Genomics:GTL Microbes for Research

March 2007*

The U.S. Department of Energy (DOE) Office of Science supports innovative, high-impact, peer-reviewed biological science to seek solutions to difficult DOE mission challenges. These challenges include cleaning up environmental waste, finding alternative sources of energy, and understanding biological carbon cycling as it relates to global climate change. The Microbial Genome Program (MGP), initiated by DOE's Office of Biological and Environmental Research (BER) in 1994, has sequenced more than 485 microbial genomes and 30 microbial communities having specialized biological capabilities. Identifying these genes will help investigators discern how gene activities in whole living systems are orchestrated to solve myriad life challenges. The Genomics:GTL (GTL) program, begun in 2001, is devoted to mechanistically understanding how microbes use a variety of energy sources, process metals, cycle carbon and nutrients such as nitrogen, and ameliorate radiation damage. Using completed genome sequences and a systems biology approach, GTL's goal is to develop a set of comprehensive principles and models showing how living systems function and to help put that knowledge to work in biotechnological solutions to DOE mission challenges. GTL research is relevant to BER's Environmental Remediation Sciences Program.

Most microbes of interest to DOE are sequenced at the DOE Joint Genome Institute (JGI). Through the DOE JGI Community Sequencing Program, researchers can propose candidates for sequencing. At the completion of a project, all data are made available to the entire community.

Program Contact

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Current Status

*Due to rapid progress, this information is continually changing. Current status available:

Joint Genome Institute
www.jgi.doe.gov

Genomics:GTL
genomicsgtl.energy.gov

Sequencing Status Key:

"New" – sequencing of organism has not started

"Pending" – DNA is waiting to enter the production process

"In production" – includes library creation and production sequencing

"In assembly" – assembly in progress

"In draft assembly" – first assembly, made without finishing the genome

"In finishing" – postproduction work not carried out for all organisms

"Incomplete" – not finished, further status unknown

"Draft" – no further work planned

"Finished" – sequencing completed

Category Key

"Bioremediation" – cleanup of toxic wastes sites

"Carbon Cycling" – understanding carbon cycle to predict sources and sinks of CO_2

"Cellulose Degradation" – efficient conversion of biomass to products such as ethanol, methane, and hydrogen

"Energy Production" – energy generation and development of renewable energy sources such as methane and hydrogen

"Biotechnology & Applied Microbiology" – production of chemicals to improve process efficiency

"Technology Development, Pilot Projects" – demonstration of feasibility or fine-tuning of sequencing technologies

References

1. DOE Joint Genome Institute http://www.jgi.doe.gov/
2. Liolios K, Tavernarakis N, Hugenholtz P, Kyrpides, NC. The Genomes On Line Database (GOLD) v.2: a monitor of genome projects worldwide NAR 34, D332-334 http://genomesonline.org/

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March 2007 Draft

	A	B	C	D	E
1	**Genome Name**	**Domain**	**Sequencing Status**	**Approximate Genome Size**	**Category**
2	*Accumulibacter phosphatis*	Bacteria	New	1 Mb	Bioremediation
3	*Acetivibrio cellulolyticus* CD2	Bacteria	New	3 Mb	
4	Acid mine drainage communities (Iron Mountain, Calif.)	Microbial Community	Draft	10.8 Mb	
5	Acidic peat bog methanogen		(unk)	24 Mb	
6	*Acidiphilium cryptum* JF 5	Bacteria	In finishing	2.4 Mb	Bioremediation
7	*Acidithiobacillus ferrooxidans*	Bacteria	Finished	2.9 Mb	Bioremediation
8	*Acidobacteria bacterium* Ellin 345	Bacteria	Finished	3 Mb	
9	*Acidobacterium* sp., Ellin 6076	Bacteria	(unk)	3 Mb	
10	*Acidobacterium Ellin* 345	Bacteria	Finished	5.6 Mb	Bioremediation
11	*Acidothermus cellulolyticus* 11B	Bacteria	Finished	6 Mb	Biotechnology & Applied Microbiology
12	*Acidovorax avenae Citrulli* AAC00-1	Bacteria	Finished	4.6 Mb	Bioremediation
13	*Acidovorax* JS42	Bacteria	Finished	4.5 Mb	Bioremediation
14	*Acremonium alcalophilum* ATCC 90507	Fungi	Pending	40 Mb	
15	*Actinobacillus succinogenes* 130Z	Bacteria	In finishing	2 Mb	Biotechnology & Applied Microbiology
16	Active methylotroph community from Lake Washington	Microbial Community	Draft		
17	*Akkermansia muciniphila*	Bacteria	In production	8 Mb	
18	Alaskan soil microbial community	Microbial Community	In production		
19	*Alkalilimnicola ehrlichei* MLHE-1	Bacteria	Finished	2-4 Mb	
20	*Alkaliphilus metalliredigenes* QYMF	Bacteria	In finishing	4.5 Mb	Bioremediation
21	*Anabaena variabilis* ATCC 29413	Bacteria	Finished	7 Mb	Energy Production
22	Anaerobic benzene-degrading methanogenic consortium	Microbial Community	Pending	192 Mb	
23	Anaerobic bioreactor granule samples some 200 BACs from Hanford PNNL site		Finished	100 Mb	
24	Anaerobic Methane Oxidizing community		In production		
25	*Anaeromyxobacter dehalogenans* 2CP-C	Bacteria	Finished	5 Mb	Bioremediation
26	*Anaeromyxobacter* strain K		In production	5 Mb	
27	Anaeromyxobacteria sp. FW109-5	Bacteria	In finishing	5 Mb	
28	*Anoplophora glabripennis* gut consortium	Microbial Community	Pending		
29	Antarctic marine bacterioplankton		Pending		
30	*Aquifex aeolicus* VF5 extremophile	Bacteria	Finished	1.5 Mb	Biotechnology & Applied Microbiology
31	ARC Deibersd Rice endophyte metagen		(unk)	100 Mb	
32	*Archaeoglobus fulgidus* VC-16	Archaea	Finished	2.1 Mb	Biotechnology & Applied Microbiology
33	*Arthrobacter chlorophenolicus* (Actinobacteria)	Bacteria	In production		
34	*Arthrobacter sp.* FB24	Bacteria	Finished	5.2 Mb	Bioremediation
35	*Arthrospira maxima* CS-328 (UTEX #2342)	Bacteria	New	5 Mb	
36	*Aspergillus niger*	Fungi	In finishing	32 Mb	Biotechnology & Applied Microbiology
37	*Aureococcus anophagefferens*	Algae	In finishing	32 Mb	Carbon Cycling
38	AWYX arctic ocean bacterial community	Microbial Community	(unk)		
39	*Azolla filiculoides*	Plant	Pending	9 Mb	
40	*Azotobacter vinelandii* AvOP	Bacteria	Finished	5.3 Mb	Carbon Cycling
41	*Bacillus anthracis* A2012	Bacteria	Finished	5.1 Mb	pathogen, human
42	*Bacillus anthracis* Ames	Bacteria	Finished	5.2 Mb	pathogen, human
43	*Bacillus anthracis* Ames Ancestor A2084	Bacteria	Finished	5.6 Mb	pathogen, human
44	*Bacillus anthracis* Sterne	Bacteria	Finished	5.2 Mb	
45	*Bacillus cereus cytotoxis* NVH 391-98	Bacteria	In finishing	3.9 Mb	
46	*Bacillus cereus* E33L	Bacteria	Finished	5.8 Mb	
47	*Bacillus coagulans* 36D1	Bacteria	In finishing	8 Mb	Energy Production

