



## Genomics:GTL Microbes for Research

May 2008\*

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 finding alternative sources of energy, understanding biological carbon cycling as it relates to global climate change, and cleaning up environmental wastes. 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 new Bioenergy Research Centers, Climate Change Research Programs, and its 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 anywhere can propose candidates for sequencing that bear on DOE missions in bioenergy, climate change, or bioremediation. Through the DOE-JGI Laboratory Science Program, scientists at DOE Laboratories are given the opportunity to propose candidates for sequencing that bear on DOE Lab missions. At the completion of any sequencing 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](http://www.jgi.doe.gov)

Genomics:GTL  
[genomicsgtl.energy.gov](http://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 of importance to the DOE, generally radionuclides, metals, and some organic compounds

“Carbon Cycling” – understanding carbon cycles in terrestrial or marine environments to predict sources and sinks of CO<sub>2</sub>

“Cellulose Degradation” – efficient conversion of biomass (cellulose, hemicellulose, or lignin) 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 or enzymes 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/>

See [microbialgenomics.energy.gov/organisms.shtml](http://microbialgenomics.energy.gov/organisms.shtml) for PDF and spreadsheet files.

Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
<i>Accumulibacter phosphatis</i>	Bacteria	New	1 Mb	Bioremediation
<i>Acetivibrio cellulolyticus</i> CD2	Bacteria	New	3 Mb	Cellulose Degradation
Acid mine drainage communities (Iron Mountain, Calif.)	Microbial Community	Finished	10.8 Mb	Bioremediation
<i>Acidiphilium cryptum</i> JF 5	Bacteria	Finished	4.0 Mb	Bioremediation
<i>Acidithiobacillus ferrooxidans</i>	Bacteria	Finished	2.9 Mb	Bioremediation
<i>Acidobacteria bacterium</i> Ellin 345	Bacteria	Finished	5.7 Mb	Technology Development, Pilot Projects
<i>Acidotherrnus cellulolyticus</i> 11B	Bacteria	Finished	2.4 Mb	Biotechnology & Applied Microbiology
<i>Acidovorax avenae Citrulli</i> AAC00-1	Bacteria	Finished	5.4 Mb	Bioremediation
<i>Acidovorax</i> JS42	Bacteria	Finished	4.6 Mb	Bioremediation
<i>Acremonium alcalophilum</i> ATCC 90507	Fungi	In production	40 Mb	Cellulose Degradation
<i>Actinobacillus succinogenes</i> 130Z	Bacteria	Finished	2.3 Mb	Biotechnology & Applied Microbiology
Active methylotroph community from Lake Washington	Microbial Community	Finished		Bioremediation
<i>Akkermansia muciniphila</i>	Bacteria	In finishing	8 Mb	Carbon Cycling
Alaskan soil microbial community	Microbial Community	Draft		Technology Development, Pilot Projects
<i>Alkalilimnicola ehrlichei</i> MLHE-1	Bacteria	Finished	3.3 Mb	Bioremediation
<i>Alkaliphilus metalliredigenes</i> QYMF	Bacteria	Finished	4.9 Mb	Bioremediation
<i>Allochromatium vinosum</i> DSM 180(T)	Bacteria	In production		Carbon Cycling
<i>Anabaena variabilis</i> ATCC 29413	Bacteria	Finished	7.1 Mb	Energy Production
Anaerobic benzene-degrading methanogenic consortium	Microbial Community	Pending	192 Mb	Bioremediation
Anaerobic bioreactor granule samples, 200 BACs from Hanford PNNL site		Finished	100 Mb	Bioremediation
Anaerobic Methane Oxidizing community		In production		Energy Production
<i>Anaeromyxobacter dehalogenans</i> 2CP-1	Bacteria	In finishing	5 Mb	Bioremediation
<i>Anaeromyxobacter dehalogenans</i> 2CP-C	Bacteria	Finished	5 Mb	Bioremediation
<i>Anaeromyxobacter</i> strain K	Bacteria	In finishing	5 Mb	Bioremediation
<i>Anaeromyxobacteria</i> sp. FW109-5	Bacteria	Finished	5.3 Mb	Bioremediation
<i>Anammoxglobus propionicus</i> (Anammox bacteria)	Bacteria	In production		Carbon Cycling
<i>Ancalomicrobium adetum</i>	Bacteria	Pending		Bioremediation
<i>Anoplophora glabripennis</i> gut consortium	Microbial Community	In production		Cellulose Degradation
Antarctic marine bacterioplankton		Pending		Carbon Cycling
<i>Aquifex aeolicus</i> VF5 extremophile	Bacteria	Finished	1.5 Mb	Biotechnology & Applied Microbiology
<i>Archaeoglobus fulgidus</i> VC-16	Archaea	Finished	2.1 Mb	Biotechnology & Applied Microbiology
<i>Arthrobacter chlorophenolicus</i> (Actinobacteria)	Bacteria	In finishing		Bioremediation
<i>Arthrobacter</i> sp. FB24	Bacteria	Finished	5.1 Mb	Bioremediation
<i>Arthrospira maxima</i>	Bacteria	In finishing	5 Mb	Bioremediation
<i>Aspergillus niger</i>	Fungi	Finished	32 Mb	Biotechnology & Applied Microbiology

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<i>Asticcacaulis biprosthicum</i>	Bacteria	Pending		Bioremediation
<i>Asticcacaulis excentricus</i>	Bacteria	In production		Bioremediation
<i>Aureococcus anophagefferens</i>	Algae	In finishing	32 Mb	Carbon Cycling
<i>Azolla</i> Cyanobacterium	Bacteria	Pending		
<i>Azospira suillum</i> strain PS	Bacteria	In production		Bioremediation
<i>Azotobacter vinelandii</i> AvOP	Bacteria	Finished	5.3 Mb	Carbon Cycling
<i>Bacillus anthracis</i> A2012	Bacteria	Finished	5.1 Mb	Pathogen, Human
<i>Bacillus anthracis</i> Ames	Bacteria	Finished	5.2 Mb	Pathogen, Human
<i>Bacillus anthracis</i> Ames Ancestor A2084	Bacteria	Finished	5.6 Mb	Pathogen, Human
<i>Bacillus anthracis</i> Sterne	Bacteria	Finished	5.2 Mb	Pathogen, Human
<i>Bacillus cereus cytotoxis</i> NVH 391-98	Bacteria	Finished	4.1 Mb	Nonpathogen for Humans; Cold-Tolerant
<i>Bacillus cereus</i> E33L	Bacteria	Finished	5.3 Mb	Technology Development, Pilot Projects
<i>Bacillus coagulans</i> 36D1	Bacteria	Draft	2.9 Mb	Energy Production
<i>Bacillus selenitireducens</i> MLS-10	Bacteria	In finishing	2-4 Mb	Bioremediation
<i>Bacillus thuringiensis</i> Al Hakam	Bacteria	Finished	5.3 Mb	Pathogen, Insect
<i>Bacillus thuringiensis konkukian</i> 97-27	Bacteria	Finished	5.3 Mb	Pathogen, Human
<i>Bacillus weihenstephanensis</i> KBAB4	Bacteria	Finished	5.6 MB	Nonpathogen for Humans; Cold-Tolerant
Bacterioplankton pool cDNA day, night, night + DOC1, night + DOC2	Microbial Community	Pending		Carbon Cycling
<i>Beggiatoa alba</i>	Bacteria	Pending	42 Mb	Bioremediation
<i>Beijerinckia indica subsp. indica</i>	Bacteria	In finishing		Energy Production
<i>Bifidobacterium longum</i> DJO10A	Bacteria	Finished	2.4 Mb	Biotechnology & Applied Microbiology
<i>Bifidobacterium longum infantis</i>	Bacteria	In finishing		
Biogas-producing microbial community	Microbial Community	Pending		Energy Production
Bison Pool, hydrothermal ecosystem	Microbial Community	Draft		
Boiling thermal pool Yellowstone National Park	Microbial Community	In production	50 Mb	Technology Development, Pilot Projects
<i>Borrelia burgdorferi</i> B31	Bacteria	Finished	1.4 Mb	Technology Development, Pilot Projects
<i>Bradyrhizobium sp.</i> BTAi1	Bacteria	Finished	8.5 Mb	Carbon Cycling
<i>Brevibacterium linens</i> BL2	Bacteria	Finished	4.5 Mb	Biotechnology & Applied Microbiology
<i>Brevundimonas subvibrioides</i>	Bacteria	In production		Bioremediation
<i>Brocadia fulgida</i> (Anammox bacteria)	Bacteria	In production		Carbon Cycling
<i>Brucella melitensis</i> 16M	Bacteria	Finished	3.3 Mb	Technology Development, Pilot Projects
<i>Brucella melitensis abortus</i> 2308	Bacteria	Finished	3.2 Mb	Pathogen, Animal
<i>Burkholderia ambifaria</i> IOP40-10	Bacteria	Pending		Carbon Cycling
<i>Burkholderia ambifaria</i> MC40-6	Bacteria	Finished	7.6 Mb	Bioremediation
<i>Burkholderia ambifaria</i> MEX-5	Bacteria	Pending		Carbon Cycling

