

Alla L Lapidus

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7385475/publications.pdf>

Version: 2024-02-01

349
papers

28,592
citations

9264

74
h-index

7518

151
g-index

360
all docs

360
docs citations

360
times ranked

30100
citing authors

#	ARTICLE	IF	CITATIONS
1	The lineage of coronavirus SARS-CoV-2 of Russian origin: Genetic characteristics and correlations with clinical parameters and severity of coronavirus infection. <i>Sibirskij Ā¼urnal KliniĀeskoj I ĀksperimentalĀnoj Mediciny</i> , 2022, 36, 132-143.	0.4	1
2	Metagenomic Data Assembly Ā€“ The Way of Decoding Unknown Microorganisms. <i>Frontiers in Microbiology</i> , 2021, 12, 613791.	3.5	67
3	Draft Genome Sequence of <i>Bordetella</i> sp. Strain FB-8, Isolated from a Former Uranium Mining Area in Germany. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
4	Elemental and Molecular Composition of Humic Acids Isolated from Soils of Tallgrass Temperate Rainforests (Chernevaya taiga) by 1H-13C HECTCOR NMR Spectroscopy. <i>Agronomy</i> , 2021, 11, 1998.	3.0	8
5	Fungal Metagenome of Chernevaya Taiga Soils: Taxonomic Composition, Differential Abundance and Factors Related to Plant Gigantism. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 908.	3.5	4
6	Genomic Variations in Drug Resistant <i>Mycobacterium tuberculosis</i> Strains Collected from Patients with Different Localization of Infection. <i>Antibiotics</i> , 2021, 10, 27.	3.7	1
7	MGnify: the microbiome analysis resource in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D570-D578.	14.5	296
8	Mixotrophic Iron-Oxidizing <i>Thiomonas</i> Isolates from an Acid Mine Drainage-Affected Creek. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	9
9	CDSnake: Snakemake pipeline for retrieval of annotated OTUs from paired-end reads using CD-HIT utilities. <i>BMC Bioinformatics</i> , 2020, 21, 303.	2.6	2
10	Extending rnaSPAdes functionality for hybrid transcriptome assembly. <i>BMC Bioinformatics</i> , 2020, 21, 302.	2.6	17
11	Using SPAdes De Novo Assembler. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e102.	25.8	1,113
12	A New Thioalkalivibrio sp. Strain Isolated from Petroleum-Contaminated Brackish Estuary Sediments: A New Candidate for Bio-Based Application for Sulfide Oxidation in Halo-Alkaline Conditions. <i>Water</i> (Switzerland), 2020, 12, 1385.	2.7	1
13	<sc>Metaviral</sc> <sc>SPAdes</sc>: assembly of viruses from metagenomic data. <i>Bioinformatics</i> , 2020, 36, 4126-4129.	4.1	149
14	Sequence Analysis. , 2019, , 292-322.		8
15	rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. <i>GigaScience</i> , 2019, 8, .	6.4	428
16	Plasmid detection and assembly in genomic and metagenomic data sets. <i>Genome Research</i> , 2019, 29, 961-968.	5.5	108
17	IonHammer: Homopolymer-Space Hamming Clustering for IonTorrent Read Error Correction. <i>Journal of Computational Biology</i> , 2019, 26, 124-127.	1.6	5
18	Draft Genome Sequence of Mn(II)-Oxidizing Bacterium <i>Oxalobacteraceae</i> sp. Strain AB_14. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4

#	ARTICLE	IF	CITATIONS
19	Autoprotobiotics as an Approach for Restoration of Personalised Microbiota. <i>Frontiers in Microbiology</i> , 2018, 9, 1869.	3.5	28
20	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	8.8	417
21	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
22	Permanent Draft Genome Sequence of <i>Desulfurococcus amylolyticus</i> Strain Z-533, a Peptide and Starch Degradator Isolated from Thermal Springs in the Kamchatka Peninsula and Kunashir Island, Russia. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
23	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
24	Complete mitochondrial genomes of Baikal oilfishes (Perciformes: Cottoidei), earth's deepest-swimming freshwater fishes. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 773-775.	0.4	2
25	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
26	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
27	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2016, 7, 238.	3.5	66
28	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , 2016, 12, e1006108.	3.5	177
29	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
30	rnaQUAST: a quality assessment tool for <i>de novo</i> transcriptome assemblies. <i>Bioinformatics</i> , 2016, 32, 2210-2212.	4.1	106
31	plasmidSPAdes: assembling plasmids from whole genome sequencing data. <i>Bioinformatics</i> , 2016, 32, 3380-3387.	4.1	468
32	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9882-9887.	7.1	302
33	Complete Genome Sequence of <i>Alkaliphilus metalliredigens</i> Strain QYMF, an Alkaliphilic and Metal-Reducing Bacterium Isolated from Borax-Contaminated Leachate Ponds. <i>Genome Announcements</i> , 2016, 4, .	0.8	10
34	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
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	Draft genome of <i>Prochlorothrix hollandica</i> CCAP 1490/1T (CALU1027), the chlorophyll a/b-containing filamentous cyanobacterium. <i>Standards in Genomic Sciences</i> , 2016, 11, 82.	1.5	0
38	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
39	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
40	Complete genome sequence of <i>Methanospirillum hungatei</i> type strain JF1. <i>Standards in Genomic Sciences</i> , 2016, 11, 2.	1.5	33
41	High quality permanent draft genome sequence of <i>Phaseolibacter flectens</i> ATCC 12775T, a plant pathogen of French bean pods. <i>Standards in Genomic Sciences</i> , 2016, 11, 4.	1.5	1
42	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
43	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
44	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
45	Sequencing, biochemical characterization, crystal structure and molecular dynamics of cellobiohydrolase Cel7A from <i>Geotrichum candidum</i> 3C. <i>FEBS Journal</i> , 2015, 282, 4515-4537.	4.7	37
46	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
47	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
48	High-quality permanent draft genome sequence of the extremely osmotolerant diphenol degrading bacterium <i>Halotalea alkalilenta</i> AW-7T, and emended description of the genus <i>Halotalea</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 52.	1.5	5
49	Genome Sequence of the Atypical Symbiotic <i>Frankia</i> R43 Strain, a Nitrogen-Fixing and Hydrogen-Producing Actinobacterium. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
50	High quality draft genome sequence of <i>Flavobacterium rivuli</i> type strain WB 3.3-2T (DSM 21788T), a valuable source of polysaccharide decomposing enzymes. <i>Standards in Genomic Sciences</i> , 2015, 10, 46.	1.5	16
51	High quality draft genome sequence of <i>Corynebacterium ulceribovis</i> type strain IMMIB-L1395T (DSM) Tj ETQq1 1 0,784314 rgBT /Overl	1.5	1
52	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
53	IgSimulator: a versatile immunosequencing simulator. <i>Bioinformatics</i> , 2015, 31, 3213-3215.	4.1	35
54	High quality draft genome sequence of <i>Leucobacter chironomi</i> strain MM2LBT (DSM 19883T) isolated from a <i>Chironomus</i> sp. egg mass. <i>Standards in Genomic Sciences</i> , 2015, 10, 21.	1.5	8

