

# Jan-Fang Cheng

## List of Publications by Citations

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270  
papers

29,805  
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49  
h-index

170  
g-index

273  
ext. papers

34,446  
ext. citations

9.5  
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5.34  
L-index

#	Paper	IF	Citations
270	Initial sequencing and analysis of the human genome. <i>Nature</i> , <b>2001</b> , 409, 860-921	50.4	17366
269	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , <b>2013</b> , 499, 431-7	50.4	1484
268	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , <b>2009</b> , 462, 1056-60	50.4	803
267	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , <b>2011</b> , 43, 476-81	36.3	638
266	Loss of silent-chromatin looping and impaired imprinting of DLX5 in Rett syndrome. <i>Nature Genetics</i> , <b>2005</b> , 37, 31-40	36.3	612
265	Dicer, Drosha, and outcomes in patients with ovarian cancer. <i>New England Journal of Medicine</i> , <b>2008</b> , 359, 2641-50	59.2	573
264	Functional screening of 2 Mb of human chromosome 21q22.2 in transgenic mice implicates minibrain in learning defects associated with Down syndrome. <i>Nature Genetics</i> , <b>1997</b> , 16, 28-36	36.3	271
263	Assembling the marine metagenome, one cell at a time. <i>PLoS ONE</i> , <b>2009</b> , 4, e5299	3.7	270
262	A genome-wide screen identifies a single beta-defensin gene cluster in the chicken: implications for the origin and evolution of mammalian defensins. <i>BMC Genomics</i> , <b>2004</b> , 5, 56	4.5	225
261	A regulatory SNP causes a human genetic disease by creating a new transcriptional promoter. <i>Science</i> , <b>2006</b> , 312, 1215-7	33.3	224
260	Narrowing and genomic annotation of the commonly deleted region of the 5q- syndrome. <i>Blood</i> , <b>2002</b> , 99, 4638-41	2.2	213
259	Comparative DNA sequence analysis of mouse and human protocadherin gene clusters. <i>Genome Research</i> , <b>2001</b> , 11, 389-404	9.7	191
258	Runx1-mediated hematopoietic stem-cell emergence is controlled by a Gata/Ets/SCL-regulated enhancer. <i>Blood</i> , <b>2007</b> , 110, 4188-97	2.2	190
257	One bacterial cell, one complete genome. <i>PLoS ONE</i> , <b>2010</b> , 5, e10314	3.7	184
256	Gene expression profiles of normal human fibroblasts after exposure to ionizing radiation: a comparative study of low and high doses. <i>Radiation Research</i> , <b>2005</b> , 164, 17-26	3.1	170
255	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , <b>2016</b> , 10, 2020-32	11.9	161
254	Characterization of human RhCG and mouse Rhcg as novel nonerythroid Rh glycoprotein homologues predominantly expressed in kidney and testis. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 25641-51	5.4	123

253	Decontamination of MDA reagents for single cell whole genome amplification. <i>PLoS ONE</i> , <b>2011</b> , 6, e26161	17	123
252	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , <b>2016</b> , 26, 1577-1584	6.3	119
251	Annotation of cis-regulatory elements by identification, subclassification, and functional assessment of multispecies conserved sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 9830-5	11.5	112
250	Computational and biological analysis of 680 kb of DNA sequence from the human 5q31 cytokine gene cluster region. <i>Genome Research</i> , <b>1997</b> , 7, 495-512	9.7	111
249	Fifty microdeletions among 112 cases of Sotos syndrome: low copy repeats possibly mediate the common deletion. <i>Human Mutation</i> , <b>2003</b> , 22, 378-87	4.7	108
248	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , <b>2019</b> , 4, 1895-1906	26.6	99
247	Construction of a panel of transgenic mice containing a contiguous 2-Mb set of YAC/P1 clones from human chromosome 21q22.2. <i>Genomics</i> , <b>1995</b> , 27, 425-34	4.3	96
246	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 12-20		94
245	Identification of a haloalkaliphilic and thermostable cellulase with improved ionic liquid tolerance. <i>Green Chemistry</i> , <b>2011</b> , 13, 2083	10	93
244	Chimeric plastid proteome in the Florida "red tide" dinoflagellate <i>Karenia brevis</i> . <i>Molecular Biology and Evolution</i> , <b>2006</b> , 23, 2026-38	8.3	93
243	The DNA sequence and comparative analysis of human chromosome 5. <i>Nature</i> , <b>2004</b> , 431, 268-74	50.4	86
242	Characterization of the dog Agouti gene and a nonagouti mutation in German Shepherd Dogs. <i>Mammalian Genome</i> , <b>2004</b> , 15, 798-808	3.2	84
241	Exploring the symbiotic pangenome of the nitrogen-fixing bacterium <i>Sinorhizobium meliloti</i> . <i>BMC Genomics</i> , <b>2011</b> , 12, 235	4.5	83
240	Isolation and characterization of a human telomere. <i>Nucleic Acids Research</i> , <b>1989</b> , 17, 6109-27	20.1	82
239	Regulation and activity of the human ABCA1 gene in transgenic mice. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 18046-51	5.4	78
238	Isolation and mapping of human chromosome 21 cDNA: progress in constructing a chromosome 21 expression map. <i>Genomics</i> , <b>1994</b> , 23, 75-84	4.3	76
237	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> , <b>2011</b> , 5, 97-111		72
236	Evolutionarily conserved sequences on human chromosome 21. <i>Genome Research</i> , <b>2001</b> , 11, 1651-9	9.7	64

