

# Natalia N Ivanova

## List of Publications by Year in descending order

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466  
papers

35,584  
citations

7568

77  
h-index

4991

167  
g-index

482  
all docs

482  
docs citations

482  
times ranked

29306  
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	27.8	2,239
2	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
3	IMG: the integrated microbial genomes database and comparative analysis system. <i>Nucleic Acids Research</i> , 2012, 40, D115-D122.	14.5	1,210
4	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	27.8	1,181
5	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009, 462, 1056-1060.	27.8	924
6	Uncovering Earth's virome. <i>Nature</i> , 2016, 536, 425-430.	27.8	880
7	IMG ER: a system for microbial genome annotation expert review and curation. <i>Bioinformatics</i> , 2009, 25, 2271-2278.	4.1	804
8	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
9	Genome sequence of <i>Bacillus cereus</i> and comparative analysis with <i>Bacillus anthracis</i> . <i>Nature</i> , 2003, 423, 87-91.	27.8	740
10	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006, 24, 1263-1269.	17.5	634
11	Microbial species delineation using whole genome sequences. <i>Nucleic Acids Research</i> , 2015, 43, 6761-6771.	14.5	609
12	IMG 4 version of the integrated microbial genomes comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D560-D567.	14.5	555
13	Dissecting biological "dark matter" with single-cell genetic analysis of rare and uncultivated TM7 microbes from the human mouth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11889-11894.	7.1	552
14	The <i>Wolbachia</i> Genome of <i>Brugia malayi</i> : Endosymbiont Evolution within a Human Pathogenic Nematode. <i>PLoS Biology</i> , 2005, 3, e121.	5.6	529
15	The genome sequence of the facultative intracellular pathogen <i>Brucella melitensis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 443-448.	7.1	513
16	Genome-Based Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2016, 7, 2003.	3.5	493
17	GenePRIMP: a gene prediction improvement pipeline for prokaryotic genomes. <i>Nature Methods</i> , 2010, 7, 455-457.	19.0	468
18	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457

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19	Complete genome sequence of DSM 30083T, the type strain (U5/41T) of <i>Escherichia coli</i> , and a proposal for delineating subspecies in microbial taxonomy. <i>Standards in Genomic Sciences</i> , 2014, 9, 2.	1.5	454
20	IMG/M: integrated genome and metagenome comparative data analysis system. <i>Nucleic Acids Research</i> , 2017, 45, D507-D516.	14.5	451
21	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018, 36, 359-367.	17.5	414
22	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
23	Symbiosis insights through metagenomic analysis of a microbial consortium. <i>Nature</i> , 2006, 443, 950-955.	27.8	396
24	The integrated microbial genomes (IMG) system. <i>Nucleic Acids Research</i> , 2006, 34, D344-D348.	14.5	355
25	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
26	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007, 4, 495-500.	19.0	322
27	Genome Sequence and Analysis of the Oral Bacterium <i>Fusobacterium nucleatum</i> Strain ATCC 25586. <i>Journal of Bacteriology</i> , 2002, 184, 2005-2018.	2.2	311
28	IMG/M: a data management and analysis system for metagenomes. <i>Nucleic Acids Research</i> , 2007, 36, D534-D538.	14.5	309
29	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
30	The Evolution of Host Specialization in the Vertebrate Gut Symbiont <i>Lactobacillus reuteri</i> . <i>PLoS Genetics</i> , 2011, 7, e1001314.	3.5	270
31	IMG/M 4 version of the integrated metagenome comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D568-D573.	14.5	270
32	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , 2008, 26, 1029-1034.	17.5	254
33	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , 2021, 6, 960-970.	13.3	248
34	IMG/M: the integrated metagenome data management and comparative analysis system. <i>Nucleic Acids Research</i> , 2012, 40, D123-D129.	14.5	242
35	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
36	The integrated microbial genomes system: an expanding comparative analysis resource. <i>Nucleic Acids Research</i> , 2010, 38, D382-D390.	14.5	237