#	ARTICLE	IF	CITATIONS
55	High-Quality Draft Genome Sequence of <i>Desulfovibrio carbinolophilus</i> FW-101-2B, an Organic Acid-Oxidizing Sulfate-Reducing Bacterium Isolated from Uranium(VI)-Contaminated Groundwater. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
56	IgRepertoireConstructor: a novel algorithm for antibody repertoire construction and immunoproteogenomics analysis. <i>Bioinformatics</i> , 2015, 31, i53-i61.	4.1	42
57	High quality draft genome sequence of <i>Meganema perideroedes</i> str. Gr1T and a proposal for its reclassification to the family Meganemaceae fam. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 23.	1.5	15
58	Consortium of the <i>Chlorobium</i> cyanobacterium <i>Chlorobium hollandicum</i> and chemoheterotrophic partner bacteria: culture and metagenome-based description. <i>Environmental Microbiology Reports</i> , 2015, 7, 623-633.	2.4	6
59	Complete Genome Sequence of <i>Anaeromyxobacter</i> sp. Fw109-5, an Anaerobic, Metal-Reducing Bacterium Isolated from a Contaminated Subsurface Environment. <i>Genome Announcements</i> , 2015, 3, .	0.8	17
60	Characterization of Cyanobacterial Hydrocarbon Composition and Distribution of Biosynthetic Pathways. <i>PLoS ONE</i> , 2014, 9, e85140.	2.5	190
61	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	5.6	190
62	ExSPAnDer: a universal repeat resolver for DNA fragment assembly. <i>Bioinformatics</i> , 2014, 30, i293-i301.	4.1	103
63	Genome-wide <i>Mycobacterium tuberculosis</i> variation (GMTV) database: a new tool for integrating sequence variations and epidemiology. <i>BMC Genomics</i> , 2014, 15, 308.	2.8	89
64	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
65	Genome sequence and emended description of <i>Leisingera nanhaiensis</i> strain DSM 24252T isolated from marine sediment. <i>Standards in Genomic Sciences</i> , 2014, 9, 585-601.	1.5	8
66	Genome sequence of the <i>Thermotoga thermarum</i> type strain (LA3T) from an African solfataric spring. <i>Standards in Genomic Sciences</i> , 2014, 9, 1105-1117.	1.5	7
67	Genome analyses of the carboxydrotrophic sulfate-reducers <i>Desulfotomaculum nigrificans</i> and <i>Desulfotomaculum carboxydvorans</i> and reclassification of <i>Desulfotomaculum carboxydvorans</i> as a later synonym of <i>Desulfotomaculum nigrificans</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 655-675.	1.5	25
68	High quality draft genome sequence of <i>Olivibacter sitiensis</i> type strain (AW-6T), a diphenol degrader with genes involved in the catechol pathway. <i>Standards in Genomic Sciences</i> , 2014, 9, 783-793.	1.5	18
69	Genome sequence of the mud-dwelling archaeon <i>Methanoplanus limicola</i> type strain (DSM 2279T), reclassification of <i>Methanoplanus petrolearius</i> as <i>Methanolacinia petrolearia</i> and emended descriptions of the genera <i>Methanoplanus</i> and <i>Methanolacinia</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 1076-1088.	1.5	22
70	High quality draft genome sequence of the slightly halophilic bacterium <i>Halomonas zhanjiangensis</i> type strain JSM 078169T (DSM 21076T) from a sea urchin in southern China. <i>Standards in Genomic Sciences</i> , 2014, 9, 1020-1030.	1.5	9
71	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. <i>Lecture Notes in Computer Science</i> , 2013, , 158-170.	1.3	439
72	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. <i>Journal of Computational Biology</i> , 2013, 20, 714-737.	1.6	1,235

#	ARTICLE	IF	CITATIONS
73	Genome Sequence of the Obligate Gammaproteobacterial Methanotroph <i>Methylomicrobium album</i> Strain BG8. <i>Genome Announcements</i> , 2013, 1, e0017013.	0.8	23
74	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
75	Correction for Morin et al., Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4146-4146.	7.1	4
76	Complete genome sequence of <i>Coriobacterium glomerans</i> type strain (PW2T) from the midgut of <i>Pyrrhocoris apterus</i> L. (red soldier bug). <i>Standards in Genomic Sciences</i> , 2013, 8, 15-25.	1.5	8
77	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
78	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
79	Complete genome sequence of the moderate thermophile <i>Anaerobaculum mobile</i> type strain (NGAT). <i>Standards in Genomic Sciences</i> , 2013, 8, 47-57.	1.5	11
80	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
81	Complete genome sequence of <i>Halorhodospira halophila</i> SL1. <i>Standards in Genomic Sciences</i> , 2013, 8, 206-214.	1.5	26
82	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
83	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
84	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
85	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
86	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 zuelzeræ</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzeræ</i> comb. nov., and emendation of the genus <i>Treponema</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 88-105.	1.5	44
87	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
88	Genome sequence of the phylogenetically isolated spirochete <i>Leptonema illini</i> type strain (3055T). <i>Standards in Genomic Sciences</i> , 2013, 8, 177-187.	1.5	5
89	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
90	Complete genome sequence of the marine methyl-halide oxidizing <i>Leisingera methylhalidivorans</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