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48	*Bacillus selenitireducens* MLMS-1	Bacteria	New		Bioremediation
49	*Bacillus selenitireducens* MLS-10	Bacteria	Draft	2-4 Mb	Bioremediation
50	*Bacillus thuringiensis* ALHakam	Bacteria	Finished		pathogen, insect
51	*Bacillus thuringiensis konkukian* 97-27	Bacteria	Finished	5.3 Mb	pathogen, insect
52	*Bacillus thuringiensis* Zebra killer	Bacteria	Finished		
53	*Bacillus weihenstephanensis* KBAB4	Bacteria	In finishing	5.6 MB	
54	Bacterioplankton pool cDNA, day	Microbial Community	Pending		
55	Bacterioplankton pool cDNA, night	Microbial Community	Pending		
56	Bacterioplankton pool cDNA, night + DOC1	Microbial Community	Pending		
57	Bacterioplankton pool cDNA, night + DOC2	Microbial Community	Pending		
58	*Beggiatoa alba*	Bacteria	Pending	42 Mb	
59	*Beijerinckia indica subsp. indica*	Bacteria	pending		
60	*Beta proteobacterium sp.* JS666	Bacteria	New	4.5 Mb	Bioremediation
61	*Bifidobacterium longum* DJO10A	Bacteria	Finished	2.4 Mb	Biotechnology & Applied Microbiology
62	Boiling thermal pool Yellowstone National Park	Microbial Community	In production	50 Mb	
63	*Borrelia burgdorferi* B31	Bacteria	Finished	1.4 Mb	Technology Development, Pilot Projects
64	*Bradyrhizobium sp.* BTAi1	Bacteria	In finishing	9.2 Mb	Carbon Cycling
65	*Brevibacterium linens* BL2	Bacteria	Finished	4.5 Mb	Biotechnology & Applied Microbiology
66	*Brucella abortus* 2308	Bacteria	Finished	3.2 Mb	
67	*Brucella melitensis* 16M	Bacteria	Finished	3.3 Mb	Technology Development, Pilot Projects
68	*Burkholderia*	Bacteria	In production (3),	576 Mb	
69	*Burkholderia ambifaria* AMMD	Bacteria	Draft	7.5 Mb	Bioremediation
70	*Burkholderia ambifaria* MC40-6	Bacteria	In finishing	7.4 Mb	Bioremediation
71	*Burkholderia cenocepacia* AU 1054	Bacteria	Finished	7.3 Mb	Bioremediation
72	*Burkholderia cenocepacia* HI2424	Bacteria	Finished	7.7 Mb	Bioremediation
73	*Burkholderia cenocepacia* MC0-3	Bacteria	In finishing	7.9 Mb	
74	*Burkholderia cepacia* AMMD	Bacteria	Finished	7.2 Mb	
75	*Burkholderia multivorans* ATCC 17616	Bacteria	In finishing	6.8 Mb	
76	*Burkholderia phymatum* STM 815	Bacteria	In finishing	8 Mb	Bioremediation
77	*Burkholderia phytofirmans* PsJN	Bacteria	In finishing	8 Mb	
78	*Burkholderia sp.* 383	Bacteria	Finished	8.8 Mb	Bioremediation
79	*Burkholderia vietnamiensis* G4	Bacteria	In finishing	8.4 Mb	Bioremediation
80	*Burkholderia xenovorans* LB400	Bacteria	Finished	8 Mb	Bioremediation
81	*Caldicellulosiruptor saccharolyticus* DSM 8903	Bacteria	In finishing	4.3 Mb	Energy Production
82	*Caldivirga maquilingensis*	Archaea	In finishing	2-3 Mb	Bioremediation
83	*Candidatus Amoebophilus asiaticus*	Bacteria	In production		
84	*Candidatus Cardinium hertigii*	Bacteria	Pending		
85	*Candidatus Chlorothrix halophila*	Bacteria	Draft	5 Mb	Carbon Cycling
86	*Candidatus Desulfococcus oleovorans* Hxd3	Bacteria	In finishing	6 Mb	
87	*Candidatus Endomicrobium trichonympha*, free-living strain Pei191		In production	110 Mb	
88	*Candidatus Ruthia magnifica* Cm (Proteobacterial symbiont of the clam *Calyptogena magnifica)*		Finished	4 Mb	
89	*Carboxydothermus hydrogenoformans*	Bacteria	Finished	2.1 Mb	Energy Production
90	*Caulobacter crescentus*	Bacteria	Finished	4 Mb	Bioremediation
91	*Caulobacter* K31	Bacteria	In finishing	4 Mb	Bioremediation
92	*Chlamydia trachomatis* Ds2923	Bacteria	Finished		pathogen, human
93	*Chlamydia trachomatis* E11023	Bacteria	Finished		pathogen, human