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37	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017, 356, 82-85.	12.6	234
38	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
39	The DOE-JGI Standard Operating Procedure for the Annotations of Microbial Genomes. <i>Standards in Genomic Sciences</i> , 2009, 1, 63-67.	1.5	218
40	The ERGOTM genome analysis and discovery system. <i>Nucleic Acids Research</i> , 2003, 31, 164-171.	14.5	207
41	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016, 1, 15032.	13.3	207
42	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019, 4, 1895-1906.	13.3	206
43	The Complete Genome Sequence of <i>Fibrobacter succinogenes</i> S85 Reveals a Cellulolytic and Metabolic Specialist. <i>PLoS ONE</i> , 2011, 6, e18814.	2.5	199
44	Genome Sequence and Analysis of the Soil Cellulolytic Actinomycete <i>Thermobifida fusca</i> YX. <i>Journal of Bacteriology</i> , 2007, 189, 2477-2486.	2.2	194
45	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476.	12.8	189
46	The Genome Sequence of <i>Psychrobacter arcticus</i> 273-4, a Psychroactive Siberian Permafrost Bacterium, Reveals Mechanisms for Adaptation to Low-Temperature Growth. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2304-2312.	3.1	184
47	The integrated microbial genomes (IMG) system in 2007: data content and analysis tool extensions. <i>Nucleic Acids Research</i> , 2007, 36, D528-D533.	14.5	179
48	The genome sequence of the psychrophilic archaeon, <i>Methanococcoides burtonii</i> : the role of genome evolution in cold adaptation. <i>ISME Journal</i> , 2009, 3, 1012-1035.	9.8	178
49	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	14.5	177
50	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
51	Targeted Discovery of Glycoside Hydrolases from a Switchgrass-Adapted Compost Community. <i>PLoS ONE</i> , 2010, 5, e8812.	2.5	170
52	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
53	Comparative Metagenomic and Metatranscriptomic Analysis of Hindgut Paunch Microbiota in Wood- and Dung-Feeding Higher Termites. <i>PLoS ONE</i> , 2013, 8, e61126.	2.5	149
54	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017, 8, 2264.	3.5	142

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55	Millimeter-scale genetic gradients and community-level molecular convergence in a hypersaline microbial mat. <i>Molecular Systems Biology</i> , 2008, 4, 198.	7.2	139
56	A metagenomic insight into freshwater methane-utilizing communities and evidence for cooperation between the <i>Methylococcaceae</i> and the <i>Methylophilaceae</i> . <i>PeerJ</i> , 2013, 1, e23.	2.0	139
57	A bacterial metapopulation adapts locally to phage predation despite global dispersal. <i>Genome Research</i> , 2008, 18, 293-297.	5.5	135
58	Architecture of thermal adaptation in an <i>Exiguobacterium sibiricum</i> strain isolated from 3 million year old permafrost: A genome and transcriptome approach. <i>BMC Genomics</i> , 2008, 9, 547.	2.8	134
59	Large-scale contamination of microbial isolate genomes by Illumina PhiX control. <i>Standards in Genomic Sciences</i> , 2015, 10, 18.	1.5	127
60	Stop codon reassignments in the wild. <i>Science</i> , 2014, 344, 909-913.	12.6	124
61	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
62	Genomic Potential of <i>Marinobacter aquaeolei</i> , a Biogeochemical "Opportunitroph". <i>Applied and Environmental Microbiology</i> , 2011, 77, 2763-2771.	3.1	120
63	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21T). <i>Standards in Genomic Sciences</i> , 2011, 5, 97-111.	1.5	115
64	Nontargeted virus sequence discovery pipeline and virus clustering for metagenomic data. <i>Nature Protocols</i> , 2017, 12, 1673-1682.	12.0	115
65	Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. <i>ISME Journal</i> , 2013, 7, 2287-2300.	9.8	113
66	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008, 9, R158.	8.8	104
67	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , 2017, 5, 140.	11.1	102
68	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). <i>Standards in Genomic Sciences</i> , 2009, 1, 12-20.	1.5	100
69	Complete genome sequence of the <i>Medicago</i> microsymbiont <i>Ensifer</i> ( <i>Sinorhizobium</i> ) <i>medicae</i> strain WSM419. <i>Standards in Genomic Sciences</i> , 2010, 2, 77-86.	1.5	100
70	Genome Sequence of "Candidatus <i>Frankia datiscae</i> " Dg1, the Uncultured Microsymbiont from Nitrogen-Fixing Root Nodules of the Dicot <i>Datisca glomerata</i> . <i>Journal of Bacteriology</i> , 2011, 193, 7017-7018.	2.2	99
71	Complete Genome Sequences of Six Strains of the Genus <i>Methylobacterium</i> . <i>Journal of Bacteriology</i> , 2012, 194, 4746-4748.	2.2	99
72	Exploring the symbiotic pangenome of the nitrogen-fixing bacterium <i>Sinorhizobium meliloti</i> . <i>BMC Genomics</i> , 2011, 12, 235.	2.8	97

