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(54) **METHOD AND SYSTEM FOR CONVERTING ELECTRICITY INTO ALTERNATIVE ENERGY RESOURCES**

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C12P 5/02 (2006.01)

(52) **U.S. Cl.** **435/167**

(57) **ABSTRACT**

A method of using electricity to produce methane includes maintaining a culture comprising living methanogenic microorganisms at a temperature above 50° C. in a reactor having a first chamber and a second chamber separated by a proton permeable barrier, the first chamber comprising a passage between an inlet and an outlet containing at least a porous electrically conductive cathode, the culture, and water, and the second chamber comprising at least an anode. The method also includes coupling electricity to the anode and the cathode, supplying carbon dioxide to the culture in the first chamber, and collecting methane from the culture at the outlet of the first chamber.

PRIOR ART

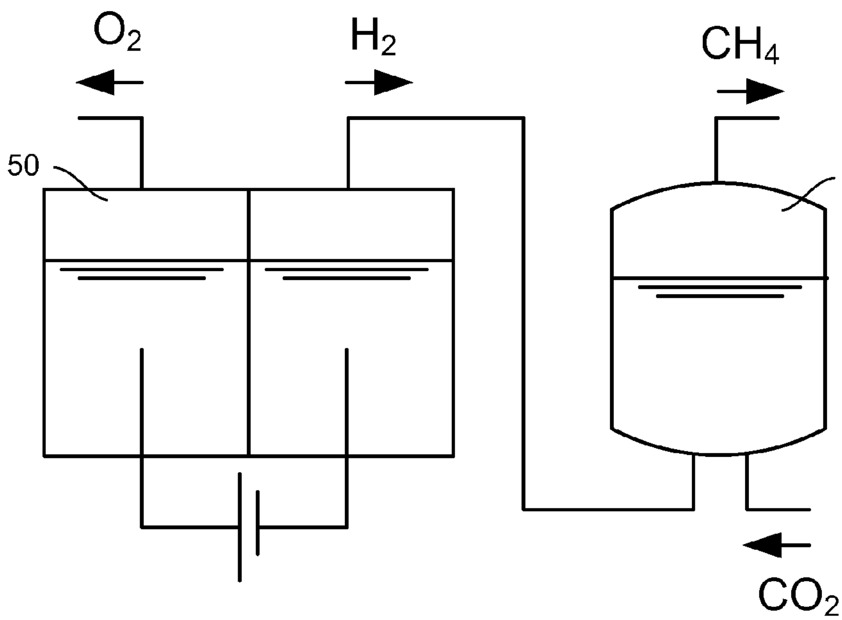

FIG. 1

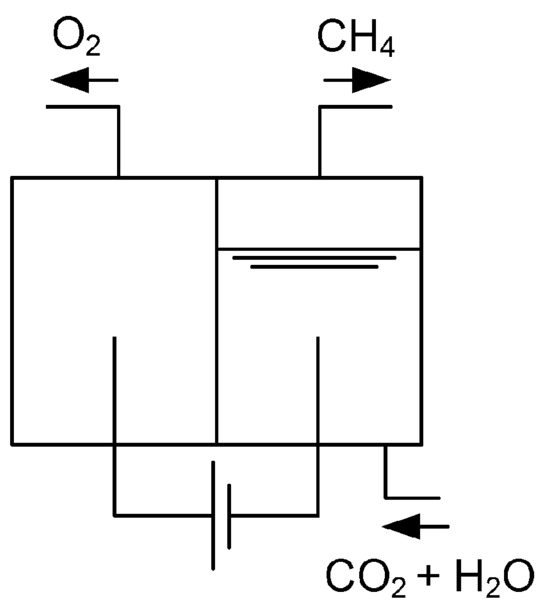

FIG. 2

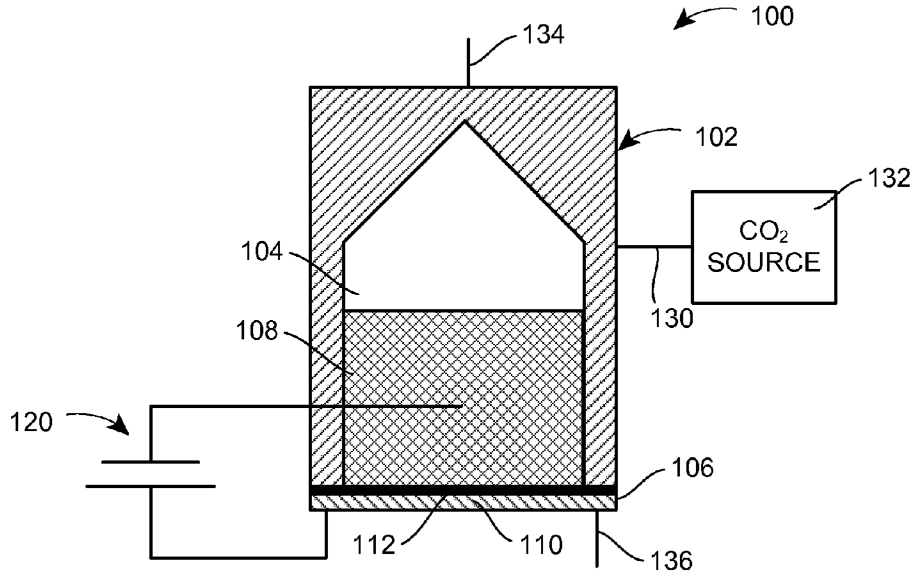
100
134
102
132
CO_2 SOURCE
104
130
108
120
106
112
110
136

FIG. 3

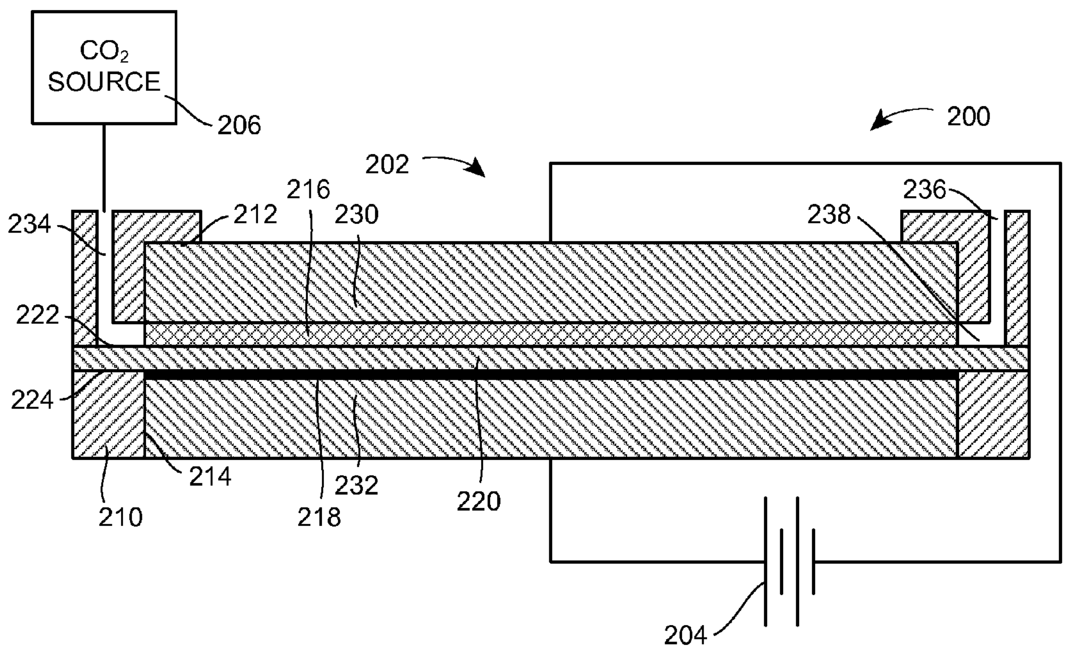
CO_2 SOURCE
206
200
202
216
230
212
236
238
234
222
224
214
232
210
218
220
204

FIG. 4

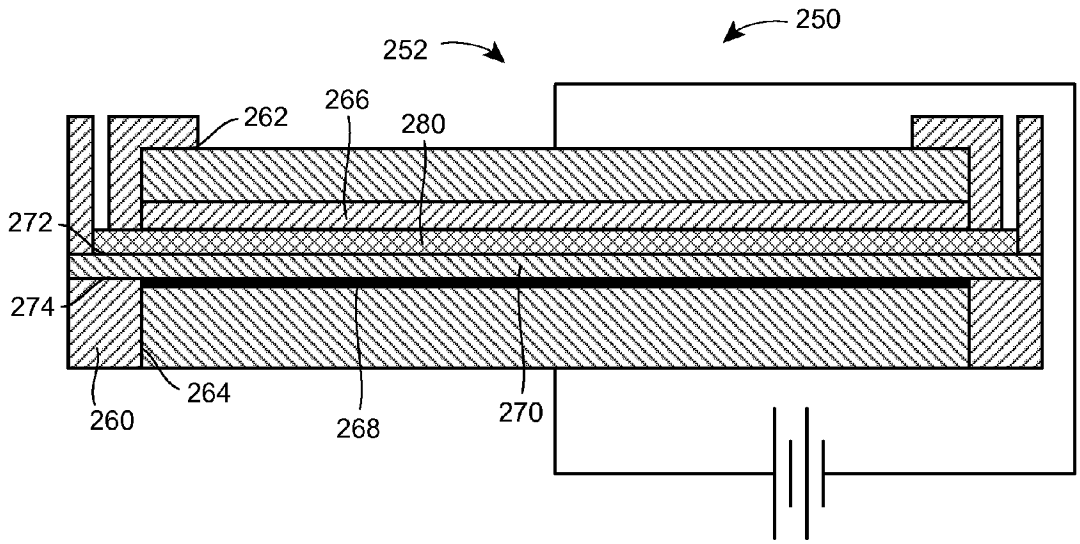
250
252
262
266
280
272
274
260
264
268
270

FIG. 5

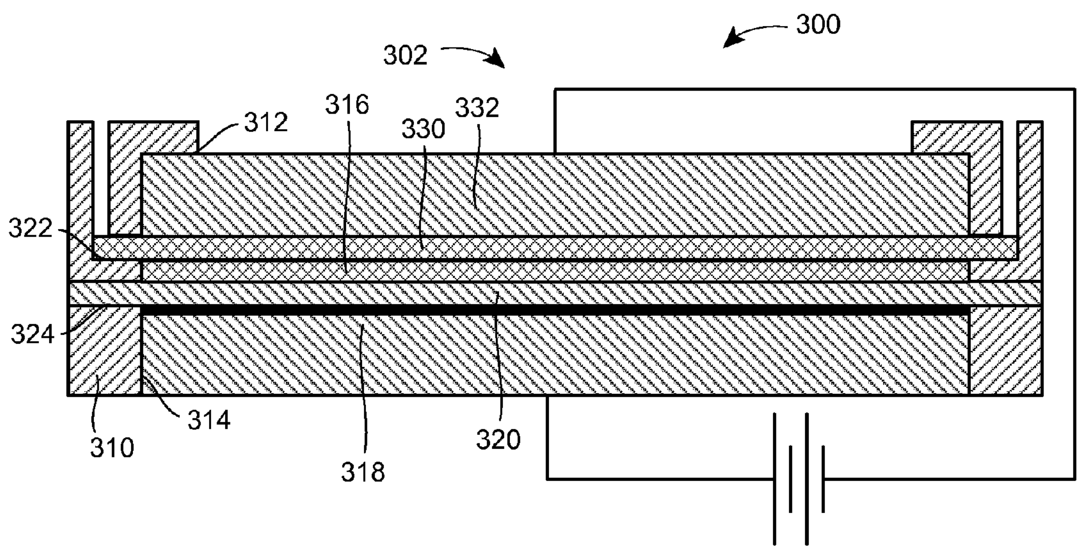
300
302
312
316
330
332
322
324
310
314
318
320