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94	*Chlamydia trachomatis* G9301	Bacteria	Finished		pathogen, human
95	*Chlamydia trachomatis* G9768	Bacteria	Finished		pathogen, human
96	*Chlamydomonas reinhardtii*	Algae	In finishing	100 Mb	Carbon Cycling
97	*Chlorella* NC64A	Algae	In production	40 Mb	
98	*Chlorella vulgaris* C-169	Algae	In production	40 Mb	
99	*Chlorobium aggregatum*	Bacteria	Finished		
100	*Chlorobium chlorochromatii* CaD3	Microbial Community	Finished	2.6 Mb	Carbon Cycling
101	*Chlorobium ferrooxidans* DSM 13031	Bacteria	In finishing	2.4 Mb	
102	*Chlorobium limicola* DSMZ 245	Bacteria	In finishing	2.4 Mb	Carbon Cycling
103	*Chlorobium phaeobacteroides* BS1	Bacteria	In finishing	2.4 Mb	
104	*Chlorobium phaeobacteroides* DSMZ 266	Bacteria	Finished	2.3 Mb	Carbon Cycling
105	*Chlorobium phaeobacteroides* MN1 Black Sea	Bacteria	New	2.2 Mb	Carbon Cycling
106	*Chlorobium tepidum*	Bacteria	Finished	2.1 Mb	Carbon Cycling
107	*Chlorobium vibrioforme f. thiosulfatophilum* DSMZ 265	Bacteria	Draft	1.9 Mb	
108	*Chlorochromatium aggregatum Lake Dagow*	Bacteria	In production		
109	*Chloroflexus aggregans* DSM 9485	Bacteria	In finishing	5 Mb	Carbon Cycling
110	*Chloroflexus aurantiacus* J-10-fl	Bacteria	In finishing	3 Mb	Carbon Cycling
111	*Chloroherpeton thalassium*	Bacteria	New	3.5 Mb	Carbon Cycling
112	*Chloronema giganteum* UdG9001	Bacteria	Pending	5 Mb	Carbon Cycling
113	*Chromohalobacter salexigens* DSM 3043	Bacteria	Finished	3.9 Mb	Bioremediation
114	*Clostridium acetobutylicum*	Bacteria	Finished	4.1 Mb	Biotechnology & Applied Microbiology
115	*Clostridium beijerincki* NCIMB 8052	Bacteria	In finishing	7.8 Mb	Energy Production
116	*Clostridium carboxidivorans* P7	Bacteria	New	3 Mb	
117	*Clostridium cellulolyticum* H10	Bacteria	In finishing	5 Mb	
118	*Clostridium cellulovorans* 743B	Bacteria	New	3 Mb	
119	*Clostridium josui* FERM P-9684	Bacteria	New	3 Mb	
120	*Clostridium papyrosolvents* DSM 2782	Bacteria	New	3 Mb	
121	*Clostridium pasteurianum* DSM 525	Bacteria	New	3 Mb	
122	*Clostridium phytofermentans* ISDg	Bacteria	In finishing	5 Mb	Energy Production
123	*Clostridium ragsdalei* P11	Bacteria	New	3 Mb	
124	*Clostridium saccharolyticum* WM1	Bacteria	New	3 Mb	
125	*Clostridium sp.* MLHE-1	Bacteria	New		Bioremediation
126	*Clostridium sp.* OhILAs	Bacteria	In finishing	2-4 Mb	Bioremediation
127	*Clostridium thermocellum* ATCC 27405	Bacteria	Finished	3.8 Mb	Cellulose Degradation
128	*Clostridium thermocellum* JW20	Bacteria	New	3 Mb	
129	*Clostridium thermocellum* LQR1	Bacteria	New	3 Mb	
130	*Clostridium ultunense*	Bacteria	New	4 Mb	
131	*Colwellia psychroerythraea* 34H	Bacteria	Finished	5.3 Mb	Carbon Cycling
132	*Comamonas testosteroni* KF-1	Bacteria	In finishing	6 Mb	
133	Contaminated groundwater	Microbial Community	In draft assembly		
134	*Crenarchaeota* community	Archaea	Pending		Carbon Cycling
135	*Crenothrix polyspora* enrichment	Bacteria	Pending	40 Mb	
136	*Crocosphaera watsonii* WH8501	Bacteria	Draft	6.4 Mb	Carbon Cycling
137	*Cthoniobacter flavus*	Bacteria	Pending	8 Mb	Carbon Cycling
138	*Cthoniobacter flavus* Ellin 428	Bacteria	Pending	8 Mb	Carbon Cycling
139	*Cupriavidus metallidurans* CH34	Bacteria	Finished	6.8 Mb	
140	*Cupriavidus necator* (*Ralstonia eutropha*) JMP134	Bacteria	Finished	7.2 Mb	
141	*Cyano* JSC-1		New	5 Mb	
142	*Cytophaga hutchinsonii* ATCC 33406	Bacteria	Finished	4.4 Mb	Cellulose Degradation
143	Dechlorinating community (KB-1)	Microbial Community	Pending	200 Mb	
144	*Dechloromonas aromatica* RCB	Bacteria	Finished	4.5 Mb	
145	*Dechloromonas* RCB	Bacteria	Draft	2 Mb	Bioremediation

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146	*Dehalococcoides ethenogenes*	Bacteria	Finished	1.5 Mb	Bioremediation
147	*Dehalococcoides* GT	Bacteria	Pending	1.5 Mb	
148	*Dehalococcoides sp.* BAV1	Bacteria	In finishing	2 Mb	Bioremediation
149	*Dehalococcoides sp.* VS	Bacteria	Draft	1.5 Mb	Bioremediation
150	*Deinococcus geothermalis* DSM 11300	Bacteria	Finished	3 Mb	Bioremediation
151	*Deinococcus radiodurans* R1	Bacteria	Finished	3 Mb	Bioremediation
152	*Delftia acidovorans* SPH-1	Bacteria	In finishing	6 Mb	
153	*Desulfatibacillum alkenivorans* AK-01	Bacteria	In production	6 Mb	
154	*Desulfitobacterium hafniense* DCB-2	Bacteria	Draft	4.7 Mb	Bioremediation
155	*Desulfotomaculum reducens* MI-1	Bacteria	In finishing	4 Mb	Bioremediation
156	*Desulfotomaculum*-like organism			2.3 Mb	
157	*Desulfovibrio desulfuricans* G20	Bacteria	Finished	3.7 Mb	Bioremediation
158	*Desulfovibrio vulgaris* Hildenborough	Bacteria	Finished	3.8 Mb	Bioremediation
159	*Desulfovibrio vulgaris* subsp. *vulgaris* DP4	Bacteria	Finished	3.6 Mb	Bioremediation
160	*Desulfuromonas acetoxidans* DSM 684	Bacteria	Draft	4.1 Mb	Bioremediation
161	*Dictyostelium purpureum*	Slime mold	In production	34 Mb	
162	*Dinoroseobacter shibae* DFL-12	Bacteria	In finishing	6 Mb	
163	*Dunaliela salina* UTEX	Algae	Pending	130 Mb	
164	*Ehrlichia canis* Jake	Bacteria	Finished	1.6 Mb	Biotechnology & Applied Microbiology
165	*Ehrlichia chaffeensis sapulpa*	Bacteria	In finishing	1.8 Mb	Biotechnology & Applied Microbiology
166	Elephant grass decomposer community	Microbial Community	Pending		
167	*Emiliania huxleyi*	Algae	In draft assembly	220 Mb	Carbon Cycling
168	Endophytic bacteria in poplar	Bacteria	In finishing	37.3 Mb	
169	*Enterobacter* sp. 638	Bacteria	In finishing	5 Mb	
170	*Enterococcus faecium* DO	Bacteria	Draft	2.8 Mb	Technology Development, Pilot Projects
171	*Escherichia coli* strain B	Bacteria	In finishing	4 Mb	
172	*Euryarchaeota* community	Microbial Community	In production		
173	*Exiguobacterium sibiricum* strain 255-15	Bacteria	Pending	2.5 Mb	
174	*Exiguobacterium sp.* 255-15	Bacteria	Draft	3.1 Mb	Technology Development, Pilot Projects
175	*Exiguobacterium* sp. strain AT1b	Bacteria	New	2.9 Mb	
176	*Ferroplasma acidarmanus* fer1	Archaea	Finished	1.8 Mb	Bioremediation
177	*Fervidobacterium nodosum*	Bacteria	In finishing	1.9 Mb	
178	*Flavobacterium johnsoniae* UW101	Bacteria	In finishing	6 Mb	Cellulose Degradation
179	*Francisella philomiragia* 2773039	Bacteria	Finished	1.9 Mb	
180	*Francisella tularensis* OR-960463	Bacteria	Finished	1.9 Mb	
181	*Francisella tularensis Wyoming*	Bacteria	Finished	1.9 Mb	
182	*Frankia sp.* CcI3	Bacteria	Finished	5.4 Mb	Carbon Cycling
183	*Frankia sp.* EAN1pec	Bacteria	Draft	10 Mb	Carbon Cycling
184	G1.1MC16		New	6 Mb	
185	*Gallionella ferruginea* (freshwater iron-oxidizing bacteria)	Bacteria	Pending		
186	*Gemmata obscuriglobus* UQM 2246	Bacteria	Finished	9 Mb	Biotechnology & Applied Microbiology
187	*Geobacter bemidjiensis* Bem (T)		In finishing		
188	*Geobacter lovleyi* SZ	Bacteria	In finishing	4 Mb	
189	*Geobacter metallireducens* GS-15	Bacteria	Finished	4.3 Mb	Bioremediation
190	*Geobacter sp.* FRC-32	Bacteria	In finishing	5 Mb	Bioremediation
191	*Geobacter sulfurreducens*	Bacteria	Finished	2.5 Mb	Bioremediation
192	*Geobacter uraniumreducens* RF4	Bacteria	In finishing	4.9 Mb	Bioremediation
193	Geobacteraceae (Environmental)		New		
194	*Geogamma barossii*		Incomplete		

