

Jan-Fang Cheng

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

270
papers

29,805
citations

49
h-index

170
g-index

273
ext. papers

34,446
ext. citations

9.5
avg, IF

5.34
L-index

#	Paper	IF	Citations
270	Protocol for single-cell isolation and genome amplification of environmental microbial eukaryotes for genomic analysis.. <i>STAR Protocols</i> , 2022 , 3, 100968	1.4	0
269	Detection of S83V GyrA mutation in quinolone-resistant <i>Shewanella</i> algae using comparative genomics. <i>Journal of Microbiology, Immunology and Infection</i> , 2021 , 54, 658-664	8.5	2
268	Evolution of trimethoprim/sulfamethoxazole resistance in <i>Shewanella</i> algae from the perspective of comparative genomics and global phylogenetic analysis. <i>Journal of Microbiology, Immunology and Infection</i> , 2021 ,	8.5	1
267	A single-cell genomics pipeline for environmental microbial eukaryotes. <i>iScience</i> , 2021 , 24, 102290	6.1	3
266	CRAGE-CRISPR facilitates rapid activation of secondary metabolite biosynthetic gene clusters in bacteria. <i>Cell Chemical Biology</i> , 2021 ,	8.2	2
265	An evolutionarily ancient mechanism for regulation of hemoglobin expression in vertebrate red cells. <i>Blood</i> , 2020 , 136, 269-278	2.2	1
264	Natural Variation in Lignin and Pectin Biosynthesis-Related Genes in Switchgrass (<i>Panicum virgatum</i> L.) and Association of SNP Variants with Dry Matter Traits. <i>Bioenergy Research</i> , 2020 , 13, 79-99 ^{3.1}	3.1	0
263	Constructing a yeast to express the largest cellulosome complex on the cell surface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 2385-2394	11.5	25
262	Bacterial genome editing by coupling Cre-lox and CRISPR-Cas9 systems. <i>PLoS ONE</i> , 2020 , 15, e0241867	3.7	2
261	Comparative genomics reveals insights into characterization and distribution of quorum sensing-related genes in <i>Shewanella</i> algae from marine environment and clinical sources. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2020 , 73, 101545	2.6	
260	Bidirectional titration of yeast gene expression using a pooled CRISPR guide RNA approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 18424-18430 ^{11.5}	11.5	9
259	Building a custom high-throughput platform at the Joint Genome Institute for DNA construct design and assembly-present and future challenges. <i>Synthetic Biology</i> , 2020 , 5, ysaa023	3.3	1
258	CRAGE-Duet Facilitates Modular Assembly of Biological Systems for Studying Plant-Microbe Interactions. <i>ACS Synthetic Biology</i> , 2020 , 9, 2610-2615	5.7	5
257	An Integrated Computer-Aided Design and Manufacturing Workflow for Synthetic Biology. <i>Methods in Molecular Biology</i> , 2020 , 2205, 3-18	1.4	1
256	Reversal of carbapenem-resistance in by CRISPR/Cas9 genome editing. <i>Journal of Advanced Research</i> , 2019 , 18, 61-69	13	11
255	Validating genome-wide CRISPR-Cas9 function improves screening in the oleaginous yeast <i>Yarrowia lipolytica</i> . <i>Metabolic Engineering</i> , 2019 , 55, 102-110	9.7	46
254	Genomic and phylogenetic characterization of <i>Shewanella xiamenensis</i> isolated from giant grouper (<i>Epinephelus lanceolatus</i>) in Taiwan. <i>Zoonoses and Public Health</i> , 2019 , 66, 679-685	2.9	4