#	ARTICLE	IF	CITATIONS
91	Genome sequence of <i>Phaeobacter caeruleus</i> type strain (DSM 24564(T)), a surface-associated member of the marine <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013, 8, 403-19.	1.5	12
92	The Genomes of the Fungal Plant Pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. <i>PLoS Genetics</i> , 2012, 8, e1003088.	3.5	226
93	Complete Genome Sequences of <i>Desulfosporosinus orientis</i> DSM765 ^T , <i>Desulfosporosinus youngiae</i> DSM17734 ^T , <i>Desulfosporosinus meridiei</i> DSM13257 ^T , and <i>Desulfosporosinus acidiphilus</i> DSM22704 ^T . <i>Journal of Bacteriology</i> , 2012, 194, 6300-6301.	2.2	73
94	Complete Genome Sequence of the Thermophilic, Piezophilic, Heterotrophic Bacterium <i>Marinitoga piezophila</i> KA3. <i>Journal of Bacteriology</i> , 2012, 194, 5974-5975.	2.2	25
95	Complete Genome Sequence of <i>Desulfurococcus fermentans</i> , a Hyperthermophilic Cellulolytic Crenarchaeon Isolated from a Freshwater Hot Spring in Kamchatka, Russia. <i>Journal of Bacteriology</i> , 2012, 194, 5703-5704.	2.2	15
96	Genome sequence of the moderately thermophilic, amino-acid-degrading and sulfur-reducing bacterium <i>Thermovirga lienii</i> type strain (Cas60314T). <i>Standards in Genomic Sciences</i> , 2012, 6, 230-239.	1.5	26
97	Genome sequence of the orange-pigmented seawater bacterium <i>Owenweeksia hongkongensis</i> type strain (UST20020801T). <i>Standards in Genomic Sciences</i> , 2012, 7, 120-130.	1.5	11
98	Complete genome sequence of the moderately thermophilic mineral-sulfide-oxidizing firmicute <i>Sulfobacillus acidophilus</i> type strain (NALT). <i>Standards in Genomic Sciences</i> , 2012, 6, 293-303.	1.5	23
99	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
100	Permanent draft genome sequence of the gliding predator <i>Saprospira grandis</i> strain Sa g1 (= HR1). <i>Standards in Genomic Sciences</i> , 2012, 6, 210-219.	1.5	3
101	Genome sequence of the soil bacterium <i>Saccharomonospora azurea</i> type strain (NA-128T). <i>Standards in Genomic Sciences</i> , 2012, 6, 220-229.	1.5	13
102	Complete genome sequence of the facultatively anaerobic, appendaged bacterium <i>Muricauda ruestringensis</i> type strain (B1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 185-193.	1.5	10
103	Complete genome sequence of <i>Dehalogenimonas lykanthroporepellens</i> type strain (BL-DC-9T) and comparison to <i>Dehalococcoides</i> strains. <i>Standards in Genomic Sciences</i> , 2012, 6, 251-264.	1.5	51
104	Complete genome sequence of <i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> type strain (QLW-P1DMWA-1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 74-83.	1.5	33
105	Complete genome sequence of the aerobic, heterotroph <i>Marinithermus hydrothermalis</i> type strain (T1T) from a deep-sea hydrothermal vent chimney. <i>Standards in Genomic Sciences</i> , 2012, 6, 21-30.	1.5	8
106	Complete genome sequence of the aquatic bacterium <i>Runella slithyformis</i> type strain (LSU 4T). <i>Standards in Genomic Sciences</i> , 2012, 6, 145-154.	1.5	24
107	Complete Genome Sequence of <i>Paenibacillus</i> strain Y4.12MC10, a Novel <i>Paenibacillus lautus</i> strain Isolated from Obsidian Hot Spring in Yellowstone National Park. <i>Standards in Genomic Sciences</i> , 2012, 6, 381-400.	1.5	32
108	Genome sequence of the ocean sediment bacterium <i>Saccharomonospora marina</i> type strain (XMU15T). <i>Standards in Genomic Sciences</i> , 2012, 6, 265-275.	1.5	5

#	ARTICLE	IF	CITATIONS
109	Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium <i>Thermodesulfator indicus</i> type strain (CIR29812T). <i>Standards in Genomic Sciences</i> , 2012, 6, 155-164.	1.5	14
110	Complete genome sequence of <i>Thauera aminoaromatica</i> strain MZ1T. <i>Standards in Genomic Sciences</i> , 2012, 6, 325-335.	1.5	53
111	Complete genome sequence of <i>Serratia plymuthica</i> strain AS12. <i>Standards in Genomic Sciences</i> , 2012, 6, 165-173.	1.5	19
112	Genome sequence of the homoacetogenic bacterium <i>Holophaga foetida</i> type strain (TMBS4T). <i>Standards in Genomic Sciences</i> , 2012, 6, 174-184.	1.5	26
113	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRPT). <i>Standards in Genomic Sciences</i> , 2012, 6, 240-250.	1.5	14
114	Complete genome sequence of the plant-associated <i>Serratia plymuthica</i> strain AS13. <i>Standards in Genomic Sciences</i> , 2012, 7, 22-30.	1.5	22
115	Complete genome sequence of <i>Syntrophobacter fumaroxidans</i> strain (MPOBT). <i>Standards in Genomic Sciences</i> , 2012, 7, 91-106.	1.5	55
116	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
117	Genome sequence of the Antarctic rhodopsins-containing flavobacterium <i>Gillisia limnaea</i> type strain (R-8282T). <i>Standards in Genomic Sciences</i> , 2012, 7, 107-119.	1.5	16
118	Complete genome sequence of the sulfate-reducing firmicute <i>Desulfotomaculum ruminis</i> type strain (DLT). <i>Standards in Genomic Sciences</i> , 2012, 7, 304-319.	1.5	22
119	Complete genome sequence of <i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> type strain (QLW-P1DMWA-1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 1-14.	1.5	30
120	Complete genome sequence of <i>Halopiger xanaduensis</i> type strain (SH-6T). <i>Standards in Genomic Sciences</i> , 2012, 6, 31-42.	1.5	9
121	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093T). <i>Standards in Genomic Sciences</i> , 2012, 7, 44-58.	1.5	16
122	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricurvum kujjense</i> type strain (YK-1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 94-103.	1.5	37
123	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17501-17506.	7.1	359
124	CD45-deficient severe combined immunodeficiency caused by uniparental disomy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10456-10461.	7.1	39
125	The genome of the xerotolerant mold <i>Wallemia sebi</i> reveals adaptations to osmotic stress and suggests cryptic sexual reproduction. <i>Fungal Genetics and Biology</i> , 2012, 49, 217-226.	2.1	103
126	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnosa</i> and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. <i>BMC Genomics</i> , 2012, 13, 444.	2.8	125

#	ARTICLE	IF	CITATIONS
127	Complete genome sequence of the rapeseed plant-growth promoting <i>Serratia plymuthica</i> strain AS9. <i>Standards in Genomic Sciences</i> , 2012, 6, 54-62.	1.5	27
128	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5458-5463.	7.1	259
129	The Fast Changing Landscape of Sequencing Technologies and Their Impact on Microbial Genome Assemblies and Annotation. <i>PLoS ONE</i> , 2012, 7, e48837.	2.5	145
130	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093T). <i>Standards in Genomic Sciences</i> , 2012, 7, 44-58.	1.5	19
131	Complete Genome of the Cellulolytic Ruminal Bacterium <i>Ruminococcus albus</i> 7. <i>Journal of Bacteriology</i> , 2011, 193, 5574-5575.	2.2	87
132	Complete genome sequence of the filamentous gliding predatory bacterium <i>Herpetosiphon aurantiacus</i> type strain (114-95T). <i>Standards in Genomic Sciences</i> , 2011, 5, 356-370.	1.5	47
133	Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13212-13217.	7.1	163
134	Complete genome sequence of <i>Leadbetterella byssophila</i> type strain (4M15T). <i>Standards in Genomic Sciences</i> , 2011, 4, 2-12.	1.5	22
135	Complete genome sequence of <i>Hydrogenobacter thermophilus</i> type strain (TK-6T). <i>Standards in Genomic Sciences</i> , 2011, 4, 131-143.	1.5	12
136	Complete genome sequence of <i>Paludibacter propionigenes</i> type strain (WB4T). <i>Standards in Genomic Sciences</i> , 2011, 4, 36-44.	1.5	30
137	Complete genome sequence of <i>Bacteroides helcogenes</i> type strain (P 36-108T). <i>Standards in Genomic Sciences</i> , 2011, 4, 45-53.	1.5	14
138	Complete genome sequence of <i>Weeksella virosa</i> type strain (9751T). <i>Standards in Genomic Sciences</i> , 2011, 4, 81-90.	1.5	15
139	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3T). <i>Standards in Genomic Sciences</i> , 2011, 4, 100-110.	1.5	51
140	Complete genome sequence of <i>Marivirga tractuosa</i> type strain (H-43T). <i>Standards in Genomic Sciences</i> , 2011, 4, 154-162.	1.5	18
141	Complete genome sequence of <i>Desulfurococcus mucosus</i> type strain (O7/1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 173-182.	1.5	10
142	Complete genome sequence of <i>Cellulophaga lytica</i> type strain (LIM-21T). <i>Standards in Genomic Sciences</i> , 2011, 4, 221-232.	1.5	33
143	Non-contiguous finished genome sequence of <i>Bacteroides coprosuis</i> type strain (PC139T). <i>Standards in Genomic Sciences</i> , 2011, 4, 233-243.	1.5	9
144	Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 293-302.	1.5	44