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195	*Geothrix fermentans*		Incomplete		
196	*Glomus intraradices*	Fungi	In production	15 Mb	Bioremediation
197	*Gluconacetobacter diazotrophicus* PAL 5	Bacteria	New	4.3 Mb	
198	*Haemophilus aphtophilus*	Bacteria	Incomplete	2 Mb	pathogen, human
199	*Haemophilus somnus* 129PT	Bacteria	Finished	2 Mb	Technology Development, Pilot Projects
200	*Haemophilus somnus* V	Bacteria	Finished		
201	Haloalkaliphilic sulfur-oxidizing bacteria	Bacteria	In production	28.8 Mb	
202	*Haloarcula marismortai* ATCC 43049	Archaea	Finished	3.4 Mb	
203	*Halobacterium halobium* plasmid	Archaea	Finished	2.3 Mb	Biotechnology & Applied Microbiology
204	*Halorhodospira halophila* SL1	Bacteria	Finished	4 Mb	Biotechnology & Applied Microbiology
205	*Halorubrum lacusprofundi*	Archaea	In finishing	2.2 Mb	Energy Production
206	*Halothermothrix orenii* H168	Bacteria	Draft	2.5 Mb	
207	*Heliothrix oregonensis*	Bacteria	New	5 Mb	Carbon Cycling
208	*Herpetosiphon aurantiacus* DSM 785	Bacteria	In finishing	5 Mb	Carbon Cycling
209	Hypersaline microbial mats	Microbial Community	In production		
210	*Ignicoccus sp.* KIN4/I	Archaea	Finished	1.3 Mb	
211	*Jannaschia sp.* CCS1	Bacteria	Finished	4.5 Mb	Carbon Cycling
212	*Kineococcus radiotolerans* nov	Bacteria	New	4.6 Mb	Bioremediation
213	*Kineococcus radiotolerans* SRS 30216	Bacteria	In finishing	4.9 Mb	
214	*Korarchaeota* community	Microbial Community	Draft		
215	*Korarchaeota SuperPure* OPF1-KOR	Archaea	(unk)		
216	*Laccaria bicolor*	Fungi	In finishing	40 Mb	Bioremediation
217	*Lactobacillus brevis* ATCC 367	Bacteria	Finished	1.8 Mb	Biotechnology & Applied Microbiology
218	*Lactobacillus buchneri* strain NRRL B 30939	Bacteria	New	5 Mb	
219	*Lactobacillus casei* ATCC 334	Bacteria	Finished	2.8 Mb	Biotechnology & Applied Microbiology
220	*Lactobacillus delbrueckii* ATCC BAA-365	Bacteria	Finished	1.6 Mb	Biotechnology & Applied Microbiology
221	*Lactobacillus gasseri* ATCC 33323	Bacteria	Finished	1.9 Mb	Biotechnology & Applied Microbiology
222	*Lactobacillus reuteri* 100-23	Bacteria	In finishing	2.17 Mb	
223	*Lactobacillus reuteri* JCM 1112	Bacteria	In finishing	1.79 Mb	
224	*Lactococcus lactis cremoris* SK11	Bacteria	Finished	2.6 Mb	Biotechnology & Applied Microbiology
225	*Leptospirillum ferroxidans* 53993	Bacteria	Incomplete	2.5 Mb	
226	*Leptospirillum ferroxidans Markosian*	Bacteria	In production	2.5 Mb	
227	*Leptothrix cholodnii* (freshwater iron-oxidizing bacteria)	Bacteria	Pending		
228	*Leuconostoc mesenteroides* ATCC 8293	Bacteria	Finished	2 Mb	Biotechnology & Applied Microbiology
229	LGT in methylobacteria	Bacteria	(unk)	40 Mb	
230	Lithifying mat communities of marine stromatolites (6 bacterial strains)	Bacteria	Pending	288 Mb	
231	Lost City *Methanosarcinales*	Archaea	Pending	3 Mb	
232	*Magnetococcus sp.* MC-1	Bacteria	Finished	4.7 Mb	Biotechnology & Applied Microbiology
233	*Magnetospirillum magnetotacticum* MS-1	Bacteria	Draft	9.2 Mb	Biotechnology & Applied Microbiology
234	*Maricaulis maris* MCS10	Bacteria	Finished	3.4 Mb	Bioremediation
235	*Marinitoga piezophila*	Bacteria	(unk)		
236	*Marinobacter aquaeolei* VT8	Bacteria	Finished	4.6 Mb	
237	*Marinomonas sp.* MWYL1	Bacteria	In finishing	5 Mb	