253	Rare earth element alcohol dehydrogenases widely occur among globally distributed, numerically abundant and environmentally important microbes. <i>ISME Journal</i> , 2019 , 13, 2005-2017	11.9	35
252	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019 , 4, 1895-1906	26.6	99
251	A toolset of constitutive promoters for metabolic engineering of <i>Rhodospiridium toruloides</i> . <i>Microbial Cell Factories</i> , 2019 , 18, 117	6.4	18
250	Shotgun metagenome data of a defined mock community using Oxford Nanopore, PacBio and Illumina technologies. <i>Scientific Data</i> , 2019 , 6, 285	8.2	36
249	CRAGE enables rapid activation of biosynthetic gene clusters in undomesticated bacteria. <i>Nature Microbiology</i> , 2019 , 4, 2498-2510	26.6	48
248	Genomic characterization of carbapenem-resistant <i>Shewanella</i> algae isolated from Asian hard clam (<i>Meretrix lusoria</i>). <i>Aquaculture</i> , 2019 , 500, 300-304	4.4	7
247	An integrated workflow for phenazine-modifying enzyme characterization. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2018 , 45, 567-577	4.2	4
246	Genome Analysis of Multidrug-Resistant Isolated From Human Soft Tissue Sample. <i>Frontiers in Pharmacology</i> , 2018 , 9, 419	5.6	15
245	Draft genome sequence of carbapenem-resistant <i>Shewanella</i> algae strain AC isolated from small abalone (<i>Haliotis diversicolor</i>). <i>Journal of Global Antimicrobial Resistance</i> , 2018 , 14, 65-67	3.4	4
244	Natural variation in genes potentially involved in plant architecture and adaptation in switchgrass (<i>Panicum virgatum</i> L.). <i>BMC Evolutionary Biology</i> , 2018 , 18, 91	3	6
243	Genome-based analysis of virulence determinants of a <i>Serratia marcescens</i> strain from soft tissues following a snake bite. <i>Future Microbiology</i> , 2018 , 13, 331-343	2.9	5
242	Whole-genome characterization of <i>Shewanella</i> algae strain SYT3 isolated from seawater reveals insight into hemolysis. <i>Future Microbiology</i> , 2018 , 13, 1709-1717	2.9	4
241	Leveraging single-cell genomics to expand the fungal tree of life. <i>Nature Microbiology</i> , 2018 , 3, 1417-1428	26.6	60
240	Genome characterization of bile-isolated ACCC. <i>Gut Pathogens</i> , 2018 , 10, 38	5.4	8
239	Repeated Cis-Regulatory Tuning of a Metabolic Bottleneck Gene during Evolution. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1968-1981	8.3	12
238	Streamlining the Design-to-Build Transition with Build-Optimization Software Tools. <i>ACS Synthetic Biology</i> , 2017 , 6, 485-496	5.7	32
237	Preparing Mate-Paired Illumina Libraries Using Cre Recombinase. <i>Methods in Molecular Biology</i> , 2017 , 1642, 247-261	1.4	1
236	Preparing Fosmid Mate-Paired Libraries Using Cre-LoxP Recombination. <i>Methods in Molecular Biology</i> , 2017 , 1642, 263-284	1.4	