235	Complete genome sequence of the cellulolytic thermophile <i>Clostridium thermocellum</i> DSM1313. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2906-7	3.5	63
234	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 200-9		62
233	Leveraging single-cell genomics to expand the fungal tree of life. <i>Nature Microbiology</i> , <b>2018</b> , 3, 1417-1428	26.6	60
232	Impact of library preparation protocols and template quantity on the metagenomic reconstruction of a mock microbial community. <i>BMC Genomics</i> , <b>2015</b> , 16, 856	4.5	59
231	Complete genome sequence of the aerobic marine methanotroph <i>Methylomonas methanica</i> MC09. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 7001-2	3.5	57
230	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 87-95		57
229	Next generation sequencing data of a defined microbial mock community. <i>Scientific Data</i> , <b>2016</b> , 3, 16008812	1.2	55
228	A previously undetected pseudogene in the human alpha globin gene cluster. <i>Nucleic Acids Research</i> , <b>1986</b> , 14, 1903-11	20.1	55
227	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 96-106		53
226	The rabbit C family of short, interspersed repeats. Nucleotide sequence determination and transcriptional analysis. <i>Journal of Molecular Biology</i> , <b>1984</b> , 176, 1-20	6.5	52
225	Massively parallel sequencing identifies the gene <i>Megf8</i> with ENU-induced mutation causing heterotaxy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 3219-24	11.5	50
224	Genome sequence of the Arctic methanotroph <i>Methylobacter tundripaludum</i> SV96. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 6418-9	3.5	50
223	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> , <b>2011</b> , 193, 1483-4	3.5	49
222	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 158-67		49
221	Decoding the fine-scale structure of a breast cancer genome and transcriptome. <i>Genome Research</i> , <b>2006</b> , 16, 394-404	9.7	48
220	CRAGE enables rapid activation of biosynthetic gene clusters in undomesticated bacteria. <i>Nature Microbiology</i> , <b>2019</b> , 4, 2498-2510	26.6	48
219	Validating genome-wide CRISPR-Cas9 function improves screening in the oleaginous yeast <i>Yarrowia lipolytica</i> . <i>Metabolic Engineering</i> , <b>2019</b> , 55, 102-110	9.7	46
218	Complete genome sequence and updated annotation of <i>Desulfovibrio alaskensis</i> G20. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 4268-9	3.5	46