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238	*Mesophilic methanococci* (five)	Archaea	(unk)	68 Mb	
239	*Mesorhizobium sp.* BNC1	Bacteria	Finished	5 Mb	Bioremediation
240	*Metallosphaera sedula* DSM 5348	Archaea	In finishing	1.9 Mb	
241	*Methanobacterium thermoautotrophicum* Delta H	Archaea	Finished	1.7 Mb	Energy Production
242	*Methanococcoides burtonii* DSM 6242	Archaea	Finished	2.6 Mb	Energy Production
243	*Methanococcus aeolicus*	Archaea	In finishing	2 Mb	
244	*Methanococcus jannaschii* DSM 2661 extremophile	Archaea	Finished	1.7 Mb	Energy Production
245	*Methanococcus maripaludis* C5	Archaea	In finishing	2 Mb	
246	*Methanococcus maripaludis* C6	Archaea	In production	2 Mb	
247	*Methanococcus maripaludis* C7	Archaea	In production	2 Mb	
248	*Methanococcus vannielii* SB	Archaea	In finishing	2 Mb	
249	*Methanococcus voltae* A3	Archaea	In production	2 Mb	
250	*Methanocorpusculum labreanum* Z		Finished	2.3 Mb	
251	*Methanocorpusculum parvum*	Archaea	(unk)		Energy Production
252	*Methanoculleus marisnigri* JR1	Archaea	Finished	1.7 Mb	Energy Production
253	*Methanomicrococcus blatticola*	Archaea	Pending	25.6 Mb	
254	*Methanopyrus kandleri* AV19	Archaea	Finished	1.7 Mb	
255	*Methanoregula boonei*	Archaea	In finishing	3 Mb	
256	*Methanosaeta thermophila* PT	Archaea	Finished	3 Mb	Energy Production
257	*Methanosarcina barkeri* Fusaro	Archaea	Finished	4.8 Mb	Energy Production
258	*Methanospirillum hungatei* JF-1	Archaea	Finished	3.7 Mb	Energy Production
259	*Methanothermobacter thermoautotophicus* Delta H	Archaea	Finished	1.7 Mb	
260	*Methanothermus fervidus*	Archaea	Pending	4.3 Mb	Energy Production
261	*Methylibium petroleiphilum* PM1	Bacteria	Finished	4.6 Mb	
262	*Methylobacillus flagellatus* KT	Bacteria	Finished	2.8 Mb	Energy Production
263	*Methylobacterium chloromethanicum* CM4	Bacteria	In production	7 Mb	
264	*Methylobacterium extorquens* PA1	Bacteria	In finishing	7 Mb	
265	*Methylobacterium nodulans* ORS 2060	Bacteria	In production	7 Mb	
266	*Methylobacterium populi* BJ001	Bacteria	In production	7 Mb	
267	*Methylobacterium radiotolerans* JCM 2831T	Bacteria	In production	7 Mb	
268	*Methylobacterium* sp. Apr-46	Bacteria	In production	7 Mb	
269	*Methylobium petroleophilum* PM1	Bacteria	Finished	4.6 Mb	Bioremediation
270	*Methylocapsa acidiphila* B2	Bacteria	pending		
271	*Methylocella silvestris* BL2	Bacteria	In production		
272	*Methylococcus capsulatus*	Bacteria	Finished	3.3 Mb	Bioremediation
273	Methylotroph strain L1N13		In production	10 Mb	
274	Microbial community in wastewater treatment plants	Microbial Community	Pending	120 Mb	
275	Microbial population from The Cedars, Calif.	Microbial Community	Pending		
276	Microbiome resident in the foregut of the tammar wallaby (*Macropus eugenii*)	Microbial Community	Pending	210 Mb	
277	*Microbulbifer degradans* 2-40	Bacteria	Finished	6 Mb	Cellulose Degradation
278	*Micrococcus luteus* (Actinobacteria)	Bacteria	In production		
279	*Micromonas pusilla ssp.* Eukarya CCMP490 (RCC 114)	Algae	New		Carbon Cycling
280	*Micromonas pusilla* CCMP 1545		In assembly	15 Mb	
281	*Micromonas pusilla* NOUM17 (RCC 299)	Algae	Finished	15 Mb	Carbon Cycling
282	*Mono Lake Deltaproteobacter* MLMS-1		Pending	6 Mb	
283	*Moorella thermoacetica* ATCC 39073	Bacteria	Finished	2.6 Mb	Carbon Cycling
284	MS024-2A	Bacteria	Pending	5 Mb	
285	MS024-3C	Bacteria	Pending	5 Mb	
286	*Mucor circinelloides* CBS277.49 (-)	Fungi	Pending	36 Mb	
287	*Mycobacterium flavescens*	Bacteria	Draft	5.9 Mb	Bioremediation
288	*Mycobacterium gilvum* PYR-GCK	Bacteria	In finishing	5 Mb	
289	*Mycobacterium sp.* JLS	Bacteria	Draft	6 Mb	Bioremediation

	A	B	C	D	E
1	**Genome Name**	**Domain**	**Sequencing Status**	**Approximate Genome Size**	**Category**
290	*Mycobacterium sp.* KMS	Bacteria	Draft	6.2 Mb	Bioremediation
291	*Mycobacterium sp.* MCS	Bacteria	Finished	5.9 Mb	Bioremediation
292	*Mycobacterium vanbaalenii* PYR-1	Bacteria	Finished	6.5 Mb	Bioremediation
293	*Mycoplasma genitalium* G-37	Bacteria	Finished	580 kb	Technology Development, Pilot Projects
294	Near-shore anoxic basin: Saanich Inlet	Microbial Community	In production	235 Mb	
295	*Nectria haematococca* MPVI	Fungi	In finishing	40 Mb	Bioremediation
296	*Nitrobacter hamburgensis* X14	Bacteria	Finished	5 Mb	Carbon Cycling
297	*Nitrobacter winogradskyi* Nb-255	Bacteria	Finished	3.4 Mb	Carbon Cycling
298	*Nitrosococcus oceani* ATCC 19707	Bacteria	Finished	3.5 Mb	Carbon Cycling
299	*Nitrosomonas europaea* ATCC 19718	Bacteria	Finished	2.8 Mb	Carbon Cycling
300	*Nitrosomonas eutropha* C71	Bacteria	Finished	2.7 Mb	Carbon Cycling
301	*Nitrosomonas* isolate IS-79	Bacteria	Pending	3 Mb	Bioremediation
302	*Nitrosomonas* oligotropha Nm45	Bacteria	Pending	3 Mb	Bioremediation
303	*Nitrosopumilus maritimus*	Archaea	In production	3 Mb	
304	*Nitrosospira multiformis* ATCC 25196	Bacteria	Finished	3.2 Mb	
305	*Nitrosospira multiformis* Surinam	Bacteria	New	3 Mb	Carbon Cycling
306	*Nocardioides sp.* JS614	Bacteria	Finished	5.5 Mb	Bioremediation
307	*Nostoc (Anabaena)* sp. PCC 7120	Bacteria	Finished	6.4 Mb	
308	*Nostoc punctiforme* ATCC 29133	Bacteria	Finished	10 Mb	Carbon Cycling
309	*Nostoc punctiforme* PCC 73102	Bacteria	Finished	9.2 Mb	
310	*Novosphingobium aromaticivorans* DSM 12444	Bacteria	Finished	4.2 Mb	
311	*Novosphingobium aromaticivorans* F199	Bacteria	Draft	3.8 Mb	Bioremediation
312	Obsidian hot spring Yellowstone	Microbial Community	Pending		
313	*Oenococcus oeni* PSU-1	Bacteria	Finished	1.8 Mb	Biotechnology & Applied Microbiology
314	*Olavius algarvensis* symbionts	Bacteria	In production		
315	*Opitutus terrae*	Bacteria	Pending	8 Mb	Carbon Cycling
316	*Orpinomyces* sp. Strain PC-2	Fungi	Pending	20 Mb	
317	*Oscillochloris* sp. UdG9002	Bacteria	Pending		
318	*Ostreococcus lucimarinus*	Algae	Finished	9.3 Mb	Carbon Cycling
319	*Ostreococcus sp.* strain CCE 9901		(unk)	9.3 Mb	
320	*Paenibacillus* sp. JDR-2	Bacteria	New	5 Mb	
321	PAH-degrading mycobacteria		In finishing		
322	*Paracoccus denitrificans* PD1222	Bacteria	Finished	3.7 Mb	Bioremediation
323	*Parvibaculum lavamentivorans* DS-1	Bacteria	In finishing	6 Mb	
324	*Pediococcus pentosaceus* ATCC 25745	Bacteria	Finished	1.8 Mb	Biotechnology & Applied Microbiology
325	*Pedomicrobium manganicum*	Bacteria	Pending	40 Mb	
326	*Pelobacter carbinolicus*	Bacteria	Finished	7.2 Mb	
327	*Pelobacter propionicus* DSM 2379	Bacteria	Finished	7.2 Mb	
328	*Pelodictyon luteolum* DSMZ 273	Bacteria	Finished	2.3 Mb	Carbon Cycling
329	*Pelodictyon phaeoclathratiforme* BU-1 (DSM 5477)	Bacteria	In finishing	2.4 Mb	Carbon Cycling
330	*Pelotomaculum schinkii* strain HH	Bacteria	Pending	3 Mb	
331	*Petrotoga mobilis*	Bacteria	In finishing	1.9 Mb	
332	*Phanerochaete carnosa*	Fungi	Pending	35 Mb	
333	*Phanerochaete chrysosporium*	Fungi	Draft	30 Mb	Cellulose Degradation
334	*Phytophthera ramorum*	Fungi	Draft	60 Mb	Biotechnology & Applied Microbiology
335	*Phytophthora sojae*	Fungi	Draft	62 Mb	Biotechnology & Applied Microbiology
336	*Pichia stipitis* CBS 6054	Fungi	Finished	12 Mb	Energy Production
337	Picoplankton BACs [Hawaii Ocean Time Series (HOTS) site]		In production	150 Mb	
338	*Polaromonas naphthalenivorans* CJ2	Bacteria	Finished	6 Mb	Bioremediation