FIG. 6

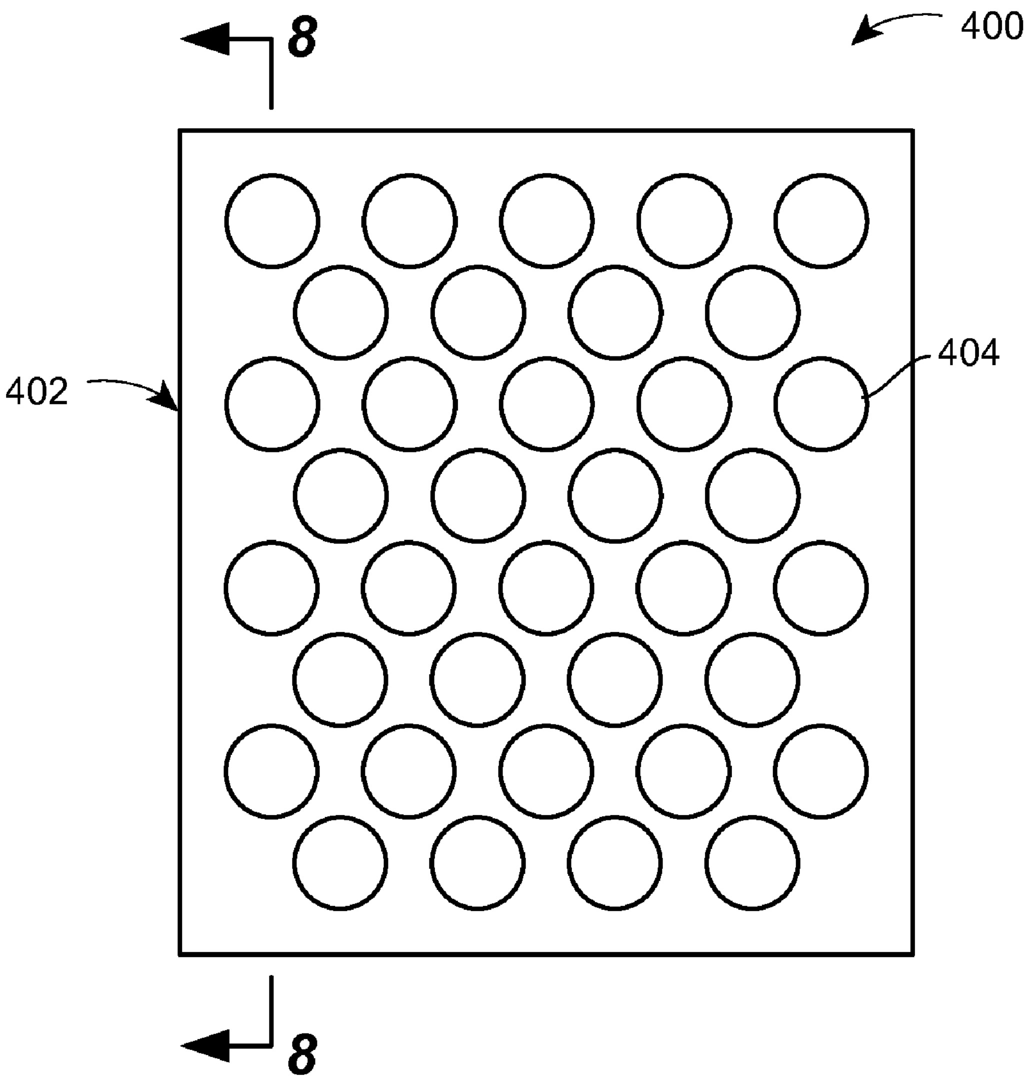

FIG. 7

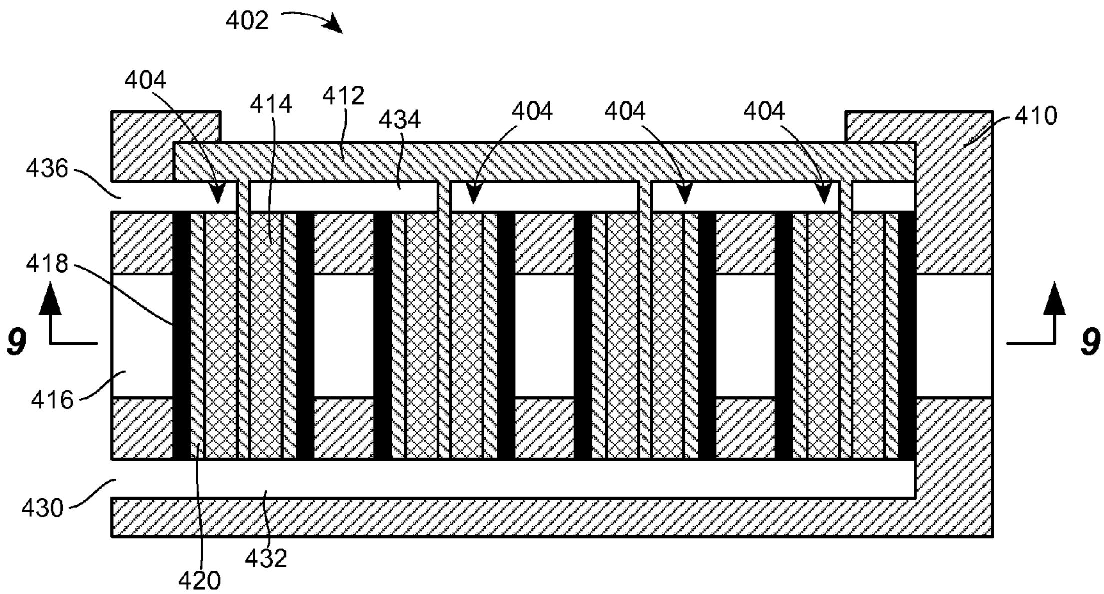

FIG. 8

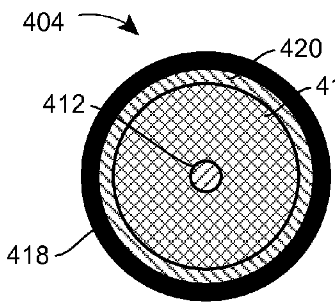

FIG. 9

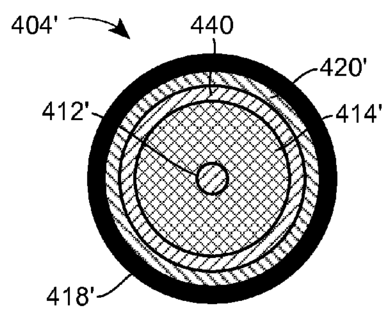

FIG. 10

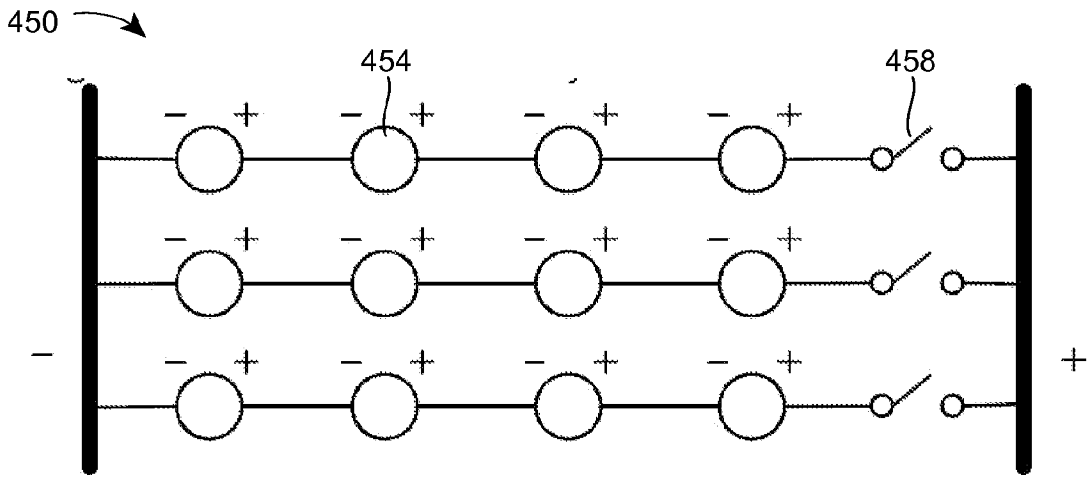

FIG. 11

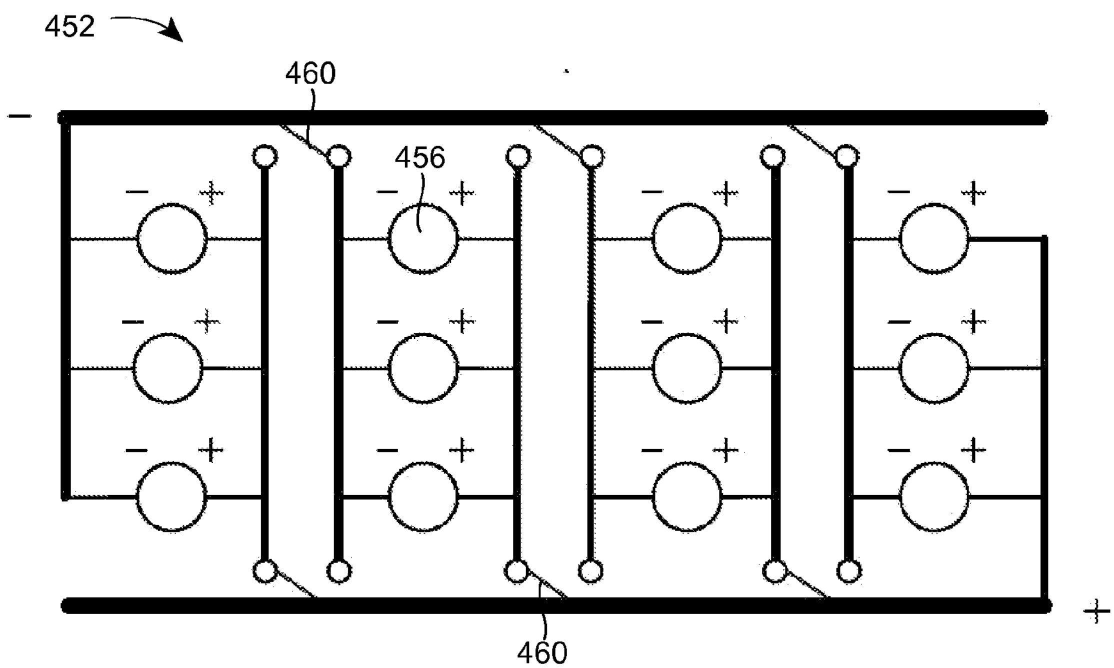

FIG. 12

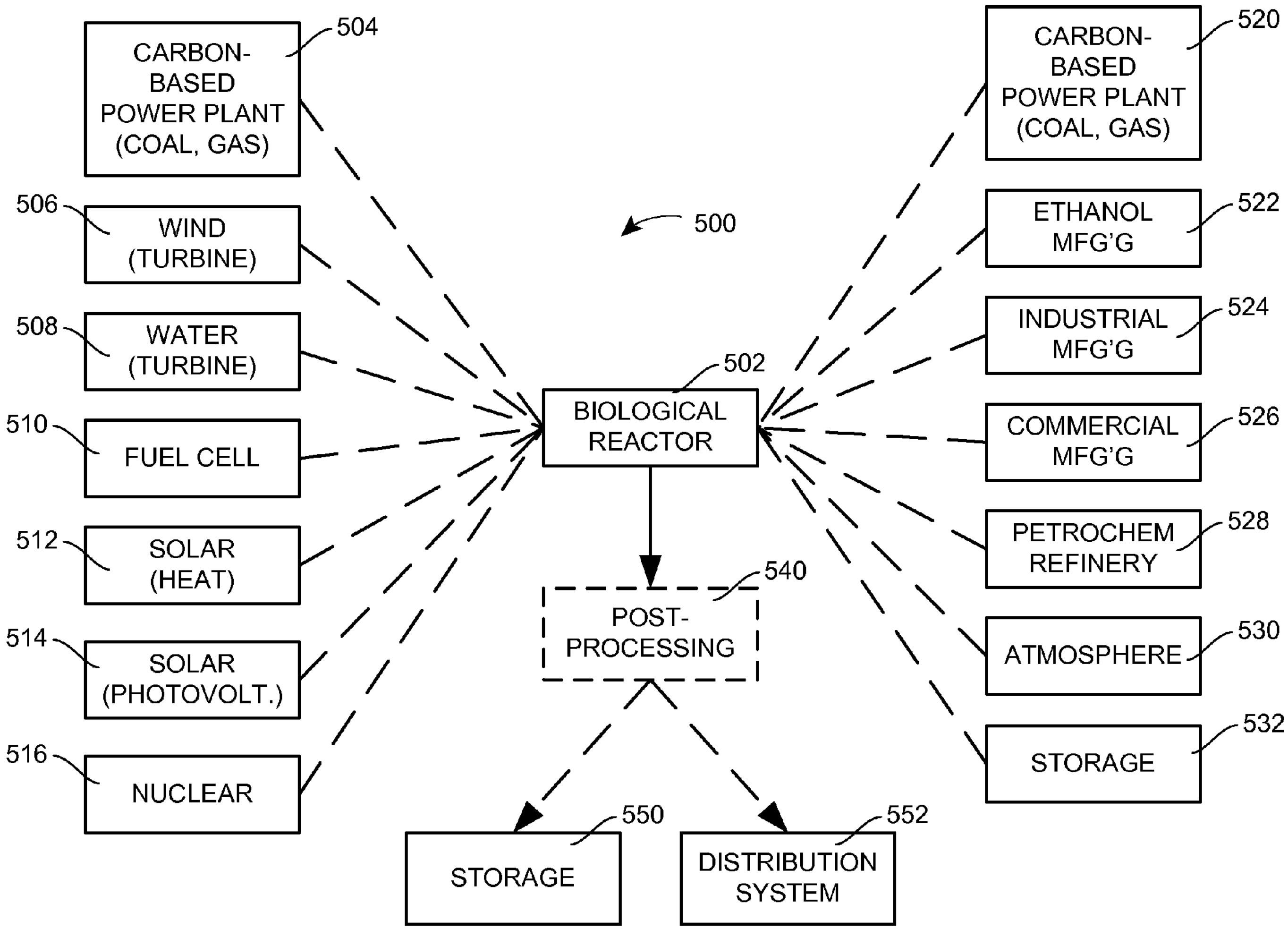
500
CARBON-BASED POWER PLANT (COAL, GAS)
504
WIND (TURBINE)
506
WATER (TURBINE)
508
FUEL CELL
510
SOLAR (HEAT)
512
SOLAR (PHOTOVOLT.)
514
NUCLEAR
516
BIOLOGICAL REACTOR
502
POST-PROCESSING
540
STORAGE
550
DISTRIBUTION SYSTEM
552
CARBON-BASED POWER PLANT (COAL, GAS)
520
ETHANOL MFG'G
522
INDUSTRIAL MFG'G
524
COMMERCIAL MFG'G
526
PETROCHEM REFINERY
528
ATMOSPHERE
530
STORAGE
532

FIG. 13

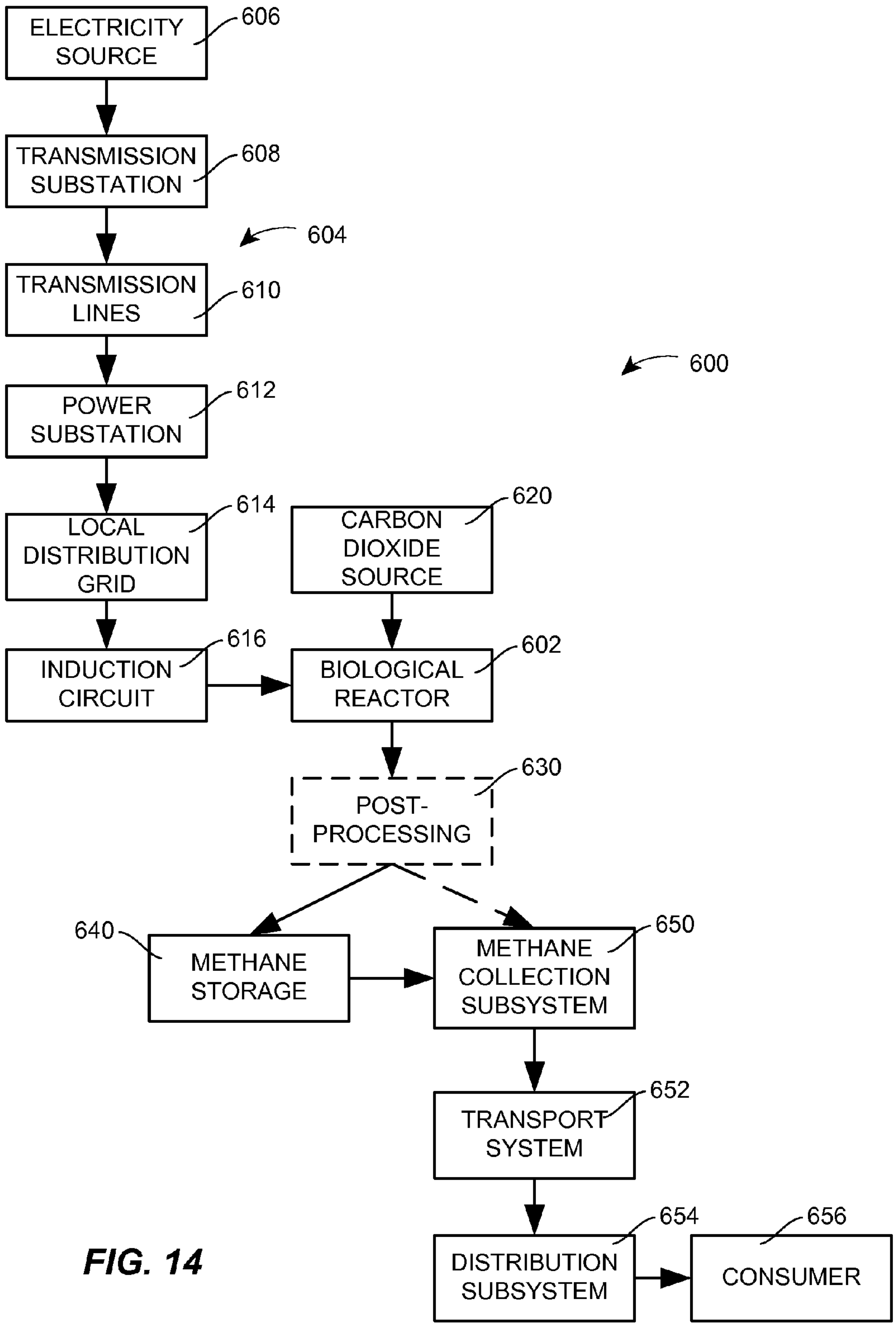
ELECTRICITY SOURCE
606
TRANSMISSION SUBSTATION
608
604
TRANSMISSION LINES
610
600
POWER SUBSTATION
612
LOCAL DISTRIBUTION GRID
614
CARBON DIOXIDE SOURCE
620
INDUCTION CIRCUIT
616
BIOLOGICAL REACTOR
602
POST-PROCESSING
630
640
METHANE STORAGE
METHANE COLLECTION SUBSYSTEM
650
TRANSPORT SYSTEM
652
DISTRIBUTION SUBSYSTEM
654
CONSUMER
656

FIG. 14

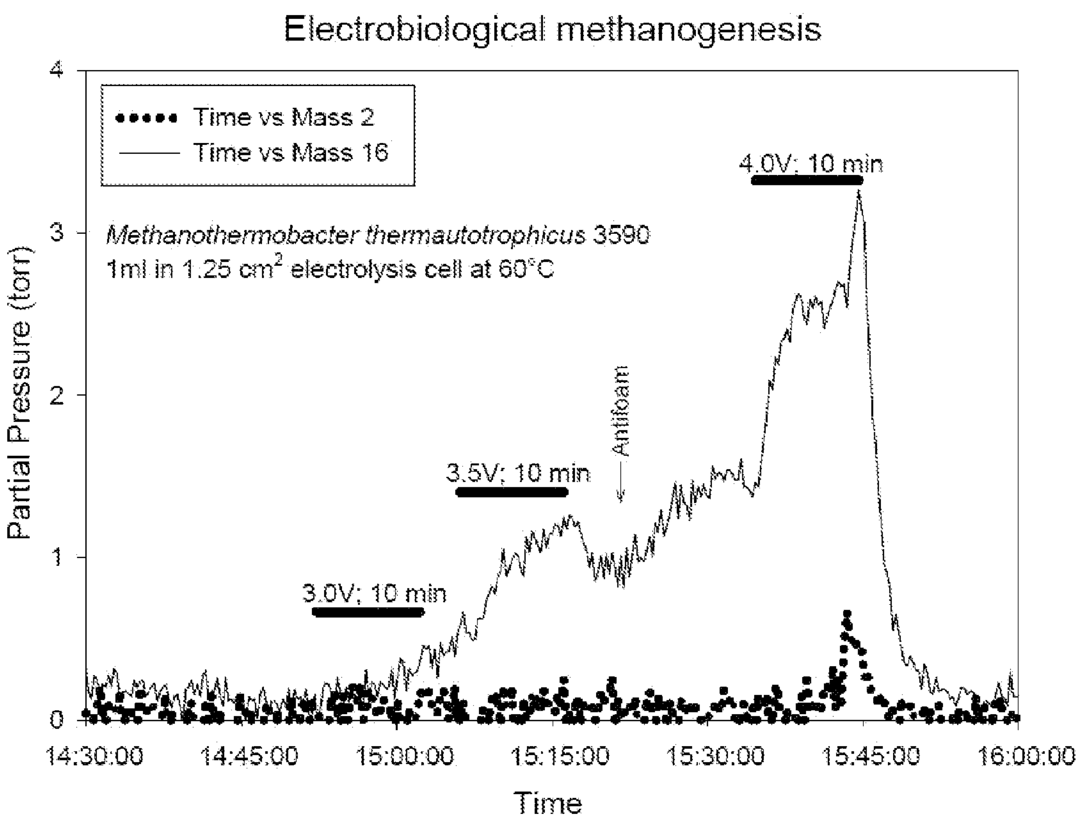
Electrobiological methanogenesis
Time vs Mass 2
Time vs Mass 16
Methanothermobacter thermautotrophicus 3590
1ml in 1.25 cm2 electrolysis cell at 60°C
3.0V; 10 min
3.5V; 10 min
Antifoam
4.0V; 10 min
Partial Pressure (torr)
0
1
2
3
4
14:30:00
14:45:00
15:00:00
15:15:00
15:30:00
15:45:00
16:00:00
Time

FIG. 15

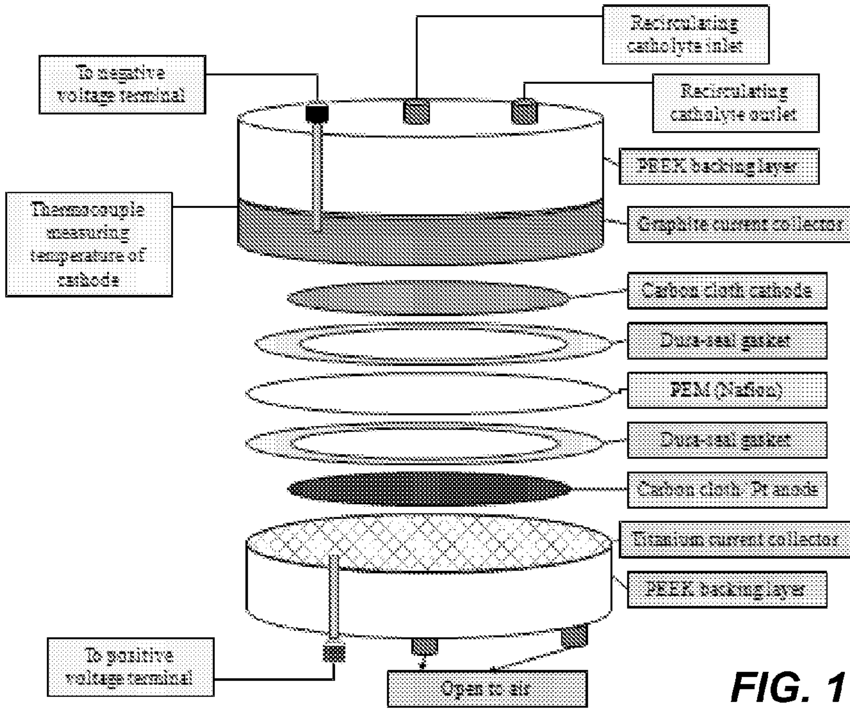
Recirculating catholyte inlet
To negative voltage terminal
Recirculating catholyte outlet
PEEK backing layer
Thermocouple measuring temperature of cathode
Graphite current collector
Carbon cloth cathode
Dura-seal gasket
PEM (Nafion)
Dura-seal gasket
Carbon cloth/ Pt anode
Titanium current collector
PEEK backing layer
To positive voltage terminal
Open to air

FIG. 16

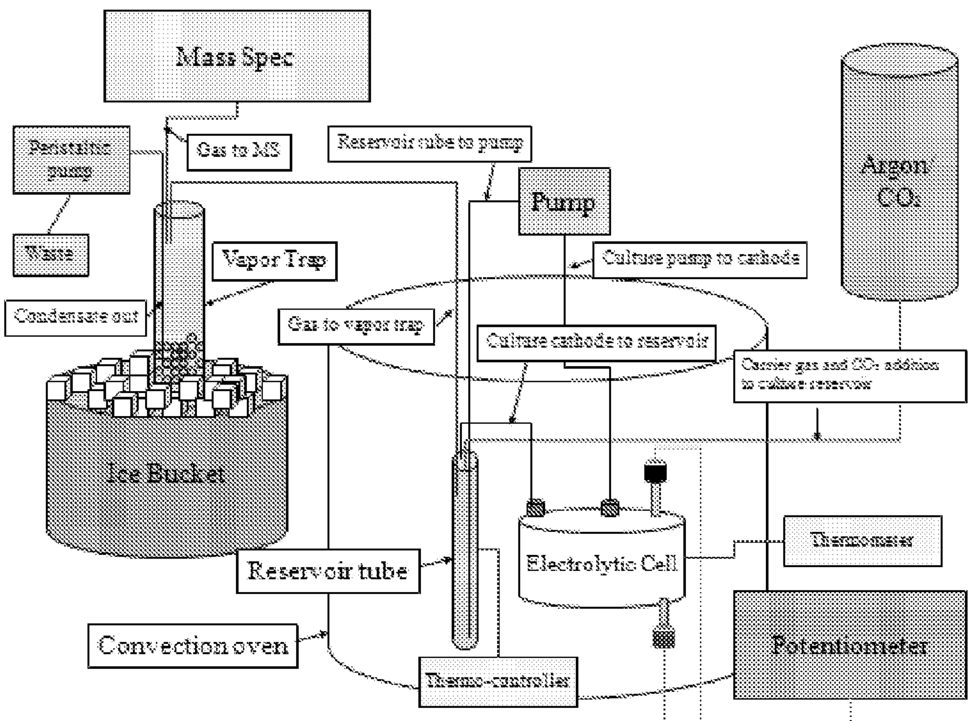
Mass Spec
Peristaltic pump
Gas to MS
Reservoir tube to pump
Argon/ CO2
Pump
Waste
Vapor Trap
Culture pump to cathode
Condensate out
Gas to vapor trap
Culture cathode to reservoir
Carrier gas and CO2 addition to culture reservoir
Ice Bucket
Thermometer
Electrolytic Cell
Reservoir tube
Convection oven
Potentiometer
Thermo-controller

FIG. 17

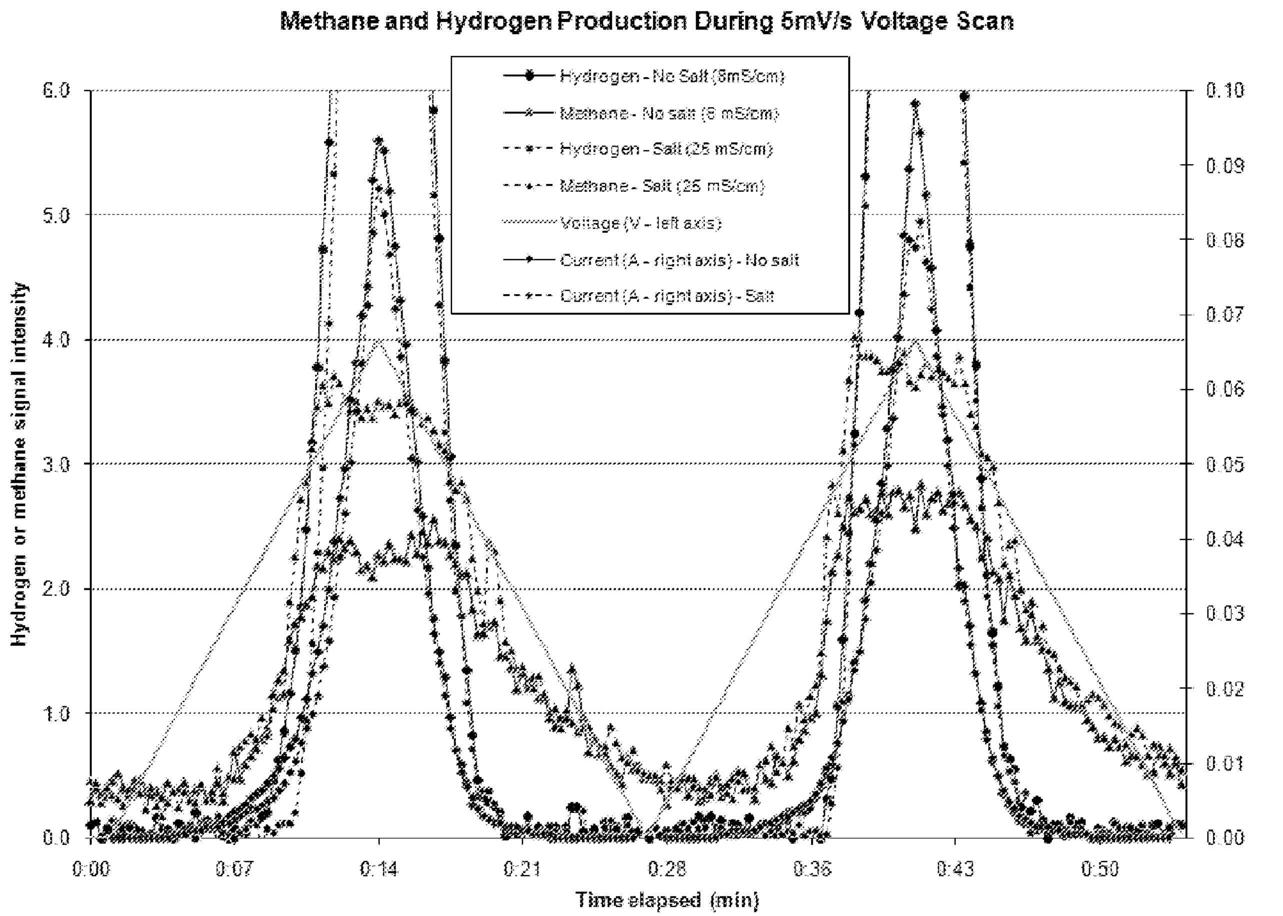
Methane and Hydrogen Production During 5mV/s Voltage Scan
Hydrogen - No Salt (8mS/cm)
Methane - No salt (8 mS/cm)
Hydrogen - Salt (25 mS/cm)
Methane - Salt (25 mS/cm)
Voltage (V - left axis)
Current (A - right axis) - No salt
Current (A - right axis) - Salt
Hydrogen or methane signal intensity
6.0
5.0
4.0
3.0
2.0
1.0
0.0
0.10
0.09
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0.00
0:00
0:07
0:14
0:21
0:28
0:36
0:43
0:50
Time elapsed (min)