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73	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6T). <i>Standards in Genomic Sciences</i> , 2011, 4, 200-209.	1.5	96
74	Whole-genome comparative analysis of three phytopathogenic <i>Xylella fastidiosa</i> strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12403-12408.	7.1	94
75	Genomics of Aerobic Cellulose Utilization Systems in Actinobacteria. <i>PLoS ONE</i> , 2012, 7, e39331.	2.5	92
76	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , 2020, 8, 22.	11.1	91
77	IMG-ABC: A Knowledge Base To Fuel Discovery of Biosynthetic Gene Clusters and Novel Secondary Metabolites. <i>MBio</i> , 2015, 6, e00932.	4.1	87
78	An experimental metagenome data management and analysis system. <i>Bioinformatics</i> , 2006, 22, e359-e367.	4.1	81
79	The Candidate Phylum Poribacteria by Single-Cell Genomics: New Insights into Phylogeny, Cell-Compartmentation, Eukaryote-Like Repeat Proteins, and Other Genomic Features. <i>PLoS ONE</i> , 2014, 9, e87353.	2.5	79
80	Genome Sequence of the Arctic Methanotroph <i>Methylobacter tundripaludum</i> SV96. <i>Journal of Bacteriology</i> , 2011, 193, 6418-6419.	2.2	78
81	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
82	Complete genome sequence of <i>Enterobacter lignolyticus</i> SCF1. <i>Standards in Genomic Sciences</i> , 2011, 5, 69-85.	1.5	76
83	Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305T), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of <i>Gimesia</i> gen. nov., <i>Planctopirus</i> gen. nov. and <i>Rubinisphaera</i> gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. <i>Standards in Genomic Sciences</i> , 2014, 9, 10.	1.5	76
84	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034T). <i>Standards in Genomic Sciences</i> , 2010, 2, 87-95.	1.5	74
85	Comparative genome analysis of <i>Bacillus cereus</i> group genomes with <i>Bacillus subtilis</i> . <i>FEMS Microbiology Letters</i> , 2005, 250, 175-184.	1.8	73
86	Metatranscriptomic array analysis of <i>Candidatus</i> <i>Accumulibacter phosphatis</i> ™-enriched enhanced biological phosphorus removal sludge. <i>Environmental Microbiology</i> , 2010, 12, 1205-1217.	3.8	73
87	Genome Analysis of <i>F. nucleatum</i> sub spp <i>vincentii</i> and Its Comparison With the Genome of <i>F. nucleatum</i> ATCC 25586. <i>Genome Research</i> , 2003, 13, 1180-1189.	5.5	72
88	Novel Insights into the Diversity of Catabolic Metabolism from Ten Haloarchaeal Genomes. <i>PLoS ONE</i> , 2011, 6, e20237.	2.5	72
89	Complete genome sequence of <i>Thioalkalivibrio sulfidophilus</i> -HL-EbGr7. <i>Standards in Genomic Sciences</i> , 2011, 4, 23-35.	1.5	72
90	Complete Genome Sequence of the Aerobic Marine Methanotroph <i>Methylomonas methanica</i> MC09. <i>Journal of Bacteriology</i> , 2011, 193, 7001-7002.	2.2	72