#	ARTICLE	IF	CITATIONS
145	Complete genome sequence of the extremely halophilic Halanaerobium praevalens type strain (GSLT). Standards in Genomic Sciences, 2011, 4, 312-321.	1.5	36
146	Complete genome sequence of Nitratifactor salsuginis type strain (E9137-1T). Standards in Genomic Sciences, 2011, 4, 322-330.	1.5	13
147	Complete genome sequence of Mahella australiensis type strain (50-1 BONT). Standards in Genomic Sciences, 2011, 4, 331-341.	1.5	7
148	Complete genome sequence of Treponema succinifaciens type strain (6091T). Standards in Genomic Sciences, 2011, 4, 361-370.	1.5	41
149	Complete genome sequence of Syntrophobotulus glycolicus type strain (FGlyRT). Standards in Genomic Sciences, 2011, 4, 371-380.	1.5	11
150	Complete genome sequence of the hyperthermophilic chemolithoautotroph Pyrolobus fumarii type strain (1AT). Standards in Genomic Sciences, 2011, 4, 381-392.	1.5	13
151	Complete genome sequence of Staphylothermus hellenicus P8T. Standards in Genomic Sciences, 2011, 5, 12-20.	1.5	7
152	Complete genome sequence of the acetate-degrading sulfate reducer Desulfobacca acetoxidans type strain (ASRB2T). Standards in Genomic Sciences, 2011, 4, 393-401.	1.5	25
153	Complete genome sequence of the thermophilic, hydrogen-oxidizing Bacillus tusciae type strain (T2T) and reclassification in the new genus, Kyrpidia gen. nov. as Kyrpidia tusciae comb. nov. and emendation of the family Alicyclobacillaceae da Costa and Rainey, 2010.. Standards in Genomic Sciences, 2011, 5, 121-134.	1.5	51
154	Complete genome sequence of the gliding, heparinolytic Pedobacter saltans type strain (113T). Standards in Genomic Sciences, 2011, 5, 30-40.	1.5	16
155	Non-contiguous finished genome sequence of the opportunistic oral pathogen Prevotella multisaccharivorax type strain (PPPA20T). Standards in Genomic Sciences, 2011, 5, 41-49.	1.5	7
156	Complete genome sequence of Tolumonas auensis type strain (TA 4T). Standards in Genomic Sciences, 2011, 5, 112-120.	1.5	6
157	Complete genome sequence of Hirschia baltica type strain (IFAM 1418T). Standards in Genomic Sciences, 2011, 5, 287-297.	1.5	12
158	Complete genome sequence of Ferroplasma placidus AEDII12DO. Standards in Genomic Sciences, 2011, 5, 50-60.	1.5	32
159	Complete genome sequence of the halophilic and highly halotolerant Chromohalobacter salexigens type strain (1H11T). Standards in Genomic Sciences, 2011, 5, 379-388.	1.5	35
160	Genome sequence of the filamentous, gliding Thiiothrix nivea neotype strain (JP2T). Standards in Genomic Sciences, 2011, 5, 398-406.	1.5	22
161	Complete genome sequence of the thermophilic sulfur-reducer Desulfurobacterium thermolithotrophum type strain (BSAT) from a deep-sea hydrothermal vent. Standards in Genomic Sciences, 2011, 5, 407-415.	1.5	11
162	Complete genome sequence of Thioalkalivibrio œsulfidophilus HL-EbGr7. Standards in Genomic Sciences, 2011, 4, 23-35.	1.5	72

#	ARTICLE	IF	CITATIONS
163	Complete genome sequence of <i>Calditerrivibrio nitroreducens</i> type strain (Yu37-1T). Standards in Genomic Sciences, 2011, 4, 54-62.	1.5	10
164	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24T). Standards in Genomic Sciences, 2011, 4, 91-99.	1.5	46
165	Complete genome sequence of <i>Bacteroides salanitronis</i> type strain (BL78T). Standards in Genomic Sciences, 2011, 4, 191-199.	1.5	11
166	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6T). Standards in Genomic Sciences, 2011, 4, 200-209.	1.5	96
167	Complete genome sequence of <i>Oceanithermus profundus</i> type strain (506T). Standards in Genomic Sciences, 2011, 4, 210-220.	1.5	4
168	Complete genome sequence of <i>Tsukamurella paurometabola</i> type strain (no. 33T). Standards in Genomic Sciences, 2011, 4, 342-351.	1.5	10
169	Complete genome sequence of <i>Mycobacterium</i> sp. strain (Spyr1) and reclassification to <i>Mycobacterium gilvum</i> Spyr1. Standards in Genomic Sciences, 2011, 5, 144-153.	1.5	22
170	Complete genome sequence of <i>Thioalkalivibrio</i> sp. K90mix. Standards in Genomic Sciences, 2011, 5, 341-355.	1.5	45
171	Complete genome sequence of <i>Arthrobacter phenanthrenivorans</i> type strain (Sphe3). Standards in Genomic Sciences, 2011, 4, 123-130.	1.5	31
172	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21T). Standards in Genomic Sciences, 2011, 5, 97-111.	1.5	115
173	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1BT). Standards in Genomic Sciences, 2011, 4, 63-71.	1.5	46
174	Complete genome sequence of <i>Cellulophaga algicola</i> type strain (IC166T). Standards in Genomic Sciences, 2011, 4, 72-80.	1.5	28
175	Complete genome sequence of <i>Riemerella anatipestifer</i> type strain (ATCC 11845T). Standards in Genomic Sciences, 2011, 4, 144-153.	1.5	33
176	Complete genome sequence of the thermophilic sulfur-reducer <i>Hippea maritima</i> type strain (MH2T). Standards in Genomic Sciences, 2011, 4, 303-311.	1.5	8
177	Complete genome sequence of <i>Haliscomenobacter hydrossis</i> type strain (OT). Standards in Genomic Sciences, 2011, 4, 352-360.	1.5	26
178	Complete genome sequence of the gliding freshwater bacterium <i>Fluviicola taffensis</i> type strain (RW262T). Standards in Genomic Sciences, 2011, 5, 21-29.	1.5	23
179	Genome sequence of the moderately thermophilic halophile <i>Flexistipes sinusarabici</i> strain (MAS10T). Standards in Genomic Sciences, 2011, 5, 86-96.	1.5	12
180	Complete genome sequence of <i>Deinococcus maricopensis</i> type strain (LB-34T). Standards in Genomic Sciences, 2011, 4, 163-172.	1.5	14