235	Next generation sequencing data of a defined microbial mock community. <i>Scientific Data</i> , 2016 , 3, 16008812	1.2	55
234	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016 , 10, 2020-32	11.9	161
233	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016 , 26, 1577-1584	6.3	119
232	High quality draft genome sequence and analysis of <i>Pontibacter roseus</i> type strain SRC-1(T) (DSM 17521(T)) isolated from muddy waters of a drainage system in Chandigarh, India. <i>Standards in Genomic Sciences</i> , 2015 , 10, 8		4
231	Impact of library preparation protocols and template quantity on the metagenomic reconstruction of a mock microbial community. <i>BMC Genomics</i> , 2015 , 16, 856	4.5	59
230	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015 , 3, 62	16.6	38
229	Complete genome sequence of the phenanthrene-degrading soil bacterium <i>Delftia acidovorans</i> Cs1-4. <i>Standards in Genomic Sciences</i> , 2015 , 10, 55		17
228	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,		1
227	Phylogenomically guided identification of industrially relevant GH1 β -glucosidases through DNA synthesis and nanostructure-initiator mass spectrometry. <i>ACS Chemical Biology</i> , 2014 , 9, 2082-91	4.9	45
226	Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305(T)), 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		39
225	Genome sequence of the <i>Thermotoga thermarum</i> type strain (LA3(T)) from an African solfataric spring. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1105-17		4
224	Genome sequence of the mud-dwelling archaeon <i>Methanoplanus limicola</i> type strain (DSM 2279(T)), 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, 1071-80		10
223	Genome complexity in the coelacanth is reflected in its adaptive immune system. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2014 , 322, 438-63	1.8	28
222	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013 , 499, 431-7	50.4	1484
221	Complete Genome Sequence of the Hyperthermophilic Sulfate-Reducing Bacterium <i>Thermodesulfobacterium geofontis</i> OPF15T. <i>Genome Announcements</i> , 2013 , 1, e0016213		4
220	Complete genome sequence of <i>Coriobacterium glomerans</i> type strain (PW2(T)) from the midgut of <i>Pyrrhocoris apterus</i> L. (red soldier bug). <i>Standards in Genomic Sciences</i> , 2013 , 8, 15-25		5
219	Complete genome sequence of the bile-resistant pigment-producing anaerobe <i>Alistipes finegoldii</i> type strain (AHN2437(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 26-36		6
218	High-quality-draft genome sequence of the yellow-pigmented flavobacterium <i>Joostella marina</i> type strain (En5(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 37-46		4

217	Complete genome sequence of the moderate thermophile <i>Anaerobaculum mobile</i> type strain (NGA(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 47-57		10
216	Genome sequence of the free-living aerobic spirochete <i>Turneriella parva</i> type strain (H(T)), and emendation of the species <i>Turneriella parva</i> . <i>Standards in Genomic Sciences</i> , 2013 , 8, 228-38		8
215	Genome sequence of the moderately thermophilic sulfur-reducing bacterium <i>Thermanaerovibrio velox</i> type strain (Z-9701(T)) and emended description of the genus <i>Thermanaerovibrio</i> . <i>Standards in Genomic Sciences</i> , 2013 , 9, 57-70		4
214	Genome sequence of <i>Frateuria aurantia</i> type strain (Kond67(T)), a xanthomonade isolated from <i>Lilium auratum</i> Lindl. <i>Standards in Genomic Sciences</i> , 2013 , 9, 83-92		1
213	Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H1(T)), reclassification of <i>Spirochaeta caldaria</i> , <i>Spirochaeta stenostrepta</i> , and <i>Spirochaeta zuelzerae</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov. and <i>Treponema zuelzerae</i> comb. nov. and emendation of the genus <i>Treponema</i> .		24
212	Complete genome sequence of the halophilic bacterium <i>Spirochaeta africana</i> type strain (Z-7692(T)) from the alkaline Lake Magadi in the East African Rift. <i>Standards in Genomic Sciences</i> , 2013 , 8, 165-76		2
211	Genome sequence of the phylogenetically isolated spirochete <i>Leptonema illini</i> type strain (3055(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 177-87		4
210	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		25
209	Generation of long insert pairs using a Cre-LoxP Inverse PCR approach. <i>PLoS ONE</i> , 2012 , 7, e29437	3.7	23
208	Complete genome sequences of <i>Desulfosporosinus orientis</i> DSM765T, <i>Desulfosporosinus youngiae</i> DSM17734T, <i>Desulfosporosinus meridiei</i> DSM13257T, and <i>Desulfosporosinus acidiphilus</i> DSM22704T. <i>Journal of Bacteriology</i> , 2012 , 194, 6300-1	3.5	46
207	Complete genome sequence of the thermophilic, piezophilic, heterotrophic bacterium <i>Marinitoga piezophila</i> KA3. <i>Journal of Bacteriology</i> , 2012 , 194, 5974-5	3.5	18
206	An independent genome duplication inferred from Hox paralogs in the American paddlefish—a representative basal ray-finned fish and important comparative reference. <i>Genome Biology and Evolution</i> , 2012 , 4, 937-53	3.9	42
205	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, 5703-4	3.5	11
204	Genome sequence of the moderately thermophilic, amino-acid-degrading and sulfur-reducing bacterium <i>Thermovirga lienii</i> type strain (Cas60314(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 230-9		21
203	Genome sequence of the orange-pigmented seawater bacterium <i>Owenweeksia hongkongensis</i> type strain (UST20020801(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 120-30		11
202	Complete genome sequence of the moderately thermophilic mineral-sulfide-oxidizing firmicute <i>Sulfobacillus acidophilus</i> type strain (NAL(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 1-13		20
201	Complete genome sequence of the termite hindgut bacterium <i>Spirochaeta coccoides</i> type strain (SPN1(T)), 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		46
200	Permanent draft genome sequence of the gliding predator <i>Saprospira grandis</i> strain Sa g1 (= HR1). <i>Standards in Genomic Sciences</i> , 2012 , 6, 210-9		1