FIG. 18

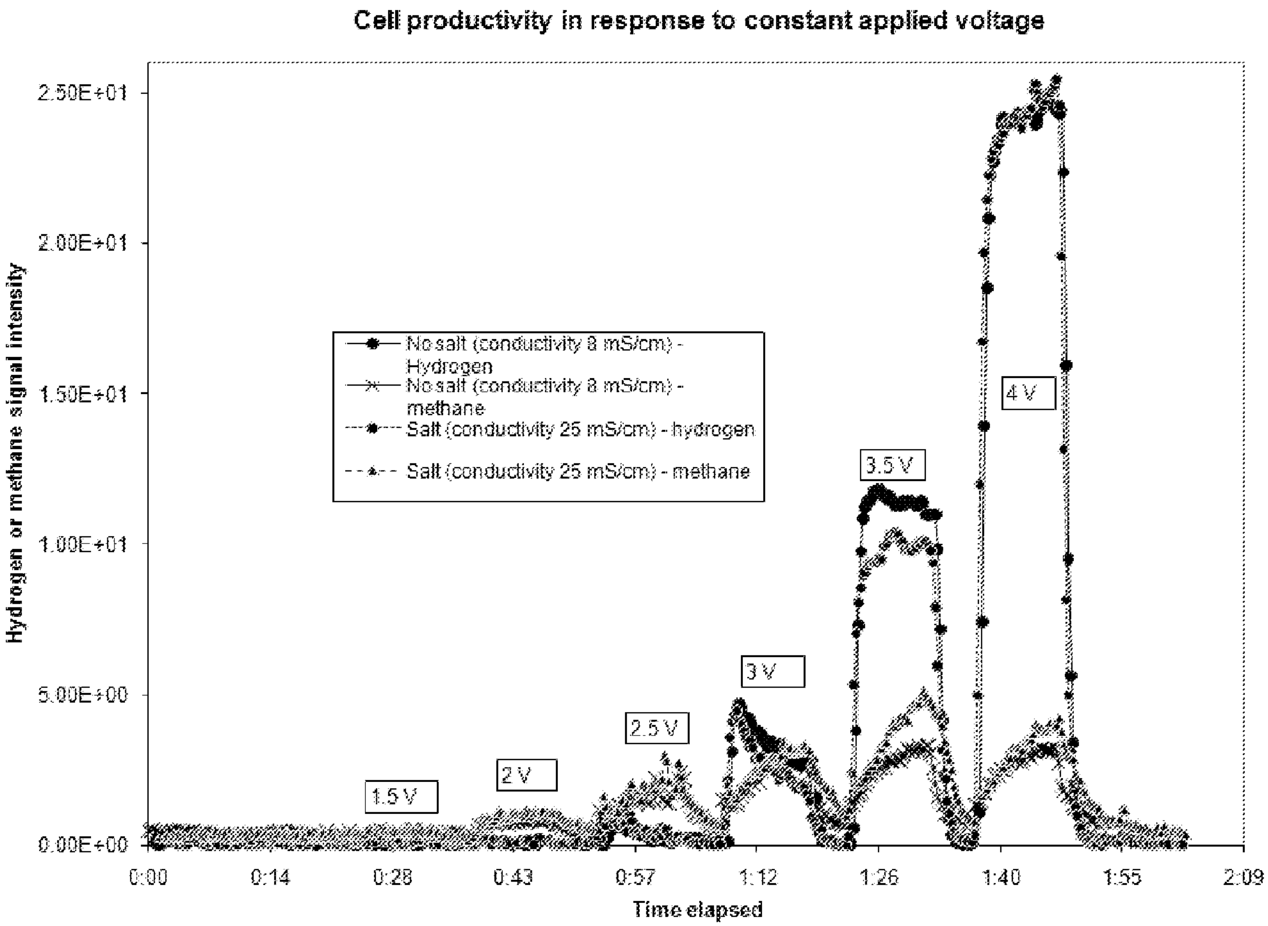
Cell productivity in response to constant applied voltage
Hydrogen or methane signal intensity
2.50E+01
2.00E+01
1.50E+01
1.00E+01
5.00E+00
0.00E+00
0:00
0:14
0:28
0:43
0:57
1:12
1:26
1:40
1:55
2:09
Time elapsed
No salt (conductivity 8 mS/cm) - Hydrogen
No salt (conductivity 8 mS/cm) - methane
Salt (conductivity 25 mS/cm) - hydrogen
Salt (conductivity 25 mS/cm) - methane
1.5 V
2 V
2.5 V
3 V
3.5 V
4 V

FIG. 19

METHOD AND SYSTEM FOR CONVERTING ELECTRICITY INTO ALTERNATIVE ENERGY RESOURCES

[0001] This application is a continuation of U.S. application Ser. No. 13/049,775, filed Mar. 16, 2011, which is a continuation-in-part of International Application No. PCT/US10/40944, filed on Jul. 2, 2010, which itself claims the benefit of U.S. Application No. 61/222,621, filed Jul. 2, 2009, and claims the benefit of U.S. Application No. 61/430,071, filed Jan. 5, 2011, all of which are hereby incorporated by reference in their entirety in the present application.

INCORPORATION BY REFERENCE OF MATERIAL SUBMITTED ELECTRONICALLY

[0002] Incorporated by reference in its entirety is a computer-readable nucleotide/amino acid sequence listing submitted concurrently herewith and identified as follows: One 6 KB ACII (Text) file named "45458C_SeqListing.txt," created on Aug. 5, 2011.

BACKGROUND

[0003] This patent is directed to the conversion of electrical energy into alternative energy resources, such as fuels. In particular, the patent relates to conversion of carbon dioxide into methane and other energy resources using electrical energy, which conversion may also create or generate other products or byproducts, such as carbon credits or oxygen, for example.

[0004] The United States annually consumes about 90 ExaJoules (EJ) of carbon-based fuels, 88% of its total energy consumption in 2008. The use of these fuels is supported by heavily capitalized processing, distribution and utilization industries.

[0005] The sustainability of these systems is questionable on two counts. First, the US imports 25% of the energy it uses, a proportion that is projected to increase substantially. Imported energy is obtained from sources that are under pressure to serve increasing demand from growing economies in other parts of the world. Second, more than 96% of the carbon-based fuels are obtained from fossil reserves, which are finite. Useful energy is obtained from carbon-based fuels by oxidizing reduced states of carbon to carbon dioxide. For fossil fuels, this process is basically open-loop, producing CO_2 with no compensating carbon reduction process to close the cycle. The consequent gradual accumulation of atmospheric CO_2 is beginning to cause changes in the global climate that threaten many aspects of our way of life. Therefore, a process that can close this carbon energy cycle for the total energy economy is needed.

[0006] An annual flux of 58,000 EJ of solar energy strikes US soil, making it our most abundant carbon-free energy resource—500 times current consumption. Solar energy has the unique advantage of being a domestic resource not just in the US, but everywhere that people live. Its widespread use as a primary resource would secure energy independence throughout the world. Nevertheless, today solar energy is only a marginal component of the energy economy, providing less than 0.1% of marketed US energy consumption. Exploitation of solar energy is limited principally because it is intermittent and cannot be relied upon to provide the base-load energy that must be available whenever needed. What is lacking is a method for storing solar energy in a stable form that can be tapped whenever needed. Ideally, such a storage form should fit smoothly into the existing energy infrastructure so that it can be quickly deployed once developed.

[0007] There is a need in the energy industry for systems to convert one form of energy into another. In particular, there is a need for systems to convert electricity into a form of energy that can be stored inexpensively on industrial scales. Many sources of electricity generation cannot be adjusted to match changing demand. For example, coal power plants run most efficiently when maintained at a constant rate and cannot be adjusted as easily as natural gas (methane) fired power plants. Likewise, wind turbines generate electricity when the wind is blowing which may not necessarily happen when electricity demand is highest.

[0008] There is also a need to convert electricity into a form that can be transported long distances without significant losses. Many opportunities for wind farms, geothermal, hydroelectric or solar based power generation facilities are not located close to major population centers, but electric power losses over hundreds of miles add significant cost to such distant power facilities.

[0009] Methane is one of the most versatile forms of energy and can be stored easily. There already exists much infrastructure for transporting and distributing methane as well as infrastructure for converting methane into electricity and for powering vehicles. Methane also has the highest energy density per carbon atom of all fossil fuels, and therefore of all fossil fuels, methane releases the least carbon dioxide per unit energy when burned. Hence, systems for converting electricity into methane would be highly useful and valuable in all energy generation and utilization industries.

[0010] In principle, it would be possible to produce methane from electric power in a two-step process, such as outlined schematically in FIG. **1**. The first step would use the electric power to make hydrogen gas from water in a standard water electrolysis system 50. In a second step, the hydrogen gas could then be pumped into a methanogenic reaction chamber 52 such as a highly specific reactor of methanogenic microbes. One such reactor is described in U.S. Publication No 2009/0130734 by Laurens Mets, which is incorporated in its entirety herein by reference.

SUMMARY

[0011] According to an aspect of the present disclosure, a system to convert electric power into methane includes a reactor having a first chamber and a second chamber separated by a proton permeable barrier. The first chamber includes a passage between an inlet and an outlet containing at least a porous electrically conductive cathode, a culture comprising living methanogenic microorganisms, and water. The second chamber includes at least an anode. The reactor has an operating state wherein the culture is maintained at a temperature above 50° C. The system also includes a source of electricity coupled to the anode and the cathode, and a supply of carbon dioxide coupled to the first chamber. The outlet of the system receives methane from the first chamber.

BRIEF DESCRIPTION OF THE DRAWINGS

[0012] It is believed that the disclosure will be more fully understood from the following description taken in conjunction with the accompanying drawings. Some of the figures may have been simplified by the omission of selected elements for the purpose of more clearly showing other elements. Such omissions of elements in some figures are not necessarily indicative of the presence or absence of particular elements in any of the exemplary embodiments, except as may be explicitly delineated in the corresponding written description. None of the drawings is necessarily to scale.

[0013] FIG. **1** is a schematic view of a system for converting carbon dioxide into methane according to the prior art;

[0014] FIG. **2** is a schematic view of a system for converting carbon dioxide into methane according to the present disclosure;

[0015] FIG. **3** is a cross-sectional view of an embodiment of a reactor for converting carbon dioxide into methane;

[0016] FIG. **4** is a cross-sectional view of another embodiment of a reactor for converting carbon dioxide into methane;

[0017] FIG. **5** is a cross-sectional view of yet another embodiment of a reactor for converting carbon dioxide into methane;

[0018] FIG. **6** is a cross-sectional view of a further embodiment of a reactor for converting carbon dioxide into methane;

[0019] FIG. **7** is a schematic view of an embodiment of a reactor with a plurality anodes and cathodes;

[0020] FIG. **8** is a cross-sectional view of the system of FIG. **7** taken along line **8-8**;

[0021] FIG. **9** is a cross-sectional view of one of the plurality of biological of FIG. **8** taken along line **9-9**;

[0022] FIG. **10** is a cross-sectional view of a variant reactor for use in the system of FIG. **7**;

[0023] FIG. **11** is a schematic view of a series arrangement of reactors according to the present disclosure;

[0024] FIG. **12** is a schematic view of a parallel arrangement of reactors according to the present disclosure;

[0025] FIG. **13** is a schematic view of a stand-alone system according to the present disclosure;

[0026] FIG. **14** is a schematic view of an integrated system according to the present disclosure; and

[0027] FIG. **15** is a graph of methane production over time with varying voltage applied across the anode and cathode of a biological reactor according to FIG. **3**;

[0028] FIG. **16** is a schematic view of a biological reactor as used in Example 2;

[0029] FIG. **17** is a schematic view of a testing system incorporating the reactor as used in Example 2;

[0030] FIG. **18** is a graph of methane and hydrogen production over time with varying voltage applied across the anode and cathode of a reactor according to FIG. **16**; and

[0031] FIG. **19** is a graph of productivity over time with varying voltage applied across the anode and cathode of a reactor according to FIG. **16**.

DETAILED DESCRIPTION OF VARIOUS EMBODIMENTS

[0032] Although the following text sets forth a detailed description of numerous different embodiments of the invention, it should be understood that the legal scope of the invention is defined by the words of the claims set forth at the end of this patent. The detailed description is to be construed as exemplary only and does not describe every possible embodiment of the invention since describing every possible embodiment would be impractical, if not impossible. Numerous alternative embodiments could be implemented, using either current technology or technology developed after the filing date of this patent, which would still fall within the scope of the claims defining the invention.

[0033] It should also be understood that, unless a term is expressly defined in this patent using the sentence "As used herein, the term '______ ' is hereby defined to mean . . . " or a similar sentence, there is no intent to limit the meaning of that term, either expressly or by implication, beyond its plain or ordinary meaning, and such term should not be interpreted to be limited in scope based on any statement made in any section of this patent (other than the language of the claims). To the extent that any term recited in the claims at the end of this patent is referred to in this patent in a manner consistent with a single meaning, that is done for sake of clarity only so as to not confuse the reader, and it is not intended that such claim term be limited, by implication or otherwise, to that single meaning. Finally, unless a claim element is defined by reciting the word "means" and a function without the recital of any structure, it is not intended that the scope of any claim element be interpreted based on the application of 35 U.S.C. §112, sixth paragraph.

[0034] The present disclosure addresses the processing or conversion of carbon dioxide into methane using an electrobiological apparatus. The apparatus may be referred to herein as a reactor, biological reactor, bioreactor, processor, converter or generator. It will be recognized that this designation is not intended to limit the role that the reactor may perform within a system including one or more reactor.

[0035] For example, the apparatus provides a non-fossil carbon-based energy resource. In this regard, the apparatus is being used to generate an energy resource that may be substituted for fossil-based carbon fuels, to reduce reliance on fossil-based carbon fuels, for example. Additionally, the apparatus converts or processes carbon dioxide to generate this energy resource. In this regard, the apparatus removes carbon dioxide from the environment, which may be a beneficial activity in and of itself. Such removal of carbon dioxide from the environment may happen by removing carbon dioxide directly from the atmosphere or by utilizing carbon dioxide from another industrial process and thereby preventing such carbon dioxide from being released into the atmosphere or into a storage system or into another process. Further, the apparatus converts or processes carbon dioxide into methane using electricity to convert electricity into another energy resource when demand for electricity may be such that the electricity would otherwise be wasted or even sold at a loss to the electricity producer, for example. In this regard, the apparatus may be viewed as part of an energy storage system. In the operation of a power grid, or an individual power plant or other power source on the grid, or as part of a facility not associated with a power grid, or in the operation of a biological reactor, available power output may be used by one or more biological reactors to consume as an input carbon dioxide, water or electrical power and to produce methane or oxygen when business conditions are favorable to provide an incentive greater than for other use of such inputs. Such conditions may exist when certain regulatory policies, power purchase agreements, carbon credits, futures trading opportunities, storage capacity, electrical demand, taxes, tax credits or abatements, contracts, customer preferences, transmission capacity, pricing conditions, or other market incentives can provide sufficient value for operation of the biological reactor to produce methane or oxygen or to consume carbon dioxide, water or electrical power. In addition to the above and other uses, the apparatus converts electrical energy or power into methane which may be transmitted via natural gas transmission pipes which on a per unit energy basis are less expensive than electrical transmission lines and in some locales the electrical transmission lines may not have as much spare transmission capacity as the natural gas transmission lines. In this regard, the apparatus may be viewed as part of an energy transmission system. All of these roles may be performed by an apparatus according to the present disclosure.

[0036] As illustrated in FIG. **2**, the biological reactor according to the present disclosure may include a container that is divided into at least a first chamber and a second chamber. At least one cathode is disposed in the first chamber, and at least one anode is disposed in the second chamber. The first chamber may have inlets that are connected to a source of carbon dioxide gas and a source of water, and an outlet that is connected, for example, to a storage device used to store methane produced in the first chamber. The first and second chambers are separated by a divider that is permeable to ions (protons) to permit them to move from the second chamber to the first chamber. This membrane also may be impermeable to the gaseous products and by-products of the conversion process to limit or prevent them from moving between the first chamber and the second chamber.

I. Description of System and Biological Reactor

[0037] Methanogenic microorganisms may be cultured, for example, in shake or stirred tank bioreactors, hollow fiber bioreactors, or fluidized bed bioreactors, and operated in a batch, fed batch, continuous, semi-continuous, or perfusion mode. In batch mode (single batch), an initial amount of medium containing nutrients necessary for growth is added to the biological reactor, and the biological reactor is operated until the number of viable cells rises to a steady-state maximum, or stationary condition. In fed-batch mode, concentrated media or selected amounts of single nutrients are added at fixed intervals to the culture. Methanogenic microorganisms can survive for years under fed batch conditions, provided that any waste products are effectively minimized or removed to prevent loss of efficiency of methane production over time. Any inhibitory waste products may be removed by continuous perfusion production processes, well known in the art. Perfusion processes may involve simple dilution by continuous feeding of fresh medium into the culture, while the same volume is continuously withdrawn from the reactor. Perfusion processes may also involve continuous, selective removal of medium by centrifugation while cells are retained in the culture or by selective removal of toxic components by dialysis, adsorption, electrophoresis, or other methods. Continuously perfused cultures may be maintained for weeks, months or years.

[0038] FIG. **3** illustrates a first embodiment of a system **100** that may be used, for example, to convert electric power into methane. The system **100** includes a biological reactor **102** having at least a first chamber **104** and a second chamber **106**. The first chamber **104** may contain at least a cathode **108**, a culture comprising living methanogenic microorganisms, and water. In particular, the culture may comprise autotrophic and/or hydrogenotrophic methanogenic archaea, and the water may be part of an aqueous electrolytic medium compatible with the living microorganisms. The second chamber may contain at least an anode **110**.

[0039] The biological reactor **102** may also include a selectively permeable barrier **112**, which may be a proton permeable barrier, separating the anode **110** from the cathode **108**. The barrier **112** may be at least gas semipermeable (e.g., certain gases may pass through, while others are limited), although according to certain embodiments, the barrier **112** is impermeable to gases. According to certain embodiments, the barrier **112** may prevent gases produced on each side of the barrier from mixing.

[0040] According to certain embodiments, the barrier **112** may be a solid polymer electrolyte membrane (PEM), such as is available under tradename Nafion from E. I. du Pont de Nemours and Company. For optimum energy conversion in the reactor according to certain embodiments, it is believed that the permeability of the barrier to hydronium ions should preferably be a minimum of two orders of magnitude greater on a molar basis than permeability of the barrier to oxygen under conditions of operation of the reactor. Other suitable PEM membranes that meet these criteria, such as sulfonated polyarylene block co-polymers (see, e.g., Bae, B., K Miyatake, and M. Watanabe. Macromolecules 43:2684-2691 (2010), which is incorporated by reference herein in its entirety) and PTFE-supported Nafion (see, e.g., G.-B. Jung, et al, J Fuel Cell Technol 4:248-255(2007), which is incorporated by reference herein in its entirety), are under active development in numerous laboratories. Suitable commercial PEM membranes, in addition to Nafion, include Gore-Select (PRIMEA), Flemion (Asahi), 3M Fluoropolymer ionomer, SPEEK (Polyfuel), Kynar blended membrane (Arkema), Fumapem (FuMA-Tech), and Solupor (Lydall).

[0041] In the biological reactor **102**, water acts as a primary net electron donor for the methanogenic microorganisms (e.g, methanogenic archaea) in the biological reactor. Accordingly, it is also believed that the barrier **112** should be permeable for hydronium ions (H_3O^+) (i.e., enable hydronium ions to cross the barrier **112** from the anode **110** to the cathode **108** and complete the electrical circuit). Nafion PEM is one example of a suitable material for such a barrier **112**.

[0042] The cathode **108** may be of a high surface to volume electrically conductive material. For example, the cathode **108** may be made of a porous electrically conductive material. In particular, the cathode **108** may be made from a reticulated vitreous carbon foam according to certain embodiments. As explained in greater detail below, other materials may be used. According to certain embodiments, the pores of the cathode may be large enough (e.g., greater than 1-2 micrometers in minimum dimension) to accommodate living methanogenic microorganisms within the pores. The electrical conductivity of the cathode matrix is preferably at least two orders of magnitude greater than the ion conductivity of the aqueous electrolytic medium contained within its pores.

[0043] It will be recognized that the role of the cathode **108** is to supply electrons to the microorganisms while minimizing side-reactions and minimizing energy loss. Additionally, it is advantageous for the cathode to be inexpensive. At the present time, it is believed that certain materials may be more or less suitable for inclusion in the reactor.

[0044] For instance, platinum cathodes may be less suitable for inclusion in the reactor. In this regard, the platinum provides a surface highly active for catalyzing hydrogen gas production from the combination of protons or hydronium ions with electrons provided by the cathode. The activity of platinum cathode catalysts for hydrogen formation in aqueous solutions is so high that the hydrogen concentration in the vicinity of the catalyst quickly rises above its solubility limit and hydrogen gas bubbles emerge. Despite the fact that the methanogenic microorganisms are evolved to consume hydrogen in the process of methane formation, hydrogen in bubbles re-dissolves only slowly in the medium and is largely unavailable to the microorganisms. Consequently, much of the energy consumed in hydrogen formation at a platinum catalyst does not contribute to methane formation. Additionally, the binding energy of hydrogen is higher than the binding energy per bond of methane. This difference results in an energetic loss when hydrogen gas is produced as an intermediate step.

[0045] On the other hand, a solid carbon cathode is an example of an inexpensive, electrically conductive material that has low activity for hydrogen formation and that can provide electrons to microorganisms. However, it will be recognized that electron transfer between microorganisms and an external electron source or sink, such as an electrode, requires some level of proximity between the microorganisms and the electrode and the total rate of electron transfer is related to the area of electrode in close contact with microorganisms. Since a porous electrode that allows the microorganisms to enter the pores has a much larger surface area in proximity to the microorganisms than a planar electrode of equivalent dimensions, the porous electrode is expected to provide superior volumetric current density.

[0046] A suitable porous cathode material may be provided by reticulated vitreous carbon foam, as demonstrated in Example 1. It is inexpensive and conductive. Its porous structure provides for electrical connections to a large number of the microorganisms allowing for a high volumetric productivity. Additionally, the vitreous nature of the carbon provides low activity for hydrogen production, which increases both energetic and Faradaic efficiency. It will also be recognized that vitreous carbon is also very resistant to corrosion.

[0047] Other suitable porous electrode materials may include, but are not limited to graphite foam (see, e.g., U.S. Pat. No. 6,033,506, which is incorporated by reference herein in its entirety), woven carbon and graphite materials, carbon, graphite or carbon nanotube impregnated paper (see, e.g., Hu, L., et al. Proc Nat Acad Sci USA 106: 21490-4 (2009), which is incorporated by reference herein in its entirety), and metal foams, or woven or non-woven mesh comprised of materials, such as titanium, that are non-reactive under the conditions of the reaction and that present a high surface to volume ratio.

[0048] Further enhancement of electron transfer between the cathode and the microorganisms may be achieved with conductive fibers. Suitable conductive fibers may consist of conductive pili generated by the microorganisms as described in more detail below. Alternatively or additionally, nanowires, such as carbon nanotubes (Iijima, S. Nature 354:56 (1991), which is incorporated by reference herein in its entirety), may be attached directly to the cathode. Wang, J. et al, J. Am. Chem. Soc. 125:2408-2409 (2003) and references therein, all of which are incorporated by reference herein in their entirety, provide techniques for modifying glassy carbon electrodes with carbon nanotubes. Additionally, conductive organic polymers may be used for this purpose (see, e.g., Jiang, P. Angewandte Chemie 43:4471-4475 (2004), which is incorporated by reference herein in its entirety). Non-conductive materials that bind the microorganisms to the surface of the electrode may also enhance electron transfer. Suitable non-conductive binders include but are not limited to polycationic polymers such as poly-lysine or poly(beta-aminosulfonamides). The living methanogenic microorganisms may also produce biological materials, such as those that support biofilm formation, that effectively bind them to the surface of the electrode.

[0049] The anode **110** may comprise a Pt-carbon catalytic layer or other materials known to provide low overpotential for the oxidation of water to oxygen.