217	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> , <b>2012</b> , 194, 6300-1	3.5	46
216	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> , <b>2012</b> , 6, 194-209		46
215	Phylogenomically guided identification of industrially relevant GH1 $\beta$ -glucosidases through DNA synthesis and nanostructure-initiator mass spectrometry. <i>ACS Chemical Biology</i> , <b>2014</b> , 9, 2082-91	4.9	45
214	Genome sequence of the methanotrophic alphaproteobacterium <i>Methylocystis</i> sp. strain Rockwell (ATCC 49242). <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2668-9	3.5	45
213	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> , <b>2012</b> , 4, 937-53	3.9	42
212	Detection of weakly conserved ancestral mammalian regulatory sequences by primate comparisons. <i>Genome Biology</i> , <b>2007</b> , 8, R1	18.3	42
211	Human Ca <sup>2+</sup> /calmodulin-dependent protein kinase kinase beta gene encodes multiple isoforms that display distinct kinase activity. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 31113-23	5.4	42
210	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1B). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 63-71		40
209	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> , <b>2014</b> , 9, 10		39
208	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 100-10		39
207	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , <b>2015</b> , 3, 62	16.6	38
206	Sequence and comparative analysis of the rabbit alpha-like globin gene cluster reveals a rapid mode of evolution in a G + C-rich region of mammalian genomes. <i>Journal of Molecular Biology</i> , <b>1991</b> , 222, 233-49	6.5	38
205	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 91-9		37
204	Shotgun metagenome data of a defined mock community using Oxford Nanopore, PacBio and Illumina technologies. <i>Scientific Data</i> , <b>2019</b> , 6, 285	8.2	36
203	Rare earth element alcohol dehydrogenases widely occur among globally distributed, numerically abundant and environmentally important microbes. <i>ISME Journal</i> , <b>2019</b> , 13, 2005-2017	11.9	35
202	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> , <b>2011</b> , 5, 121-34		35
201	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 176-85		35
200	Genome sequence of the mercury-methylating strain <i>Desulfovibrio desulfuricans</i> ND132. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2078-9	3.5	33

199	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 242-53		33
198	Streamlining the Design-to-Build Transition with Build-Optimization Software Tools. <i>ACS Synthetic Biology</i> , <b>2017</b> , 6, 485-496	5-7	32
197	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 46-53		32
196	Complete genome sequence of <i>Arcobacter nitrofigilis</i> type strain (CI). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 300-8		32
195	Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 194-202		32
194	The genome sequence of <i>Methanohalophilus mahii</i> SLP(T) reveals differences in the energy metabolism among members of the Methanosarcinaceae inhabiting freshwater and saline environments. <i>Archaea</i> , <b>2010</b> , 2010, 690737	2	31
193	Complete genome sequence of <i>Cellulomonas flavigena</i> type strain (134). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 15-25		31
192	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricum kujiense</i> type strain (YK-1(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 94-103		31
191	Complete genome sequence of <i>Eggerthella lenta</i> type strain (IPP VPI 0255). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 174-82		31
190	Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (X). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 29-37		30
189	Complete genome sequence of <i>Halomicrobium mukohataei</i> type strain (arg-2). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 270-7		30
188	A sequence-based survey of the complex structural organization of tumor genomes. <i>Genome Biology</i> , <b>2008</b> , 9, R59	18.3	30
187	Human and mouse ABCA1 comparative sequencing and transgenesis studies revealing novel regulatory sequences. <i>Genomics</i> , <b>2001</b> , 73, 66-76	4.3	30
186	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 57-65		29
185	Genome complexity in the coelacanth is reflected in its adaptive immune system. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , <b>2014</b> , 322, 438-63	1.8	28
184	Complete genome sequence of <i>Planctomyces limnophilus</i> type strain (M <sup>2</sup> 90). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 47-56		28
183	Complete genome sequence of <i>Meiothermus ruber</i> type strain (21). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 26-36		28
182	Complete genome sequence of <i>Haloterrigena turkmenica</i> type strain (4k). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 107-16		28

181	Complete genome sequence of <i>Nakamurella multipartita</i> type strain (Y-104). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 168-75		28
180	Complete genome sequence of <i>Ferroglobus placidus</i> AEDII12DO. <i>Standards in Genomic Sciences</i> , <b>2011</b> , 5, 50-60		27
179	Complete genome sequence of <i>Nocardioopsis dassonvillei</i> type strain (IMRU 509). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 325-36		27
178	Complete genome sequence of <i>Olsenella uli</i> type strain (VPI D76D-27C). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 76-84		27
177	Complete genome sequence of <i>Desulfarculus baarsii</i> type strain (2st14). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 276-84		27
176	Complete genome sequence of <i>Aminobacterium colombiense</i> type strain (ALA-1). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 280-9		27
175	Structural and transcriptional analysis of a human subtelomeric repeat. <i>Nucleic Acids Research</i> , <b>1991</b> , 19, 149-54	20.1	27
174	Complete genome sequence of <i>Riemerella anatipestifer</i> type strain (ATCC 11845T). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 144-153		26
173	Complete genome sequence of <i>Pirellula staleyi</i> type strain (ATCC 27377). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 308-16		26
172	LPA and PLG sequence variation and kringle IV-2 copy number in two populations. <i>Human Heredity</i> , <b>2008</b> , 66, 199-209	1.1	26
171	Imprinting of opossum <i>Igf2r</i> in the absence of differential methylation and air. <i>Epigenetics</i> , <b>2006</b> , 1, 49-54.7		26
170	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> , <b>2020</b> , 117, 2385-2394	11.5	25
169	Complete genome sequence of the rapeseed plant-growth promoting <i>Serratia plymuthica</i> strain AS9. <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 54-62		25
168	Complete genome sequence of <i>Streptosporangium roseum</i> type strain (NI 9100). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 29-37		25
167	The mammalian alphaD-globin gene lineage and a new model for the molecular evolution of alpha-globin gene clusters at the stem of the mammalian radiation. <i>Molecular Phylogenetics and Evolution</i> , <b>2006</b> , 38, 439-48	4.1	25
166	Identification and analysis of the human and murine putative chromatin structure regulator SUPT6H and Supt6h. <i>Genomics</i> , <b>1996</b> , 34, 328-33	4.3	25
165	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 zuelzeriae</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzeriae</i> comb. nov., and emendation of the genus <i>Treponema</i> .		24
164	Complete genome sequence of <i>Paludibacter propionigenes</i> type strain (WB4). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 36-44		24