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91	Draft Sequencing and Comparative Genomics of <i>Xylella fastidiosa</i> Strains Reveal Novel Biological Insights. <i>Genome Research</i> , 2002, 12, 1556-1563.	5.5	70
92	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2T). <i>Standards in Genomic Sciences</i> , 2010, 2, 96-106.	1.5	70
93	Uncultivated thermophiles: current status and spotlight on "Aigarchaeota". <i>Current Opinion in Microbiology</i> , 2015, 25, 136-145.	5.1	70
94	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020, 14, 659-675.	9.8	69
95	Genomes of Three Methylophilids from a Single Niche Reveal the Genetic and Metabolic Divergence of the Methylophilaceae. <i>Journal of Bacteriology</i> , 2011, 193, 3757-3764.	2.2	66
96	Complete Genome Sequence of the Cellulolytic Thermophile <i>Clostridium thermocellum</i> DSM1313. <i>Journal of Bacteriology</i> , 2011, 193, 2906-2907.	2.2	66
97	Genomic Analysis of <i>Caldithrix abyssi</i> , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum Caldithrichaeota. <i>Frontiers in Microbiology</i> , 2017, 8, 195.	3.5	66
98	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
99	ProDeGe: a computational protocol for fully automated decontamination of genomes. <i>ISME Journal</i> , 2016, 10, 269-272.	9.8	65
100	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
101	Genome Sequences for Six <i>Rhodanobacter</i> Strains, Isolated from Soils and the Terrestrial Subsurface, with Variable Denitrification Capabilities. <i>Journal of Bacteriology</i> , 2012, 194, 4461-4462.	2.2	62
102	The Expanded Diversity of Methylophilaceae from Lake Washington through Cultivation and Genomic Sequencing of Novel Ecotypes. <i>PLoS ONE</i> , 2014, 9, e102458.	2.5	62
103	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv <i>trifolii</i> strain WSM2304, an effective microsymbiont of the South American clover <i>Trifolium polymorphum</i> . <i>Standards in Genomic Sciences</i> , 2010, 2, 66-76.	1.5	60
104	Genome Analysis of the Anaerobic Thermohalophilic Bacterium <i>Halothermothrix orenii</i> . <i>PLoS ONE</i> , 2009, 4, e4192.	2.5	58
105	Complete genome sequence of the termite hindgut bacterium <i>Spirochaeta coccoides</i> type strain (SPN1T), reclassification in the genus <i>Sphaerochaeta</i> as <i>Sphaerochaeta coccoides</i> comb. nov. and emendations of the family Spirochaetaceae and the genus <i>Sphaerochaeta</i> . <i>Standards in Genomic Sciences</i> , 2012, 6, 194-209.	1.5	58
106	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20T). <i>Standards in Genomic Sciences</i> , 2010, 2, 158-167.	1.5	56
107	Functional Genomics of Novel Secondary Metabolites from Diverse Cyanobacteria Using Untargeted Metabolomics. <i>Marine Drugs</i> , 2013, 11, 3617-3631.	4.6	56
108	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015, 3, 62.	11.1	56

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109	DOE JGI Metagenome Workflow. MSystems, 2021, 6, .	3.8	56
110	A Genomic Encyclopedia of the Root Nodule Bacteria: assessing genetic diversity through a systematic biogeographic survey. Standards in Genomic Sciences, 2015, 10, 14.	1.5	55
111	Complete Genome Sequences for the Anaerobic, Extremely Thermophilic Plant Biomass-Degrading Bacteria <i>Caldicellulosiruptor hydrothermalis</i> , <i>Caldicellulosiruptor kristjanssonii</i> , <i>Caldicellulosiruptor kronotskyensis</i> , <i>Caldicellulosiruptor owensensis</i> , and <i>Caldicellulosiruptor lactoaceticus</i> . Journal of Bacteriology, 2011, 193, 1483-1484.	2.2	54
112	Improving Microbial Genome Annotations in an Integrated Database Context. PLoS ONE, 2013, 8, e54859.	2.5	54
113	Supporting community annotation and user collaboration in the integrated microbial genomes (IMG) system. BMC Genomics, 2016, 17, 307.	2.8	54
114	Facile Recoding of Selenocysteine in Nature. Angewandte Chemie - International Edition, 2016, 55, 5337-5341.	13.8	54
115	Gene Context Analysis in the Integrated Microbial Genomes (IMG) Data Management System. PLoS ONE, 2009, 4, e7979.	2.5	54
116	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM1325, an effective microsymbiont of annual Mediterranean clovers.. Standards in Genomic Sciences, 2010, 2, 347-356.	1.5	53
117	Diversity, evolution, and classification of virophages uncovered through global metagenomics. Microbiome, 2019, 7, 157.	11.1	53
118	VPF-Class: taxonomic assignment and host prediction of uncultivated viruses based on viral protein families. Bioinformatics, 2021, 37, 1805-1813.	4.1	53
119	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3T). Standards in Genomic Sciences, 2011, 4, 100-110.	1.5	51
120	Complete genome sequence of the thermophilic, hydrogen-oxidizing <i>Bacillus tusciae</i> type strain (T2T) and reclassification in the new genus, <i>Kyrpidia</i> gen. nov. as <i>Kyrpidia tusciae</i> comb. nov. and emendation of the family Alicyclobacillaceae da Costa and Rainey, 2010.. Standards in Genomic Sciences, 2011, 5, 121-134.	1.5	51
121	Draft Genome Sequence of <i>Frankia</i> sp. Strain CN3, an Atypical, Noninfective (Nod <sup>+</sup> ) Ineffective (Fix <sup>-</sup> ) Isolate from <i>Coriaria nepalensis</i> . Genome Announcements, 2013, 1, e0008513.	0.8	51
122	Complete genome sequence of the filamentous gliding predatory bacterium <i>Herpetosiphon aurantiacus</i> type strain (114-95T). Standards in Genomic Sciences, 2011, 5, 356-370.	1.5	47
123	Microbiome Data Science: Understanding Our Microbial Planet. Trends in Microbiology, 2016, 24, 425-427.	7.7	47
124	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24T). Standards in Genomic Sciences, 2011, 4, 91-99.	1.5	46
125	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1BT). Standards in Genomic Sciences, 2011, 4, 63-71.	1.5	46
126	Complete genome sequence of <i>Rhodothermus marinus</i> type strain (R-10T). Standards in Genomic Sciences, 2009, 1, 283-290.	1.5	45