[0050] As illustrated in FIG. **3**, a source of electricity **120** is coupled to the anode **110** and the cathode **108**. As mentioned above, the source **120** may be generated from carbon-free, renewable sources. In particular, the source **120** may be generated from carbon-free, renewable sources such as solar sources (e.g., photovoltaic cell arrays) and wind sources (e.g., wind turbines). However, according to other embodiments, the source **120** may be a coal power plant, a fuel cell, a nuclear power plant. According to still further embodiments, the source **120** may be a connector to an electrical transmission grid. Further details are provided below.

[0051] Based upon dynamic computational models of porous electrodes containing aqueous electrolyte, the optimal conductivity of the cathode electrolyte is believed to be preferably in the range of 100 mS/cm to 250 mS/cm or higher in the operating state of the reactor, although according to embodiments of the present disclosure, the range may be from about 5 mS/cm to about 100 mS/cm or from about 100 mS/cm to about 250 mS/cm. Higher conductivity of the electrolyte may reduce ohmic losses in the reactor and hence may increase energy conversion efficiency. Computational models further suggest that the optimal thickness of the porous cathode (perpendicular to the planes of the reactor layers) may be between 0.2 cm and 0.01 cm, or less. Thinner cathode layers may have lower ohmic resistance under a given set of operating conditions and hence may have an increased energy conversion efficiency. It will be recognized, however, that thicker cathodes may also be used.

[0052] The biological reactor **102** may operate at an electrical current density above 6 mA/cm^2. For example, the biological reactor **102** may operate at an electrical current density of between 6 and 10 mA/cm^2. According to certain embodiments, the biological reactor **102** may operate at electrical current densities at least one order of magnitude higher (e.g., 60-100 mA/cm^2). The current may be supplied as direct current, or may be supplied as pulsed current such as from rectified alternating current. The frequency of such pulsed current is not constrained by the properties of the reactor. The frequency of the pulsed current may be variable, such as that generated by variable speed turbines, for example wind turbines lacking constant-speed gearing.

[0053] The living methanogenic microorganisms (e.g., autotrophic and/or hydrogenotrophic methanogenic archaea) may be impregnated into the cathode **108**. Alternatively or in combination, the living methanogenic microorganisms may pass through the cathode **108** along with the circulating medium, electrolytic medium, or electrolyte (which may also be referred to as a catholyte, where the medium passes through, at least in part, the cathode **108**). While various embodiments and variants of the microorganisms are described in greater detail in the following section, it is noted that the microorganisms may be a strain of archaea adapted to nearly stationary growth conditions according to certain embodiments of the present disclosure. In addition, according to certain embodiments of the present disclosure, the microorganisms may be Archaea of the subkingdom Euryarchaeota, in particular, the microorganisms may consist essentially of *Methanothermobacter thermautotrophicus.*

[0054] As explained in greater detail below, the biological reactor **102** may have an operating state wherein the culture is maintained at a temperature above 50° C., although certain embodiments may have an operating state in the range of between approximately 60° C. and 100° C. The biological reactor **102** may also have a dormant state wherein electricity and/or carbon dioxide is not supplied to the reactor **102**. According to such a dormant state, the production of methane may be significantly reduced relative to the operating state, such that the production may be several orders of magnitude less than the operating state, and likewise the requirement for input electrical power and for input carbon dioxide may be several orders of magnitude less than the operating state. According to certain embodiments of the present disclosure, the biological reactor **102** may change between the operating state and the dormant state or between dormant state and operating state without addition of microorganisms to the reactor **102**. Additionally, according to certain embodiments, the reactor **102** may change between dormant and operating state rapidly, and the temperature of the reactor **102** may be maintained during the dormant state to facilitate the rapid change.

[0055] The biological reactor **102** may have an inlet **130** connected to the first chamber for receiving gaseous carbon dioxide. The inlet **130** may be coupled to a supply of carbon dioxide **132** to couple the supply of carbon dioxide to the first chamber **104**. The biological reactor **102** may also have an outlet **134** to receive methane from the first chamber.

[0056] The biological reactor **102** may also have an outlet **136** connected to the second chamber **106** for receiving byproducts. For example, gaseous oxygen may be generated in the second chamber **106** as a byproduct of the production of methane in the first chamber **104**. According to certain embodiments, oxygen may be the only gaseous byproduct of the biological reactor **102**. In either event, the gaseous oxygen may be received by the outlet **134** connected to the second chamber **106**.

[0057] In keeping with the disclosure of FIG. **3**, a method of the present disclosure may include supplying electricity to the anode **110** and the cathode **108** of the biological reactor **102** having at least the first chamber **104** containing at least the cathode **108**, a culture comprising living methanogenic microorganisms (e.g., autotrophic and/or hydrogenotrophic methanogenic archaea), and water (e.g., as part of an aqueous electrolytic medium compatible with the living microorganisms), and the second chamber **106** containing at least the anode **110**, wherein the culture is maintained at a temperature above 50° C. Further, the method may include generating electricity from carbon-free, renewable sources, such as from solar and wind sources, as noted above. According to certain embodiments, electricity may be supplied during a non-peak demand period. Further details are provided in section III, below.

[0058] The method may also include supplying carbon dioxide to the first chamber **104**. As noted above, the method may include recycling carbon dioxide from at least a concentrated industrial source or atmospheric carbon dioxide, which carbon dioxide is supplied to the first chamber **104**.

[0059] The method may further include collecting methane from the first chamber **104**. The method may further include storing and transporting the methane. The method may also include collecting other gaseous products or byproducts of the biological reactor; for example, the method may include collecting oxygen from the second chamber **106**.

[0060] It will be recognized that while the system of FIG. **3** may be viewed as operating to convert electricity into methane, it is also possible to view the system of FIG. **3** as operating to create or earn carbon credits, as an alternative to carbon sequestration for example. According to such a method, the method would include supplying electricity to the anode **110** and the cathode **108** of biological reactor **102** having at least the first chamber **104** containing at least the cathode **108**, methanogenic microorganisms (e.g., methanogenic archaea), and water (e.g., as part of an aqueous electrolytic medium compatible with the living microorganisms), and a second chamber containing at least the anode, wherein the culture is maintained at a temperature above 50° C. The method would also include supplying carbon dioxide to the first chamber **104**. Finally, the method would include receiving carbon credits for the carbon dioxide converted in the biological reactor **102** into methane. According to such a method, the carbon dioxide may be recycled from a concentrated industrial source.

[0061] It will be recognized that the system **100** is only one such embodiment of a system according to the present disclosure. Additional embodiments and variants of the system **100** are illustrated in FIGS. **4-10**, and will be described in the following section. While these embodiments are generally shown in cross-section, assuming a generally cylindrical shape for the reactor and disc-like shapes for the anode and cathode, which may be arranged parallel to one another as illustrated, it will be appreciated that other geometries may be used instead.

[0062] FIG. **4** illustrates a system **200** that includes a biological reactor **202**, a source of electricity **204** and a source of carbon dioxide **206**. As illustrated, the source of electricity **204** and the source of carbon dioxide **206** are both coupled to the biological reactor **202**. The biological reactor **202** uses a circulating liquid/gas media, as explained in greater detail below.

[0063] The biological reactor **202** includes a housing **210** that defines, in part, first and second chambers **212**, **214**. The reactor **202** also includes a cathode **216** disposed in the first chamber **212**, and an anode **218** disposed in the second chamber **214**. The first and second chambers **212**, **214** are separated by proton permeable, gas impermeable barrier **220**, the barrier **220** having surfaces **222**, **224** which also define in part the first and second chambers **212**, **214**.

[0064] The biological reactor **202** also includes current collectors **230**, **232**, one each for the cathode **216** and the anode **218** (which in turn may, according to certain embodiments, either be backed with a barrier impermeable to fluid, gas, and ions or be replaced by with a barrier impermeable to fluid, gas, and ions). The current collector **230** for the cathode **216** may be made as a solid disc of material, so as to maintain a sealed condition within the chamber **212** between an inlet **234** for the carbon dioxide and an outlet **236** for the methane (and potentially byproducts). The inlet **234** and the outlet **236** may be defined in the housing **210**. The current collector **232** for the anode **218** may also define a porous gas diffusion layer, on which the anode catalyst layer is disposed. It will be recognized that a porous gas diffusion layer should be provided so as to permit gaseous byproducts to exit the second chamber **214**, because the barrier **220** prevents their exit through the outlet **236** via the first chamber **212**.

[0065] In keeping with the disclosure above, the cathode **216** is made of a porous material, such as a reticulated carbon foam. The cathode **216** is impregnated with the methanogenic microorganisms and with the aqueous electrolytic medium. The methanogenic microorganisms (e.g., archaea) are thus in a passage **238** formed between the barrier **220** and the current collector **230** between the inlet **234** and the outlet **236**.

[0066] In operation, carbon dioxide is dissolved into the aqueous electrolytic medium and is circulated through the cathode **216**. The methanogenic microorganisms may reside within the circulating electrolytic medium or may be bound to the porous cathode **216**. In the presence of an electric current, the methanogenic microorganisms process the carbon dioxide to generate methane. The methane is carried by the electrolytic medium out of the reactor **202** via the outlet **236**. According to such an embodiment, post-processing equipment, such as a liquid/gas separator, may be connected to the outlet to extract the methane from the solution.

[0067] FIG. **5** illustrates a system **250** including a reactor **252** that is a variant of that illustrated in FIG. **4**. Similar to the reactor **202**, the reactor **252** includes a housing **260** that defines, in part, first and second chambers **262**, **264**. The reactor **252** also includes a cathode **266** disposed in the first chamber **262**, and an anode **268** disposed in the second chamber **264**. The first and second chambers **262**, **264** are separated by proton permeable, gas impermeable barrier **270**, the barrier **270** having surfaces **272**, **274** that also define in part the first and second chambers **262**, **264**.

[0068] Unlike the embodiment illustrated in FIG. **4**, the embodiment illustrated in FIG. **5** also includes a porous, proton conducting gas diffusion layer **280**. The gas diffusion layer **280** is disposed between the cathode **266** and the barrier **270**. Using this gas diffusion layer **280**, gaseous carbon dioxide may enter the first chamber **212** through the gas diffusion layer **280** and then diffuse into the cathode **266**, while gaseous methane produced by the microorganisms may diffuse from the cathode **266** into the layer **280** and then out of the first chamber **212**. Proton-conducting gas diffusion layers suitable for use as layer **280** may be produced by coating porous materials with proton-conducting ionomer, by incorporating ionomer directly into the porous matrix, or by chemical derivitization of porous matrix materials with sulfate, phosphate, or other groups that promote proton-conduction, for example.

[0069] It will thus be recognized that the carbon dioxide and the methane are not carried by a circulating liquid media according to the embodiment of FIG. **5**. Instead, the culture and the media are contained in the first chamber **262**, while only the gaseous carbon dioxide and the methane circulate between inlet and outlet. Such an embodiment may present certain advantages relative to the reactor **202** of FIG. **4**, in that the handling of the methane post-processing or generation may be simplified. Further, the absence of a circulating liquid media in the reactor **202** may simplify the serial connection between multiple reactors, as illustrated in FIG. **11**. However, while the circulating media in the embodiment of FIG. **4** provided any water required by the culture, it may be necessary to couple equipment to the reactor to provide water vapor to the culture, in addition to the gaseous carbon dioxide. The electrolytic medium and microorganisms may be retained within the pores of the cathode **266** by surface tension or alternatively by including materials within the electrolyte that increase its viscosity or form a gel.

[0070] FIG. **6** illustrates a system **300** including a reactor **302** that is a variant of that illustrated in FIG. **5**. Similar to the reactors **202** and **252**, the reactor **302** includes a housing **310** that defines, in part, first and second chambers **312**, **314**. The reactor **302** also includes a cathode **316** disposed in the first chamber **312**, and an anode **318** disposed in the second chamber **314**. The first and second chambers **312**, **314** are separated by proton permeable, gas impermeable barrier **320**, the barrier **320** having surfaces **322**, **324** that also define in part the first and second chambers **312**, **314**.

[0071] Moreover, similar to the embodiment illustrated in FIG. **5**, the embodiment illustrated in FIG. **6** also includes a porous, proton conducting gas diffusion layer **330**. However, the gas diffusion layer **330** is not disposed between the cathode **316** and the barrier **320**, but instead is disposed between the cathode **316** and the current collector **332**. In this arrangement, the gas diffusion layer **330** is current-conducting rather than proton-conduction like the gas diffusion layer **280** in reactor **252**. Current would pass through the layer **330** into the cathode **316**. As in the reactor **252**, the carbon dioxide still would enter the first chamber **312** passes through the gas diffusion layer **330** and diffuse into the cathode **316**, while methane produced by the microorganisms would diffuse from the cathode **316** through the layer **330**.

[0072] As a result, the embodiment of FIG. **6** illustrates a reactor wherein the gaseous carbon dioxide enters the cathode from a side or along a path opposite that of the protons. By comparison, the embodiment of FIG. **5** illustrates a reactor wherein the gaseous carbon dioxide and the protons enter the cathode from the same side or along a similar path. The counter-diffusion of the embodiment of FIG. **6** may provide slower production than that of FIG. **5**, but may provide acceptable production levels. As to the material used for the barrier **320** according to such an embodiment, it is believed that a porous carbon foam impregnated with Nafion particles may be suitable.

[0073] FIGS. **7-10** illustrate a system **400** including a biological reactor **402** that highlights several aspects of the present disclosure over and above those illustrated in FIGS. **2-6**. In particular, while the general nature of the reactor (with first and second chambers, anode, cathode, barrier, microorganisms, and aqueous electrolytic medium) has much in common with the systems illustrated in FIGS. **2-6**, the reactor **402** illustrates new geometries, as well as a reactor in which a plurality of anodes and a plurality of cathodes are present.

[0074] In particular, as illustrated in FIG. **7**, the reactor **402** includes a number of tubular reactor subunits **404** that may be arranged in a matrix format. It will be recognized that the particular arrangement of the subunits **404** utilizes an offset relative to the arrangement of adjacent rows of subunits **404**, so as to increase the number of subunits **404** within a volume. It will also be recognized that adjacent rows of subunits **404** may be aligned with each other instead. It will also be recognized that while four rows of five subunits **404** each and four rows of four subunits **404** each have been illustrated, this should not be taken as limiting the reactor **402** thereby.

[0075] FIG. **8** illustrates a plurality of subunits in cross-section, so as to appreciate the similarities and differences with the systems illustrated in FIGS. **2-6** above. While it need not be the case for all embodiments, each of the subunits **404** illustrated in FIG. **8** is identical, such that discussion of any one of the subunits **404** would be inclusive of remarks that may be made relative to the other subunits **404** as well.

[0076] As seen in FIG. **8**, the reactor **402** includes a housing **410**, in which the subunits **404** are disposed. It will be recognized that the housing **410** is sealed against leakage of products and byproducts as explained in greater detail below. Disposed at one end of the housing **410** is a common current collector **412** that is connected to a generally tubular cathode **414** of each of the subunits **404**. In a similar fashion, the reactor **402** includes a porous gas diffusion layer/current collector **416** that is connected to a generally tubular anode **418** of each subunit **404**. Disposed between the cathode **414** and the anode **418** is a generally tubular proton-permeable, gas impermeable barrier **420**, as is discussed in greater detail above. This arrangement is also illustrated in FIG. **9**.

[0077] According to this embodiment, the carbon dioxide enters the reactor **402** via an inlet **430** and moves along a passage **432**. The carbon dioxide then passes along the porous cathode **414**, which is impregnated with methanogenic microorganisms and aqueous electrolytic medium. The methane produced in the cathode **414** then is collected in a space **434** that is connected to the outlet **436**.

[0078] FIG. **10** illustrates a variant to the subunit **404** illustrated relative to the system **400** in FIGS. **7** and **8**. Given the similarities between the subunit **404** and its variant, the common structures will be designated with a prime.

[0079] As illustrated in FIG. **10**, the subunit **404'** includes a tubular cathode **414'**, a tubular anode **418'** and a tubular barrier **420'**. As in the subunit **404**, the tubular cathode **414'** is disposed centrally of the subunit **404'**, with the anode **418'** disposed radially outward of the cathode **416'** and the barrier **420'** disposed therebetween. However, similar to the variants described in FIG. **5**, the subunit **404'** includes a porous, proton-conducting gas diffusion layer **440**. This layer **440** may be in communication with the passage **432** and the space **434** in a reactor **402**, instead of the cathode **414'**. As such, carbon dioxide would pass from the inlet **430** through the layer **440** to the cathode **414'**, while methane would pass from the cathode **414'** through the layer **440** to the outlet **436**. An arrangement similar to FIG. **10**, but with an electrically conductive gas diffusion layer arranged as in FIG. **6** between the cathode **414'** and the current collector **412'** is also possible.

[0080] FIGS. **11** and **12** illustrate two different power management options that may be used with any of the reactors described above. In this regard, it will be recognized that each of the systems **450**, **452** illustrated in FIGS. **11** and **12** may include a plurality of individual reactors **454**, **456**.

[0081] In FIG. **11**, the individual reactors **454** are connected in series to match a fixed or constant voltage. The system **450** accommodates a variable current by providing a plurality of switches **458** to permit additional series chains of reactors **454** to be switched into the circuit to match variable current. In FIG. **12**, the individual reactors **456** are connected in parallel to match a fixed or constant current. The system **452** accommodates a variable voltage by providing pairs of switches **460** to permit additional parallel planes of reactors **456** to be switched into the circuit to match variable voltage. It will be recognized that it may also be possible to address variable current and variable voltage applications with addressable switching so as to build dynamic parallel reactor planes and to adjust the lengths of series chains as needed.

II. Cultures Comprising Methanogenic Microorganisms

Cultures

[0082] With regard to the present invention, the reactor (also referred to herein as the electromethanogenic reactor, the electrobiological methanogenesis reactor, the biological reactor, the bioreactor, etc.) comprises a culture comprising methanogenic microorganisms (a term used interchangeably with "methanogens"). The term "culture" as used herein refers to a population of live microorganisms in or on culture medium. When part of the reactor, the culture medium also serves as the electrolytic medium facilitating electrical conduction within the reactor.

Monocultures, Substantially Pure Cultures

[0083] In some embodiments, the culture is a monoculture and/or is a substantially-pure culture. As used herein the term "monoculture" refers to a population of microorganisms derived or descended from a single species (which may encompass multiple strains) or a single strain of microorganism. The monoculture in some aspects is "pure," i.e., nearly homogeneous, except for (a) naturally-occurring mutations that may occur in progeny and (b) natural contamination by non-methanogenic microorganisms resulting from exposure to non-sterile conditions. Organisms in monocultures can be grown, selected, adapted, manipulated, modified, mutated, or transformed, e.g. by selection or adaptation under specific conditions, irradiation, or recombinant DNA techniques, without losing their monoculture nature.

[0084] As used herein, a "substantially-pure culture" refers to a culture that substantially lacks microorganisms other than the desired species or strain(s) of microorganism. In other words, a substantially-pure culture of a strain of microorganism is substantially free of other contaminants, which can include microbial contaminants (e.g., organisms of different species or strain). In some embodiments, the substantially-pure culture is a culture in which greater than or about 70%, greater than or about 75%, greater than or about 80%, greater than or about 85%, greater than or about 90%, greater than or about 91%, greater than or about 92%, greater than or about 93%, greater than or about 94%, greater than or about 95%, greater than or about 96%, greater than or about 97%, greater than or about 98%, greater than or about 99% of the total population of the microorganisms of the culture is a single, species or strain of methanogenic microorganism. By way of example, in some embodiments, the substantially-pure culture is a culture in which greater than 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more of the total population of microorganisms of the culture is a single methanogenic microorganism species, e.g.,

Methanothermobacter Thermautotrophicus.

[0085] When initially set up, the biological reactor is inoculated with a pure or substantially pure monoculture. As the culture is exposed to non-sterile conditions during operation, the culture may be contaminated by other non-methanogenic microorganisms in the environment without significant impact on operating efficiency over a period of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 months, or 1.5 or 2 years.

Mixed Cultures

[0086] In other embodiments, the culture comprises a plurality of (e.g., a mixture or combination of two or more) different species of methanogenic microorganisms. In some aspects, the culture comprises two, three, four, five, six, seven, eight, nine, ten, or more different species of methanogenic microorganisms. In some aspects, the culture comprises a plurality of different species of methanogenic microorganisms, but the culture is substantially free of any non-methanogenic microorganism.

[0087] In yet other embodiments, the culture comprises a plurality of microorganisms of different species, in which at least one is a methanogenic microorganism. In some aspects of this embodiment, the culture comprises at least one species of methanogenic microorganism and further comprises at least one selected non-methanogenic microorganism. In some aspects, the culture comprises two or more different species of methanogens, and, optionally comprises at least one selected non-methanogenic microorganism.

[0088] Suitable cultures of mixtures of two or more microbes are also readily isolated from the specified environmental sources (Bryant et al. Archiv Microbiol 59:20-31 (1967) "Methanobacillus omelianskii, a symbiotic association of two species of bacteria.", which is incorporated by reference herein in its entirety). Suitable mixtures may be consortia in which cells of two or more species are physically associated or they may be syntrophic mixtures in which two or more species cooperate metabolically without physical association. Also, suitable mixtures may be consortia in which cells of two or more species are physically associated or they may be syntrophic mixtures in which two or more species cooperate metabolically with physical association. Mixed cultures may have useful properties beyond those available from pure cultures of known hydrogenotrophic methanogens. These properties may include, for instance, resistance to contaminants in the gas feed stream, such as oxygen, ethanol, or other trace components, or aggregated growth, which may increase the culture density and volumetric gas processing capacity of the culture. Another contaminant in the gas feed stream may be carbon monoxide.

[0089] Suitable cultures of mixed organisms may also be obtained by combining cultures isolated from two or more sources. One or more of the species in a suitable mixed culture should be an Archaeal methanogen. Any non-Archael species may be bacterial or eukaryotic.

[0090] Mixed cultures have been described in the art. See, for example, Cheng et al., U.S. 2009/0317882, and Zeikus US 2007/7250288, each of which is incorporated by reference in its entirety.

Reactor States and Growth Phases

[0091] As described herein, the reactor may be in a dormant (e.g., off) state or in an operating (e.g., on) state with regard to the production of methane, and, consequently, the reactor may be turned "on" or "off" as desired in accordance with the need or desire for methane production. In some embodiments, the methanogenic microorganisms of the culture are in a state which accords with the state of the reactor. Therefore, in some embodiments, the methanogenic microorganisms are in a dormant state in which the methanogenic microorganisms are not producing methane (e.g., not producing methane at a detectable level). In alternative embodiments, the methanogenic microorganisms are in an operating state in which the methanogenic microorganisms are producing methane (e.g., producing methane at a detectable level).