	A	B	C	D	E
1	**Genome Name**	**Domain**	**Sequencing Status**	**Approximate Genome Size**	**Category**
339	*Polaromonas sp.* JS666	Bacteria	Finished	5.2 Mb	
340	*Polynucleobacter necessarius* STIR1	Bacteria	In production	1.7 Mb	
341	*Polynucleobacter sp.* QWL-P1DMWA-1	Bacteria	In finishing	2.2 Mb	
342	*Postia placenta*	Fungi	In finishing	40 Mb	Cellulose Degradation
343	*Prochlorococcus* [HOTS site]	Bacteria	(unk)	2000 Mb	
344	*Prochlorococcus* ACM A12II	Bacteria	Draft		
345	*Prochlorococcus isolate* NATL2	Bacteria	Finished	2.4 Mb	Carbon Cycling
346	*Prochlorococcus marinus* HOT_152-C11		In production		
347	*Prochlorococcus marinus* MED4	Bacteria	Finished	1.6 Mb	Carbon Cycling
348	*Prochlorococcus marinus* MIT 9312	Bacteria	Finished	2.4 Mb	Carbon Cycling
349	*Prochlorococcus marinus* MIT 9313	Bacteria	Finished	2.4 Mb	Carbon Cycling
350	*Prochlorococcus marinus* NATL2A	Bacteria	Finished	2 Mb	
351	*Prochlorococcus marinus pastoris* CCMP 1986	Bacteria	Finished	1.6 Mb	
352	*Prochlorococcus sp.* CC9605 (oligotrophic)	Bacteria	Finished	2.5 Mb	
353	*Prochlorococcus sp.* CC9902 (coastal)	Bacteria	Finished	2.2 Mb	
354	Prokaryotic plasmids		In finishing	7 Mb	
355	*Prosthecochloris aestuarii* DSM 271	Bacteria	In finishing	2.5 Mb	Carbon Cycling
356	*Prosthecochloris vibrioformis* DSM 265	Bacteria	Finished	2.4 Mb	
357	Proteorhodopsin-carrying Flavobacterium-1	Bacteria	Pending	5 Mb	
358	Proteorhodopsin-carrying Flavobacterium-2	Bacteria	Pending	5 Mb	
359	Proteorhodopsin-carrying Flavobacterium-3	Bacteria	Pending	5 Mb	
360	*Pseudoalteromonas atlantica* T6c	Bacteria	Finished	3.5 Mb	Bioremediation
361	*Pseudomonas fluorescens* PfO-1	Bacteria	Finished	6.7 Mb	Bioremediation
362	*Pseudomonas mendocina* ymp	Bacteria	In finishing	4.6 Mb	
363	*Pseudomonas putida* F1	Bacteria	In finishing	6.2 Mb	Bioremediation
364	*Pseudomonas putida* GB-1	Bacteria	Finished	6 Mb	
365	*Pseudomonas putida* KT2440	Bacteria	Finished	6.1 Mb	Bioremediation
366	*Pseudomonas putida* PRSI	Bacteria	Incomplete	6.1 Mb	
367	*Pseudomonas syringae* B728a	Bacteria	Finished	6.1 Mb	Biotechnology & Applied Microbiology
368	*Pseudonitschia*	Algae	(unk)	250 Mb	
369	*Pseudo-nitzschia* (diatom)		In production	250 Mb	
370	*Psychrobacter arcticus* 273-4	Bacteria	Finished	2.5 Mb	Technology Development, Pilot Projects
371	*Psychrobacter cryohalolentis* K5	Bacteria	Finished	3.2 Mb	
372	*Psychrobacter sp.* PRwf-1	Bacteria	Draft	2.9 Mb	
373	*Psychromonas ingrahamii*	Bacteria	Finished	4 Mb	Biotechnology & Applied Microbiology
374	*Pyrobaculum aerophilum* IM2	Archaea	Finished	2.2 Mb	Biotechnology & Applied Microbiology
375	*Pyrobaculum aresenaticum*	Archaea	In finishing	2.2 Mb	Bioremediation
376	*Pyrobaculum calidifontis*	Archaea	In finishing	2.2 Mb	Bioremediation
377	*Pyrobaculum islandicum*	Archaea	Finished	2.2 Mb	Bioremediation
378	*Pyrococcus furiosus*	Archaea	Finished	2.1 Mb	Biotechnology & Applied Microbiology
379	*Ralstonia eutropha* JMP-134	Bacteria	Finished	7.2 Mb	Bioremediation
380	*Ralstonia metallidurans* CH34	Bacteria	Finished	6.9 Mb	Bioremediation
381	*Ralstonia pickettii* 12D	Bacteria	In production	3 Mb	
382	*Ralstonia pickettii* 12J	Bacteria	In finishing	3.5 Mb	
383	*Rhizobium leguminosarum bv trifolii* (strains WSM1325 and WSM2304)	Bacteria	In production	128 Mb	
384	*Rhodobacter* sp. str. SW2 (freshwater iron-oxidizing bacteria)	Bacteria	Pending		
385	*Rhodobacter sphaeroides* 2.4.1	Bacteria	Finished	4.6 Mb	Bioremediation
386	*Rhodobacter sphaeroides* ATCC 17025	Bacteria	In finishing	4.5 Mb	
387	*Rhodobacter sphaeroides* ATCC 17029	Bacteria	Draft	4.5 Mb	
388	*Rhodocyclus*-like polyphosphate accum.		In draft assembly		