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127	Complete genome sequence of <i>Thioalkalivibrio</i> sp. K90mix. <i>Standards in Genomic Sciences</i> , 2011, 5, 341-355.	1.5	45
128	A centimeter-long bacterium with DNA contained in metabolically active, membrane-bound organelles. <i>Science</i> , 2022, 376, 1453-1458.	12.6	45
129	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3T). <i>Standards in Genomic Sciences</i> , 2010, 2, 57-65.	1.5	44
130	Complete genome sequence of <i>Dehalobacter restrictus</i> PER-K23T. <i>Standards in Genomic Sciences</i> , 2013, 8, 375-388.	1.5	44
131	Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H11), 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
132	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
133	Complete genome sequence of <i>Olsenella uli</i> type strain (VPI D76D-27CT). <i>Standards in Genomic Sciences</i> , 2010, 3, 76-84.	1.5	43
134	IMG/M-HMP: A Metagenome Comparative Analysis System for the Human Microbiome Project. <i>PLoS ONE</i> , 2012, 7, e40151.	2.5	43
135	Genome sequence and description of the anaerobic lignin-degrading bacterium <i>Tolumonas lignolytica</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 106.	1.5	43
136	Complete genome sequence of the phenanthrene-degrading soil bacterium <i>Delftia acidovorans</i> Cs1-4. <i>Standards in Genomic Sciences</i> , 2015, 10, 55.	1.5	43
137	Complete genome sequence of <i>Nitrosomonas</i> sp. Is79, an ammonia oxidizing bacterium adapted to low ammonium concentrations. <i>Standards in Genomic Sciences</i> , 2013, 7, 469-482.	1.5	43
138	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
139	Ecological and genomic analyses of candidate phylum WPS bacteria in an unvegetated soil. <i>Environmental Microbiology</i> , 2020, 22, 3143-3157.	3.8	42
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144	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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#	ARTICLE	IF	CITATIONS
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398	Genome sequence of the chemoheterotrophic soil bacterium <i>Saccharomonospora cyanea</i> type strain (NA-134T). Standards in Genomic Sciences, 2013, 9, 28-41.	1.5	4
399	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain SRDI565.. Standards in Genomic Sciences, 2013, 9, 220-231.	1.5	4
400	Genome sequence of the South American clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM597. Standards in Genomic Sciences, 2013, 9, 264-272.	1.5	4
401	High quality draft genome sequence of <i>Bacteroides barnesiae</i> type strain BL2T (DSM 18169T) from chicken caecum. Standards in Genomic Sciences, 2015, 10, 48.	1.5	4
402	Draft Genome Sequence of the Cellulolytic and Xylanolytic Thermophile <i>Clostridium clariflavum</i> Strain 4-2a. Genome Announcements, 2015, 3, .	0.8	4
403	High-Quality Draft Genome Sequence of <i>Kallotenuis papyrolyticum</i> JKG1 T Reveals Broad Heterotrophic Capacity Focused on Carbohydrate and Amino Acid Metabolism. Genome Announcements, 2015, 3, .	0.8	4
404	Genome Sequence of <i>Polycyclovorans algicola</i> Strain TG408, an Obligate Polycyclic Aromatic Hydrocarbon-Degrading Bacterium Associated with Marine Eukaryotic Phytoplankton. Genome Announcements, 2015, 3, .	0.8	4
405	High-quality permanent draft genome sequence of <i>Ensifer meliloti</i> strain 4H41, an effective salt- and drought-tolerant microsymbiont of <i>Phaseolus vulgaris</i> . Standards in Genomic Sciences, 2015, 10, 34.	1.5	4
406	Genomic Prospecting for Microbial Biodiesel Production. , 0, , 405-418.		4
407	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FIGlyR). Standards in Genomic Sciences, 2011, 4, 371-80.	1.5	4
408	Permanent draft genome sequence of the gliding predator <i>Saprospira grandis</i> strain Sa g1 (= HR1). Standards in Genomic Sciences, 2012, 6, 210-219.	1.5	3
409	Genome sequence of the <i>Trifolium rueppellianum</i> -nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM2012.. Standards in Genomic Sciences, 2013, 9, 283-293.	1.5	3
410	Genome sequence of <i>Frateuria aurantia</i> type strain (KondÅ´ 67T), a xanthomonade isolated from <i>Lilium auratum</i> Lindl.. Standards in Genomic Sciences, 2013, 9, 83-92.	1.5	3
411	Genome sequence of the lupin-nodulating <i>Bradyrhizobium</i> sp. strain WSM1417. Standards in Genomic Sciences, 2013, 9, 273-282.	1.5	3
412	Genome sequence of the acid-tolerant <i>Burkholderia</i> sp. strain WSM2230 from Karijini National Park, Australia. Standards in Genomic Sciences, 2013, 9, 551-561.	1.5	3
413	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. Standards in Genomic Sciences, 2013, 8, 165-176.	1.5	3
414	Genome sequence of the dark pink pigmented <i>Listia bainesii</i> microsymbiont <i>Methylobacterium</i> sp. WSM2598. Standards in Genomic Sciences, 2014, 9, 5.	1.5	3