[0092] When the methanogenic microorganisms are in the operating state, the methanogenic microorganisms may be in one of a variety of growth phases, which differ with regard to the growth rate of the microorganisms (which can be expressed, e.g., as doubling time of microorganism number or cell mass). The phases of growth typically observed include a lag phase, an active growth phase (also known as exponential or logarithmic phase when microorganisms multiply rapidly), a stationary phase, and a death phase (exponential or logarithmic decline in cell numbers). In some aspects, the methanogenic microorganisms of the biological reactor are in a lag phase, an active growth phase, a stationary phase, or a nearly stationary phase.

Active Growth Phase

[0093] In some embodiments, the methanogenic microorganisms are in an active growth phase in which the methanogenic microorganisms are actively multiplying at a rapid rate.

[0094] In some aspects, during operation of the biological reactor, the doubling time of the microorganisms may be rapid or similar to that observed during the growth phase in its natural environment or in a nutrient-rich environment. For example, the doubling time of many methanogenic microorganisms in the active growth phase is about 15 minutes, about 20 minutes, about 30 minutes, about 45 minutes, about 60 minutes, about 75 minutes, about 80 minutes, about 90 minutes, or about 2 hours.

Stationary Growth Phase, Nearly Stationary Growth Phase

[0095] Stationary phase represents a growth phase in which, after the logarithmic or active growth phase, the rate of cell division and the rate of cell death are in equilibrium or near equilibrium, and thus a relatively constant concentration of microorganisms is maintained in the reactor. (See, Eugene W. Nester, Denise G. Anderson, C. Evans Roberts Jr., Nancy N. Pearsall, Martha T. Nester; Microbiology: A Human Perspective, 2004, Fourth Edition, Chapter 4, which is incorporated by reference herein in its entirety).

[0096] In other embodiments, the methanogenic microorganisms are in an stationary growth phase or nearly stationary growth phase in which the methanogenic microorganisms are not rapidly growing or have a substantially reduced growth rate. In some aspects, the doubling time of the methanogenic microorganisms is about 1 week or greater, including about 2, 3, 4 weeks or greater, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 months or greater.

[0097] In some embodiments, the reactor comprises a culture comprising methanogenic microorganisms, which microorganisms are initially in an active growth phase, and subsequently in a stationary or nearly stationary phase. In some embodiments, the reactor comprises a culture comprising methanogenic microorganisms which cycle between a dormant and an operating state.

Methanogenesis

[0098] As used herein, the term "methanogenic" refers to microorganisms that produce methane as a metabolic byproduct. In some embodiments, the reactor (also referenced herein interchangeably as electromethanogenic reactor, biological reactor or bioreactor, etc.) comprises a culture comprising hydrogenotrophic methanogenic microorganisms. As used herein, the term "hydrogenotrophic" refers to a microorganism capable of converting hydrogen to another compound as part of its metabolism. Hydrogenotrophic methanogenic microorganisms are capable of utilizing hydrogen in the production of methane. In some embodiments, the reactor comprises a culture comprising autotrophic methanogenic microorganisms. As used herein, the term "autotrophic" refers to a microorganism capable of using carbon dioxide and a source of reducing power to provide all carbon and energy necessary for growth and maintenance of the cell (e.g., microorganism). Suitable sources of reducing power may include but are not limited to hydrogen, hydrogen sulfide, sulfur, formic acid, carbon monoxide, reduced metals, sugars (e.g., glucose, fructose), acetate, photons, or cathodic electrodes or a combination thereof. In some aspects, the methanogenic microorganisms produce methane from carbon dioxide, electricity, and water, a process referred to as electrobiological methanogenesis.

[0099] The methanogenic microorganisms produce substantial amounts of methane in the operating state, as described herein. In some aspects, the methanogenic microorganisms produce methane in an active growth phase or stationary growth phase or nearly stationary growth phase.

[0100] The efficiency of methane production per molecule of carbon dioxide (CO_2) by the methanogenic microorganisms may be any efficiency suitable for the purposes herein. It has been reported that naturally-occurring methanogenic microorganisms in the active growth phase produce methane at a ratio of about 8 CO_2 molecules converted to methane per molecule of CO_2 converted to cellular material, ranging up to a ratio of about 20 CO_2 molecules converted to methane per molecule of CO_2 converted to cellular material. In some embodiments, the methanogenic microorganisms of the biological reactor of the present invention demonstrate an increased efficiency, particularly when adapted to stationary phase growth conditions. Accordingly, in some aspects, the ratio of the number of CO_2 molecules converted to methane to the number of CO_2 molecules converted to cellular material is higher than the ratio of naturally-occurring methanogenic microorganisms in the active growth phase. In exemplary embodiments, the ratio of the number of CO_2 molecules converted to methane to the number of CO_2 molecules converted to cellular material is N:1, wherein N is a number greater than 20, e.g. about 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, or higher. In some aspects, N is less than 500, less than 400, less than 300, or less than 200. In some aspects, N ranges from about 40 to about 150.

Archaea

Naturally-Occurring Archaea

[0101] In some embodiments, the methanogenic microorganisms, e.g., the autotrophic methanogenic microorganisms, are archaea. The term "Archaea" refers to a categorization of organisms of the division *Mendosicutes,* typically found in unusual environments and distinguished from the rest of the prokaryotes by several criteria, including ether-linked membrane lipids and lack of muramic acid in cell walls. On the basis of ssrRNA analysis, the Archaea consist of two phylogenetically-distinct groups: *Crenarchaeota* and *Euryarchaeota.* On the basis of their physiology, the Archaea can be organized into three partially overlapping groupings: methanogens (prokaryotes that produce methane); extreme halophiles (prokaryotes that live at very high concentrations of salt (NaCl); and extreme (hyper) thermophiles (prokaryotes that live at very high temperatures—e.g., 50-122° C.). Besides the unifying archaeal features that distinguish them from bacteria (i.e., no murein in cell wall, ether-linked membrane lipids, etc.), these prokaryotes exhibit unique structural or biochemical attributes which adapt them to their particular habitats. The *Crenarchaeota* consist mainly of hyperthermophilic sulfur-dependent prokaryotes and the *Euryarchaeota* contain the methanogens and extreme halophiles.

[0102] Methanogens (or methanobacteria) suitable for practice of the invention are readily obtainable from public collections of organisms or can be isolated from a variety of environmental sources. Such environmental sources include anaerobic soils and sands, bogs, swamps, marshes, estuaries, dense algal mats, both terrestrial and marine mud and sediments, deep ocean and deep well sites, sewage and organic waste sites and treatment facilities, and animal intestinal tracts and feces. Examples of suitable organisms have been classified into four different genera within the Methanobacteria class (e.g. Methanobacterium alcaliphilum, Methanobacterium bryantii, Methanobacterium congolense, Methanobacterium defluvii, Methanobacterium espanolae, Methanobacterium formicicum, Methanobacterium ivanovii, Methanobacterium palustre, Methanobacterium thermaggregans, Methanobacterium uliginosum, Methanobrevibacter acididurans, Methanobrevibacter arboriphilicus, Methanobrevibacter gottschalkii, Methanobrevibacter olleyae, Methanobrevibacter rum inantium, Methanobrevibacter smithii, Methanobrevibacter woesei, Methanobrevibacter wolinii, Methanothermobacter marburgensis, Methanothermobacter thermautotrophicum (also known as Methanothermobacter thermautotrophicus, Methanobacterium thermalcaliphilum, Methanobacterium thermoformicicum, Methanobacterium thermautotrophicum, Methanobacterium thermoalcaliphilum, Methanobacterium thermoautotrophicum), Methanothermobacter thermoflexus, Methanothermobacter thermophilus, Methanothermobacter wolfeii, Methanothermus sociabilis), 5 different genera within the Methanomicrobia class (e.g. Methanocorpusculum bavaricum, Methanocorpusculum parvum, Methanoculleus chikuoensis, Methanoculleus submarinus, Methanogenium frigidum, Methanogenium liminatans, Methanogenium marinum, Methanosarcina acetivorans, Methanosarcina barkeri, Methanosarcina mazei, Methanosarcina thermophila, Methanomicrobium mobile), 7 different genera within the Methanococci class (e.g. Methanocaldococcus jannaschii, Methanococcus aeolicus, Methanococcus maripaludis, Methanococcus vannielii, Methanococcus voltaei, Methanothermococcus thermolithotrophicus, Methanocaldococcus fervens, Methanocaldococcus indicus, Methanocaldococcus infernus, Methanocaldococcus vulcanius), and one genus within the Methanopyri class (e.g. *Methanopyrus kandleri*). Suitable cultures are available from public culture collections (e.g. the American Type Culture Collection, the Deutsche Sammlung von Mikroorganismen and Zellkulturen GmbH, and the Oregon Collection of Methanogens). In some embodiments, the methanogen is selected from the group consisting of Methanosarcinia barkeri, Methanococcus maripaludis, and Methanothermobacter thermautotrophicus.

[0103] Additional species of methanogens suitable for purposes of the present invention include, but are not limited to, *Methanobacterium formicum, Methanobrevibacter ruminantium, Methanocalculus chunghsingensis, Methanococcoides burtonii, Methanococcus deltae, Methanocorpusculum labreanum, Methanoculleus bourgensis* (*Methanogenium olentangyi, Methanogenium bourgense*), *Methanoculleus marisnigri, Methangenium cariaci, Methanogenium organophilum, Methanopyrus kandleri, Methanoregula boonei.* In some embodiments, the biological reactor comprises a culture (e.g. monoculture or substantially pure culture) of thermophilic or hyperthermophilic microorganisms, which may also be halophiles. In some embodiments, the methanogenic microorganism is from the phylum *Euryarchaeota.* Examples of species of thermophilic or hyperthermophilic autotrophic methanogens suitable for the purposes of the present invention include *Methanocaldococcus fervens, Methanocaldococcus indicus, Methanocaldococcus infernos, Methanocaldococcus jannaschii, Methanocaldococcus vulcanius, Methanopyrus kandleri, Methanothermobacter defluvii, Methanothermobacter marburgensis, Methanothermobacter thermautotrophicus, Methanothermobacter thermoflexus, Methanothermobacter thermophilus, Methanothermobacter wolfeii, Methanothermococcus okinawensis, Methanothermococcus thermolithotrophicus, Methanothermus fervidus, Methanothermus sociabilis, Methanotorris formicicus,* and *Methanotorris.*

[0104] In accordance with the foregoing, in some embodiments, the methanogenic microorganisms are of the superkingdom Archaea, formerly called Archaebacteria. In certain aspects, the archaea are of the phylum:*Crenarchaeota, Euryarchaeota, Korarchaeota, Nanoarchaeota, or Thaumarchaeota. In some aspects, the Crenarchaeota are of the class Thermoprotei. In some aspects, the Euryarchaeota are of the class: archaeoglobi, halobacteria, methanobacteria, methanococci, methanomicrobia, methanopyri, thermococci, thermoplasmata. In some embodiments, the Korarchaeota are of the class: Candidatus Korarchaeum or korarchaeote SRI-*306. In some aspects, the Nanoarchaeota are of the class nanoarchaeum. In some aspects, the Thaumarchaeota is of the class Cenarchaeales or marine archaeal group 1.

[0105] In some embodiments, the methanogenic microorganisms are of the order: Candidatus Korarchaeum, Nanoarchaeum, Caldisphaerales, Desulfurococcales, Fervidicoccales, Sulfolobales, Thermoproteales, Archaeoglobales, Halobacteriales, Methanobacteriales, Methanococcales, Methanocellales, Methanomicrobiales, Methanosarcinales, Methanopyrales, Thermococcales, Thermoplasmatales, Cenarchaeales, or Nitrosopumilales.

[0106] In some embodiments, the culture comprises a classified species of the Archaea phylum Euryarchaeota, including, but not limited to, any of those set forth in Table 1. In some embodiments, the culture comprises an unclassified species of Euryarchaeota, including, but not limited to, any of those set forth in Table 2. In some embodiments, the culture comprises an unclassified species of Archaea, including, but not limited to, any of those set forth in Table 3.

[0107] In some embodiments, the culture comprises a classified species of the Archaea phylum Crenarchaeota, including but not limited to any of those set forth in Table 4. In some embodiments, the culture comprises an unclassified species of the Archaea phylum Crenarchaeota, including, but not limited to, any of those set forth in Table 5.

[0108] The archaea listed in Tables 1-5 are known in the art. See, for example, the entries for "Archaea" in the Taxonomy Browser of the National Center for Biotechnological Information (NCBI) website.

Modified Archaea

[0109] Any of the above naturally-occurring methanogenic microorganisms may be modified. Accordingly, in some embodiments, the culture of the reactor comprises methanogenic microorganisms that have been modified (e.g., adapted in culture, genetically modified) to exhibit or comprise certain characteristics or features, which, optionally, may be specific to a given growth phase (active growth phase, stationary growth phase, nearly stationary growth phase) or reactor state (e.g., dormant state, operating state). For example, in some embodiments, the culture of the reactor comprises a methanogenic microorganism that has been modified to survive and/or grow in a desired culture condition which is different from a prior culture condition in which the methanogenic microorganism survived and/or grew, e.g., the natural environment from which the microorganism was isolated, or a culture condition previously reported in literature. The desired culture conditions may differ from the prior environment in temperature, pH, pressure, cell density, volume, humidity, salt content, conductivity, carbon content, nitrogen content, vitamin-content, amino acid content, mineral-content, or a combination thereof. In some embodiments, the culture of the biological reactor comprises a methanogenic microorganism, which, before adaptation in culture or genetic modification, is one that is not a halophile and/or not a thermophile or hyperthermophile, but, through adaptation in culture or genetic modification, has become a halophile and/or thermophile or hyperthermophile. Also, for example, in some embodiments, the methanogenic microorganism before genetic modification is one which does not express a protein, but through genetic modification has become a methanogenic microorganism which expresses the protein. Further, for example, in some embodiments, the methanogenic microorganism before adaptation in culture or genetic modification, is one which survives and/or grows in the presence of a particular carbon source, nitrogen source, amino acid, mineral, salt, vitamin, or combination thereof but through adaptation in culture or genetic modification, has become a methanogenic microorganism which survives and/or grows in the substantial absence thereof. Alternatively or additionally, in some embodiments, the methanogenic microorganism before adaptation in culture or genetic modification, is one which survives and/or grows in the presence of a particular amount or concentration of carbon source, nitrogen source, amino acid, mineral, salt, vitamin, but through adaptation in culture or genetic modification, has become a methanogenic microorganism which survives and/or grows in a different amount or concentration thereof.

[0110] In some embodiments, the methanogenic microorganisms are adapted to a particular growth phase or reactor state. Furthermore, for example, the methanogenic microorganism in some embodiments is one which, before adaptation in culture or genetic modification, is one which survives and/or grows in a given pH range, but through adaptation in culture becomes a methanogenic microorganism that survives and/or grows in different pH range. In some embodiments, the methanogenic microorganisms (e.g., archaea) are adapted in culture to a nearly stationary growth phase in a pH range of about 3.5 to about 10 (e.g., about 5.0 to about 8.0, about 6.0 to about 7.5). Accordingly, in some aspects, the methanogenic microorganisms are adapted in culture to a nearly stationary growth phase at a pH of about 3.5, 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8.0, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9.0, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, or 10.0. In some embodiments, the methanogenic microorganisms (e.g., archaea) are adapted in culture to an active growth phase in a pH range of about 6.5 to about 7.5 (e.g., about 6.8 to about 7.3). Accordingly, in some aspects, the methanogenic microorganisms are adapted in culture to a nearly stationary growth phase at a pH of about 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, or 7.5.

[0111] As used herein, the term "adaptation in culture" refers to a process in which microorganisms (e.g., naturally-occurring archaea) are cultured under a set of desired culture conditions (e.g., high salinity, high temperature, substantial absence of any carbon source, low pH, etc.), which differs from prior culture conditions. The culturing under the desired conditions occurs for a period of time which is sufficient to yield modified microorganisms (progeny of the parental line (i.e. the unadapted microorganisms)) which survive and/or grow (and/or produce methane) under the desired condition (s). The period of time of adaptation in some aspects is 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 2 weeks, 3 weeks 4 weeks, 5 weeks, 6 weeks 1 month, 2 months, 3 months, 4 months, 5 months 6 months, 7 months, 8 months, 9 months, 10 months, 12 months, 1 year, 2 years. The process of adapting in culture selects for microorganisms that can survive and/or grow and/or produce methane in the desired culture conditions; these selected microorganisms remain in the culture, whereas the other microorganisms that cannot survive and/or grow and/or produce methane in the desired culture conditions eventually die in the culture. In some embodiments, as a result of the adaptation in culture, the methanogenic microorganisms produce methane at a higher efficiency, e.g., at a ratio of the number of carbon dioxide molecules converted to methane to the number of carbon dioxide molecules converted to cellular materials which is higher than N:1, wherein N is a number greater than 20, as further described herein.

[0112] In some embodiments, the adaptation process occurs before the microorganisms are placed in the reactor. In some embodiments, the adaptation process occurs after the microorganisms are placed in the reactor. In some embodiments, the microorganisms are adapted to a first set of conditions and then placed in the reactor, and, after placement into the biological reactor, the microorganisms are adapted to another set of conditions.

[0113] For purposes of the present invention, in some embodiments, the culture of the reactor comprises a methanogenic microorganism (e.g., archaea) which has been adapted in culture to survive and/or grow in a high salt and/or high conductivity culture medium. For example, the culture of the biological reactor comprises a methanogenic microorganism (e.g., archaea) which has been adapted in culture to survive and/or grow in a culture medium having a conductivity of about 1 to about 25 S/m.

[0114] In alternative or additional embodiments, the culture of the reactor comprises a methanogenic microorganism (e.g., archaea) which has been adapted in culture to survive and/or grow at higher temperature (e.g., a temperature which is between about 1 and about 15 degrees C. greater than the temperature that the microorganisms survives and/or grows before adaptation). In exemplary embodiments, the methanogenic microorganisms are adapted to survive and/or grow in a temperature which is greater than 50° C., e.g., greater than 55° C., greater than 60° C., greater than 65° C., greater than 70° C., greater than 75° C., greater than 80° C., greater than 85° C., greater than 90° C., greater than 95° C., greater than 100° C., greater than 105° C., greater than 110° C., greater than 115° C., greater than 120° C.

[0115] In some embodiments, the culture comprises a methanogenic microorganism (e.g., archaea) which has been adapted in culture to grow and/or survive in conditions which are low in or substantially absent of any vitamins. In some aspects, the culture comprises a methanogenic microorganism (e.g., archaea) which has been adapted in culture to grow and/or survive in conditions which are low in or substantially absent of any organic carbon source. In some embodiments, the culture comprises a methanogenic microorganism which has been adapted in culture to grow and/or survive in conditions with substantially reduced amounts of carbon dioxide. In these embodiments, the methanogenic microorganisms may be adapted to exhibit an increased methanogenesis efficiency, producing the same amount of methane (as compared to the unadapted microorganism) with a reduced amount of carbon dioxide. In some embodiments, the culture comprises a methanogenic microorganism which has been adapted in culture to survive in conditions which substantially lacks carbon dioxide. In these embodiments, the methanogenic microorganisms may be in a dormant phase in which the microorganisms survive but do not produce detectable levels of methane. In some embodiments, the methanogenic microorganisms have been adapted to grow and/or survive in conditions which are low in or substantially absent of any hydrogen. In some embodiments, the methanogenic microorganisms have been adapted to grow and/or survive in conditions which are low in or substantially absent of any external source of water, e.g., the conditions do not comprise a dilution step.

[0116] In exemplary embodiments, the methanogens are adapted in culture to a nearly stationary growth phase. Such methanogens favor methane production over cell growth as measured, e.g., by the ratio of the number of CO_2 molecules converted to methane to the number of CO_2 molecules converted to cellular materials. This ratio is increased as compared to unadapted methanogens (which may exhibit, e.g., a ratio ranging from about 8:1 to about 20:1). In some embodiments, the methanogens are adapted in culture to a nearly stationary growth phase by being deprived of one or more nutrients otherwise required for optimal growth for a prolonged period of time (e.g., 1 week, 2 week, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 2 years, 3 years, 4 years, 5 years or more). In some embodiments, the methanogens are deprived of inorganic nutrients (e.g., hydrogen or electrons) necessary for optimum growth. In some embodiments, depriving the methanogens of hydrogen or electrons is achieved by sparging the media with an insert gas mixture such as $Ar:CO_2$ at a flow rate of 250 mL/min for several hours until neither hydrogen nor methane appear in the effluent gas stream. In some embodiments, the methanogenic microorganisms have been adapted to a nearly stationary growth phase in conditions which are low in or substantially absent of any external source of water, e.g., the adaptation conditions do not comprise a dilution step.

[0117] In some aspects, the culture comprises a methanogenic microorganism which has been adapted in culture to grow and/or survive in the culture medium set forth herein as Medium 1 and/or Medium 2 or a medium which is substantially similar to Medium 1 or Medium 2.

Genetically Modified Archaea

[0118] In some embodiments, the culture comprises methanogenic microorganisms which have been purposefully or intentionally genetically modified to become suitable, e.g., more suitable, for the purposes of the present invention. Suitable cultures may also be obtained by genetic modification of non-methanogenic organisms in which genes essential for supporting autotrophic methanogenesis are transferred from a methanogenic microbe or from a combination of microbes that may or may not be methanogenic on their own. Suitable genetic modification may also be obtained by enzymatic or chemical synthesis of the necessary genes.

[0119] In exemplary embodiments, a host cell that is not naturally methanogenic is intentionally genetically modified to express one or more genes that are known to be important for methanogenesis. For example, the host cell in some aspects is intentionally genetically modified to express one or more coenzymes or cofactors involved in methanogenesis. In some specific aspects, the coenzymes or cofactors are selected from the group consisting of F420, coenzyme B, coenzyme M, methanofuran, and methanopterin, the structures of which are known in the art. In some aspects the organisms are modified to express the enzymes, well known in the art, that employ these cofactors in methanogenesis.

[0120] In some embodiments, the host cells that are intentionally modified are extreme halophiles. In other embodiments, the host cells that are intentionally modified are thermophiles or hyperthermophiles. In other embodiments, the host cells that are intentionally modified are non-autotrophic methanogens. In some aspects, the host cells that are intentionally modified are methanogens that are not autotrophic. In some aspects, the host cells that are intentionally modified are cells which are neither methanogenic nor autotrophic. In other embodiments, the host cells that are intentionally modified are host cells comprising synthetic genomes. In some aspects, the host cells that are intentionally modified are host cells which comprise a genome which is not native to the host cell.