#	ARTICLE	IF	CITATIONS
181	Exploring the symbiotic pangenome of the nitrogen-fixing bacterium <i>Sinorhizobium meliloti</i> . <i>BMC Genomics</i> , 2011, 12, 235.	2.8	97
182	Complete genome sequence of the filamentous anoxygenic phototrophic bacterium <i>Chloroflexus aurantiacus</i> . <i>BMC Genomics</i> , 2011, 12, 334.	2.8	90
183	Genome Sequence of the <i>Verrucomicrobium Opitutus terrae</i> PB90-1, an Abundant Inhabitant of Rice Paddy Soil Ecosystems. <i>Journal of Bacteriology</i> , 2011, 193, 2367-2368.	2.2	44
184	Genome Sequence of <i>Victivallis vadensis</i> ATCC BAA-548, an Anaerobic Bacterium from the Phylum Lentisphaerae, Isolated from the Human Gastrointestinal Tract. <i>Journal of Bacteriology</i> , 2011, 193, 2373-2374.	2.2	14
185	Genomes of Three Methylophils 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
186	Complete Genome Sequence of the Cellulose-Degrading Bacterium <i>Cellulosilyticum lentocellum</i> . <i>Journal of Bacteriology</i> , 2011, 193, 2357-2358.	2.2	28
187	Genome Sequence of the Arctic Methanotroph <i>Methylobacter tundripaludum</i> SV96. <i>Journal of Bacteriology</i> , 2011, 193, 6418-6419.	2.2	78
188	The Evolution of Host Specialization in the Vertebrate Gut Symbiont <i>Lactobacillus reuteri</i> . <i>PLoS Genetics</i> , 2011, 7, e1001314.	3.5	270
189	Genome Sequence of the 1,4-Dioxane-Degrading <i>Pseudonocardia dioxanivorans</i> Strain CB1190. <i>Journal of Bacteriology</i> , 2011, 193, 4549-4550.	2.2	56
190	Genome Sequence of the Ethene- and Vinyl Chloride-Oxidizing Actinomycete <i>Nocardioides</i> sp. Strain JS614. <i>Journal of Bacteriology</i> , 2011, 193, 3399-3400.	2.2	17
191	Complete Genome Sequence of the Thermophilic Bacterium <i>Exiguobacterium</i> sp. AT1b. <i>Journal of Bacteriology</i> , 2011, 193, 2880-2881.	2.2	47
192	Genome Sequence of <i>Chthoniobacter flavus</i> Ellin428, an Aerobic Heterotrophic Soil Bacterium. <i>Journal of Bacteriology</i> , 2011, 193, 2902-2903.	2.2	52
193	Genome Sequence of <i>Pedospira parvula</i> Ellin514, an Aerobic Verrucomicrobial Isolate from Pasture Soil. <i>Journal of Bacteriology</i> , 2011, 193, 2900-2901.	2.2	28
194	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
195	Complete Genome Sequence and Updated Annotation of <i>Desulfovibrio alaskensis</i> G20. <i>Journal of Bacteriology</i> , 2011, 193, 4268-4269.	2.2	56
196	Massive Changes in Genome Architecture Accompany the Transition to Self-Fertility in the Filamentous Fungus <i>Neurospora tetrasperma</i> . <i>Genetics</i> , 2011, 189, 55-69.	2.9	69
197	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> . <i>Journal of Bacteriology</i> , 2011, 193, 1483-1484.	2.2	54
198	Complete Genome Sequence of the Cellulolytic Thermophile <i>Clostridium thermocellum</i> DSM1313. <i>Journal of Bacteriology</i> , 2011, 193, 2906-2907.	2.2	66

#	ARTICLE	IF	CITATIONS
199	Genome Sequence of the Methanotrophic Alphaproteobacterium <i>Methylocystis</i> sp. Strain Rockwell (ATCC 49242). <i>Journal of Bacteriology</i> , 2011, 193, 2668-2669.	2.2	55
200	The Plant Cell Wallâ€œDecomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	12.6	512
201	Genome Sequence of the Mercury-Methylating Strain <i>Desulfovibrio desulfuricans</i> ND132. <i>Journal of Bacteriology</i> , 2011, 193, 2078-2079.	2.2	41
202	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9T). <i>Standards in Genomic Sciences</i> , 2011, 4, 13-22.	1.5	35
203	Complete genome sequence of <i>Riemerella anatipestifer</i> type strain (ATCC 11845). <i>Standards in Genomic Sciences</i> , 2011, 4, 144-53.	1.5	20
204	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FIGlyR). <i>Standards in Genomic Sciences</i> , 2011, 4, 371-80.	1.5	4
205	Complete genome sequence of <i>Planctomyces limnophilus</i> type strain (MÃ¼ 290T). <i>Standards in Genomic Sciences</i> , 2010, 3, 47-56.	1.5	31
206	Permanent draft genome sequence of <i>Dethiosulfovibrio peptidovorans</i> type strain (SEBR 4207T). <i>Standards in Genomic Sciences</i> , 2010, 3, 85-92.	1.5	9
207	Complete genome sequence of <i>Ferrimonas balearica</i> type strain (PATT). <i>Standards in Genomic Sciences</i> , 2010, 3, 174-182.	1.5	14
208	Non-contiguous finished genome sequence of <i>Aminomonas paucivorans</i> type strain (GLU-3T). <i>Standards in Genomic Sciences</i> , 2010, 3, 285-293.	1.5	9
209	Complete genome sequence of <i>Ilyobacter polytropus</i> type strain (CuHbu1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 304-314.	1.5	10
210	Complete genome sequence of <i>Nocardioopsis dassonvillei</i> type strain (IMRU 509T). <i>Standards in Genomic Sciences</i> , 2010, 3, 325-336.	1.5	32
211	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3T). <i>Standards in Genomic Sciences</i> , 2010, 2, 57-65.	1.5	44
212	Complete genome sequence of <i>Kribbella flavida</i> type strain (IFO 14399T). <i>Standards in Genomic Sciences</i> , 2010, 2, 185-192.	1.5	11
213	Complete genome sequence of <i>Conexibacter woesei</i> type strain (ID131577T). <i>Standards in Genomic Sciences</i> , 2010, 2, 212-219.	1.5	24
214	Complete genome sequence of <i>Thermocrinis albus</i> type strain (HI 11/12T). <i>Standards in Genomic Sciences</i> , 2010, 2, 194-202.	1.5	18
215	Complete genome sequence of <i>Meiothermus silvanus</i> type strain (VI-R2T). <i>Standards in Genomic Sciences</i> , 2010, 3, 37-46.	1.5	19
216	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