163	Complete genome sequence of the extremely halophilic <i>Halanaerobium praevalens</i> type strain (GSL). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 312-21		24
162	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 13-22		24
161	Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 149-57		24
160	Haplotypes in the APOA1-C3-A4-A5 gene cluster affect plasma lipids in both humans and baboons. <i>Human Molecular Genetics</i> , <b>2004</b> , 13, 1049-56	5.6	24
159	Generation of long insert pairs using a Cre-LoxP Inverse PCR approach. <i>PLoS ONE</i> , <b>2012</b> , 7, e29437	3.7	23
158	Complete genome sequence of <i>Cellulophaga lytica</i> type strain (LIM-21). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 221-32		23
157	Genome sequence of the homoacetogenic bacterium <i>Holophaga foetida</i> type strain (TMBS4(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 174-84		23
156	Complete genome sequence of <i>Cellulophaga algicola</i> type strain (IC166). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 72-80		22
155	Complete genome sequence of <i>Halogeometricum borinquense</i> type strain (PR3). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 150-9		22
154	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> , <b>2012</b> , 6, 230-9		21
153	Complete genome sequence of <i>Halorhabdus utahensis</i> type strain (AX-2). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 218-25		21
152	Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 141-9		21
151	Complete genome sequence of <i>Atopobium parvulum</i> type strain (IPP 1246). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 166-73		21
150	Complete genome sequence of <i>Treponema succinifaciens</i> type strain (6091). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 361-70		20
149	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> , <b>2012</b> , 6, 1-13		20
148	Complete genome sequence of <i>Rhodothermus marinus</i> type strain (R-10). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 283-90		20
147	Complete genome sequence of <i>Alicyclobacillus acidocaldarius</i> type strain (104-IA). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 9-18		20
146	Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 49-56		20



145	Complete genome sequence of <i>Archaeoglobus profundus</i> type strain (AV18). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 327-46		20
144	Complete genome sequence of the acetate-degrading sulfate reducer <i>Desulfobacca acetoxidans</i> type strain (ASRB2). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 393-401		19
143	Complete genome sequence of the gliding freshwater bacterium <i>Fluviicola taffensis</i> type strain (RW262). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 5, 21-9		19
142	Complete genome sequence of <i>Catenulispora acidiphila</i> type strain (ID 139908). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 119-25		19
141	Complete genome sequence of <i>Pedobacter heparinus</i> type strain (HIM 762-3). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 54-62		19
140	Complete genome sequence of <i>Brachybacterium faecium</i> type strain (Schefferle 6-10). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 3-11		19
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4	Genome sequence of the flexirubin-pigmented soil bacterium <i>Niabella soli</i> type strain (JS13-8(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 7, 210-20		0
3	Protocol for single-cell isolation and genome amplification of environmental microbial eukaryotes for genomic analysis.. <i>STAR Protocols</i> , <b>2022</b> , 3, 100968	1.4	0
2	Preparing Fosmid Mate-Paired Libraries Using Cre-LoxP Recombination. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1642, 263-284	1.4	



- 1 Comparative genomics reveals insights into characterization and distribution of quorum sensing-related genes in *Shewanella* algae from marine environment and clinical sources. *Comparative Immunology, Microbiology and Infectious Diseases*, **2020**, 73, 101545 2.6