199	Complete genome sequence of the facultatively anaerobic, appendaged bacterium <i>Muricauda ruestringensis</i> type strain (B1(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 185-93	8
198	Complete genome sequence of the aerobic, heterotroph <i>Marinithermus hydrothermalis</i> type strain (T1(T)) from a deep-sea hydrothermal vent chimney. <i>Standards in Genomic Sciences</i> , 2012 , 6, 21-30	6
197	Complete genome sequence of the aquatic bacterium <i>Runella slithyformis</i> type strain (LSU 4(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 145-54	16
196	Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium <i>Thermodesulfator indicus</i> type strain (CIR29812(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 155-64	9
195	Complete genome sequence of <i>Serratia plymuthica</i> strain AS12. <i>Standards in Genomic Sciences</i> , 2012 , 6, 165-73	15
194	Genome sequence of the homoacetogenic bacterium <i>Holophaga foetida</i> type strain (TMBS4(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 174-84	23
193	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRP(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 240-50	7
192	Complete genome sequence of the plant-associated <i>Serratia plymuthica</i> strain AS13. <i>Standards in Genomic Sciences</i> , 2012 , 7, 22-30	16
191	Genome sequence of the flexirubin-pigmented soil bacterium <i>Niabella soli</i> type strain (JS13-8(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 210-20	0
190	Genome sequence of the Antarctic rhodopsins-containing flavobacterium <i>Gillisia limnaea</i> type strain (R-8282(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 107-19	9
189	Complete genome sequence of the sulfate-reducing firmicute <i>Desulfotomaculum ruminis</i> type strain (DL(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 304-19	18
188	Complete genome sequence of <i>Halopiger xanaduensis</i> type strain (SH-6(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 31-42	7
187	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricurvum kujiense</i> type strain (YK-1(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 94-103	31
186	Identification of a haloalkaliphilic and thermostable cellulase with improved ionic liquid tolerance. <i>Green Chemistry</i> , 2011 , 13, 2083	10 93
185	Complete genome sequence of <i>Leadbetterella byssophila</i> type strain (4M15). <i>Standards in Genomic Sciences</i> , 2011 , 4, 2-12	15
184	Complete genome sequence of <i>Hydrogenobacter thermophilus</i> type strain (TK-6). <i>Standards in Genomic Sciences</i> , 2011 , 4, 131-43	8
183	Complete genome sequence of <i>Paludibacter propionigenes</i> type strain (WB4). <i>Standards in Genomic Sciences</i> , 2011 , 4, 36-44	24
182	Complete genome sequence of <i>Bacteroides helcogenes</i> type strain (P 36-108). <i>Standards in Genomic Sciences</i> , 2011 , 4, 45-53	7