	A	B	C	D	E
1	**Genome Name**	**Domain**	**Sequencing Status**	**Approximate Genome Size**	**Category**
389	*Rhodoferax ferrireducens* DSM 15236	Bacteria	Finished	4.9 Mb	
390	*Rhodopseudomonas palustris* (freshwater iron-oxidizing bacteria)	Bacteria	Pending		
391	*Rhodopseudomonas palustris* BisA53	Bacteria	Finished	5.5 Mb	Carbon Cycling
392	*Rhodopseudomonas palustris* BisB18	Bacteria	Finished	5.5 Mb	Carbon Cycling
393	*Rhodopseudomonas palustris* BisB5	Bacteria	Finished	4.9 Mb	Carbon Cycling
394	*Rhodopseudomonas palustris* CGA009	Bacteria	Finished	5.5 Mb	Carbon Cycling
395	*Rhodopseudomonas palustris* HaA2	Bacteria	Finished	5.5 Mb	Carbon Cycling
396	*Rhodospirillum rubrum* ATCC 11170	Bacteria	Finished	4.4 Mb	Carbon Cycling
397	*Rhodosporidium babjevae* WP1	Fungi	New	20 Mb	
398	Rice endophyte metagenome		Pending	100 Mb	
399	*Roseiflexus castenholzii* DSM 13941	Bacteria	In finishing	5 Mb	Carbon Cycling
400	*Roseiflexus sp.* strain RS-1	Bacteria	In finishing	5 Mb	Carbon Cycling
401	*Roseobacter* strain TM1040	Bacteria	New	4.5 Mb	Carbon Cycling
402	*Rubrivivax gelatinosus* PM1	Bacteria	Draft	4.6 Mb	
403	*Rubrobacter xylanophilus* DSM 9941	Bacteria	Finished	3.2 Mb	Cellulose Degradation
404	*Saccharophagus degradans* 2-40	Bacteria	Finished	5.1 Mb	
405	*Salinospora arenicola* (marine actinomycetes)	Bacteria	In finishing	7.7 Mb	
406	*Salinospora tropicalis* (marine actinomycetes)	Bacteria	In finishing	7.7 Mb	
407	Sargasso Sea community	Microbial Community	New		
408	*Schizophyllum* commune	Microbial Community	In production	38 Mb	
409	*Serpula lacrymans*	Fungi	Pending	25 Mb	
410	*Shewanella amazonensis* SB2B	Bacteria	Finished	4.4 Mb	Bioremediation
411	*Shewanella baltica* OS155	Bacteria	Finished	5.2 Mb	Bioremediation
412	*Shewanella baltica* OS195	Bacteria	In finishing	5 Mb	Bioremediation
413	*Shewanella denitrificans* OS217	Bacteria	Finished	4.7 Mb	
414	*Shewanella denitrificans* OS220	Bacteria	New	3.1 Mb	Bioremediation
415	*Shewanella frigidimarina* NCIMB400	Bacteria	Finished	4.9 Mb	Bioremediation
416	*Shewanella halifaxensis* HAW-EB4T	Bacteria	In finishing	5 Mb	
417	*Shewanella oneidensis* MR-1	Bacteria	Finished	4.5 Mb	Bioremediation
418	*Shewanella pealeana* ATCC 700345	Bacteria	In finishing	5 Mb	
419	*Shewanella putrefaciens* 200	Bacteria	In finishing	4.5 Mb	Bioremediation
420	*Shewanella putrefaciens* CN-32	Bacteria	Finished	4.5 Mb	Bioremediation
421	*Shewanella putrefaciens* ML-S2	Bacteria	New	5 Mb	Bioremediation
422	*Shewanella putrefaciens* W3-6-1	Bacteria	New	5 Mb	Bioremediation
423	*Shewanella sediminis* HAW-EB3T	Bacteria	In finishing	5 Mb	
424	*Shewanella sp.* ANA-3	Bacteria	Finished	5 Mb	Bioremediation
425	*Shewanella sp.* MR-4	Bacteria	Finished	5 Mb	Bioremediation
426	*Shewanella sp.* MR-7	Bacteria	Finished	5 Mb	Bioremediation
427	*Shewanella sp.* PV-4	Bacteria	Finished	4.5 Mb	Bioremediation
428	*Shewanella sp.* W3-18-1	Bacteria	Finished	5 Mb	
429	*Shewanella woodyi* ATCC 51908	Bacteria	In finishing	5 Mb	
430	*Sideroxydans lithotrophicus* (freshwater iron-oxidizing bacteria)	Bacteria	Pending		
431	*Silicibacter sp.* TM1040	Bacteria	Finished	3.2 Mb	
432	*Sinorhizobium medicae* WSM 419	Bacteria	In finishing	6.8 Mb	
433	Six Cyanothece strains	Bacteria	Pending (4), In pr	300 Mb	
434	Soil: Diversa Silage	Microbial Community	Draft	152 Mb	
435	*Solibacter usitatus* Ellin6076	Bacteria	Finished	10.2 Mb	
436	South African Gold Mine Metagenome (*Desulforudis audaxviator*)		In finishing		
437	*Sphingomonas wittichii* RW1	Bacteria	In finishing	5 Mb	
438	*Sphingopyxis alaskensis* RB2256	Bacteria	Finished	3.2 Mb	Carbon Cycling
439	*Sporotrichum thermophile* ATCC 42464	Fungi	Pending	43 Mb	
440	*Staphylococcus aureus subsp. aureus* JH1	Bacteria	In finishing	2.9 Mb	

