxidizing bacterium from agricultural soil. <i>Standards in Genomic Sciences</i> , 2016, 11, 46.	1.5	22
92	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016, 1, 15032.	13.3	207
93	High-Quality Draft Genome Sequence of <i>Thermocrinis jamiesonii</i> GBS1 Isolated from Great Boiling Spring, Nevada. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
94	Draft Genome Sequence of Heavy Metal-Resistant <i>Cupriavidus alkaliphilus</i> ASC-732 T , Isolated from Agave Rhizosphere in the Northeast of Mexico. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
95	High quality draft genome sequences of <i>Pseudomonas fulva</i> DSM 17717T, <i>Pseudomonas parafulva</i> DSM 17004T and <i>Pseudomonas cremoricolorata</i> DSM 17059T type strains. <i>Standards in Genomic Sciences</i> , 2016, 11, 55.	1.5	30
96	An improved high-quality draft genome sequence of <i>Carnobacterium inhibens</i> subsp. <i>inhibens</i> strain K1T. <i>Standards in Genomic Sciences</i> , 2016, 11, 65.	1.5	2
97	Complete genome sequence of the Antarctic <i>Halorubrum lacusprofundi</i> type strain ACAM 34. <i>Standards in Genomic Sciences</i> , 2016, 11, 70.	1.5	21
98	High-quality permanent draft genome sequence of <i>Ensifer</i> sp. PC2, isolated from a nitrogen-fixing root nodule of the legume tree (<i>Khejri</i>) native to the Thar Desert of India. <i>Standards in Genomic Sciences</i> , 2016, 11, 43.	1.5	7
99	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
100	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
101	Permanent draft genome sequence of <i>Desulfurococcus mobilis</i> type strain DSM 2161, a thermoacidophilic sulfur-reducing crenarchaeon isolated from acidic hot springs of Hveravellir, Iceland. <i>Standards in Genomic Sciences</i> , 2016, 11, 3.	1.5	2
102	The standard operating procedure of the DOE-JGI Metagenome Annotation Pipeline (MAP v.4). <i>Standards in Genomic Sciences</i> , 2016, 11, 17.	1.5	161
103	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
104	Supporting community annotation and user collaboration in the integrated microbial genomes (IMG) system. <i>BMC Genomics</i> , 2016, 17, 307.	2.8	54
105	Complete genome sequence of <i>Methanospirillum hungatei</i> type strain JF1. <i>Standards in Genomic Sciences</i> , 2016, 11, 2.	1.5	33
106	High-quality draft genome sequence of the <i>Thermus amyloliquefaciens</i> type strain YIM 77409T with an incomplete denitrification pathway. <i>Standards in Genomic Sciences</i> , 2016, 11, 20.	1.5	7
107	Facile Recoding of Selenocysteine in Nature. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 5337-5341.	13.8	54
108	Metagenomic investigation of the geologically unique Hellenic Volcanic Arc reveals a distinctive ecosystem with unexpected physiology. <i>Environmental Microbiology</i> , 2016, 18, 1122-1136.	3.8	37

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109	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476.	12.8	189
110	ProDeGe: a computational protocol for fully automated decontamination of genomes. <i>ISME Journal</i> , 2016, 10, 269-272.	9.8	65
111	Discovery of Novel Plant Interaction Determinants from the Genomes of 163 Root Nodule Bacteria. <i>Scientific Reports</i> , 2015, 5, 16825.	3.3	33
112	High quality draft genome sequence of <i>Brachymonas chironomi</i> AIMA4T (DSM 19884T) isolated from a <i>Chironomus</i> sp. egg mass. <i>Standards in Genomic Sciences</i> , 2015, 10, 29.	1.5	2
113	High-quality permanent draft genome sequence of the <i>Parapiptadenia rigida</i> -nodulating <i>Burkholderia</i> sp. strain UYPR1.413. <i>Standards in Genomic Sciences</i> , 2015, 10, 31.	1.5	2
114	High quality draft genome sequence of <i>Bacteroides barnesiae</i> type strain BL2T (DSM 18169T) from chicken caecum. <i>Standards in Genomic Sciences</i> , 2015, 10, 48.	1.5	4
115	High-quality permanent draft genome sequence of the <i>Lebeckia</i> - nodulating <i>Burkholderia dilworthii</i> strain WSM3556T. <i>Standards in Genomic Sciences</i> , 2015, 10, 64.	1.5	1
116	High-quality draft genome sequence of <i>Gracilimonas tropica</i> CL-CB462T (DSM 19535T), isolated from a <i>Synechococcus</i> culture. <i>Standards in Genomic Sciences</i> , 2015, 10, 98.	1.5	3
117	High-quality permanent draft genome sequence of the <i>Lebeckia ambigua</i> -nodulating <i>Burkholderia</i> sp. strain WSM4176. <i>Standards in Genomic Sciences</i> , 2015, 10, 79.	1.5	5
118	The standard operating procedure of the DOE-JGI Microbial Genome Annotation Pipeline (MGAP v.4). <i>Standards in Genomic Sciences</i> , 2015, 10, 86.	1.5	287
119	Partial genome sequence of <i>Thioalkalivibrio thiocyanodenitrificans</i> ARhD 1T, a chemolithoautotrophic haloalkaliphilic sulfur-oxidizing bacterium capable of complete denitrification. <i>Standards in Genomic Sciences</i> , 2015, 10, 84.	1.5	2
120	High-quality permanent draft genome sequence of the <i>Parapiptadenia rigida</i> -nodulating <i>Cupriavidus</i> sp. strain UYPR2.512. <i>Standards in Genomic Sciences</i> , 2015, 10, 13.	1.5	6
121	Large-scale contamination of microbial isolate genomes by Illumina PhiX control. <i>Standards in Genomic Sciences</i> , 2015, 10, 18.	1.5	127
122	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. strain WSM1743 - an effective microsymbiont of an <i>Indigofera</i> sp. growing in Australia. <i>Standards in Genomic Sciences</i> , 2015, 10, 87.	1.5	1
123	Draft genome sequence of <i>Halomonas lutea</i> strain YIM 91125T (DSM 23508T) isolated from the alkaline Lake Ebinur in Northwest China. <i>Standards in Genomic Sciences</i> , 2015, 10, 1.	1.5	65
124	High quality draft genome sequence and analysis of <i>Pontibacter roseus</i> type strain SRC-1T (DSM 17521T) isolated from muddy waters of a drainage system in Chandigarh, India. <i>Standards in Genomic Sciences</i> , 2015, 10, 8.	1.5	6
125	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015, 3, 62.	11.1	56
126	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

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130	Genome sequence and description of the anaerobic lignin-degrading bacterium <i>Tolumonas lignolytica</i> sp. nov.. Standards in Genomic Sciences, 2015, 10, 106.	1.5	43
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