181	Complete genome sequence of <i>Weeksella virosa</i> type strain (9751). <i>Standards in Genomic Sciences</i> , 2011 , 4, 81-90	8
180	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3). <i>Standards in Genomic Sciences</i> , 2011 , 4, 100-10	39
179	Complete genome sequence of <i>Marivirga tractuosa</i> type strain (H-43). <i>Standards in Genomic Sciences</i> , 2011 , 4, 154-62	15
178	Complete genome sequence of <i>Desulfurococcus mucosus</i> type strain (O7/1). <i>Standards in Genomic Sciences</i> , 2011 , 4, 173-82	9
177	Complete genome sequence of <i>Cellulophaga lytica</i> type strain (LIM-21). <i>Standards in Genomic Sciences</i> , 2011 , 4, 221-32	23
176	Non-contiguous finished genome sequence of <i>Bacteroides coprosuis</i> type strain (PC139). <i>Standards in Genomic Sciences</i> , 2011 , 4, 233-43	4
175	Complete genome sequence of the extremely halophilic <i>Halanaerobium praevalens</i> type strain (GSL). <i>Standards in Genomic Sciences</i> , 2011 , 4, 312-21	24
174	Complete genome sequence of <i>Nitratifactor salsuginis</i> type strain (E9I37-1). <i>Standards in Genomic Sciences</i> , 2011 , 4, 322-30	10
173	Complete genome sequence of <i>Mahella australiensis</i> type strain (50-1 BON). <i>Standards in Genomic Sciences</i> , 2011 , 4, 331-41	6
172	Complete genome sequence of <i>Treponema succinifaciens</i> type strain (6091). <i>Standards in Genomic Sciences</i> , 2011 , 4, 361-70	20
171	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FIGlyRT). <i>Standards in Genomic Sciences</i> , 2011 , 4, 371-380	9
170	Complete genome sequence of the hyperthermophilic chemolithoautotroph <i>Pyrolobus fumarii</i> type strain (1A). <i>Standards in Genomic Sciences</i> , 2011 , 4, 381-92	10
169	Complete genome sequence of <i>Staphylothermus hellenicus</i> P8. <i>Standards in Genomic Sciences</i> , 2011 , 5, 12-20	5
168	Complete genome sequence of the acetate-degrading sulfate reducer <i>Desulfobacca acetoxidans</i> type strain (ASRB2). <i>Standards in Genomic Sciences</i> , 2011 , 4, 393-401	19
167	Complete genome sequence of the thermophilic, hydrogen-oxidizing <i>Bacillus tusciae</i> type strain (T2) 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. <i>Standards in Genomic Sciences</i> , 2011 , 5, 121-34	35
166	Complete genome sequence of the gliding, heparinolytic <i>Pedobacter saltans</i> type strain (113). <i>Standards in Genomic Sciences</i> , 2011 , 5, 30-40	11
165	Non-contiguous finished genome sequence of the opportunistic oral pathogen <i>Prevotella multisaccharivorax</i> type strain (PPPA20). <i>Standards in Genomic Sciences</i> , 2011 , 5, 41-9	2
164	Complete genome sequence of <i>Ferroglobus placidus</i> AEDII12DO. <i>Standards in Genomic Sciences</i> , 2011 , 5, 50-60	27