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415	Genome sequence of the <i>Medicago-nodulating Ensifer meliloti</i> commercial inoculant strain RRI128. <i>Standards in Genomic Sciences</i> , 2014, 9, 602-613.	1.5	3
416	Genome sequence of the <i>Wenxinia marina</i> type strain (DSM 24838T), a representative of the <i>Roseobacter</i> group isolated from oilfield sediments. <i>Standards in Genomic Sciences</i> , 2014, 9, 855-865.	1.5	3
417	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
418	High-quality permanent draft genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> strain GB30; an effective microsymbiont of <i>Pisum sativum</i> growing in Poland. <i>Standards in Genomic Sciences</i> , 2015, 10, 36.	1.5	3
419	Genome sequence of <i>Bradyrhizobium</i> sp. WSM1253; a microsymbiont of <i>Ornithopus compressus</i> from the Greek Island of Sifnos. <i>Standards in Genomic Sciences</i> , 2015, 10, 113.	1.5	3
420	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
421	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
422	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
423	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
424	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
425	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
426	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
427	Genome sequence of the flexirubin-pigmented soil bacterium <i>Niabella soli</i> type strain (JS13-8T). <i>Standards in Genomic Sciences</i> , 2012, 7, 210-220.	1.5	2
428	Genome sequence of <i>Ensifer medicae</i> strain WSM1115; an acid-tolerant <i>Medicago-nodulating</i> microsymbiont from Samothraki, Greece. <i>Standards in Genomic Sciences</i> , 2013, 9, 514-526.	1.5	2
429	Genome sequence of the acid-tolerant <i>Burkholderia</i> sp. strain WSM2232 from Karjijini National Park, Australia. <i>Standards in Genomic Sciences</i> , 2013, 9, 1168-1180.	1.5	2
430	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
431	High-quality permanent draft genome sequence of the <i>Parapiptadenia rigida-nodulating Burkholderia</i> sp. strain UYPR1.413. <i>Standards in Genomic Sciences</i> , 2015, 10, 31.	1.5	2
432	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