	A	B	C	D	E
1	**Genome Name**	**Domain**	**Sequencing Status**	**Approximate Genome Size**	**Category**
441	*Staphylococcus aureus subsp. aureus* JH9	Bacteria	In finishing	2.9 Mb	
442	*Staphylothermus marinus* F1	Archaea	In finishing	2.2 Mb	
443	*Streptococcus suis* 1591	Bacteria	Draft	2.2 Mb	Technology Development, Pilot Projects
444	*Streptococcus suis* 89/1591	Bacteria	In finishing	2 Mb	
445	*Streptococcus thermophilus* LMD-9	Bacteria	Finished	1.8 Mb	Biotechnology & Applied Microbiology
446	*Sulfolobus islandicus* strains (8)	Archaea	In production	24 Mb	
447	Symbiont from the basal clade of the *Frankiaceae*	Bacteria	Pending	64 Mb	
448	*Synechococcus elongates* PCC7942	Bacteria	Finished	2.7 Mb	Carbon Cycling
449	*Synechococcus elongatus* BP-1	Bacteria	Finished	2.6 Mb	
450	*Synechococcus sp.* C9902 (coastal)	Bacteria	Finished	2.5 Mb	Carbon Cycling
451	*Synechococcus sp.* Cc9605 (oligotrophic)	Bacteria	Finished	2.5 Mb	Carbon Cycling
452	*Synechococcus sp.* WH8102	Bacteria	Finished	2.4 Mb	Carbon Cycling
453	*Syntrophobacter fumaroxidans* MPOB	Bacteria	Finished	3.3 Mb	Energy Production
454	*Syntrophomonas wolfei* Göttingen (DSM 2245B)	Bacteria	Finished	3 Mb	Energy Production
455	*Syntrophomonas zehnderi* sp. nov.	Bacteria	Pending	3 Mb	
456	*Terephthalate* (TA) degrading community	Microbial Community	Pending		
457	Termite gut microbial community	Microbial Community	Finished		
458	*Thalassiosira pseudonana* CCMP1335	Algae	In finishing	32 Mb	Carbon Cycling
459	*Thauera* sp. MZ1T	Bacteria	In production	32 Mb	
460	*Thermacetogenium phaeum*	Bacteria	New	4 Mb	
461	*Thermoanaerobacter brockii subsp. Finnii* Ako-1	Bacteria	New	3 Mb	
462	*Thermoanaerobacter ethanolicus* 39E	Bacteria	In finishing	3 Mb	
463	*Thermoanaerobacter ethanolicus* CCSD_DF2450_M1_68 isolate 1	Bacteria	New	3 Mb	
464	*Thermoanaerobacter ethanolicus* FB14	Bacteria	New	3 Mb	
465	*Thermoanaerobacter ethanolicus* JW200	Bacteria	New	3 Mb	
466	*Thermoanaerobacter ethanolicus* X513	Bacteria	New	3 Mb	
467	*Thermoanaerobacter ethanolicus* X514	Bacteria	In finishing	3 Mb	
468	*Thermoanaerobacter ethanolicus* X561	Bacteria	New	3 Mb	
469	*Thermoanaerobacter italicus* Ab9	Bacteria	New	3 Mb	
470	*Thermoanaerobacterium polysaccharolyticum* KMTHCJ	Bacteria	New	3 Mb	
471	*Thermoanaerobacterium saccharolyticum* JW/SL	Bacteria	New	24 Mb	
472	*Thermoanaerobacterium thermosaccharolyticum* DSM571	Bacteria	New	3 Mb	
473	*Thermoanaerobacterium xylanolyticum* LXII	Bacteria	New	3 Mb	
474	*Thermobifida fusca* YX	Bacteria	Finished	3.6 Mb	Cellulose Degradation
475	*Thermofilum pendens*	Archaea	Finished	1.7 Mb	
476	*Thermofilum pendens* Hrk5	Archaea	Draft	1.8 Mb	
477	*Thermolithobacter ferrireducens*		Pending	48 Mb	
478	*Thermoproteus neutrophilus*	Archaea	In production	3 Mb	
479	*Thermosinus carboxydivorans* Nor 1	Bacteria	In finishing	3 Mb	
480	*Thermosipho melanesiensis* BI429	Bacteria	In finishing	1.9 Mb	
481	*Thermotoga letingae*	Bacteria	In production	1.9 Mb	
482	*Thermotoga maritima* M5B8	Bacteria	Finished	1.8 Mb	Biotechnology & Applied Microbiology
483	*Thermotoga naphthophila*	Bacteria	(unk)	1.9 Mb	
484	*Thermotoga neopolitana* ATCC 49045	Bacteria	Finished	1.8 Mb	Energy Production
485	*Thermotoga petrophila* RKU-1	Bacteria	In finishing	1.9 Mb	
486	*Thermotoga* RQ2		Pending		
487	*Thiobacillus denitrificans* ATCC 23644	Bacteria	Finished	2 Mb	Carbon Cycling
488	*Thiobacillus denitrificans* ATCC 25259	Bacteria	Finished	3 Mb	

	A	B	C	D	E
1	**Genome Name**	**Domain**	**Sequencing Status**	**Approximate Genome Size**	**Category**
489	*Thiomicrospira crunogena* XCL-2	Bacteria	Finished	2.4 Mb	Carbon Cycling
490	*Thiomicrospira denitrificans* ATCC 33889	Bacteria	Finished	2.2 Mb	Carbon Cycling
491	*Tipula abdominalis* gut microbial consortium	Microbial Community	Pending		
492	*Trichoderma atroviride*	Fungi	In production	40 Mb	
493	*Trichoderma reesei*	Fungi	In finishing	30 Mb	Cellulose Degradation
494	*Trichodesmium erythraeum* IMS101	Bacteria	Finished	7.8 Mb	Carbon Cycling
495	Tropical picophytoeukaryotes site 1		Pending		
496	Tropical picophytoeukaryotes site 2		Pending		
497	Tropical picophytoeukaryotes site 3		Pending		
498	Two sulfur-reducing delta proteobacteria	Bacteria	(unk)	122 Mb	
499	Uncultured methylotrophs	Bacteria	(unk)	80 Mb	
500	Uncultured microbes in soil environments	Microbial Community	New		
501	*Verminephrobacter eiseniae* EF01-2 (*Acidovorax* symbiont)		Finished	2.3 Mb	
502	*Verrucomicrobium sp.* TAV2	Bacteria	In finishing	4 Mb	Carbon Cycling
503	*Vibrio furnissi*	Bacteria	New	5 Mb	
504	*Victivallis vadensis*	Bacteria	In finishing	3 Mb	
505	Viruses infecting globally distributed microalgae	Virus	New		
506	WCH70		New	6 Mb	
507	*Xanthobacter autotrophicus* Py2	Bacteria	In finishing	5 Mb	Bioremediation
508	*Xylella fastidiosa* Ann-1	Bacteria	In finishing	5.1 Mb	Technology Development, Pilot Projects
509	*Xylella fastidiosa* Dixon	Bacteria	In finishing	2.6 Mb	Technology Development, Pilot Projects
510	*Xylella fastidiosa XYA*	Bacteria	(unk)	2.4 Mb	
511	*Xylella fastidiosa XYB*	Bacteria	(unk)	2.7 Mb	
512	Y4.12MC10		New	6 Mb	
513	*Yersinia pestis* Antiqua	Bacteria	Finished	4.9 Mb	
514	*Yersinia pestis* Nepal516	Bacteria	Finished	4.6 Mb	
515	*Yersinia pseudotuberculosis* IP 32953	Bacteria	Finished	4.8 Mb	