163	Genome sequence of the filamentous, gliding <i>Thiothrix nivea</i> neotype strain (JP2(T)). <i>Standards in Genomic Sciences</i> , 2011 , 5, 398-406	9
162	Complete genome sequence of the thermophilic sulfur-reducer <i>Desulfurobacterium thermolithotrophum</i> type strain (BSA(T)) from a deep-sea hydrothermal vent. <i>Standards in Genomic Sciences</i> , 2011 , 5, 407-15	10
161	Complete genome sequence of <i>Calditerrivibrio nitroreducens</i> type strain (Yu37-1). <i>Standards in Genomic Sciences</i> , 2011 , 4, 54-62	9
160	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24). <i>Standards in Genomic Sciences</i> , 2011 , 4, 91-9	37
159	Complete genome sequence of <i>Bacteroides salanitronis</i> type strain (BL78). <i>Standards in Genomic Sciences</i> , 2011 , 4, 191-9	8
158	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6). <i>Standards in Genomic Sciences</i> , 2011 , 4, 200-9	62
157	Complete genome sequence of <i>Oceanithermus profundus</i> type strain (506). <i>Standards in Genomic Sciences</i> , 2011 , 4, 210-20	3
156	Complete genome sequence of <i>Tsukamurella paurometabola</i> type strain (no. 33). <i>Standards in Genomic Sciences</i> , 2011 , 4, 342-51	8
155	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21). <i>Standards in Genomic Sciences</i> , 2011 , 5, 97-111	72
154	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1B). <i>Standards in Genomic Sciences</i> , 2011 , 4, 63-71	40
153	Complete genome sequence of <i>Cellulophaga algicola</i> type strain (IC166). <i>Standards in Genomic Sciences</i> , 2011 , 4, 72-80	22
152	Complete genome sequence of <i>Riemerella anatipestifer</i> type strain (ATCC 11845T). <i>Standards in Genomic Sciences</i> , 2011 , 4, 144-153	26
151	Complete genome sequence of the thermophilic sulfur-reducer <i>Hippea maritima</i> type strain (MH(2)). <i>Standards in Genomic Sciences</i> , 2011 , 4, 303-11	6
150	Complete genome sequence of <i>Haliscomenobacter hydrossis</i> type strain (O). <i>Standards in Genomic Sciences</i> , 2011 , 4, 352-60	17
149	Complete genome sequence of the gliding freshwater bacterium <i>Fluviicola taffensis</i> type strain (RW262). <i>Standards in Genomic Sciences</i> , 2011 , 5, 21-9	19
148	Genome sequence of the moderately thermophilic halophile <i>Flexistipes sinusarabici</i> strain (MAS10). <i>Standards in Genomic Sciences</i> , 2011 , 5, 86-96	8
147	Complete genome sequence of <i>Deinococcus maricopensis</i> type strain (LB-34). <i>Standards in Genomic Sciences</i> , 2011 , 4, 163-72	11
146	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011 , 43, 476-81	36.3 638

145	Exploring the symbiotic pangenome of the nitrogen-fixing bacterium <i>Sinorhizobium meliloti</i> . <i>BMC Genomics</i> , 2011 , 12, 235	4.5	83
144	Genome sequence of the Arctic methanotroph <i>Methylobacter tundripaludum</i> SV96. <i>Journal of Bacteriology</i> , 2011 , 193, 6418-9	3.5	50
143	Complete genome sequence of the aerobic marine methanotroph <i>Methylomonas methanica</i> MC09. <i>Journal of Bacteriology</i> , 2011 , 193, 7001-2	3.5	57
142	Complete genome sequence and updated annotation of <i>Desulfovibrio alaskensis</i> G20. <i>Journal of Bacteriology</i> , 2011 , 193, 4268-9	3.5	46
141	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, 1483-4	3.5	49
140	Complete genome sequence of the cellulolytic thermophile <i>Clostridium thermocellum</i> DSM1313. <i>Journal of Bacteriology</i> , 2011 , 193, 2906-7	3.5	63
139	Genome sequence of the methanotrophic alphaproteobacterium <i>Methylocystis</i> sp. strain Rockwell (ATCC 49242). <i>Journal of Bacteriology</i> , 2011 , 193, 2668-9	3.5	45
138	Genome sequence of the mercury-methylating strain <i>Desulfovibrio desulfuricans</i> ND132. <i>Journal of Bacteriology</i> , 2011 , 193, 2078-9	3.5	33
137	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9). <i>Standards in Genomic Sciences</i> , 2011 , 4, 13-22		24
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1 Cryptic inoviruses are pervasive in bacteria and archaea across Earth's biomes

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