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434	High-quality permanent draft genome sequence of the Mimosa asperata - nodulating Cupriavidus sp. strain AMP6. Standards in Genomic Sciences, 2015, 10, 80.	1.5	2
435	High-quality permanent draft genome sequence of Bradyrhizobium sp. Th.b2, a microsymbiont of Amphicarpaea bracteata collected in Johnson City, New York. Standards in Genomic Sciences, 2015, 10, 24.	1.5	2
436	High-Quality draft genome sequence of the Lotus spp. microsymbiont Mesorhizobium loti strain CJ3Sym. Standards in Genomic Sciences, 2015, 10, 54.	1.5	2
437	Application of Long Sequence Reads To Improve Genomes for Clostridium thermocellum AD2, Clostridium thermocellum LQRI, and Pelosinus fermentans R7. Genome Announcements, 2016, 4, .	0.8	2
438	An improved high-quality draft genome sequence of Carnobacterium inhibens subsp. inhibens strain K1T. Standards in Genomic Sciences, 2016, 11, 65.	1.5	2
439	Permanent draft genome sequence of Desulfurococcus mobilis type strain DSM 2161, a thermoacidophilic sulfur-reducing crenarchaeon isolated from acidic hot springs of Hveravellir, Iceland. Standards in Genomic Sciences, 2016, 11, 3.	1.5	2
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442	High-quality draft genome sequence of Rhizobium mesoamericanum strain STM6155, a Mimosa pudica microsymbiont from New Caledonia. Standards in Genomic Sciences, 2017, 12, 7.	1.5	2
443	High-Quality Draft Genome Sequence of the Siderophilic and Thermophilic <i>Leptolyngbyaceae</i> Cyanobacterium JSC-12. Microbiology Resource Announcements, 2021, 10, e0049521.	0.6	2
444	Metagenomes and Metatranscriptomes of a Glucose-Amended Agricultural Soil. Microbiology Resource Announcements, 2020, 9, .	0.6	2
445	The Genome of the Acid Soil-Adapted Strain Rhizobium favelukesii OR191 Encodes Determinants for Effective Symbiotic Interaction With Both an Inverted Repeat Lacking Clade and a Phaseoloid Legume Host. Frontiers in Microbiology, 2022, 13, 735911.	3.5	2
446	SOP for pathway inference in Integrated Microbial Genomes (IMG). Standards in Genomic Sciences, 2010, 5, 420-423.	1.5	1
447	Genome sequence of Ensifer medicae strain WSM1369; an effective microsymbiont of the annual legume Medicago sphaerocarpos. Standards in Genomic Sciences, 2013, 9, 420-430.	1.5	1
448	High-quality permanent draft genome sequence of the Lebeckia - nodulating Burkholderia dilworthii strain WSM3556T. Standards in Genomic Sciences, 2015, 10, 64.	1.5	1
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452	High-quality permanent draft genome sequence of <i>Ensifer medicae</i> strain WSM244, a microsymbiont isolated from <i>Medicago polymorpha</i> growing in alkaline soil. <i>Standards in Genomic Sciences</i> , 2015, 10, 126.	1.5	1
453	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
454	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
455	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
456	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
457	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
458	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
459	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
460	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
461	Complete genome sequence of <i>Mesorhizobium australicum</i> type strain (WSM2073T). <i>Standards in Genomic Sciences</i> , 2013, 9, 1-15.	1.5	1
462	<i>Sodalis ligni</i> Strain 159R Isolated from an Anaerobic Lignin-Degrading Consortium. <i>Microbiology Spectrum</i> , 2022, 10, e0234621.	3.0	1
463	Genome sequence of the <i>Ornithopus/Lupinus</i> -nodulating <i>Bradyrhizobium</i> sp. strain WSM471. <i>Standards in Genomic Sciences</i> , 2013, 9, 254-263.	1.5	0
464	Genome sequence of <i>Ensifer medicae</i> Di28; an effective N <sub>2</sub> -fixing microsymbiont of <i>Medicago murex</i> and <i>M. polymorpha</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 4.	1.5	0
465	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
466	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