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<i>Burkholderia cenocepacia</i> AU 1054	Bacteria	Finished	7.3 Mb	Bioremediation
<i>Burkholderia cenocepacia</i> HI2424	Bacteria	Finished	7.7 Mb	Bioremediation
<i>Burkholderia cenocepacia</i> MC0-3	Bacteria	Finished	7.9 Mb	Technology Development, Pilot Projects
<i>Burkholderia cepacia</i> AMMD	Bacteria	Finished	7.5 Mb	Bioremediation
<i>Burkholderia graminis</i> C4D1M	Bacteria	In finishing		Carbon Cycling
<i>Burkholderia multivorans</i> ATCC 17616	Bacteria	Finished	7 Mb	Technology Development, Pilot Projects
<i>Burkholderia phymatum</i> STM 815	Bacteria	In finishing	8.6 Mb	Bioremediation
<i>Burkholderia phytofirmans</i> PsJN	Bacteria	In finishing	8.1 Mb	Carbon Cycling
<i>Burkholderia</i> sp. 383	Bacteria	Finished	8.7 Mb	Bioremediation
<i>Burkholderia</i> sp. SEMIA 6167	Bacteria	Pending		Carbon Cycling
<i>Burkholderia</i> sp. strain 131	Bacteria	Pending		Carbon Cycling
<i>Burkholderia</i> sp. strain 144F	Bacteria	Pending		Carbon Cycling
<i>Burkholderia</i> sp. strain H160	Bacteria	Pending		Carbon Cycling
<i>Burkholderia</i> UFLA 4-5-1 (Amazon strain)	Bacteria	Pending		Carbon Cycling
<i>Burkholderia vietnamiensis</i> G4	Bacteria	Finished	8.4 Mb	Bioremediation
<i>Burkholderia xenovorans</i> LB400	Bacteria	Finished	9.7 Mb	Bioremediation
<i>Caldicellulosiruptor saccharolyticus</i> DSM 8903	Bacteria	Finished	3 Mb	Energy Production
<i>Caldivirga maquilingsensis</i> IC-167	Archaea	Finished	2.1 Mb	Bioremediation
<i>Candidatus Amoebophilus asiaticus</i>	Bacteria	In finishing		Technology Development, Pilot Projects
<i>Candidatus Cardinium hertigii</i>	Bacteria	Pending		Technology Development, Pilot Projects
<i>Candidatus Chlorothrix halophila</i>	Bacteria	Draft	5 Mb	Carbon Cycling
<i>Candidatus Endomicrobium trichonymphae</i>		In finishing	110 Mb	Cellulose Degradation
<i>Candidatus Ruthia magnifica</i> Cm (Proteobacterial symbiont of the clam <i>Calyptogena magnifica</i> )	Bacteria	Finished	1.2 Mb	Carbon Cycling
<i>Candidatus Nitrosopumilus maritimus</i> SCM1	Archaea	Finished	3 Mb	Carbon Cycling
<i>Carboxydotherrnus hydrogenoformans</i>	Bacteria	Finished	2.1 Mb	Energy Production
<i>Caulobacter crescentus</i>	Bacteria	Finished	4 Mb	Bioremediation
<i>Caulobacter</i> sp. K31	Bacteria	Finished	5.9 Mb	Bioremediation
<i>Chlamydia trachomatis</i> Ds2923	Bacteria	Finished		Carbon Cycling; Plant Homologue
<i>Chlamydia trachomatis</i> E11023	Bacteria	Finished		Carbon Cycling; Plant Homologue
<i>Chlamydia trachomatis</i> G9301	Bacteria	Finished		Carbon Cycling; Plant Homologue
<i>Chlamydia trachomatis</i> G9768	Bacteria	Finished		Carbon Cycling; Plant Homologue
<i>Chlamydomonas reinhardtii</i>	Algae	In finishing	100 Mb	Carbon Cycling
<i>Chlorella</i> NC64A	Algae	Draft	40 Mb	Carbon Cycling
<i>Chlorella vulgaris</i> C-169	Algae	Draft	40 Mb	Carbon Cycling
<i>Chlorobium aggregatum</i>	Microbial Community	Finished		Carbon Cycling

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<i>Chlorobium chlorochromatii</i> CaD3	Microbial Community	Finished	2.5 Mb	Carbon Cycling
<i>Chlorobium ferrooxidans</i> DSM 13031	Bacteria	In finishing	2.5 Mb	Energy Production
<i>Chlorobium limicola</i> DSM 245	Bacteria	In finishing	2.8 Mb	Carbon Cycling
<i>Chlorobium luteolum</i> DSM 273	Bacteria	Finished	2.4 Mb	Carbon Cycling
<i>Chlorobium phaeobacteroides</i> BS1	Bacteria	In finishing	4.9 Mb	Carbon Cycling
<i>Chlorobium phaeobacteroides</i> DSM 266	Bacteria	Finished	3.1 Mb	Carbon Cycling
<i>Chlorobium tepidum</i>	Bacteria	Finished	2.1 Mb	Carbon Cycling
<i>Chlorobium vibrioforme f. thiosulfatophilum</i> DSMZ 265	Bacteria	Draft	1.9 Mb	Carbon Cycling
<i>Chlorochromatium aggregatum</i> Lake Dagow	Bacteria	Draft		Biotechnology & Applied Microbiology
<i>Chloroflexus aggregans</i> DSM 9485	Bacteria	In finishing	4.6 Mb	Carbon Cycling
<i>Chloroflexus aurantiacus</i> J-10-fl	Bacteria	Finished	5.2 Mb	Carbon Cycling
<i>Chloroherpeton thalassium</i>	Bacteria	In finishing	3.5 Mb	Carbon Cycling
<i>Chloronema giganteum</i> UdG9001	Bacteria	Pending	5 Mb	Carbon Cycling
<i>Chromohalobacter salexigens</i> DSM 3043	Bacteria	Finished	3.7 Mb	Bioremediation
<i>Chthoniobacter flavus</i> Ellin428	Bacteria	In finishing		Carbon Cycling
<i>Chthoniobacter flavus</i> Ellin514	Bacteria	In finishing		Carbon Cycling
<i>Clostridium acetobutylicum</i>	Bacteria	Finished	4.1 Mb	Biotechnology & Applied Microbiology
<i>Clostridium beijerincki</i> NCIMB 8052	Bacteria	Finished	6 Mb	Energy Production
<i>Clostridium carboxidivorans</i>	Bacteria	In production	3 Mb	Energy Production
<i>Clostridium cellulolyticum</i> H10	Bacteria	In finishing	4 Mb	Cellulose Degradation
<i>Clostridium cellulovorans</i> 743B	Bacteria	In production	3 Mb	Cellulose Degradation
<i>Clostridium josui</i> FERM P-9684	Bacteria	In production	3 Mb	Cellulose Degradation
<i>Clostridium papyrosolvents</i> DSM 2782	Bacteria	In production	3 Mb	Cellulose Degradation
<i>Clostridium pasteurianum</i> DSM 525	Bacteria	In production	3 Mb	Energy Production
<i>Clostridium phytofermentans</i> ISDg	Bacteria	Finished	4.5 Mb	Energy Production
<i>Clostridium ragsdalei</i> P11	Bacteria	In production	3 Mb	Carbon Cycling
<i>Clostridium saccharolyticum</i> WM1	Bacteria	In production	3 Mb	Energy Production
<i>Clostridium sp.</i> MLHE-1	Bacteria	In production		Bioremediation
<i>Clostridium sp.</i> OhILAs	Bacteria	In production	3 Mb	Bioremediation
<i>Clostridium thermocellum</i> ATCC 27405	Bacteria	Finished	3.8 Mb	Cellulose Degradation
<i>Clostridium thermocellum</i> JW20 DSM4150	Bacteria	In production	3 Mb	Energy Production
<i>Clostridium thermocellum</i> LQR1 DSM2360	Bacteria	In production	3 Mb	Energy Production
<i>Clostridium ultunense</i>	Bacteria	In production	4 Mb	Energy Production
<i>Colwellia psychoerythraea</i> 34H	Bacteria	Finished	5.3 Mb	Carbon Cycling
<i>Comamonas testosteroni</i> KF-1	Bacteria	In finishing	5.9 Mb	Bioremediation
Contaminated groundwater	Microbial Community	Draft		Bioremediation
<i>Crenarchaeota</i> community	Archaea	In production		Carbon Cycling
<i>Crenothrix polyspora</i> enrichment	Bacteria	In production	40 Mb	Carbon Cycling
<i>Crocospaera watsonii</i> WH8501	Bacteria	Draft	6.2 Mb	Carbon Cycling
<i>Cupriavidus metallidurans</i> CH34	Bacteria	Finished	6.9 Mb	Bioremediation
<i>Cupriavidus metallidurans</i> CH34	Bacteria	Finished	6.9 Mb	Bioremediation
<i>Cyano bacterium</i> JSC-1		In production	5 Mb	Cellulose Degradation
<i>Cyanothece</i> (six strains)	Bacteria	In finishing	300 Mb	Carbon Cycling
<i>Cytophaga hutchinsonii</i> ATCC 33406	Bacteria	Finished	4.4 Mb	Cellulose Degradation

Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
Dechlorinating community (KB-1)	Microbial Community	Pending	200 Mb	Bioremediation
<i>Dechloromonas aromatica</i> RCB	Bacteria	Finished	4.5 Mb	Bioremediation
<i>Dehalococcoides ethenogenes</i>	Bacteria	Finished	1.5 Mb	Bioremediation
<i>Dehalococcoides</i> GT	Bacteria	Pending	1.5 Mb	Bioremediation
<i>Dehalococcoides</i> sp. BAV1	Bacteria	Finished	1.3 Mb	Bioremediation
<i>Dehalococcoides</i> sp. VS	Bacteria	Draft	1.5 Mb	Bioremediation
<i>Deinococcus geothermalis</i> DSM 11300	Bacteria	Finished	3 Mb	Bioremediation
<i>Deinococcus radiodurans</i> R1	Bacteria	Finished	3 Mb	Bioremediation
<i>Delftia acidovorans</i> SPH-1	Bacteria	Finished	6.7 Mb	Bioremediation
<i>Desulfatibacillum alkenivorans</i> AK-01	Bacteria	Draft	6 Mb	Bioremediation
<i>Desulfitobacterium hafniense</i> DCB-2	Bacteria	Draft	5.3 Mb	Bioremediation
<i>Desulfococcus oleovorans</i> Hxd3	Bacteria	Finished	3.8 Mb	Bioremediation
<i>Desulfonatovirga dismutans</i> ASO3-1	Bacteria	In production		Energy Production
<i>Desulfotomaculum reducens</i> MI-1	Bacteria	Finished	3.6 Mb	Bioremediation
<i>Desulfovibrio alkaliphilus</i> AHT2	Bacteria	In production		Energy Production
<i>Desulfovibrio desulfuricans</i> 27774	Bacteria	In production		Bioremediation
<i>Desulfovibrio desulfuricans</i> G20	Bacteria	Finished	3.7 Mb	Bioremediation
<i>Desulfovibrio vulgaris</i> Hildenborough	Bacteria	Finished	3.8 Mb	Bioremediation
<i>Desulfovibrio vulgaris</i> Miyazaki F	Bacteria	In finishing	3.57 Mb	Bioremediation
<i>Desulfovibrio vulgaris</i> subsp. <i>vulgaris</i> DP4	Bacteria	Finished	3.7 Mb	Bioremediation
<i>Desulfuromonas acetoxidans</i> DSM 684	Bacteria	Draft	3.8 Mb	Bioremediation
<i>Dethiobacter alkaliphilus</i> AHT1	Bacteria	In production		Energy Production
<i>Diaphorobacter</i> sp. strain TPSY	Bacteria	In production		Bioremediation
<i>Dictyostelium purpureum</i>	Slime mold	Draft	34 Mb	Biotechnology & Applied Microbiology
<i>Dinoroseobacter shibae</i> DFL-12	Bacteria	Finished	4.3 Mb	Carbon Cycling
<i>Dunaliella salina</i> UTEX	Algae	In production	130 Mb	Carbon Cycling
<i>Ehrlichia canis</i> Jake	Bacteria	Finished	1.3 Mb	Biotechnology & Applied Microbiology
<i>Ehrlichia chaffeensis</i> sapulpa	Bacteria	In finishing	1.0 Mb	Biotechnology & Applied Microbiology
Elephant grass decomposer community	Microbial Community	Pending		Cellulose Degradation
<i>Elusimicrobium minutum</i> Pei191		In finishing		Cellulose Degradation
<i>Emiliana huxleyi</i>	Algae	Draft	220 Mb	Carbon Cycling
<i>Enterobacter</i> sp. 638	Bacteria	Finished	4.7 Mb	Carbon Cycling
<i>Enterobacter</i> sp. R558-1 (Poplar endophytic bacteria)	Bacteria	In finishing		Carbon Cycling
<i>Enterococcus faecium</i> DO	Bacteria	Draft	2.8 Mb	Technology Development, Pilot Projects
<i>Escherichia coli</i> C str. ATCC 8739	Bacteria	Finished	4 Mb	Biotechnology & Applied Microbiology
<i>Euryarchaeota</i> community (acid mine drainage)	Microbial Community	In assembly		Bioremediation
<i>Exiguobacterium sibiricum</i> strain 255-15	Bacteria	Finished	3.1 Mb	Carbon Cycling
<i>Exiguobacterium</i> sp. strain AT1b	Bacteria	In finishing	2.9 Mb	Carbon Cycling
Extreme microbial habitats across the Yellowstone geothermal ecosystem	Microbial Community	In production		Energy Production

Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
<i>Ferroplasma acidarmanus</i> fer1	Archaea	Finished	1.8 Mb	Bioremediation
<i>Ferrutens nitratireducens</i> strain 2002	Bacteria	In production		Bioremediation
<i>Fervidobacterium nodosum</i> Rt17-B1	Bacteria	Finished	1.9 Mb	Energy Production
<i>Flavobacteria</i> sp. MS024-2A	Bacteria	In finishing		Biotechnology & Applied Microbiology
<i>Flavobacteria</i> sp. MS0243-3C	Bacteria	In finishing		Biotechnology & Applied Microbiology
<i>Flavobacteria</i> sp. MS190-1F	Bacteria	In production		Biotechnology & Applied Microbiology
<i>Flavobacteria</i> sp. MS311-3	Bacteria	In production		Biotechnology & Applied Microbiology
<i>Flavobacterium johnsoniae</i> UW101	Bacteria	Finished	6.1 Mb	Cellulose Degradation
<i>Francisella philomiragia</i> subsp. <i>philomiragia</i> ATCC 25017	Bacteria	Finished	1.9 Mb	Pathogen, Animal
<i>Francisella tularensis</i> OR-960463	Bacteria	Finished	1.9 Mb	Pathogen, Human
<i>Francisella tularensis</i> Wyoming	Bacteria	Finished	1.9 Mb	Pathogen, Human
<i>Frankia</i> sp. Ccl3	Bacteria	Finished	5.4 Mb	Carbon Cycling
<i>Frankia</i> sp. EAN1pec	Bacteria	Finished	8.9 Mb	Carbon Cycling
<i>Frankia</i> strain AmMr	Bacteria	Pending		Carbon Cycling, Bioremediation
<i>Frankia</i> strain BCU110501	Bacteria	Pending		Carbon Cycling, Bioremediation
<i>Frankia</i> strain BMG5.12	Bacteria	Pending		Carbon Cycling, Bioremediation
<i>Frankia</i> strain Eul1c,	Bacteria	Pending		Carbon Cycling, Bioremediation
<i>Frankia</i> strain R43	Bacteria	Pending		Carbon Cycling, Bioremediation
<i>Gallionella ferruginea</i> (freshwater iron-oxidizing bacteria)	Bacteria	Pending		Carbon Cycling
<i>Gemmata obscuriglobus</i> UQM 2246	Bacteria	Finished	9 Mb	Biotechnology & Applied Microbiology
<i>Geobacillus</i> sp. G11MC16		In finishing	6 Mb	Carbon Cycling
<i>Geobacillus</i> sp. WCH70		In finishing	6 Mb	Carbon Cycling
<i>Geobacillus</i> sp. Y4.12MC10		In finishing	6 Mb	Carbon Cycling
<i>Geobacter bemidjiensis</i> Bem	Bacteria	In finishing	4.5 Mb	Bioremediation
<i>Geobacter lovleyi</i> SZ	Bacteria	In finishing	3.9 Mb	Bioremediation
<i>Geobacter metallireducens</i> GS-15	Bacteria	Finished	4 Mb	Bioremediation
<i>Geobacter</i> sp. FRC-32	Bacteria	In finishing	4 Mb	Bioremediation
<i>Geobacter</i> sp. M21	Bacteria	In production		Bioremediation
<i>Geobacter sulfurreducens</i>	Bacteria	Finished	2.5 Mb	Bioremediation
<i>Geobacter uraniumreducens</i> RF4	Bacteria	Finished	5.1 Mb	Bioremediation
<i>Geogemma barossii</i>	Archaea	Incomplete		Biotechnology & Applied Microbiology
<i>Geothrix fermentans</i>	Bacteria	Incomplete		Bioremediation
<i>Glomus intraradices</i>	Fungi	In production	15 Mb	Bioremediation
<i>Gluconacetobacter diazotrophicus</i> PAL 5	Bacteria	In production	4.3 Mb	Carbon Cycling
<i>Haemophilus aphrophilus</i>	Bacteria	Incomplete	2 Mb	Pathogen, Human



Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
<i>Haemophilus somnus</i> 129PT	Bacteria	Finished	2 Mb	Technology Development, Pilot Projects
<i>Haemophilus somnus</i> 2336	Bacteria	Finished		Biotechnology & Applied Microbiology
Haloalkaliphilic sulfur-oxidizing bacteria ( <i>Thioalkalivibrio</i> )	Bacteria	In production	28.8 Mb	Bioremediation
<i>Haloarcula marismortui</i> ATCC 43049	Archaea	Finished	3.4 Mb	Energy Production
<i>Halobacterium halobium</i> plasmid	Archaea	Finished	2.3 Mb	Biotechnology & Applied Microbiology
<i>Halorhodospira halophila</i> SL1	Bacteria	Finished	2.7 Mb	Biotechnology & Applied Microbiology
<i>Halorubrum lacusprofundi</i> ATCC 49239	Archaea	In finishing	2.8 Mb	Energy Production
<i>Halothermothrix orenii</i> H168	Bacteria	Draft	2.5 Mb	Energy Production
<i>Halothiobacillus neapolitanus</i>	Bacteria	In production		Carbon Cycling
<i>Herpetosiphon aurantiacus</i> DSM 785	Bacteria	Finished	6.6 Mb	Carbon Cycling
Hypersaline microbial mats	Microbial Community	Draft		Biotechnology & Applied Microbiology
<i>Hyphomicrobium denitrificans</i>	Bacteria	Pending		Bioremediation
<i>Ignicoccus</i> sp. KIN4-1	Archaea	Finished	1.3 Mb	Biotechnology & Applied Microbiology
<i>Jannaschia</i> sp. CCS1	Bacteria	Finished	4.4 Mb	Carbon Cycling
<i>Kineococcus radiotolerans</i> SRS 30216	Bacteria	Finished	5 Mb	Bioremediation
<i>Korarchaeota</i> community	Microbial Community	Draft		Biotechnology & Applied Microbiology
<i>Laccaria bicolor</i>	Fungi	In finishing	40 Mb	Bioremediation; Carbon Cycling
<i>Lactobacillus brevis</i> ATCC 367	Bacteria	Finished	2.3 Mb	Biotechnology & Applied Microbiology; Energy Production
<i>Lactobacillus buchneri</i> B-30929	Bacteria	In finishing	5 Mb	Cellulose Degradation
<i>Lactobacillus buchneri</i> NRRL B30929	Bacteria	Draft	5 Mb	Cellulose Degradation
<i>Lactobacillus casei</i> ATCC 334	Bacteria	Finished	2.9 Mb	Biotechnology & Applied Microbiology
<i>Lactobacillus delbrueckii</i> ATCC BAA-365	Bacteria	Finished	1.9 Mb	Biotechnology & Applied Microbiology
<i>Lactobacillus gasserii</i> ATCC 33323	Bacteria	Finished	1.9 Mb	Biotechnology & Applied Microbiology
<i>Lactobacillus reuteri</i> 100-23	Bacteria	In finishing	2.2 Mb	Biotechnology & Applied Microbiology
<i>Lactobacillus reuteri</i> F275	Bacteria	Finished	2.0 Mb	Biotechnology & Applied Microbiology
<i>Lactococcus lactis cremoris</i> SK11	Bacteria	Finished	2.6 Mb	Biotechnology & Applied Microbiology
<i>Leptospirillum ferrooxidans</i> Markosian	Bacteria	In finishing	2.5 Mb	Bioremediation
<i>Leptospirillum ferrooxidans</i> 53993	Bacteria	Incomplete	2.5 Mb	Bioremediation
<i>Leptothrix cholodnii</i> (freshwater iron-oxidizing bacteria)	Bacteria	In finishing		Bioremediation
<i>Leuconostoc mesenteroides</i> ATCC 8293	Bacteria	Finished	2.1 Mb	Biotechnology & Applied Microbiology

Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
Lithifying mat communities of marine stromatolites (6 bacterial strains)	Bacteria	Pending	288 Mb	Carbon Cycling
Lost City <i>Methanosarcinales</i>	Archaea	In assembly	3 Mb	Energy Production
Lynne Flavobacteria sp. MS220-5C	Bacteria	In production		Biotechnology & Applied Microbiology
<i>Magnetococcus</i> sp. MC-1	Bacteria	Finished	4.7 Mb	Biotechnology & Applied Microbiology
<i>Magnetospirillum magnetotacticum</i> MS-1	Bacteria	Draft	9.2 Mb	Biotechnology & Applied Microbiology
<i>Maricaulis maris</i> MCS10	Bacteria	Finished	3.4 Mb	Bioremediation
<i>Marinobacter aquaeolei</i> VT8	Bacteria	Finished	4.8 Mb	Carbon Cycling
<i>Marinomonas</i> sp. MWYL1	Bacteria	Finished	5.1 Mb	Carbon Cycling
<i>Mesorhizobium</i> sp. BNC1	Bacteria	Finished	4.9 Mb	Bioremediation
<i>Metallosphaera sedula</i> DSM 5348	Archaea	Finished	2.2 Mb	Bioremediation
<i>Methanobacterium thermoautotrophicum</i> Delta H	Archaea	Finished	1.7 Mb	Energy Production
<i>Methanocaldococcus fervens</i> AG86	Archaea	In production		Energy Production
<i>Methanocaldococcus infernus</i> ME	Archaea	In production		Energy Production
<i>Methanocaldococcus</i> strain FS406-22	Archaea	Pending		Energy Production
<i>Methanocaldococcus vulcanius</i> M7	Archaea	Pending		Energy Production
<i>Methanococcoides burtonii</i> DSM 6242	Archaea	Finished	2.6 Mb	Energy Production
<i>Methanococcus aeolicus</i> Nankai-3	Archaea	Finished	1.6 Mb	Energy Production
<i>Methanococcus jannaschii</i> DSM 2661 extremophile	Archaea	Finished	1.7 Mb	Energy Production
<i>Methanococcus maripaludis</i> C5	Archaea	Finished	1.8 Mb	Energy Production
<i>Methanococcus maripaludis</i> C6	Archaea	Finished	2 Mb	Energy Production
<i>Methanococcus maripaludis</i> C7	Archaea	Finished	1.8 Mb	Energy Production
<i>Methanococcus vanniellii</i> SBC5	Archaea	Finished	1.7 Mb	Energy Production
<i>Methanococcus voltae</i> A3	Archaea	In finishing	2 Mb	Energy Production
<i>Methanocorpusculum labreanum</i> Z	Archaea	Finished	1.8 Mb	Energy Production
<i>Methanoculleus marisnigri</i> JR1	Archaea	Finished	2.5 Mb	Energy Production
<i>Methanomicrococcus blatticola</i>	Archaea	Pending	25.6 Mb	Carbon Cycling
<i>Methanopyrus kandleri</i> AV19	Archaea	Finished	1.7 Mb	Energy Production
<i>Methanoregula boonei</i> 6A8	Archaea	Finished	3 Mb	Energy Production
<i>Methanosaeta thermophila</i> PT	Archaea	Finished	1.9 Mb	Energy Production
<i>Methanosarcina barkeri</i> Fusaro	Archaea	Finished	4.9 Mb	Energy Production
<i>Methanosphaerula palustris</i> E1-9c		In production		
<i>Methanospirillum hungatei</i> JF-1	Archaea	Finished	3.5 Mb	Energy Production
<i>Methanothermobacter thermoautotrophicus</i> Delta H	Archaea	Finished	1.7 Mb	Energy Production
<i>Methanothermococcus okinawensis</i> IH1	Archaea	Pending		Energy Production
<i>Methanothermus fervidus</i>	Archaea	Pending	4.3 Mb	Energy Production
<i>Methanotorris formicicus</i> Mc-S-70	Archaea	Pending		Energy Production
<i>Methanotorris igneus</i> Kol 5	Archaea	In production		Energy Production
<i>Methylibium petroleiphilum</i> PM1	Bacteria	Finished	4.6 Mb	Bioremediation
<i>Methylobacillus flagellatus</i> KT	Bacteria	Finished	3 Mb	Energy Production
<i>Methylobacterium chloromethanicum</i> CM4	Bacteria	In finishing	7 Mb	Carbon Cycling
<i>Methylobacterium extorquens</i> PA1	Bacteria	Finished	5.5 Mb	Carbon Cycling
<i>Methylobacterium nodulans</i> ORS 2060	Bacteria	In finishing	7 Mb	Carbon Cycling
<i>Methylobacterium populi</i> BJ001	Bacteria	In finishing	7 Mb	Carbon Cycling
<i>Methylobacterium radiotolerans</i> JCM 2831T	Bacteria	Finished	7 Mb	Carbon Cycling

Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
<i>Methylobacterium</i> sp. 4-46	Bacteria	Finished	7.9 Mb	Carbon Cycling
<i>Methylobium petroleophilum</i> PM1	Bacteria	Finished	4.6 Mb	Bioremediation
<i>Methylocapsa acidiphila</i> B2	Bacteria	Pending		Energy Production
<i>Methylocella silvestris</i> BL2	Bacteria	In finishing		Energy Production
<i>Methylococcus capsulatus</i>	Bacteria	Finished	3.3 Mb	Bioremediation
<i>Methylomicrobium album</i> BG8	Bacteria	In production		Carbon Cycling
<i>Methylosinus trichosporium</i> OB3b	Bacteria	In production		Carbon Cycling
Methylotroph strain L1N13		Pending	10 Mb	Carbon Cycling
Microbial community in wastewater treatment plants	Microbial Community	In assembly	120 Mb	Biotechnology & Applied Microbiology
Microbial population from The Cedars, Calif.	Microbial Community	Pending		Biotechnology & Applied Microbiology
Microbiome resident in foregut of tammar wallaby ( <i>Macropus eugenii</i> )	Microbial Community	In production	210 Mb	Cellulose Degradation
<i>Micrococcus luteus</i> (Actinobacteria)	Bacteria	In finishing		Bioremediation
<i>Micromonas pusilla</i> CCMP 1545	Algae	In finishing	15 Mb	Carbon Cycling
<i>Micromonas pusilla</i> NOUM17 (RCC 299)	Algae	Draft	15 Mb	Carbon Cycling
<i>Micromonosporas aurantiaca</i>	Bacteria	Pending		Cellulose Degradation
<i>Micromonosporas</i> L5	Bacteria	Pending		Cellulose Degradation
<i>Mono Lake Deltaproteobacter</i> MLMS-1		Pending	6.1 Mb	Carbon Cycling
<i>Moorella thermoacetica</i> ATCC 39073	Bacteria	Finished	2.6 Mb	Carbon Cycling
<i>Mucor circinelloides</i> CBS277.49 (-)	Fungi	In finishing	36 Mb	Energy Production
<i>Mycobacterium gilvum</i> PYR-GCK	Bacteria	Finished	6 Mb	Bioremediation
<i>Mycobacterium</i> sp. JLS	Bacteria	Finished	6 Mb	Bioremediation
<i>Mycobacterium</i> sp. KMS	Bacteria	Finished	6.3 Mb	Bioremediation
<i>Mycobacterium</i> sp. MCS	Bacteria	Finished	5.9 Mb	Bioremediation
<i>Mycobacterium vanbaalenii</i> PYR-1	Bacteria	Finished	6.5 Mb	Bioremediation
<i>Mycoplasma genitalium</i> G-37	Bacteria	Finished	580 kb	Technology Development, Pilot Projects
<i>Natrialba magadii</i> ATCC 43099	Archaea	In production		Technology Development, Pilot Projects
Near-shore anoxic basin: Saanich Inlet	Microbial Community	In assembly	235 Mb	Carbon Cycling
<i>Nectria haematococca</i> MPVI	Fungi	Finished	40 Mb	Bioremediation
<i>Nitrobacter hamburgensis</i> X14	Bacteria	Finished	5 Mb	Carbon Cycling
<i>Nitrobacter winogradskyi</i> Nb-255	Bacteria	Finished	3.4 Mb	Carbon Cycling
<i>Nitrosococcus oceani</i> ATCC 19707	Bacteria	Finished	3.5 Mb	Carbon Cycling
<i>Nitrosomonas europaea</i> ATCC 19718	Bacteria	Finished	2.8 Mb	Carbon Cycling
<i>Nitrosomonas eutropha</i> C91	Bacteria	Finished	2.8 Mb	Carbon Cycling
<i>Nitrosomonas</i> isolate IS-79	Bacteria	Pending	3 Mb	Bioremediation
<i>Nitrosomonas oligotropha</i> Nm45	Bacteria	Pending	3 Mb	Bioremediation
<i>Nitrosospira multiformis</i> ATCC 25196	Bacteria	Finished	3.2 Mb	Carbon Cycling
<i>Nocardioides</i> sp. JS614	Bacteria	Finished	5.3 Mb	Bioremediation
<i>Nostoc (Anabaena)</i> sp. PCC 7120	Bacteria	Finished	6.4 Mb	Carbon Cycling
<i>Nostoc punctiforme</i> ATCC 29133	Bacteria	Finished	10 Mb	Carbon Cycling
<i>Nostoc punctiforme</i> PCC 73102	Bacteria	Finished	9 Mb	Carbon Cycling
<i>Novosphingobium aromaticivorans</i> DSM 12444	Bacteria	Finished	4.2 Mb	Bioremediation
<i>Novosphingobium aromaticivorans</i> F199	Bacteria	Draft	3.8 Mb	Bioremediation

Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
Obsidian hot spring Yellowstone	Microbial Community	Draft		Biotechnology & Applied Microbiology
<i>Oenococcus oeni</i> PSU-1	Bacteria	Finished	1.8 Mb	Biotechnology & Applied Microbiology
<i>Olavius algarvensis</i> symbionts	Bacteria	In production		Biotechnology & Applied Microbiology
<i>Opitutaceae</i> bacterium TAV2	Bacteria	In finishing	4 Mb	Carbon Cycling
<i>Opitutus terrae</i>	Bacteria	In finishing	8 Mb	Carbon Cycling
<i>Orpinomyces</i> sp. Strain PC-2	Fungi	Pending	20 Mb	Cellulose Degradation
<i>Oscillochloris</i> sp. UdG9002	Bacteria	Pending		Carbon Cycling
<i>Ostreococcus</i> (low-light strain)	Algae	Finished	12 Mb	Biotechnology & Applied Microbiology
<i>Ostreococcus lucimarinus</i>	Algae	Finished	9.3 Mb	Carbon Cycling
<i>Paenibacillus</i> sp. JDR-2	Bacteria	In finishing	5 Mb	Cellulose Degradation
<i>Paracoccus denitrificans</i> PD1222	Bacteria	Finished	5.2 Mb	Bioremediation
<i>Parvibaculum lavamentivorans</i> DS-1	Bacteria	Finished	3.9 Mb	Bioremediation
<i>Pediococcus pentosaceus</i> ATCC 25745	Bacteria	Finished	1.8 Mb	Biotechnology & Applied Microbiology
<i>Pedomicrobium manganicum</i>	Bacteria	Pending	40 Mb	Bioremediation
<i>Pelobacter carbinolicus</i>	Bacteria	Finished	3.7 Mb	Bioremediation
<i>Pelobacter propionicus</i> DSM 2379	Bacteria	Finished	4.2 Mb	Energy Production
<i>Pelodictyon phaeoclathratiforme</i> BU-1	Bacteria	In finishing	3 Mb	Carbon Cycling
<i>Pelotomaculum schinkii</i> strain HH	Bacteria	In production	3 Mb	Bioremediation
<i>Petrotoga mobilis</i> SJ95	Bacteria	Finished	2.1 Mb	Biotechnology & Applied Microbiology
<i>Phakopsora pachyrhizi</i> (soybean rust pathogen)	Fungi	Draft	50 Mb	Biotechnology & Applied Microbiology
<i>Phanerochaete carnososa</i>	Fungi	In production	35 Mb	Cellulose Degradation
<i>Phanerochaete chrysosporium</i>	Fungi	Done	30 Mb	Cellulose Degradation
<i>Phytophthora ramorum</i>	Stramenopiles	Done	60 Mb	Biotechnology & Applied Microbiology
<i>Phytophthora sojae</i>	Fungi	Done	62 Mb	Biotechnology & Applied Microbiology
<i>Pichia stipitis</i> CBS 6054	Fungi	Finished	12 Mb	Energy Production
Picoplankton BACs [Hawaii Ocean Time Series (HOTS) site]		In production	150 Mb	Carbon Cycling
<i>Polaromonas naphthalenivorans</i> CJ2	Bacteria	Finished	5.4 Mb	Bioremediation
<i>Polaromonas</i> sp. JS666	Bacteria	Finished	5.9 Mb	Bioremediation
<i>Polynucleobacter necessarius</i> STIR1	Bacteria	In finishing	1.7 Mb	Carbon Cycling
<i>Polynucleobacter</i> sp. QWL-P1DMWA-1	Bacteria	Finished	2.2 Mb	Carbon Cycling
<i>Postia placenta</i>	Fungi	Finished	40 Mb	Cellulose Degradation
<i>Prochlorococcus</i> ACM A12II	Bacteria	Draft		Carbon Cycling
<i>Prochlorococcus marinus</i> HOT_152-C11		In production		Carbon Cycling
<i>Prochlorococcus marinus</i> MED4	Bacteria	Finished	1.6 Mb	Carbon Cycling
<i>Prochlorococcus marinus</i> MIT 9312	Bacteria	Finished	1.7 Mb	Carbon Cycling
<i>Prochlorococcus marinus</i> MIT 9313	Bacteria	Finished	2.4 Mb	Carbon Cycling
<i>Prochlorococcus marinus</i> NATL2A	Bacteria	Finished	1.8 Mb	Carbon Cycling
<i>Prochlorococcus marinus pastoris</i> CCMP 1986	Bacteria	Finished	1.7 Mb	Carbon Cycling
<i>Prochlorococcus</i> sp. CC9605 (oligotrophic)	Bacteria	Finished	2.5 Mb	Carbon Cycling
<i>Prochlorococcus</i> sp. CC9902 (coastal)	Bacteria	Finished	2.2 Mb	Carbon Cycling

Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
Prokaryotic plasmids		Various	7 Mb	Biotechnology & Applied Microbiology
<i>Prosthecochloris aestuarii</i> DSM 271	Bacteria	In finishing	2.5 Mb	Carbon Cycling
<i>Prosthecochloris vibrioformis</i> DSM 265	Bacteria	Finished	2.0 Mb	Biotechnology & Applied Microbiology
<i>Pseudoalteromonas atlantica</i> T6c	Bacteria	Finished	5.2 Mb	Bioremediation
<i>Pseudomonas fluorescens</i> PfO-1	Bacteria	Finished	6.4 Mb	Bioremediation
<i>Pseudomonas mendocina</i> ymp	Bacteria	Finished	5.1 Mb	Bioremediation
<i>Pseudomonas putida</i> F1	Bacteria	Finished	6.0 Mb	Bioremediation
<i>Pseudomonas putida</i> GB-1	Bacteria	Finished	6.1 Mb	Bioremediation
<i>Pseudomonas putida</i> KT2440	Bacteria	Finished	6.1 Mb	Bioremediation
<i>Pseudomonas putida</i> PRSI	Bacteria	Incomplete	6.1 Mb	Bioremediation
<i>Pseudomonas putida</i> W619 (Poplar endophytic bacteria)	Bacteria	Finished	5.8 Mb	Carbon Cycling
<i>Pseudomonas syringae</i> B728a	Bacteria	Finished	6.1 Mb	Biotechnology & Applied Microbiology
<i>Pseudo-nitzschia</i> (diatom)		In production	250 Mb	Biotechnology & Applied Microbiology
<i>Pseudonocardia dioxanivorans</i> CB1190	Bacteria	In production		Bioremediation
<i>Psychrobacter arcticus</i> 273-4	Bacteria	Finished	2.7 Mb	Technology Development, Pilot Projects
<i>Psychrobacter cryohalolentis</i> K5	Bacteria	Finished	3.1 Mb	Technology Development, Pilot Projects
<i>Psychrobacter</i> sp. PRwf-1	Bacteria	Finished	3.0 Mb	Technology Development, Pilot Projects
<i>Psychromonas ingrahamii</i> 37	Bacteria	Finished	4.6 Mb	Biotechnology & Applied Microbiology
<i>Pyrobaculum aerophilum</i> IM2	Archaea	Finished	2.2 Mb	Biotechnology & Applied Microbiology
<i>Pyrobaculum aresenaticum</i> DSM 13514	Archaea	Finished	2.1 Mb	Bioremediation
<i>Pyrobaculum calidifontis</i> JCM 11548	Archaea	Finished	2.0 Mb	Bioremediation
<i>Pyrobaculum islandicum</i> DSM 4184	Archaea	Finished	1.8 Mb	Bioremediation
<i>Pyrococcus furiosus</i>	Archaea	Finished	2.1 Mb	Biotechnology & Applied Microbiology
<i>Ralstonia eutropha</i> JMP-134	Bacteria	Finished	7.3 Mb	Bioremediation
<i>Ralstonia pickettii</i> 12D	Bacteria	In finishing	2.1 Mb	Bioremediation
<i>Ralstonia pickettii</i> 12J	Bacteria	In finishing	5.3 Mb	Bioremediation
<i>Rhizobium leguminosarum</i> bv <i>trifolii</i> (strains WSM1325 and WSM2304)	Bacteria	In finishing	128 Mb	Carbon Cycling
<i>Rhodobacter</i> sp. str. SW2 (freshwater iron-oxidizing bacteria)	Bacteria	In production		Bioremediation
<i>Rhodobacter sphaeroides</i> 2.4.1	Bacteria	Finished	4.6 Mb	Bioremediation
<i>Rhodobacter sphaeroides</i> ATCC 17025	Bacteria	Finished	4.6 Mb	Biotechnology & Applied Microbiology
<i>Rhodobacter sphaeroides</i> ATCC 17029	Bacteria	Finished	4.5 Mb	Biotechnology & Applied Microbiology

Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
<i>Rhodocyclus</i> -like polyphosphate accumulating organism		In draft assembly		Biotechnology & Applied Microbiology
<i>Rhodoferax ferrireducens</i> DSM 15236	Bacteria	Finished	5.0 Mb	Bioremediation
<i>Rhodomicrobium vannielii</i>	Bacteria	Pending		Bioremediation
<i>Rhodopseudomonas palustris</i> (freshwater iron-oxidizing bacteria)	Bacteria	In finishing		Carbon Cycling
<i>Rhodopseudomonas palustris</i> BisA53	Bacteria	Finished	5.5 Mb	Carbon Cycling
<i>Rhodopseudomonas palustris</i> BisB18	Bacteria	Finished	5.5 Mb	Carbon Cycling
<i>Rhodopseudomonas palustris</i> BisB5	Bacteria	Finished	4.9 Mb	Carbon Cycling
<i>Rhodopseudomonas palustris</i> CGA009	Bacteria	Finished	5.5 Mb	Carbon Cycling
<i>Rhodopseudomonas palustris</i> HaA2	Bacteria	Finished	5.3 Mb	Carbon Cycling
<i>Rhodospirillum rubrum</i> ATCC 11170	Bacteria	Finished	4.4 Mb	Carbon Cycling
<i>Rhodospiridium babjevae</i> WP1	Fungi	In production	20 Mb	Biotechnology & Applied Microbiology
Rice endophyte metagenome		In production	100 Mb	Carbon Cycling
<i>Roseiflexus castenholzii</i> HL08	Bacteria	Finished	5.7 Mb	Carbon Cycling
<i>Roseiflexus</i> sp. strain RS-1	Bacteria	Finished	5.8 Mb	Carbon Cycling
<i>Rubrobacter xylanophilus</i> DSM 9941	Bacteria	Finished	3.2 Mb	Cellulose Degradation
<i>Saccharophagus degradans</i> 2-40	Bacteria	Finished	5.1 Mb	Cellulose Degradation
<i>Salinispora arenicola</i> CNS205 (marine actinomycetes)	Bacteria	Finished	5.7 Mb	Biotechnology & Applied Microbiology
<i>Salinispora tropica</i> CNB-440 (marine actinomycetes)	Bacteria	Finished	5.2 Mb	Biotechnology & Applied Microbiology
Sargasso Sea community	Microbial Community	Various		Energy Production
<i>Scalindua marina</i> (Anammox bacteria)	Bacteria	In production		Carbon Cycling
<i>Schizophyllum commune</i>	Microbial Community	In production	38 Mb	Cellulose Degradation
<i>Selenospirillum indicus</i>	Bacteria	Pending		Technology Development, Pilot Projects
<i>Serpula lacrymans</i>	Fungi	In production	25 Mb	Cellulose Degradation
<i>Serratia proteamaculans</i> 568 (Poplar endophytic bacteria)	Bacteria	Finished	5.5 Mb	Carbon Cycling
<i>Shewanella amazonensis</i> SB2B	Bacteria	Finished	4.3 Mb	Bioremediation
<i>Shewanella baltica</i> OS155	Bacteria	Finished	5.3 Mb	Bioremediation
<i>Shewanella baltica</i> OS185	Bacteria	Finished	5.3 Mb	Bioremediation
<i>Shewanella baltica</i> OS195	Bacteria	Finished	5.3 Mb	Bioremediation
<i>Shewanella baltica</i> OS223	Bacteria	In finishing	5.1 Mb	Bioremediation
<i>Shewanella denitrificans</i> OS217	Bacteria	Finished	4.5 Mb	Bioremediation
<i>Shewanella frigidimarina</i> NCIMB400	Bacteria	Finished	4.8 Mb	Bioremediation
<i>Shewanella halifaxensis</i> HAW-EB4T	Bacteria	In finishing	5 Mb	Bioremediation
<i>Shewanella loihica</i> PV-4	Bacteria	Finished	4.6 Mb	Bioremediation
<i>Shewanella oneidensis</i> MR-1	Bacteria	Finished	4.5 Mb	Bioremediation
<i>Shewanella pealeana</i> ATCC 700345	Bacteria	Finished	5.0 Mb	Bioremediation
<i>Shewanella putrefaciens</i> 200	Bacteria	In finishing	4.7 Mb	Bioremediation
<i>Shewanella putrefaciens</i> CN-32	Bacteria	Finished	4.7 Mb	Bioremediation
<i>Shewanella sediminis</i> HAW-EB3	Bacteria	Finished	5.4 Mb	Bioremediation
<i>Shewanella</i> sp. ANA-3	Bacteria	Finished	5.3 Mb	Bioremediation
<i>Shewanella</i> sp. MR-4	Bacteria	Finished	4.7 Mb	Bioremediation

Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
<i>Shewanella</i> sp. MR-7	Bacteria	Finished	4.8 Mb	Bioremediation
<i>Shewanella</i> sp. W3-18-1	Bacteria	Finished	4.7 Mb	Bioremediation
<i>Shewanella woodyi</i> ATCC 51908	Bacteria	Finished	5.8 Mb	Bioremediation
<i>Sideroxydans lithotrophicus</i> (freshwater iron-oxidizing bacteria)	Bacteria	In production		Bioremediation
<i>Silicibacter</i> sp. TM1040	Bacteria	Finished	4.2 Mb	Carbon Cycling
<i>Sinorhizobium medicae</i> WSM 419	Bacteria	Finished	6.8 Mb	Carbon Cycling
<i>Solibacter usitatus</i> Ellin6076	Bacteria	Finished	10.0 Mb	Bioremediation
South African Gold Mine Metagenome ( <i>Desulforudis audaxviator</i> )		Finished		Bioremediation
<i>Sphingomonas wittichii</i> RW1	Bacteria	Finished	5.9 Mb	Bioremediation
<i>Sphingopyxis alaskensis</i> RB2256	Bacteria	Finished	3.4 Mb	Carbon Cycling
<i>Sporotrichum thermophile</i> ATCC 42464	Fungi	Pending	43 Mb	Cellulose Degradation
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> JH1	Bacteria	Finished	2.9 Mb	Biotechnology & Applied Microbiology
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> JH9	Bacteria	Finished	2.9 Mb	Biotechnology & Applied Microbiology
<i>Staphylothermus marinus</i> F1	Archaea	Finished	1.6 Mb	Biotechnology & Applied Microbiology
<i>Starkeya novella</i>	Bacteria	In production		Carbon Cycling
<i>Stenotrophomonas maltophilia</i> R551-3 (Poplar endophytic bacteria)	Bacteria	In finishing	4.5 Mb	Carbon Cycling
<i>Streptococcus suis</i> 89/1591	Bacteria	In finishing	1.9 Mb	Technology Development, Pilot Projects
<i>Streptococcus thermophilus</i> LMD-9	Bacteria	Finished	1.9 Mb	Biotechnology & Applied Microbiology
<i>Sulfolobus islandicus</i> (8 strains)	Archaea	In finishing	24 Mb	Biotechnology & Applied Microbiology
Symbiont from the basal clade of the <i>Frankiaceae</i>	Bacteria	Pending	64 Mb	Carbon Cycling
<i>Synechococcus elongates</i> PCC7942 ( <i>elongatus</i> )	Bacteria	Finished	2.7 Mb	Carbon Cycling
<i>Synechococcus</i> sp. CC9605 (oligotrophic)	Bacteria	Finished	2.5 Mb	Carbon Cycling
<i>Synechococcus</i> sp. CC9902 (coastal)	Bacteria	Finished	2.2 Mb	Carbon Cycling
<i>Synechococcus</i> sp. WH8102	Bacteria	Finished	2.4 Mb	Carbon Cycling
<i>Syntrophobacter fumaroxidans</i> MPOB	Bacteria	Finished	5.0 Mb	Energy Production
<i>Syntrophomonas wolfei</i> subsp. <i>Wolfei</i> Göttingen (DSM 2245B)	Bacteria	Finished	3.0 Mb	Energy Production
<i>Syntrophomonas zehnderi</i> sp. nov.	Bacteria	Pending	3 Mb	Energy Production
Terephthalate (TA) degrading community	Microbial Community	Draft		Bioremediation
Termite gut microbial community	Microbial Community	Draft		Cellulose Degradation
<i>Thalassiosira pseudonana</i> CCMP1335	Diatom	In finishing	32 Mb	Carbon Cycling
<i>Thauera</i> sp. MZ1T	Bacteria	In finishing	32 Mb	Carbon Cycling
<i>Thermacetogenium phaeum</i>	Bacteria	In production	4 Mb	Cellulose Degradation
<i>Thermoanaerobacter brockii</i> subsp. <i>Finnii</i> Ako-1	Bacteria	New	3 Mb	Energy Production
<i>Thermoanaerobacter ethanolicus</i> CCSD_DF2450_M1_68 isolate 1	Bacteria	New	3 Mb	Energy Production

Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
<i>Thermoanaerobacter ethanolicus</i> FB14	Bacteria	New	3 Mb	Energy Production
<i>Thermoanaerobacter ethanolicus</i> JW200	Bacteria	New	3 Mb	Energy Production
<i>Thermoanaerobacter ethanolicus</i> X513	Bacteria	In production	3 Mb	Energy Production
<i>Thermoanaerobacter ethanolicus</i> X514	Bacteria	Finished	2.5 Mb	Energy Production
<i>Thermoanaerobacter ethanolicus</i> X561	Bacteria	In production	3 Mb	Energy Production
<i>Thermoanaerobacter italicus</i> Ab9 DSM9252	Bacteria	In production	3 Mb	Energy Production
<i>Thermoanaerobacter pseudoethanolicus</i> 39E	Bacteria	Finished	2.3 Mb	Energy Production
<i>Thermoanaerobacterium polysaccharolyticum</i> KMTHCJ	Bacteria	New	3 Mb	Energy Production
<i>Thermoanaerobacterium thermosaccharolyticum</i>	Bacteria	In production	3 Mb	Energy Production
<i>Thermoanaerobacterium xylanolyticum</i> LXII DSM7097	Bacteria	In production	3 Mb	Cellulose Degradation
<i>Thermobifida fusca</i> YX	Bacteria	Finished	3.6 Mb	Cellulose Degradation
<i>Thermofilum pendens</i> Hrk5	Archaea	Finished	1.8 Mb	Biotechnology & Applied Microbiology
<i>Thermolithobacter ferrireducens</i>	Bacteria	Pending	48 Mb	Bioremediation
<i>Thermoproteus neutrophilus</i>	Archaea	In finishing	3 Mb	Bioremediation
<i>Thermosinus carboxydivorans</i> Nor 1	Bacteria	In finishing	2.9 Mb	Energy Production
<i>Thermosipho melanesiensis</i> BI429	Bacteria	Finished	1.9 Mb	Biotechnology & Applied Microbiology
<i>Thermotoga letingae</i>	Bacteria	Finished	1.9 Mb	Biotechnology & Applied Microbiology
<i>Thermotoga maritima</i> M5B8	Bacteria	Finished	1.8 Mb	Biotechnology & Applied Microbiology
<i>Thermotoga naphthophila</i>	Bacteria	In production	1.9 Mb	Biotechnology & Applied Microbiology
<i>Thermotoga neopolitana</i> ATCC 49045	Bacteria	Finished	1.8 Mb	Energy Production
<i>Thermotoga petrophila</i> RKU-1	Bacteria	Finished	1.8 Mb	Biotechnology & Applied Microbiology
<i>Thermotoga</i> RQ2		Finished		Bioremediation
<i>Thermovibrio ammonificans</i> DSM 15698	Bacteria	Pending		Carbon Cycling
<i>Thiobacillus denitrificans</i> ATCC 23644	Bacteria	Finished	2 Mb	Carbon Cycling
<i>Thiobacillus denitrificans</i> ATCC 25259	Bacteria	Finished	2.9 Mb	Bioremediation
<i>Thiomicrospira crunogena</i> XCL-2	Bacteria	Finished	2.4 Mb	Carbon Cycling
<i>Thiomicrospira denitrificans</i> ATCC 33889	Bacteria	Finished	2.2 Mb	Carbon Cycling
<i>Thiomonas intermedia</i>	Bacteria	In production		Carbon Cycling
<i>Tipula abdominalis</i> gut microbial consortium	Microbial Community	In production		Cellulose Degradation
<i>Trichoderma atroviride</i>	Fungi	In finishing	40 Mb	Biotechnology & Applied Microbiology
<i>Trichoderma reesei</i>	Fungi	Draft	30 Mb	Cellulose Degradation
<i>Trichodesmium erythraeum</i> IMS101	Bacteria	Finished	7.8 Mb	Carbon Cycling
Tropical picophytoeukaryotes site 1		In production		Carbon Cycling
Tropical picophytoeukaryotes site 2		In production		Carbon Cycling
Tropical picophytoeukaryotes site 3		In production		Carbon Cycling
Type I Accumulibacter	Microbial Community	In production		Biotechnology & Applied Microbiology
Uncultivated methane-oxidizing archaeon ANME-1	Archaea	Pending		Carbon Cycling
<i>Variovorax paradoxus</i> strain EPS	Bacteria	In production		Bioremediation



Genome Name	Domain	Sequencing Status	Approximate Genome Size	Category
<i>Variovorax paradoxus</i> strains S110	Bacteria	In production		Bioremediation
<i>Verminephrobacter eiseniae</i> EF01-2 ( <i>Acidovorax</i> symbiont)		Finished	5.6 Mb	Bioremediation
<i>Vibrio furnissii</i>	Bacteria	Pending	5 Mb	Energy Production
<i>Victivallis vadensis</i> ATCC BAA-548	Bacteria	In finishing	4.6 Mb	Carbon Cycling
<i>Xanthobacter autotrophicus</i> Py2	Bacteria	Finished	5.6 Mb	Bioremediation
<i>Xylella fastidiosa</i> Ann-1	Bacteria	Draft	5.1 Mb	Technology Development, Pilot Projects
<i>Xylella fastidiosa</i> Dixon	Bacteria	Draft	2.6 Mb	Technology Development, Pilot Projects
<i>Yersinia pestis</i> Antiqua	Bacteria	Finished	4.9 Mb	Technology Development, Pilot Projects
<i>Yersinia pestis</i> Nepal516	Bacteria	Finished	4.6 Mb	Technology Development, Pilot Projects
<i>Yersinia pestis</i> Pestoides F	Bacteria	Finished	4.7 Mb	Biotechnology & Applied Microbiology
<i>Yersinia pseudotuberculosis</i> IP 32953	Bacteria	Finished	4.8 Mb	Technology Development, Pilot Projects
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ATCC 10988	Bacteria	In production		Energy Production
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ATCC 29191	Bacteria	In production		Energy Production
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> CP4	Bacteria	In production		Energy Production
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> recifencis, industrial strain	Bacteria	Pending		Energy Production
<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ZM4 (ATCC 31821)	Bacteria	In production		Energy Production
<i>Zymomonas mobilis</i> subsp. <i>pomaceae</i> ATCC 29192	Bacteria	In production		Energy Production
<i>Zymomonas mobilis</i> subsp. <i>Pomaceae</i> NCIB11163	Bacteria	In production		Energy Production