#	ARTICLE	IF	CITATIONS
217	Complete genome sequence of <i>Acidaminococcus fermentans</i> type strain (VR4T). <i>Standards in Genomic Sciences</i> , 2010, 3, 1-14.	1.5	31
218	Complete genome sequence of <i>Meiothermus ruber</i> type strain (21T). <i>Standards in Genomic Sciences</i> , 2010, 3, 26-36.	1.5	33
219	Complete genome sequence of <i>Acetohalobium arabaticum</i> type strain (Z-7288T). <i>Standards in Genomic Sciences</i> , 2010, 3, 57-65.	1.5	24
220	Complete genome sequence of <i>Ignisphaera aggregans</i> type strain (AQ1.S1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 66-75.	1.5	15
221	Complete genome sequence of <i>Vulcanisaeta distributa</i> type strain (IC-017T). <i>Standards in Genomic Sciences</i> , 2010, 3, 117-125.	1.5	10
222	Complete genome sequence of <i>Arcanobacterium haemolyticum</i> type strain (11018T). <i>Standards in Genomic Sciences</i> , 2010, 3, 126-135.	1.5	8
223	Complete genome sequence of <i>Thermosediminibacter oceani</i> type strain (JW/IW-1228PT). <i>Standards in Genomic Sciences</i> , 2010, 3, 108-116.	1.5	12
224	Complete genome sequence of <i>Spirochaeta smaragdinae</i> type strain (SEBR 4228T). <i>Standards in Genomic Sciences</i> , 2010, 3, 1-9.	1.5	18
225	Complete genome sequence of <i>Thermobaculum terrenum</i> ™ type strain (YNP1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 153-162.	1.5	11
226	Complete genome sequence of <i>Syntrophothermus lipocalidus</i> type strain (TGB-C1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 268-275.	1.5	13
227	Complete genome sequence of <i>Desulfarculus baarsii</i> type strain (2st14T). <i>Standards in Genomic Sciences</i> , 2010, 3, 276-284.	1.5	37
228	Complete genome sequence of <i>Intrasporangium calvum</i> type strain (7 KIPT). <i>Standards in Genomic Sciences</i> , 2010, 3, 294-303.	1.5	7
229	Complete genome sequence of <i>Methanothermus fervidus</i> type strain (V24ST). <i>Standards in Genomic Sciences</i> , 2010, 3, 315-324.	1.5	17
230	Complete genome sequence of <i>Thermaerobacter marianensis</i> type strain (7p75aT). <i>Standards in Genomic Sciences</i> , 2010, 3, 337-345.	1.5	10
231	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
232	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
233	Complete genome sequence of <i>Xylanimonas cellulositytica</i> type strain (XIL07T). <i>Standards in Genomic Sciences</i> , 2010, 2, 1-8.	1.5	10
234	Complete genome sequence of <i>Alicyclobacillus acidocaldarius</i> type strain (104-IAT). <i>Standards in Genomic Sciences</i> , 2010, 2, 9-18.	1.5	24

#	ARTICLE	IF	CITATIONS
235	Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022T). Standards in Genomic Sciences, 2010, 2, 49-56.	1.5	27
236	Complete genome sequence of <i>Streptosporangium roseum</i> type strain (NI 9100T). Standards in Genomic Sciences, 2010, 2, 29-37.	1.5	27
237	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034T). Standards in Genomic Sciences, 2010, 2, 87-95.	1.5	74
238	Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175T). Standards in Genomic Sciences, 2010, 2, 149-157.	1.5	29
239	Complete genome sequence of <i>Haloterrigena turkmenica</i> type strain (4kT). Standards in Genomic Sciences, 2010, 2, 107-116.	1.5	32
240	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2T). Standards in Genomic Sciences, 2010, 2, 96-106.	1.5	70
241	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20T). Standards in Genomic Sciences, 2010, 2, 158-167.	1.5	56
242	Complete genome sequence of <i>Nakamurella multipartita</i> type strain (Y-104T). Standards in Genomic Sciences, 2010, 2, 168-175.	1.5	35
243	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1T). Standards in Genomic Sciences, 2010, 2, 176-184.	1.5	40
244	Complete genome sequence of <i>Segniliparus rotundus</i> type strain (CDC 1076T). Standards in Genomic Sciences, 2010, 2, 203-211.	1.5	10
245	Complete genome sequence of <i>Sebaldella termitidis</i> type strain (NCTC 11300T). Standards in Genomic Sciences, 2010, 2, 220-227.	1.5	34
246	Complete genome sequence of <i>Thermosphaera aggregans</i> type strain (M11TLT). Standards in Genomic Sciences, 2010, 2, 245-259.	1.5	14
247	Complete genome sequence of <i>Brachyspira murdochii</i> type strain (56-150T). Standards in Genomic Sciences, 2010, 2, 260-269.	1.5	20
248	Complete genome sequence of <i>Aminobacterium colombiense</i> type strain (ALA-1T). Standards in Genomic Sciences, 2010, 2, 280-289.	1.5	32
249	Complete genome sequence of <i>Arcobacter nitrofigilis</i> type strain (CIT). Standards in Genomic Sciences, 2010, 2, 300-308.	1.5	40
250	Complete genome sequence of <i>Coralimargarita akajimensis</i> type strain (04OKA010-24T). Standards in Genomic Sciences, 2010, 2, 290-299.	1.5	28
251	Complete genome sequence of <i>Thermobispora bispora</i> type strain (R51T). Standards in Genomic Sciences, 2010, 2, 318-326.	1.5	23
252	Complete genome sequence of <i>Desulfohalobium retbaense</i> type strain (HR100T). Standards in Genomic Sciences, 2010, 2, 38-48.	1.5	22

#	ARTICLE	IF	CITATIONS
253	Complete genome sequence of <i>Archaeoglobus profundus</i> type strain (AV18T). <i>Standards in Genomic Sciences</i> , 2010, 2, 327-346.	1.5	26
254	Complete genome sequence of <i>Denitrovibrio acetiphilus</i> type strain (N2460T). <i>Standards in Genomic Sciences</i> , 2010, 2, 270-279.	1.5	16
255	Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410T). <i>Standards in Genomic Sciences</i> , 2010, 2, 19-28.	1.5	26
256	The Complete Genome Sequence of <i>Cupriavidus metallidurans</i> Strain CH34, a Master Survivalist in Harsh and Anthropogenic Environments. <i>PLoS ONE</i> , 2010, 5, e10433.	2.5	275
257	A genomic perspective on the potential of <i>Actinobacillus succinogenes</i> for industrial succinate production. <i>BMC Genomics</i> , 2010, 11, 680.	2.8	100
258	The genome of <i>Syntrophomonas wolfei</i> : new insights into syntrophic metabolism and biohydrogen production. <i>Environmental Microbiology</i> , 2010, 12, 2289-2301.	3.8	158
259	The Genome Sequence of <i>Methanohalophilus mahii</i> SLP ^T Reveals Differences in the Energy Metabolism among Members of the <i>Methanosarcinaceae</i> Inhabiting Freshwater and Saline Environments. <i>Archaea</i> , 2010, 2010, 1-16.	2.3	35
260	Genome Sequence of the Fleming Strain of <i>Micrococcus luteus</i> , a Simple Free-Living Actinobacterium. <i>Journal of Bacteriology</i> , 2010, 192, 841-860.	2.2	68
261	Complete genome sequence of <i>Cellulomonas flavigena</i> type strain (134T). <i>Standards in Genomic Sciences</i> , 2010, 3, 15-25.	1.5	38
262	Complete Genome Sequence of the Photosynthetic Purple Nonsulfur Bacterium <i>Rhodobacter capsulatus</i> SB 1003. <i>Journal of Bacteriology</i> , 2010, 192, 3545-3546.	2.2	90
263	Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. <i>Journal of Bacteriology</i> , 2010, 192, 6494-6496.	2.2	81
264	The Complete Multipartite Genome Sequence of <i>Cupriavidus necator</i> JMP134, a Versatile Pollutant Degrader. <i>PLoS ONE</i> , 2010, 5, e9729.	2.5	112
265	One Bacterial Cell, One Complete Genome. <i>PLoS ONE</i> , 2010, 5, e10314.	2.5	215
266	Genome Erosion in a Nitrogen-Fixing Vertically Transmitted Endosymbiotic Multicellular Cyanobacterium. <i>PLoS ONE</i> , 2010, 5, e11486.	2.5	178
267	Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10T). <i>Standards in Genomic Sciences</i> , 2010, 3, 194-202.	1.5	37
268	Complete genome sequence of <i>Methanoplanus petrolearius</i> type strain (SEBR 4847T). <i>Standards in Genomic Sciences</i> , 2010, 3, 203-211.	1.5	14
269	Genome Analysis of the Anaerobic Thermohalophilic Bacterium <i>Halothermothrix orenii</i> . <i>PLoS ONE</i> , 2009, 4, e4192.	2.5	58
270	The genomic basis of trophic strategy in marine bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15527-15533.	7.1	685