[0121] In some embodiments, the culture comprises microorganisms that have been purposefully or intentionally genetically modified to express pili or altered pili, e.g., altered pili that promote cell adhesion to the cathode or other components of the electrobiological methanogenesis reactor or pili altered to become electrically conductive. Pili are thin filamentous protein complexes that form flexible filaments that are made of proteins called pilins. Pili traverse the outer membrane of microbial cells and can extend from the cell surface to attach to a variety of other surfaces. Pili formation facilitates such disparate and important functions as surface adhesion, cell-cell interactions that mediate processes such as aggregation, conjugation, and twitching motility. Recent in silico analyses of more than twenty archaeal genomes have identified a large number of archaeal genes that encode putative proteins resembling type IV pilins (Szabó et al. 2007, which is incorporated by reference herein in its entirety). The expression of several archaeal pilin-like proteins has since been confirmed in vivo (Wang et al. 2008; Zolghadr et al. 2007; Fröls et al. 2007, 2008, which are incorporated by reference herein in their entirety). The sequence divergence of these proteins as well as the differential expression of the operons encoding these proteins suggests they play a variety of roles in distinct biological processes.

[0122] Certain microorganisms such as *Geobacter* and *Rhodoferax* species, have highly conductive pili that can function as biologically produced nanowires as described in US 20060257985, which is incorporated by reference herein in its entirety. Many methanogenic organisms, including most of the Methanocaldococcus species and the Methanotorris species, have native pili and in some cases these pili are used for attachment. None of these organisms are known to have natively electrically conductive pili.

[0123] In certain embodiments of the present invention the pili of a methanogenic organism and/or surfaces in contact with pili of a methanogenic organism or other biological components can be altered in order to promote cell adhesion to the cathode or other components of the electrobiological methanogenesis reactor. Pili of a methanogenic organism can be further engineered to optimize their electrical conductivity. Pilin proteins can be engineered to bind to various complexes. For example, pilin proteins can be engineered to bind iron, mimicking the pili of *Geobacter* species or alternatively, they can be engineered to bind a low potential ferredoxin-like iron-sulfur cluster that occurs naturally in many hyperthermophilic methanogens. The desired complex for a particular application will be governed by the midpoint potential of the redox reaction.

[0124] The cells may be genetically modified, e.g., using recombinant DNA technology. For example, cell or strain variants or mutants may be prepared by introducing appropriate nucleotide changes into the organism's DNA. The changes may include, for example, deletions, insertions, or substitutions of, nucleotides within a nucleic acid sequence of interest. The changes may also include introduction of a DNA sequence that is not naturally found in the strain or cell type. One of ordinary skill in the art will readily be able to select an appropriate method depending upon the particular cell type being modified. Methods for introducing such changes are well known in the art and include, for example, oligonucleotide-mediated mutagenesis, transposon mutagenesis, phage transduction, transformation, random mutagenesis (which may be induced by exposure to mutagenic compounds, radiation such as X-rays, UV light, etc.), PCR-mediated mutagenesis, DNA transfection, electroporation, etc.

[0125] The ability of the pili of the methanogenic organisms to adhere to the cathode coupled with an increased ability to conduct electrons, will enable the organisms to receive directly electrons passing through the cathode from the negative electrode of the power source. The use of methanogenic organisms with genetically engineered pili attached to the cathode will greatly increase the efficiency of conversion of electric power to methane.

Culture Media

[0126] The culture comprising the methanogenic microorganisms, e.g., the methanogenic archaea, may be maintained in or on a culture medium. In some embodiments, the culture medium is a solution or suspension (e.g., an aqueous solution). In other embodiments, the culture medium is a solid or semisolid. In yet other embodiments, the culture medium comprises or is a gel, a gelatin, or a paste.

[0127] In some embodiments, the culture medium is one that encourages the active growth phase of the methanogenic microorganisms. In exemplary aspects, the culture medium comprises materials, e.g., nutrients, in non-limiting amounts that support relatively rapid growth of the microorganisms. The materials and amounts of each material of the culture medium that supports the active phase of the methanogenic microorganisms will vary depending on the species or strain of the microorganisms of the culture. However, it is within the skill of the ordinary artisan to determine the contents of culture medium suitable for supporting the active phase of the microorganisms of the culture. In some embodiments, the culture medium encourages or permits a stationary phase of the methanogenic microorganisms. Exemplary culture medium components and concentrations are described in further detail below. Using this guidance, alternative variations can be selected for particular species for electrobiological methanogenesis in the operating state of the biological reactor using well known techniques in the field.

Inorganic Materials: Inorganic Elements, Minerals, and Salts

[0128] In some embodiments, the medium for culturing archaea comprises one or more nutrients that are inorganic elements, or salts thereof. Common inorganic elements include but are not limited to sodium, potassium, magnesium, calcium, iron, chloride, sulfur sources such as hydrogen sulfide or elemental sulfur, phosphorus sources such as phosphate and nitrogen sources such as ammonium, nitrogen gas or nitrate. Exemplary sources include NaCl, $NaHCO_3$, KCl, $MgCl_2$, $MgSO_4$, $CaCl_2$, ferrous sulfate, Na_2HPO_4, NaH_2PO_4 H_2O, H_2S, Na_2S, NH_4OH, N_2, and $NaNO_3$. In some embodiments, the culture medium further comprises one or more trace elements selected from the group consisting of ions of barium, bromium, boron, cobalt, iodine, manganese, chromium, copper, nickel, selenium, vanadium, titanium, germanium, molybdenum, silicon, iron, fluorine, silver, rubidium, tin, zirconium, cadmium, zinc, tungsten and aluminum. These ions may be provided, for example, in trace element salts, such as H_3BO_3, $Ba(C_2H_3O_2)_2$, KBr, $CoCl_2$-$6H_2O$, KI, $MnCl_2$-$2H_2O$, $Cr(SO_4)_3$-$15H_2O$, $CuSO_4$-$5H_2O$, $NiSO_4$-$6H_2O$, H_2SeO_3, $NaVO_3$, $TiCl_4$, GeO_2, $(NH_4)6Mo_7O_{24}$-$4H_2O$, Na_2SiO_3-$9H_2O$, $FeSO_4$-$7H_2O$, NaF, $AgNO_3$, RbCl, $SnCl_2$, $ZrOCl_2$-$8H_2O$, $CdSO_4$-$8H_2O$, $ZnSO_4$-$7H_2O$, $Fe(NO_3)_3$-$9H_2ONa_2WO_4$, $AlCl_3$-$6H_2O$.

[0129] In some embodiments, the medium comprises one or more minerals selected from the group consisting of nickel, cobalt, sodium, magnesium, iron, copper, manganese, zinc, boron, phosphorus, sulfur, nitrogen, selenium, tungsten, aluminum and potassium including any suitable non-toxic salts thereof. Thus, in some embodiments, the minerals in the medium are provided as mineral salts. Any suitable salts or hydrates may be used to make the medium. For example, and in some embodiments, the media comprises one or more of the following mineral salts: Na_3nitrilotriacetate, nitrilotriacetic acid, $NiCl_2$-$6H_2O$, $CoCl_2$-$6H_2O$, Na_2MoO_4-H_2O, $MgCl_2$-$6H_2O$, $FeSO_4$-H_2O, Na_2SeO_3, Na_2WO_4, KH_2PO_4, and NaCl. In some embodiments, L-cysteine may be added as a redox buffer to support early phases of growth of a low-density culture. In some embodiments, the medium comprises nickel, optionally $NiCl_2$-$6H_2O$ in an amount of about 0.001 mM to about 0.01 mM, e.g. 0.002 mM, 0.003 mM, 0.004 mM, 0.005 mM, 0.006 mM, 0.007 mM, 0.008 mM, 0.009 mM, or any combination of the foregoing range endpoints. In some embodiments, the media comprises a nitrogen source, e.g., ammonium hydroxide or ammonium chloride in an amount of about 1 mM to about 10 mM, e.g. 2 mM, 3 mM, 4 mM, 5 mM, 6 mM, 7 mM, 8 mM, 9 mM, or any combination of the foregoing range endpoints. In some embodiments, the media comprises cobalt, e.g. $CoCl_2$-$6H_2O$, in an amount of about 0.001 mM to about 0.01 mM, e.g., 0.002 mM, 0.003 mM, 0.004 mM, 0.005 mM, 0.006 mM, 0.007 mM, 0.008 mM, 0.009 mM, or any combination of the foregoing range endpoints. In some embodiments, the media comprises molybdenum, a molybdenum source or molybdate, e.g. Na_2MoO_4-H_2O, in an amount of about 0.005 mM to about 0.05 mM, e.g., 0.006 mM, 0.007 mM, 0.008 mM, 0.009 mM, 0.01 mM, 0.02 mM, 0.03 mM, 0.04 mM, or any combination of the foregoing range endpoints. In some embodiments, the media comprises magnesium, e.g. $MgCl_2$-$6H_2O$, in an amount of about 0.5 mM to about 1.5 mM, e.g., 0.6 mM, 0.7 mM, 0.8 mM, 0.9 mM, 1.0 mM, 1.1 mM, 1.2 mM, 1.3 mM, 1.4 mM, or any combination of the foregoing range endpoints. In some embodiments, the media comprises iron, e.g. $FeSO_4$-H_2O, in an amount of about 0.05 mM to about 0.5 mM, e.g., 0.06 mM, 0.07 mM, 0.08 mM, 0.09 mM, 0.1 mM, 0.2 mM, 0.3 mM, 0.4 mM, or any combination of the foregoing range endpoints. In some embodiments, the media comprises a sulfur source or sulfate in an amount of about 0.05 mM to about 0.5 mM, e.g., 0.06 mM, 0.07 mM, 0.08 mM, 0.09 mM, 0.1 mM, 0.2 mM, 0.3 mM, 0.4 mM, or any combination of the foregoing range endpoints. In some embodiments, the media comprises selenium, a selenium source or selenate, e.g. Na_2SeO_3, in an amount of about 0.005 mM to about 0.05 mM, e.g., 0.006 mM, 0.007 mM, 0.008 mM, 0.009 mM, 0.01 mM, 0.02 mM, 0.03 mM, 0.04 mM, or any combination of the foregoing range endpoints. In some embodiments, the media comprises tungsten, a tungsten source or tungstate, e.g. Na_2WO_4, in an amount of about 0.005 mM to about 0.05 mM, e.g., 0.006 mM, 0.007 mM, 0.008 mM, 0.009 mM, 0.01 mM, 0.02 mM, 0.03 mM, 0.04 mM, or any combination of the foregoing range endpoints. In some embodiments, the media comprises potassium, e.g. KH_2PO_4, in an amount of about 5 mM to about 15 mM, e.g., 6 mM, 7 mM, 8 mM, 9 mM, 10 mM, 11 mM, 12 mM, 13 mM, 14 mM, or any combination of the foregoing range endpoints. In some embodiments, the media comprises phosphorus, a phosphorus source, or phosphate, e.g. KH_2PO_4, in an amount of about 5 mM to about 15 mM, e.g., 6 mM, 7 mM, 8 mM, 9 mM, 10 mM, 11 mM, 12 mM, 13 mM, 14 mM, or any combination of the foregoing range endpoints. In some embodiments, the media comprises NaCl in an amount of about 5 mM to about 15 mM, e.g., 6 mM, 7 mM, 8 mM, 9 mM, 10 mM, 11 mM, 12 mM, 13 mM, 14 mM, or any combination of the foregoing range endpoints.

[0130] In some embodiments, the microorganism is adapted to prefer high salt conditions, e.g. about 1.5M to about 5.5 M NaCl, or about 3 M to about 4 M NaCl. In some embodiments, the microorganism is adapted to growth in higher salt conditions than their normal environment.

[0131] In some embodiments, the culture medium serves more than one purpose. Accordingly, in some aspects, the culture medium supports the growth and/or survival of the microorganisms of the culture and serves as the cathode electrolytic medium within the reactor. An electrolyte is a substance that, when dissolved in water, permits current to flow through the solution. The conductivity (or specific conductance) of an electrolytic medium is a measure of its ability to conduct electricity. The SI unit of conductivity is siemens per meter (S/m), and unless otherwise qualified, it is measured at a standard temperature of 25° C. Deionized water may have a conductivity of about 5.5 μS/m, while sea water has a conductivity of about 5 S/m (i.e., sea water's conductivity is one million times higher than that of deionized water).

[0132] Conductivity is traditionally determined by measuring the AC resistance of the solution between two electrodes or by torroidal inductance meters.

[0133] Limiting ion conductivity in water at 298 K for exemplary ions:

Cations	λ + 0/mS m^2mol^{-1}	anions	λ − 0/mS m^2mol^{-1}
H^+	34.96	OH	19.91
Li^+	3.869	Cl	7.634
Na^+	5.011	Br	7.84

-continued

Cations	λ + 0/mS m^2mol^{-1}	anions	λ − 0/mS m^2mol^{-1}
K^+	7.350	I	7.68
Mg^{2+}	10.612	SO42	15.96
Ca^{2+}	11.900	NO_3	7.14

[0134] In some embodiments, the culture medium comprises a high salt concentration for purposes of increasing the conductivity of the culture medium/reactor cathode electrolyte. Conductivity is readily adjusted, for example, by adding NaCl until the desired conductivity is achieved. In exemplary embodiments, the conductivity of the medium/electrolyte is in the range of about 5 mS/cm to about 100 mS/cm. This conductivity is readily achieved within the range of salt concentrations that are compatible with living methanogenic Archaea. In some embodiments, the conductivity of the medium/electrolyte is in the range of about 100 mS/cm to about 250 mS/cm, which is exemplary of a high conductivity medium.

Vitamins

[0135] In some embodiments, vitamins are substantially absent from the culture medium, to reduce contamination by non-methanogens and/or to decrease the cost of the culture medium, and thus, the overall cost of the biological reactor. However, it is possible to operate the biological reactor using media supplemented with one or more vitamins selected from the group consisting of ascorbic acid, biotin, choline chloride; D-Ca^{++}pantothenate, folic acid, i-inositol, menadione, niacinamide, nicotinic acid, paraaminobenzoic acid (PABA), pyridoxal, pyridoxine, riboflavin, thiamine-HCl, vitamin A acetate, vitamin B_{12} and vitamin D_2. In some embodiments, the medium is supplemented with a vitamin that is essential to survival of the methanogenic microorganism, but other vitamins are substantially absent.

Other Materials

[0136] The culture medium in some embodiments comprises materials other than inorganic compounds and salts. For example, the culture medium in some embodiments, comprises a chelating agent. Suitable chelating agents are known in the art and include but not limited to nitrilotriacetic acid and/or salts thereof. Also, in some aspects, the culture medium comprises a redox buffer, e.g., cystine, to support an early active growth phase in a low-density culture.

Carbon Sources

[0137] In some aspects, the culture medium comprises a carbon source, e.g., carbon dioxide, formic acid, or carbon monoxide. In some embodiments, the culture medium comprises a plurality of these carbon sources in combination. Preferably, organic carbon sources are substantially absent, to reduce contamination by non-methanogens.

Nitrogen Sources

[0138] In some embodiments, the culture medium comprises a nitrogen source, e.g., ammonium, anhydrous ammonia, ammonium salts and the like. In some embodiments, the culture medium may comprise nitrate or nitrite salts as a nitrogen source, although chemically reduced nitrogen compounds are preferable. In some aspects, the culture medium substantially lacks an organic nitrogen source, e.g., urea, corn steep liquor, casein, peptone yeast extract, and meat extract. In some embodiments diatomic nitrogen (N_2) may serve as a nitrogen source, either alone or in combination with other nitrogen sources.

Oxygen

[0139] Methanogens that are primarily anaerobic may still be capable of surviving prolonged periods of oxygen stress, e.g. exposure to ambient air for at least 6, 12, 18, or 24 hours, or 2 days, 3 days, 4 days, 5 days, 6 days, 1 week or more. Ideally, exposure to air is for 4 days or less, or 3 days or less, or 2 days or less, or 24 hours or less. Methane production may continue in the presence of oxygen concentrations as high as 2-3% of the gas phase for extended periods (at least days). However, anaerobic organisms will grow optimally in conditions of low oxygen. In some embodiments, the biological reactor substantially excludes oxygen to promote high levels of methane production.

[0140] In some embodiments, the system comprises various methods and/or features that reduce the presence of oxygen in the CO_2 stream that is fed into the biological reactor. When obligate anaerobic methanogenic microorganisms are used to catalyze methane formation, the presence of oxygen may be detrimental to the performance of the process and contaminates the product gas. Therefore, reduction of the presence of oxygen in the CO_2 stream is helpful for improving the process. In one embodiment, the oxygen is removed by pre-treatment of the gas stream in a biological reactor. In this embodiment, the reductant may be provided either by provision of a source of organic material (e.g. glucose, starch, cellulose, fermentation residue from an ethanol plant, whey residue, etc.) that can serve as substrate for an oxidative fermentation. The microbial biological catalyst is chosen to oxidatively ferment the chosen organic source, yielding CO_2 from the contaminant oxygen. In another embodiment, oxygen removal is accomplished in the main fermentation vessel via a mixed culture of microbes that includes one capable of oxidative fermentation of an added organic source in addition to the autotrophic methanogen necessary for methane production. An example of a suitable mixed culture was originally isolated as "Methanobacillus omelianskii" and is readily obtained from environmental sources (Bryant et al. Archiv Microbiol 59:20-31 (1967) "Methanobacillus omelianskii, a symbiotic association of two species of bacteria.", which is incorporated by reference herein in its entirety). In another embodiment, carbon dioxide in the input gas stream is purified away from contaminating gases, including oxygen, buy selective absorption or by membrane separation. Methods for preparing carbon dioxide sufficiently free of oxygen are well known in the art.

Exemplary Media

[0141] In some embodiments, the culture medium comprises the following components: Na_3nitrilotriacetate, nitrilotriacetic acid, $NiCl_2$-$6H_2O$, $CoCl_2$-$6H_2O$, Na_2MoO_4-H_2O, $MgCl_2$-$6H_2O$, $FeSO_4$-H_2O, Na_2SeO_3, Na_2WO_4, KH_2PO_4, and NaCl. In some embodiments, L-cysteine may be added as a redox buffer to support early phases of growth of a low-density culture. In some embodiments, the media comprises Na_3nitrilotriacetate (0.81 mM), nitrilotriacetic acid (0.4 mM), $NiCl_2$-$6H_2O$ (0.005 mM), $CoCl_2$-$6H_2O$ (0.0025 mM),

Na_2MoO_4-H_2O (0.0025 mM), $MgCl_2$-$6H_2O$ (1.0 mM), $FeSO_4$-H_2O (0.2 mM), Na_2SeO_3 (0.001 mM), Na_2WO_4 (0.01 mM), KH_2PO_4 (10 mM), and NaCl (10 mM). L-cysteine (0.2 mM) may be included.

[0142] In some embodiments, the culture medium comprises the following components: KH_2PO_4, NH_4Cl, NaCl, Na_3nitrilotriacetate, $NiCl_2$-$6H_2O$, $CoCl_2$-H_2O, Na_2MoO_4-$2H_2O$, $FeSO_4$-$7H_2O$, $MgCl_2$-$6H_2O$, Na_2SeO_3, Na_2WO_4, Na_2S-$9H_2O$. A culture medium comprising these components may be referred to herein as Medium 1, which is capable of supporting survival and/or growth of methanogenic microorganisms originally derived from a terrestrial environment, e.g., a *Methanothermobacter* species. Thus, in some embodiments, the biological reactor comprises a culture of *Methanothermobacter* and a culture medium of Medium 1. In some aspects, the culture medium is adjusted with NH_4OH to a pH between about 6.8 and about 7.3. In some embodiments, the culture medium not only supports growth of and/or survival of and/or methane production by the methanogenic microorganisms but also serves as the cathode electrolytic medium suitable for conducting electricity within the reactor. Accordingly, in some aspects, the conductivity of the culture medium is in the range of about 5 mS/cm to about 100 mS/cm or about 100 mS/cm to about 250 mS/cm.

[0143] In some embodiments, the KH_2PO_4 is present in the medium at a concentration within the range of about 1 mM to about 100 mM, e.g., about 2 mM, about 50 mM, about 5 mM to about 20 mM.

[0144] In some embodiments, the NH_4Cl is present in the culture medium at a concentration within the range of about 10 mM to about 1500 mM, e.g., about 20 mM to about 600 mM, about 60 mM to about 250 mM.

[0145] In some embodiments, the NaCl is present in the culture medium within the range of about 1 mM to about 100 mM, e.g., about 2 mM, about 50 mM, about 5 mM to about 20 mM.

[0146] In some embodiments, the Na_3nitrilotriacetate is present in the culture medium within the range of about 0.1 mM to about 10 mM, e.g., 0.20 mM to about 6 mM, about 0.5 to about 2.5 mM.

[0147] In some embodiments, the $NiCl_2$-$6H_2O$ is present in the culture medium within the range of about 0.00025 to about 0.025 mM, e.g., about 0.005 mM to about 0.0125 mM, about 0.0005 mM to about 0.005 mM.

[0148] In some embodiments, the $CoCl_2$-H_2O is present in the culture medium within the range of about 0.0005 mM to about 0.05 mM, e.g., about 0.001 mM to about 0.025 mM, about 0.0025 mM to about 0.01 mM.

[0149] In some embodiments, the Na_2MoO_4-$2H_2O$ is present in the culture medium within the range of about 0.00025 mM to about 0.025 mM, e.g., about 0.0005 mM to about 0.0125 mM, about 0.00125 mM to about 0.005 mM.

[0150] In some embodiments, the $FeSO_4$-$7H_2O$ is present in the culture medium within the range of about 0.02 mM to about 2 mM, e.g., about 0.04 mM to about 1 mM, about 0.1 mM to about 0.4 mM.

[0151] In some embodiments, the $MgCl_2$-$6H_2O$ is present in the culture medium within the range of about 0.1 mM to about 10 mM, e.g., about 0.2 mM to about 5 mM, about 0.5 mM to about 2 mM.

[0152] In some embodiments, the Na_2SeO_3 is present in the culture medium within the range of about 0.0001 mM to about 0.01 mM, e.g., about 0.0002 mM to about 0.005 mM, about 0.0005 mM to about 0.002 mM.

[0153] In some embodiments, the Na_2WO_4 is present in the culture medium within the range of about 0.001 mM to about 0.1 mM, e.g., about 0.05 mM to about 0.05 mM, about 0.005 mM to about 0.02 mM.