#	ARTICLE	IF	CITATIONS
271	Complete genome sequence of Capnocytophaga ochracea type strain (VPI 2845T). Standards in Genomic Sciences, 2009, 1, 101-109.	1.5	14
272	Complete genome of the cellulolytic thermophile <i>Acidothermus cellulolyticus</i> 11B provides insights into its ecophysiological and evolutionary adaptations. Genome Research, 2009, 19, 1033-1043.	5.5	109
273	Novel Features of the Polysaccharide-Digesting Gliding Bacterium <i>Flavobacterium johnsoniae</i> as Revealed by Genome Sequence Analysis. Applied and Environmental Microbiology, 2009, 75, 6864-6875.	3.1	212
274	The complete genome sequence of Staphylothermus marinus reveals differences in sulfur metabolism among heterotrophic Crenarchaeota. BMC Genomics, 2009, 10, 145.	2.8	26
275	Metabolic analysis of the soil microbe Dechloromonas aromatica str. RCB: indications of a surprisingly complex life-style and cryptic anaerobic pathways for aromatic degradation. BMC Genomics, 2009, 10, 351.	2.8	155
276	The genome sequence of Geobacter metallireducens: features of metabolism, physiology and regulation common and dissimilar to Geobacter sulfurreducens. BMC Microbiology, 2009, 9, 109.	3.3	145
277	The genome sequence of the psychrophilic archaeon, <i>Methanococcoides burtonii</i> : the role of genome evolution in cold adaptation. ISME Journal, 2009, 3, 1012-1035.	9.8	178
278	Genomic islands link secondary metabolism to functional adaptation in marine Actinobacteria. ISME Journal, 2009, 3, 1193-1203.	9.8	175
279	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. Nature, 2009, 462, 1056-1060.	27.8	924
280	Complete genome sequence of Halorhabdus utahensis type strain (AX-2T). Standards in Genomic Sciences, 2009, 1, 218-225.	1.5	22
281	Complete genome sequence of Methanoculleus marisnigri Romesser et al. 1981 type strain JR1. Standards in Genomic Sciences, 2009, 1, 189-196.	1.5	34
282	Complete genome sequence of Beutenbergia cavernae type strain (HKI 0122T). Standards in Genomic Sciences, 2009, 1, 21-28.	1.5	12
283	Complete genome sequence of Cryptobacterium curtum type strain (12-3T). Standards in Genomic Sciences, 2009, 1, 93-100.	1.5	17
284	Complete genome sequence of Desulfomicrobium baculatum type strain (XT). Standards in Genomic Sciences, 2009, 1, 29-37.	1.5	36
285	Complete genome sequence of Acidimicrobium ferrooxidans type strain (ICPT). Standards in Genomic Sciences, 2009, 1, 38-45.	1.5	32
286	Complete genome sequence of Sanguibacter keddiei type strain (ST-74T). Standards in Genomic Sciences, 2009, 1, 110-118.	1.5	16
287	Complete genome sequence of Catenulispora acidiphila type strain (ID 139908T). Standards in Genomic Sciences, 2009, 1, 119-125.	1.5	24
288	Complete genome sequence of Leptotrichia buccalis type strain (C-1013-bT). Standards in Genomic Sciences, 2009, 1, 126-132.	1.5	24

#	ARTICLE	IF	CITATIONS
289	Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 141-149.	1.5	24
290	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 46-53.	1.5	38
291	Complete genome sequence of <i>Pedobacter heparinus</i> type strain (HIM 762-3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 54-62.	1.5	25
292	Complete genome sequence of <i>Halogeometricum borinquense</i> type strain (PR3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 150-158.	1.5	23
293	Complete genome sequence of <i>Anaerococcus prevotii</i> type strain (PC1T). <i>Standards in Genomic Sciences</i> , 2009, 1, 159-165.	1.5	25
294	Complete genome sequence of <i>Atopobium parvulum</i> type strain (IPP 1246T). <i>Standards in Genomic Sciences</i> , 2009, 1, 166-173.	1.5	30
295	Complete genome sequence of <i>Staphylothermus marinus</i> Stetter and Fiala 1986 type strain F1. <i>Standards in Genomic Sciences</i> , 2009, 1, 183-188.	1.5	8
296	Complete genome sequence of <i>Eggerthella lenta</i> type strain (VPI 0255T). <i>Standards in Genomic Sciences</i> , 2009, 1, 174-182.	1.5	37
297	Complete genome sequence of <i>Methanocorpusculum labreanum</i> type strain Z. <i>Standards in Genomic Sciences</i> , 2009, 1, 197-203.	1.5	29
298	Complete genome sequence of <i>Kangiella koreensis</i> type strain (SW-125T). <i>Standards in Genomic Sciences</i> , 2009, 1, 226-233.	1.5	28
299	Complete genome sequence of <i>Jonesia denitrificans</i> type strain (Prevot 55134T). <i>Standards in Genomic Sciences</i> , 2009, 1, 262-269.	1.5	14
300	Complete genome sequence of <i>Halomicrobium mukohataei</i> type strain (arg-2T). <i>Standards in Genomic Sciences</i> , 2009, 1, 270-277.	1.5	31
301	Complete genome sequence of <i>Rhodothermus marinus</i> type strain (R-10T). <i>Standards in Genomic Sciences</i> , 2009, 1, 283-290.	1.5	45
302	Complete genome sequence of <i>Streptobacillus moniliformis</i> type strain (9901T). <i>Standards in Genomic Sciences</i> , 2009, 1, 300-307.	1.5	21
303	Complete genome sequence of <i>Brachybacterium faecium</i> type strain (Schefferle 6-10T). <i>Standards in Genomic Sciences</i> , 2009, 1, 3-11.	1.5	25
304	Complete genome sequence of <i>Pirellula staleyi</i> type strain (ATCC 27377T). <i>Standards in Genomic Sciences</i> , 2009, 1, 308-316.	1.5	34
305	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). <i>Standards in Genomic Sciences</i> , 2009, 1, 12-20.	1.5	100
306	Complete genome sequence of <i>Dyadobacter fermentans</i> type strain (NS114T). <i>Standards in Genomic Sciences</i> , 2009, 1, 133-140.	1.5	25