[0154] In some embodiments, Medium 1 is supplemented with components, such as sulfide, that support the active growth phase or relatively rapid multiplication of the microorganism. Accordingly, in some aspects, the culture medium comprises a higher sulfide concentration, e.g. 0.1 mM to about 10 mM (e.g., about 0.2 mM to about 5 mM, about 0.5 mM to about 2 mM), about 0.5 to 5 mM, or about 1 mM Na_2S-$9H_2O$, and preferably greater than 0.01 mM Na_2S-$9H_2O$, optionally with a pH between about 6.8 and about 7.0. In other embodiments, Medium 1 supports the inactive or stationary or nearly-stationary growth phase of the microorganism and the medium comprises a lower sulfide concentration. Accordingly, in some aspects, the culture comprises about 0.01 mM or less Na_2S-$9H_2O$, and not 1 mM Na_2S-$9H_2O$. optionally with a pH between about 7.2 and about 7.4.

[0155] In some embodiments, the culture medium comprises the following components: KH_2PO_4, NaCl, NH_4Cl, Na_2CO_3, $CaCl_2 \times 2H_2O$, $MgCl_2 \times 6H_2O$, $FeCl_2 \times 4H_2O$, $NiCl_2 \times 6H_2O$, $Na_2SeO_3 \times 5\ H_2O$, $Na_2WO_4 \times H_2O$, $MnCl_2 \times 4H_2O$, $ZnCl_2$, H_3BO_3, $CoCl_2 \times 6H_2O$, $CuCl_2 \times 2H_2O$, $Na_2MoO_4 \times 2H_2O$, Nitrilotriacetic acid, Na_3nitrilotriacetic acid, $KAl(SO_4)_2 \times 12\ H_2O$, $Na_2S \times 9H_2O$. A culture medium comprising these components may be referred to herein as Medium 2, which is capable of supporting survival and/or growth of methanogenic microorganisms originally derived from a marine environment, e.g., a *Methanocaldooccus* species, *Methanotorris* species, *Methanopyrus* species, or *Methanothermococcus* species. In some aspects, the culture medium is adjusted with NH_4OH to a pH between about 6.3 and about 6.8 (e.g., about 6.4 to about 6.6). In some embodiments, the culture medium not only supports growth of and/or survival of and/or methane production by the methanogenic microorganisms but also serves as the cathode electrolytic medium suitable for conducting electricity within the reactor. Accordingly, in some aspects, the conductivity of the culture medium is in the range of about 5 mS/cm to about 100 mS/cm or about 100 mS/cm to about 250 mS/cm.

[0156] In some embodiments, the KH_2PO_4 is present in the culture medium at a concentration within the range of about 0.35 mM to about 37 mM, e.g., about 0.7 mM to about 0.75 mM, about 1.75 mM to about 7.5 mM.

[0157] In some embodiments, the NaCl is present in the culture medium at a concentration within the range of about 17 mM to about 1750 mM, e.g., about 30 mM to about 860 mM, about 80 mM to about 350 mM.

[0158] In some embodiments, the NH_4Cl is present in the culture medium at a concentration within the range of about 0.7 mM to about 750 mM, e.g., about 1.5 mM to about 40 mM, about 3.75 mM to about 15 mM.

[0159] In some embodiments, the Na_2CO_3 is present in the culture medium at a concentration within the range of about 5 mM to about 600 mM, e.g., 10 mM to about 300 mM, about 30 mM to about 150 mM.

[0160] In some embodiments, the $CaCl_2 \times 2H_2O$ is present in the culture medium at a concentration within the range of about 0.05 to about 50 mM, e.g., 0.2 mM to about 5 mM, about 0.5 mM to about 2 mM.

[0161] In some embodiments, the $MgCl_2 \times 6H_2O$ is present in the culture medium at a concentration within the range of about 3 mM to about 350 mM, e.g., about 6.5 mM to about 175 mM, about 15 mM to about 70 mM.

[0162] In some embodiments, the $FeCl_2 \times 4H_2O$ is present in the culture medium at a concentration within the range of about 0.003 mM to about 0.3 mM, e.g., about 0.006 mM to about 0.15 mM, about 0.015 mM to about 0.06 mM.

[0163] In some embodiments, the $NiCl_2 \times 6H_2O$ is present in the culture medium at a concentration within the range of about 0.0005 mM to about 0.007 mM, e.g., 0.0012 mM to about 0.03 mM, about 0.003 mM to about 0.012 mM.

[0164] In some embodiments, the $Na_2SeO_3 \times 5\ H_2O$ is present in the culture medium at a concentration within the range of about 0.0001 mM to about 0.01 mM, e.g., about 0.00025 mM to about 0.01 mM, about 0.001 mM to about 0.005 mM.

[0165] In some embodiments, the $Na_2WO_4 \times H_2O$ is present in the culture medium at a concentration within the range of about 0.0005 mM to about 0.007 mM, e.g., 0.0012 mM to about 0.03 mM, about 0.003 mM to about 0.012 mM.

[0166] In some embodiments, the $MnCl_2 \times 4H_2O$ is present in the culture medium at a concentration within the range of about 0.003 mM to about 0.4 mM, e.g., about 0.08 mM to about 2 mM, about 0.02 mM to about 0.08 mM.

[0167] In some embodiments, the $ZnCl_2$ is present in the culture medium at a concentration within the range of about 0.0005 mM to about 0.007 mM, e.g., 0.0012 mM to about 0.03 mM, about 0.003 mM to about 0.012 mM.

[0168] In some embodiments, the H_3BO_3 is present in the culture medium at a concentration within the range of about 0.0001 mM to about 0.01 mM, e.g., about 0.00025 mM to about 0.01 mM, about 0.001 mM to about 0.005 mM.

[0169] In some embodiments, the $CoC_{12} \times 6H_2O$ is present in the culture medium at a concentration within the range of about 0.0005 mM to about 0.007 mM, e.g., 0.0012 mM to about 0.03 mM, about 0.003 mM to about 0.012 mM.

[0170] In some embodiments, the $CuCl_2 \times 2H_2O$ is present in the culture medium at a concentration within the range of about 0.00004 mM to about 0.004 mM, e.g., 0.00008 mM to about 0.002 mM, about 0.0002 mM to about 0.0008 mM.

[0171] In some embodiments, the $Na_2MoO_4 \times 2H_2O$ is present in the culture medium at a concentration within the range of about 0.00004 mM to about 0.004 mM, e.g., 0.00008 mM to about 0.002 mM, about 0.0002 mM to about 0.0008 mM.

[0172] In some embodiments, the Nitrilotriacetic acid is present in the culture medium at a concentration within the range of about 0.003 mM to about 0.7 mM, e.g., about 0.12 mM to about 0.3 mM, about 0.03 mM to about 0.12 mM.

[0173] In some embodiments, the Na_3nitrilotriacetic acid is present in the culture medium at a concentration within the range of about 0.002 mM to about 0.2 mM, e.g., about 0.004 mM to about 0.1 mM, about 0.01 mM to about 0.04 mM.

[0174] In some embodiments, the $KAl(SO_4)_2 \times 12\ H_2O$ is present in the culture medium at a concentration within the range of about 0.00004 mM to about 0.004 mM, e.g., 0.00008 mM to about 0.002 mM, about 0.0002 mM to about 0.0008 mM.

[0175] In some embodiments, the salt concentration in Medium 2 is adjusted upward to the range of 400 to 800 mM for formulation of the electrolyte in the reactor. Additionally, the sulfide concentration of relatively stationary cultures is adjusted downward to the range of <0.01mM (<1 ppm sulfide in the exit gas stream).

[0176] In some examples, the media is sparged with a H_2:CO_2 gas mixture in a 4:1 ratio. The gas mixture can, in some embodiments, be generated with mass flow controllers at a total flow of 250 ml/minute. In some embodiments, the medium should be replenished at a rate suitable to maintain a useful concentration of essential minerals and to eliminate any metabolic products that may inhibit methanogenesis. Dilution rates below 0.1 culture volume per hour are suitable, since they yield high volumetric concentrations of active methane generation capacity.

Culture Conditions

[0177] The microorganisms may be cultured under any set of conditions suitable for the survival and/or methane production. Suitable conditions include those described below.

Temperature

[0178] In some embodiments, the temperature of the culture is maintained near the optimum temperature for growth of the organism used in the culture (e.g. about 35° C. to about 37° C. for mesophilic organisms such as *Methanosarcinia barkeri* and *Methanococcus maripaludis* or about 60° C. to about 65° C. for thermophiles such as *Methanothermobacter thermoautotrophicus* and *Methanothermobacter marburgensis,* and about 85° C. to about 90° C. for organisms such as *Methanocaldococcus jannaschii, Methanocaldococcus fervens, Methanocaldococcus indicus, Methanocaldococcus infernus,* and *Methanocaldococcus vulcanius*). However, it is envisioned that temperatures above or below the temperatures for optimal growth may be used. In fact, higher conversion rates of methane may be obtained at temperatures above the optimal growth rate temperature. Temperatures of about 50° C. or higher are contemplated, e.g., about 51° C. or higher, about 52° C. or higher, about 53° C. or higher, about 54° C. or higher, about 55° C. or higher, about 56° C. or higher, about 57° C. or higher, about 58° C. or higher, about 59° C. or higher, about 60° C. to about 150° C., about 60° C. to about 120° C., about 60° C. to about 100° C., about 60° C. to about 80° C. Temperatures of about 40° C. or higher, or about 50° C. or higher are contemplated, e.g. about 40° C. to about 150° C., about 50° C. to about 150° C., about 40° C. to about 120° C., about 50° C., to about 120° C., about 40° C. to about 100° C., or about 50° C. to about 100° C.

[0179] In view of the foregoing, the temperature at which the culture is maintained may be considered as a description of the methanogenic microorganisms contemplated herein. For example, when the temperature of the culture is maintained at a temperature between 55° C. and 120° C., the methanogenic microorganism is considered as one that can be cultured at this temperature. Accordingly, the methanogenic microorganism in some embodiments is a thermophile or a hyperthermophile. In some aspects, the culture of the biological reactor comprises an autotrophic thermophilic methanogenic microorganism or an autotrophic hyperthermophilic methanogenic microorganism. In some aspects, the culture of the biological reactor comprises an autotrophic thermophilic methanogenic microorganism or an autotrophic hyperthermophilic methanogenic microorganism, either of which is tolerant to high conductivity culture medium (e.g., about 100 mS/cm to about 250 mS/cm), as described herein, e.g., a halophile.

[0180] Archaea may be capable of surviving extended periods at suboptimal temperatures. In some embodiments, a culture of archaea can naturally survive or are adapted to survive at room temperature (e.g. 22-28° C.) for a period of at least 3 weeks to 1, 2, 3, 4, 5 or 6 months.

[0181] In some embodiments, the organisms in the culture are not mesophilic. In some embodiments, the culture is not maintained at a temperature below or about 37° C. With respect to thermophilic or hyperthermophilic organisms (including, but not limited to, Methanothermobacter thermoautotrophicus, Methanothermobacter marburgensis, Methanocaldococcus jannaschii, Methanocaldococcus fervens, Methanocaldococcus indicus, Methanocaldococcus infernus, and Methanocaldococcus vulcanius), in some embodiments, the temperature of the culture is e.g. about 60° C. to about 150° C., about 60° C. to about 120° C., about 60° C. to about 100° C., or about 60° C. to about 80° C.

pH

[0182] Archaea can also survive under a wide range of pH conditions. In some embodiments, the pH of the culture comprising methanogenic microorganisms is between about 3.5 and about 10.0, although for growth conditions, the pH may be between about 6.5 and about 7.5. For example, the pH of the culture may be about 3.5, about 3.6., about 3.7, about 3.8, about 3.9, about 4.0, about 4.5, about 5.0, about 5.5, about 6.0, about 6.5, about 7.0, about 7.5, about 8.0, about 8.5, about 9.0, about 9.5, about 10.0. In some embodiments, the pH of the media is acidic, e.g. about 0.1 to about 5.5, about 0.1 to about 4, about 0.1 to about 3, about 1 to about 3, or about 2 to about 3. In some embodiments, the pH of the media is close to neutral, e.g. about 6 to about 8. In some embodiments, the pH of the media is alkaline, e.g. about 8.5 to about 11, or about 8 to about 10. The pH of the media can be altered by means known in the art. For example, the pH can be controlled by sparging CO_2 and/or by adding acid (e.g., HCL) or base (e.g., NaOH or NH_4OH) as needed.

Pressure and Other Conditions

[0183] In some embodiments, suitably pressures within the biological reactor range from about 0.5 atmospheres to about 500 atmospheres. The biological reactor can also contain a source of intermittent agitation of the culture. Also in one embodiment, the methane gas removed from the biological reactor suitably comprises less than about **450** ppm hydrogen sulfide, or alternatively less than about 400 ppm, 300 ppm, 200 ppm, 150 ppm, 100 ppm, 50 ppm or 20 ppm of hydrogen sulfide. Total gas delivery rates (CO_2) in the range of 0.2 to 4 volume of gas (STP) per volume of culture per minute are suitable, since they both maintain and exploit high volumetric concentrations of active methane generation capacity. Phrased in different terms, the carbon dioxide concentration of the electrolytic medium at the entrance to the passage is maintained at 0.1 mM or higher according to certain embodiments, and at 1.0 nM or higher according to other embodiments; in either case, according to certain embodiments, the carbon dioxide concentration of the electrolytic medium at the entrance to the passage is maintained at not more than 70 mM (although it will be understood that this limit is dependent upon temperature and pressure). In one embodiment, the redox potential is maintained below −100 mV or lower during methanogenesis. The method of the present invention encompasses conditions in which the redox potential is transiently increased to above −100 MV, as for example when air is added to the system.

Culture Containers

[0184] A biological reactor, also known as a fermentor vessel, bioreactor, or simply reactor, as set forth herein may be any suitable vessel in which methanogenesis can take place. Suitable biological reactors to be used in the present invention should be sized relative to the volume of the CO_2 source. Typical streams of 2,200,000 lb CO_2/day from a 100,000,000 gal/yr ethanol plant would require a CO_2 recovery/methane production fermentor of about 750,000 gal total capacity. Fermentor vessels similar to the 750,000 gal individual fermentor units installed in such an ethanol plant would be suitable.

Culture Volume and Density

[0185] The concentration of living cells in the culture medium (culture density) is in some embodiments maintained above 1 g dry weight/L. In certain embodiments, the density may be 30 g dry weight/L or higher. The volume of the culture is based upon the pore volume within the porous cathode structure within the reactor, plus any volume needed to fill any ancillary components of the reactor system, such as pumps and liquid/gas separators.

Culture Medium For Reducing Contamination By Non-Methanogens

[0186] The term "non-methanogen" as used herein refers to any microorganism that is not a methanogen or is not a host cell expressing genes that permit methanogenesis. For example, in some embodiments, the archaea are cultured under conditions wherein the temperature, pH, salinity, sulfide concentration, carbon source, hydrogen concentration or electric source is altered such that growth of non-methanogens is significantly retarded under such conditions. For example, in some embodiments, the methanogens are cultured at a temperature that is higher than 37° C. In some aspects, the methanogenic microorganisms are cultured at a temperature of at least 50° C. or higher, as discussed herein, e.g., 100° C. or more, to avoid contamination by mesophilic non-methanogens. In other embodiments, the methanogens are cultured under conditions of high salinity (e.g., >75%) to avoid contamination by non-methanogens that are not capable of growing under high salt conditions. In still other embodiments, the methanogens are cultured under conditions in which the pH of the culture media is altered to be more acidic or more basic in order to reduce or eliminate contamination by non-methanogens that are not capable of growing under such conditions.

[0187] Contamination by non-methanogens can also be accomplished by minimizing amounts of organic carbon nutrients (e.g., sugars, fatty acids, oils, etc.) in the media. For example, in some embodiments, organic nutrients are substantially absent from the medium.

[0188] In some embodiments, components required for the growth of non-methanogenic organisms are substantially absent from the media. Such components include, but are not limited to, one or more organic carbon sources, and/or one or more organic nitrogen sources, and/or one or more vitamins. In some embodiments, formate, acetate, ethanol, methanol, methylamine, and any other metabolically available organic materials are substantially absent from the media.

[0189] In some embodiments, high salt conditions that permit survival of methanogens can retard growth of contaminating organisms.

[0190] In some embodiments, high temperatures that permit survival of methanogens can retard growth of contaminating organisms.

[0191] The term "substantially lacks" or "substantially absent" or "substantially excludes" as used herein refers to the qualitative condition of lacking an amount of a particular component significant enough to contribute to the desired function (e.g. growth of microorganisms, production of methane). In some embodiments, the term "substantially lacks" when applied to a given component of the media means that the media contains less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, 0.1% or less of that component. In some embodiments, the media does not contain detectable amounts of a given component.

Exemplary Strain

[0192] The present disclosures provide microorganisms that produce methane from carbon dioxide via a process called methanogenesis. Accordingly, the microorganisms of the present disclosures are methanogenic microorganisms, also known as methanogens. As used herein, the term "methanogenic" refers to microorganisms that produce methane as a metabolic byproduct. In exemplary aspects, the microorganism produces methane from carbon dioxide, electricity, and water, via a process called electrobiological methanogenesis. In exemplary aspects, the microorganism utilizes hydrogen in the production of methane via a process called hydrogenotrophic methanogenesis. Accordingly, in exemplary aspects, the presently disclosed microorganism is a hydrogenotrophic methanogenic microorganism. In exemplary aspects, the microorganism of the present disclosures has the capacity to produce methane via electrobiological methanogenesis or via hydrogenotrophic methanogenesis. In exemplary aspects, the *Methanothermobacter* microorganism produces methane at a pH within a range of about 6.5 to about 7.5, at a temperature within a range of about 55° C. to about 69° C., and/or in a medium having a conductivity within a range of about 5 mS/cm to about 100 mS/cm.

[0193] In exemplary aspects, the presently disclosed microorganism belong to the genus *Methanothermobacter*. The characteristics of this genus are known in the art. See, e.g., Reeve et al., J Bacteriol 179: 5975-5986 (1997) and Wasserfallen et al., Internatl J Systematic Evol Biol 50: 43-53 (2000). Accordingly, in exemplary aspects, the microorganism expresses a 16S rRNA which has at least 90% (e.g., at least 95%, at least 98%, at least 99%) sequence identity to the full length of the sequence of 16S rRNA of *M. thermautotrophicum* Delta H, which is publicly available from the under European Molecular Biology Laboratory (EMBL) sequence database as Accession No. X68720, and which is set forth herein as SEQ ID NO: 1. In exemplary aspects, the *Methanothermobacter* microorganism is a microorganism of the species *thermautotrophicus* which is also known as *thermoautotrophicus*. In exemplary aspects, the *Methanothermobacter* microorganism is a microorganism of the species *marburgensis*.

[0194] In exemplary aspects, the *Methanothermobacter* microorganism of the present disclosures exhibits the phenotypic characteristics described herein. In exemplary aspects, the *Methanothermobacter* microorganism is (1) autotrophic and either thermophilic or hyperthermophilic; and (2) capable of returning to at least 80% (e.g., 90%, 95%, 98%) of the methane productivity level in the operating state within 20 minutes, after an exposure of at least 10 minutes to oxygen (e.g. oxygen in ambient air) or carbon monoxide; and any one or more of the following:

[0195] (3) capable of exhibiting a methane production efficiency per molecule of carbon dioxide (CO_2) that is at least or about 25 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material (e.g., at least or about 40, 50, 60, or 70 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material), optionally while exhibiting a doubling time of at least or about 72 hours;

[0196] (4) capable of surviving in a stationary phase or a nearly stationary phase having a doubling time of at least or about 72 hours (e.g., a doubling time of at least or about 80, 90, or 100 hours) for at least 30 days (e.g., for at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 months);

[0197] (5) capable of continuously maintaining a methane production efficiency of (3) for at least 30 days (e.g., for at least or about 6 months, at least or about 12 months), optionally while in a stationary phase or a nearly stationary phase having a doubling time of at least or about 72 hours (e.g., a doubling time of at least or about 80, 90, or 100 hours); and

[0198] (6) capable of returning to at least 80% (e.g., 90%, 95%, 98%) of the methane productivity in the operating state within 20 minutes of re-supplying hydrogen or electricity, after being in a dormant state for at least 2 hours as induced by interrupting or ceasing hydrogen supply or electricity.

[0199] In any of the exemplary embodiments described herein, the microorganism may be isolated. As used herein, the term "isolated" means having been removed from its natural environment, not naturally-occurring, and/or substantially purified from contaminants that are naturally associated with the microorganism.

Microorganisms: Strain UC120910

[0200] In exemplary embodiments, the *Methanothermobacter* microorganism of the present disclosures is a microorganism of strain UC120910, deposited on Dec. 22, 2010, with the American Type Culture Collection (ATCC) under Accession No. PTA-11561.

Microorganisms: Progeny

[0201] In alternative exemplary embodiments, the isolated *Methanothermobacter* microorganism of the present disclosures is a progeny of the microorganism of strain UC120910, which progeny retains the phenotypic characteristics of a microorganism of strain UC120910, as further described herein.

[0202] Accordingly, the present disclosures also provide an isolated progeny of a *Methanothermobacter* microorganism of strain UC120910, deposited on Dec. 22, 2010, with the American Type Culture Collection (ATCC) under Accession No. PTA-11561, that retains the phenotypic characteristics of said strain.

[0203] As used herein, the term "progeny" refers to any microorganism resulting from the reproduction or multiplication of a microorganism of strain UC120910. In this regard, "progeny" means any descendant of a microorganism of strain UC120910. In exemplary embodiments, the progeny are genetically identical to a microorganism of strain UC120910, and, as such, the progeny may be considered as a "clone" of the microorganism of strain UC120910. In alternative exemplary embodiments, the progeny are substantially genetically identical to a microorganism of strain UC120910, such that the sequences of the genome of the progeny are different from the genome of the microorganism of strain UC120910, but the phenotype of the progeny are substantially the same as the phenotype of a microorganism of strain UC120910. In exemplary embodiments, the progeny are progeny as a result of culturing the microorganisms of strain UC120910 under the conditions set forth herein, e.g., Example 1 or 2.

Microorganisms: Variants

[0204] In exemplary embodiments, the isolated *Methanothermobacter* microorganism of the present disclosures is a variant of a microorganism of strain UC120910, which variant retains the phenotypic characteristics of the microorganism of strain UC120910, as further described herein.

[0205] Accordingly, the present disclosures also provide an isolated variant of a *Methanothermobacter* microorganism of strain UC120910, deposited on Dec. 22, 2010, with the American Type Culture Collection (ATCC) under Accession No. PTA-11561, that retains the phenotypic characteristics of said strain.

[0206] As used herein, the term "variant" refers to any microorganism resulting from modification of a microorganism of strain UC120910. In exemplary aspects, the variant is a microorganism resulting from adapting in culture a microorganism of strain UC120910, as described herein. In alternative aspects, the variant is a microorganism resulting from genetically modifying a microorganism of strain UC120910, as described herein.