#	ARTICLE	IF	CITATIONS
307	Complete genome sequence of <i>Thermanaerovibrio acidaminovorans</i> type strain (Su883T). <i>Standards in Genomic Sciences</i> , 2009, 1, 254-261.	1.5	23
308	Complete genome sequence of <i>Slackia heliotrinireducens</i> type strain (RHS 1T). <i>Standards in Genomic Sciences</i> , 2009, 1, 234-241.	1.5	20
309	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575T). <i>Standards in Genomic Sciences</i> , 2009, 1, 242-253.	1.5	35
310	Complete genome sequence of <i>Stackebrandtia nassauensis</i> type strain (LLR-40K-21T). <i>Standards in Genomic Sciences</i> , 2009, 1, 292-299.	1.5	23
311	Localized Plasticity in the Streamlined Genomes of Vinyl Chloride Respiring <i>Dehalococcoides</i> . <i>PLoS Genetics</i> , 2009, 5, e1000714.	3.5	162
312	Genomic Characterization of Methanomicrobiales Reveals Three Classes of Methanogens. <i>PLoS ONE</i> , 2009, 4, e5797.	2.5	103
313	Environmental Genomics Reveals a Single-Species Ecosystem Deep Within Earth. <i>Science</i> , 2008, 322, 275-278.	12.6	474
314	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , 2008, 26, 1029-1034.	17.5	254
315	Extending the <i>Bacillus cereus</i> group genomics to putative food-borne pathogens of different toxicity. <i>Chemico-Biological Interactions</i> , 2008, 171, 236-249.	4.0	140
316	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
317	A Bioinformatician's Guide to Metagenomics. <i>Microbiology and Molecular Biology Reviews</i> , 2008, 72, 557-578.	6.6	361
318	The Genetically Remote Pathogenic Strain NVH391-98 of the <i>Bacillus cereus</i> Group Is Representative of a Cluster of Thermophilic Strains. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1276-1280.	3.1	41
319	A korarchaeal genome reveals insights into the evolution of the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8102-8107.	7.1	253
320	Genome of the Epsilonproteobacterial Chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 1145-1156.	3.1	228
321	Genome Sequence of <i>Thermofilum pendens</i> Reveals an Exceptional Loss of Biosynthetic Pathways without Genome Reduction. <i>Journal of Bacteriology</i> , 2008, 190, 2957-2965.	2.2	53
322	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
323	Patterns and Implications of Gene Gain and Loss in the Evolution of <i>Prochlorococcus</i> . <i>PLoS Genetics</i> , 2007, 3, e231.	3.5	469
324	Genome of <i>Methylobacillus flagellatus</i> , Molecular Basis for Obligate Methylophily, and Polyphyletic Origin of Methylophily. <i>Journal of Bacteriology</i> , 2007, 189, 4020-4027.	2.2	107

#	ARTICLE	IF	CITATIONS
325	Genome sequencing reveals complex secondary metabolome in the marine actinomycete <i>Salinispora tropica</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10376-10381.	7.1	502
326	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007, 4, 495-500.	19.0	322
327	<i>Deinococcus geothermalis</i> : The Pool of Extreme Radiation Resistance Genes Shrinks. <i>PLoS ONE</i> , 2007, 2, e955.	2.5	212
328	The <i>Methanosarcina barkeri</i> Genome: Comparative Analysis with <i>Methanosarcina acetivorans</i> and <i>Methanosarcina mazei</i> Reveals Extensive Rearrangement within Methanosarcinal Genomes. <i>Journal of Bacteriology</i> , 2006, 188, 7922-7931.	2.2	158
329	The Genome of Deep-Sea Vent Chemolithoautotroph <i>Thiomicrospira crunogena</i> XCL-2. <i>PLoS Biology</i> , 2006, 4, e383.	5.6	144
330	Living with Genome Instability: the Adaptation of Phytoplasmas to Diverse Environments of Their Insect and Plant Hosts. <i>Journal of Bacteriology</i> , 2006, 188, 3682-3696.	2.2	356
331	Facile Recovery of Individual High-Molecular-Weight, Low-Copy-Number Natural Plasmids for Genomic Sequencing. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4899-4906.	3.1	44
332	Genome characteristics of facultatively symbiotic <i>Frankia</i> sp. strains reflect host range and host plant biogeography. <i>Genome Research</i> , 2006, 17, 7-15.	5.5	352
333	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
334	Fishing for biodiversity: novel methanopterin-linked C ₁ transfer genes deduced from the Sargasso Sea metagenome. <i>Environmental Microbiology</i> , 2005, 7, 1909-1916.	3.8	12
335	How to be moderately halophilic with broad salt tolerance: clues from the genome of <i>Chromohalobacter salexigens</i> . <i>Extremophiles</i> , 2005, 9, 275-279.	2.3	69
336	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
337	Whole-Genome Shotgun Optical Mapping of <i>Rhodospirillum rubrum</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 5511-5522.	3.1	62
338	Comparison of the complete genome sequences of <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a and pv. <i>tomato</i> DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11064-11069.	7.1	399
339	What We Can Deduce about Metabolism in the Moderate Halophile <i>Chromohalobacter Saalexigens</i> from its Genomic Sequence. , 2005, , 267-285.		4
340	The Enigmatic Planctomycetes May Hold a Key to the Origins of Methanogenesis and Methylotrophy. <i>Molecular Biology and Evolution</i> , 2004, 21, 1234-1241.	8.9	123
341	Complete sequence and comparative genome analysis of the dairy bacterium <i>Streptococcus thermophilus</i> . <i>Nature Biotechnology</i> , 2004, 22, 1554-1558.	17.5	485
342	Complete genome sequence of the industrial bacterium <i>Bacillus licheniformis</i> and comparisons with closely related <i>Bacillus</i> species. <i>Genome Biology</i> , 2004, 5, r77.	9.6	319

#	ARTICLE	IF	CITATIONS
343	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
344	Methylotrophy in <i>Methylobacterium extorquens</i> AM1 from a Genomic Point of View. <i>Journal of Bacteriology</i> , 2003, 185, 2980-2987.	2.2	262
345	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
346	Co-linear scaffold of the <i>Bacillus licheniformis</i> and <i>Bacillus subtilis</i> genomes and its use to compare their competence genes. <i>FEMS Microbiology Letters</i> , 2002, 209, 23-30.	1.8	23
347	The <i>Rhodobacter capsulatus</i> genome. <i>Photosynthesis Research</i> , 2001, 70, 43-52.	2.9	35
348	Use of a dual-origin temperature-controlled amplifiable replicon for optimization of human interleukin-1 β synthesis in <i>Escherichia coli</i> . <i>Gene</i> , 1991, 97, 259-266.	2.2	8
349	TGATG vector: a new expression system for cloned foreign genes in <i>Escherichia coli</i> cells. <i>Gene</i> , 1990, 88, 121-126.	2.2	18