[0207] In exemplary embodiments, the variant is a microorganism of strain UC120910 modified to exhibit or comprise certain characteristics or features, which, optionally, may be specific to a given growth phase (active growth phase, stationary growth phase, nearly stationary growth phase) or state (e.g., dormant state, operating state). For example, in some embodiments, the microorganism of strain UC 120910 has been modified to survive and/or grow in a desired culture condition which is different from a prior culture condition in which the methanogenic microorganism of strain UC120910 survived and/or grew. The desired culture conditions may differ from the prior environment in temperature, pH, pressure, cell density, volume, humidity, salt content, conductivity, carbon content, nitrogen content, vitamin-content, amino acid content, mineral-content, or a combination thereof. In some embodiments, the methanogenic microorganism, before adaptation in culture or genetic modification, is one that is not a halophile but, through adaptation in culture or genetic modification, has become a halophile. As used herein, "halophile" or "halophilic" refers to a microorganism that survives and grows in a medium comprising a salt concentration higher than 100 g/L. Also, for example, in some embodiments, the methanogenic microorganism before genetic modification is one which does not express a protein, but through genetic modification has become a methanogenic microorganism which expresses the protein. Further, for example, in some embodiments, the methanogenic microorganism before adaptation in culture or genetic modification, is one which survives and/or grows in the presence of a particular carbon source, nitrogen source, amino acid, mineral, salt, vitamin, or combination thereof but through adaptation in culture or genetic modification, has become a methanogenic microorganism which survives and/or grows in the substantial absence thereof. Alternatively or additionally, in some embodiments, the methanogenic microorganism before adaptation in culture or genetic modification, is one which survives and/or grows in the presence of a particular amount or concentration of carbon source, nitrogen source, amino acid, mineral, salt, vitamin, but through adaptation in culture or genetic modification, has become a methanogenic microorganism which survives and/or grows in a different amount or concentration thereof.

[0208] In some embodiments, the methanogenic microorganisms are adapted to a particular growth phase or state. Furthermore, for example, the methanogenic microorganism in some embodiments is one which, before adaptation in culture or genetic modification, is one which survives and/or grows in a given pH range, but through adaptation in culture becomes a methanogenic microorganism that survives and/or grows in different pH range. In some embodiments, the methanogenic microorganisms are adapted in culture to a nearly stationary growth phase in a pH range of about 3.5 to about 10 (e.g., about 5.0 to about 8.0, about 6.0 to about 7.5). Accordingly, in some aspects, the methanogenic microorganisms are adapted in culture to a nearly stationary growth phase at a pH of about 3.5, 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8.0, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9.0, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, or 10.0. In some embodiments, the methanogenic microorganisms are adapted in culture to an active growth phase in a pH range of about 6.5 to about 7.5 (e.g., about 6.8 to about 7.3). Accordingly, in some aspects, the methanogenic microorganisms are adapted in culture to a nearly stationary growth phase at a pH of about 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, or 7.5.

[0209] As used herein, the term "adaptation in culture" refers to a process in which microorganisms are cultured under a set of desired culture conditions (e.g., high salinity, high temperature, substantial absence of any carbon source, low pH, etc.), which differs from prior culture conditions. The culturing under the desired conditions occurs for a period of time which is sufficient to yield modified microorganisms (progeny of the parental line (i.e. the unadapted microorganisms)) which survive and/or grow (and/or produce methane) under the desired condition(s). The period of time of adaptation in some aspects is 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 2 weeks, 3 weeks 4 weeks, 5 weeks, 6 weeks, 1 month, 2 months, 3 months, 4 months, 5 months 6 months, 7 months, 8 months, 9 months, 10 months, 12 months, 1 year, 2 years. The process of adapting in culture selects for microorganisms that can survive and/or grow and/or produce methane in the desired culture conditions; these selected microorganisms remain in the culture, whereas the other microorganisms that cannot survive and/or grow and/or produce methane in the desired culture conditions eventually die in the culture. In some embodiments, as a result of the adaptation in culture, the methanogenic microorganisms produce methane at a higher efficiency, e.g., at a ratio of the number of carbon dioxide molecules converted to methane to the number of carbon dioxide molecules converted to cellular materials which is higher than N:1, wherein N is a number greater than 20, as further described herein.

[0210] For purposes of the present invention, in some embodiments, the methanogenic microorganism (e.g., of strain UC120910) has been adapted in culture to survive and/or grow in a high salt and/or high conductivity culture medium. For example, the methanogenic microorganism which has been adapted in culture to survive and/or grow in a culture medium having a conductivity of about 5 mS/cm to about 100 mS/cm.

[0211] In alternative or additional embodiments, the methanogenic microorganism (e.g., of strain UC 120910) has been adapted in culture to survive and/or grow at higher temperature (e.g., a temperature which is between about 1 and about 15 degrees C. greater than the temperature that the microorganisms survives and/or grows before adaptation). In exemplary embodiments, the methanogenic microorganisms are adapted to survive and/or grow in a temperature which is greater than 50° C., e.g., greater than 55° C., greater than 60° C., greater than 65° C., greater than 70° C., greater than 75° C., greater than 80° C., greater than 85° C., greater than 90° C., greater than 95° C., greater than 100° C., greater than 105° C., greater than 110° C., greater than 115° C., greater than 120° C.

[0212] In some embodiments, the presently disclosed methanogenic microorganism (e.g., of strain UC120910) has been adapted in culture to grow and/or survive in conditions which are low in or substantially absent of any vitamins. In some aspects, the methanogenic microorganism (e.g., of strain UC120910) has been adapted in culture to grow and/or survive in conditions which are low in or substantially absent of any organic carbon source. In some embodiments, the methanogenic microorganism has been adapted in culture to grow and/or survive in conditions with substantially reduced amounts of carbon dioxide. In these embodiments, the methanogenic microorganisms may be adapted to exhibit an increased methanogenesis efficiency, producing the same amount of methane (as compared to the unadapted microorganism) with a reduced amount of carbon dioxide. In some embodiments, the methanogenic microorganism has been adapted in culture to survive in conditions which substantially lacks carbon dioxide. In these embodiments, the methanogenic microorganisms may be in a dormant phase in which the microorganisms survive but do not produce detectable levels of methane. In some embodiments, the methanogenic microorganisms have been adapted to grow and/or survive in conditions which are low in or substantially absent of any hydrogen. In some embodiments, the methanogenic microorganisms have been adapted to grow and/or survive in conditions which are low in or substantially absent of any external source of water, e.g., the conditions depend only upon water produced by the metabolism of the organisms and do not comprise a step involving dilution with externally added water.

[0213] In exemplary embodiments, the methanogens are adapted in culture to a nearly stationary growth phase. Such methanogens favor methane production over cell growth as measured, e.g., by the ratio of the number of CO_2 molecules converted to methane to the number of CO_2 molecules converted to cellular materials. This ratio is increased as compared to unadapted methanogens (which may exhibit, e.g., a ratio ranging from about 8:1 to about 20:1). In exemplary embodiments, the methanogens are adapted in culture to a nearly stationary growth phase by being deprived of one or more nutrients otherwise required for optimal growth for a prolonged period of time (e.g., 1 week, 2 week, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 2 years, 3 years, 4 years, 5 years or more). In exemplary embodiments, the methanogens are deprived of inorganic nutrients (e.g., hydrogen or electrons) necessary for optimum growth. In exemplary embodiments, depriving the methanogens of hydrogen or electrons is achieved by sparging the media with an insert gas mixture such as $Ar:CO_2$ at a flow rate of 250 mL/min for several hours until neither hydrogen nor methane appear in the effluent gas stream. In exemplary embodiments, the methanogenic microorganisms have been adapted to a nearly stationary growth phase in conditions which are low in or substantially absent of any external source of water, e.g., the adaptation conditions do not comprise a dilution step.

[0214] In exemplary aspects, the methanogenic microorganism has been adapted in culture to grow and/or survive in the culture medium set forth herein as Medium 1 and/or Medium 2 or a medium which is substantially similar to Medium 1 or Medium 2.

[0215] In exemplary embodiments, the variant expresses an 16S rRNA which has at least or about 90% (e.g., at least or about 95%, at least or about 98%, at least or about 99%) sequence identity to the 16S rRNA of the parent microorganism (e.g., a microorganism of strain UC120910). In exemplary embodiments, the variant expresses an 16S rRNA which has at least or about 90% (e.g., at least or about 95%, at least or about 98%, at least or about 99%) sequence identity to the 16S rRNA of a Delta H *M. thermautotrophicus*, which sequence is set forth herein as SEQ ID NO: 1. In exemplary embodiments, the variant expresses an 16S rRNA which has at least or about 90% (e.g., at least or about 95%, at least or about 98%, at least or about 99%) sequence identity to the 16S rRNA of the microorganism of strain UC120910 and which has at least or about 90% (e.g., at least or about 95%, at least or about 98%, at least or about 99%) sequence identity to SEQ ID NO: 1.

Genetically Modified Archaea

[0216] In exemplary embodiments, the methanogenic microorganisms have been purposefully or intentionally genetically modified to become suitable, e.g., more suitable, for the purposes of the present disclosures. Suitable microorganisms may also be obtained by genetic modification of non-methanogenic organisms in which genes essential for supporting autotrophic methanogenesis are transferred from a methanogenic microbe or from a combination of microbes that may or may not be methanogenic on their own. Suitable genetic modification may also be obtained by enzymatic or chemical synthesis of the necessary genes.

[0217] In exemplary embodiments, a host cell that is not naturally methanogenic is intentionally genetically modified to express one or more genes that are known to be important for methanogenesis. For example, the host cell in some aspects is intentionally genetically modified to express one or more coenzymes or cofactors involved in methanogenesis. In some specific aspects, the coenzymes or cofactors are selected from the group consisting of F420, coenzyme B, coenzyme M, methanofuran, and methanopterin, the structures of which are known in the art. In exemplary aspects, the organisms are modified to express the enzymes, well known in the art, that employ these cofactors in methanogenesis.

[0218] In exemplary embodiments, the host cells that are intentionally modified are extreme halophiles. In exemplary embodiments, the host cells that are intentionally modified are thermophiles or hyperthermophiles. In exemplary embodiments, the host cells that are intentionally modified are non-autotrophic methanogens. In some aspects, the host cells that are intentionally modified are methanogens that are not autotrophic. In some aspects, the host cells that are intentionally modified are cells which are neither methanogenic nor autotrophic. In other embodiments, the host cells that are intentionally modified are host cells comprising synthetic genomes. In some aspects, the host cells that are intentionally modified are host cells which comprise a genome which is not native to the host cell.

[0219] In some embodiments, the methanogenic microorganisms have been purposefully or intentionally genetically modified to express pili or altered pili, e.g., altered pili that promote cell adhesion to the cathode or other components of the electrobiological methanogenesis reactor or pili altered to become electrically conductive. Pili are thin filamentous protein complexes that form flexible filaments that are made of proteins called pilins. Pili traverse the outer membrane of microbial cells and can extend from the cell surface to attach to a variety of other surfaces. Pili formation facilitates such disparate and important functions as surface adhesion, cell-cell interactions that mediate processes such as aggregation, conjugation, and twitching motility. Recent in silico analyses of more than twenty archaeal genomes have identified a large number of archaeal genes that encode putative proteins resembling type IV pilins (Szabó et al. 2007, which is incorporated by reference herein in its entirety). The expression of several archaeal pilin-like proteins has since been confirmed in vivo (Wang et al. 2008; Zolghadr et al. 2007; Fröls et al. 2007, 2008, which are incorporated by reference herein in their entirety). The sequence divergence of these proteins as well as the differential expression of the operons encoding these proteins suggests they play a variety of roles in distinct biological processes.

[0220] Certain microorganisms such as *Geobacter* and *Rhodoferax* species, have highly conductive pili that can function as biologically produced nanowires as described in U.S. Publication No. 2006/0257985, which is incorporated by reference herein in its entirety. Many methanogenic organisms, including most of the *Methanocaldococcus* species and the *Methanotorris* species, have native pili and in some cases these pili are used for attachment. None of these organisms are known to have natively electrically conductive pili.

[0221] In exemplary embodiments of the present disclosures, the pili of a methanogenic organism and/or surfaces in contact with pili of a methanogenic organism or other biological components are altered in order to promote cell adhesion to the cathode or other components of the electrobiological methanogenesis reactor. Pili of a methanogenic organism can be further engineered to optimize their electrical conductivity. Pilin proteins can be engineered to bind to various complexes. For example, pilin proteins can be engineered to bind iron, mimicking the pili of *Geobacter* species or alternatively, they can be engineered to bind a low potential ferredoxin-like iron-sulfur cluster that occurs naturally in many hyperthermophilic methanogens. The desired complex for a particular application will be governed by the midpoint potential of the redox reaction.

[0222] The microorganisms may be genetically modified, e.g., using recombinant DNA technology. For example, cell or strain variants or mutants may be prepared by introducing appropriate nucleotide changes into the organism's DNA. The changes may include, for example, deletions, insertions, or substitutions of, nucleotides within a nucleic acid sequence of interest. The changes may also include introduction of a DNA sequence that is not naturally found in the strain or cell type. One of ordinary skill in the art will readily be able to select an appropriate method depending upon the particular cell type being modified. Methods for introducing such changes are well known in the art and include, for example, oligonucleotide-mediated mutagenesis, transposon mutagenesis, phage transduction, transformation, random mutagenesis (which may be induced by exposure to mutagenic compounds, radiation such as X-rays, UV light, etc.), PCR-mediated mutagenesis, DNA transfection, electroporation, etc.

[0223] The ability of the pili of the methanogenic organisms to adhere to the cathode coupled with an increased ability to conduct electrons, enable the organisms to receive directly electrons passing through the cathode from the negative electrode of the power source. The use of methanogenic organisms with genetically engineered pili attached to the cathode will greatly increase the efficiency of conversion of electric power to methane.

Phenotypic Characteristics

[0224] As used herein, "phenotypic characteristics" of a methanogen or *Methanobacter* microorganism refers to:

[0225] (1) autotrophic and either thermophilic or hyperthermophilic; and

[0226] (2) capable of returning to at least 80% (e.g., 90%, 95%, 98%) of the methane productivity level in the operating state within 20 minutes, after an exposure of at least 10 minutes to oxygen (e.g. oxygen in ambient air) or carbon monoxide;

[0227] and any one or more of the following:

[0228] (3) capable of exhibiting a methane production efficiency per molecule of carbon dioxide (CO_2) that is at least or about 25 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material (e.g., at least or about 40, 50, 60, or 70 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material), optionally while exhibiting a doubling time of at least or about 72 hours;

[0229] (4) capable of surviving in a stationary phase or a nearly stationary phase having a doubling time of at least or about 72 hours (e.g., a doubling time of at least or about 80, 90, or 100 hours) for at least 30 days (e.g., for at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 months);

[0230] (5) capable of continuously maintaining a methane production efficiency of (3) for at least 30 days (e.g., for at least or about 6 months, at least or about 12 months), optionally while in a stationary phase or a nearly stationary phase having a doubling time of at least or about 72 hours (e.g., a doubling time of at least or about 80, 90, or 100 hours); and

[0231] (6) capable of returning to at least 80% (e.g., 90%, 95%, 98%) of the methane productivity in the operating state within 20 minutes of re-supplying hydrogen or electricity, after being in a dormant state for at least 2 hours as induced by interrupting or ceasing hydrogen supply or electricity.

[0232] In exemplary aspects, the *Methanothermobacter* microorganism is (1) autotrophic and either thermophilic or hyperthermophilic; and (2) capable of returning to at least 80% (e.g., 90%, 95%, 98%) of the methane productivity level in the operating state within 20 minutes, after an exposure of at least 10 minutes to oxygen (e.g. oxygen in ambient air) or carbon monoxide; and any one or more of the following:

[0233] (3) capable of exhibiting a methane production efficiency per molecule of carbon dioxide (CO_2) that is at least or about 40 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material (e.g., at least or about 70 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material), optionally while exhibiting a doubling time of at least or about 100 hours;

[0234] (4) capable of surviving in a stationary phase or a nearly stationary phase having a doubling time of at least or about 100 hours for at least 6 months (e.g., for at least about 7, 8, 9, 10, 11 or 12 months);

[0235] (5) capable of continuously maintaining a methane production efficiency of (3) for at least 30 days (e.g., for at least or about 6 months, at least or about 12 months), optionally while in a stationary phase or a nearly stationary phase having a doubling time of at least or about 100 hours; and

[0236] (6) capable of returning to at least 80% (e.g., 90%, 95%, 98%) of the methane productivity in the operating state within 10 minutes of re-supplying hydrogen or electricity, after being in a dormant state for at least 2 hours as induced by interrupting or ceasing hydrogen supply or electricity.

[0237] Autotrophic. In exemplary aspects, the microorganisms of the present disclosures are autotrophic. As used herein, the term "autotrophic" refers to a microorganism capable of using carbon dioxide, formic acid, and/or carbon monoxide, and a source of reducing power to provide all carbon and energy necessary for growth and maintenance of the cell (e.g., microorganism). Suitable sources of reducing power may include but are not limited to hydrogen, hydrogen sulfide, sulfur, formic acid, carbon monoxide, reduced metals, sugars (e.g., glucose, fructose), acetate, photons, or cathodic electrodes or a combination thereof. In exemplary aspects, the autotrophic microorganisms of the present disclosures obtain reducing power from a cathode or hydrogen.

[0238] Thermophilic or Hyperthermophilic. In exemplary aspects, the microorganisms of the present disclosures are thermophilic or hyperthermophilic. As used herein, the term "thermophilic" refers to an organism which has an optimum growth temperature of about 50° C. or more, e.g., within a range of about 50° C. to about 80° C., about 55° C. to about 75° C., or about 60° C. to about 70° C. (e.g., about 60° C. to about 65° C., about 65° C. to about 70° C.). As used herein, the term "hyperthermophilic" refers to organism which has an optimum growth temperature of about 80° C. or more, e.g., within a range of about 80° C. to about 105° C.

[0239] Resilience to Oxygen or Carbon Monoxide. Methanogenic organisms are regarded as extremely strict anaerobes. Oxygen is known as an inhibitor of the enzyme catalysts of both hydrogen uptake and methanogenesis. A low oxidation-reduction potential (ORP) in the growth medium is regarded as important to methanogenesis. In exemplary embodiments, the *Methanothermobacter* microorganism of the present disclosures is substantially resilient to oxygen exposure, inasmuch as the microorganism returns to a methane productivity level which is substantially the same as the methane productivity level exhibited before oxygen exposure within a relatively short period of time. In exemplary embodiments, the microorganism of the present disclosures is capable of returning to a level of methane productivity level which is at least 80% (e.g., at least 85%, at least 90%, at least 95%, at least 98%, 100%) of the methane productivity level in the operating state (e.g., before oxygen exposure) within 20 minutes after an exposure of at least 10 minutes to oxygen (e.g. oxygen in ambient air). In exemplary embodiments, the microorganism of the present disclosures is capable of returning to a level of methane productivity level which is at least 80% (e.g., at least 85%, at least 90%, at least 95%, at least 98%, 100%) of the methane productivity level in the operating state (e.g., before oxygen exposure) within 10 minutes after an exposure of at least 10 minutes to oxygen (e.g. oxygen in ambient air). In exemplary embodiments, the microorganism of the present disclosures capable of returning to a level of methane productivity level which is at least 80% (e.g., at least 85%, at least 90%, at least 95%, at least 98%, 100%) of the methane productivity level in the operating state (e.g., before oxygen exposure) within 5 minutes or within 2 minutes after an exposure of at least 10 minutes to oxygen (e.g. oxygen in ambient air). In exemplary aspects, the exposure to oxygen is at least 30 minutes, at least 60 minutes, at least 90 minutes, 2 hours, 4 hours, 6 hours, 8 hours, 10 hours, 15 hours, 24 hours, 48 hours, 72 hours, or more. In exemplary embodiments, the methane productivity level in the operating state is within a range of about 300 VVD to about 500 VVD. Resilience to oxygen exposure may be tested in accordance with methods known in the art or as described in Example 4.

[0240] Carbon monoxide (CO) is another known inhibitor of enzymes involved in both hydrogen uptake and methanogenesis. In exemplary embodiments, the *Methanothermobacter* microorganism of the present disclosures is substantially resilient to CO exposure, inasmuch as the microorganism returns to a methane productivity level which is substantially the same as the methane productivity level exhibited before CO exposure within a relatively short period of time. In exemplary embodiments, the microorganism of the present disclosures is capable of returning to a level of methane productivity level which is at least 80% (e.g., at least 85%, at least 90%, at least 95%, at least 98%, 100%) of the methane productivity level in the operating state (e.g., before CO exposure) within 20 minutes after an exposure of at least 10 minutes to CO. In exemplary embodiments, the microorganism of the present disclosures is capable of returning to a level of methane productivity level which is at least 80% (e.g., at least 85%, at least 90%, at least 95%, at least 98%, 100%) of the methane productivity level in the operating state (e.g., before CO exposure) within 10 minutes after an exposure of at least 10 minutes to CO. In exemplary embodiments, the microorganism of the present disclosures is capable of returning to a level of methane productivity level which is at least 80% (e.g., at least 85%, at least 90%, at least 95%, at least 98%, 100%) of the methane productivity level in the operating state (e.g., before CO exposure) in within 5 minutes or within 2 minutes after an exposure of at least 10 minutes to CO. In exemplary aspects, the exposure to CO is at least 30 minutes, at least 60 minutes, at least 90 minutes, 2 hours, 4 hours, 6 hours, 8 hours, 10 hours, 15 hours, 24 hours, 48 hours, 72 hours, or more. In exemplary embodiments, the methane productivity level in the operating state is within a range of about 300 VVD to about 500 VVD. Resilience to CO exposure may be tested in accordance with methods known in the art or as described in Example 4.

[0241] Methane Production Efficiency. It has been reported that naturally-occurring methanogenic microorganisms in the active growth phase produce methane at a ratio of about 8 CO_2 molecules converted to methane per molecule of CO_2 converted to cellular material, ranging up to a ratio of about 20

CO_2 molecules converted to methane per molecule of CO_2 converted to cellular material. In exemplary embodiments, the presently disclosed microorganisms demonstrate an increased efficiency, particularly when adapted in culture to stationary phase growth conditions. Accordingly, in exemplary aspects, the ratio of the number of CO_2 molecules converted to methane to the number of CO_2 molecules converted to cellular material of the presently disclosed microorganisms is higher than the ratio of naturally-occurring methanogenic microorganisms in the active growth phase. In exemplary embodiments, the ratio of the number of CO_2 molecules converted to methane to the number of CO_2 molecules converted to cellular material of the microorganisms of the present disclosures is N:1, wherein N is a number greater than 20, e.g. about 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, or higher. In some aspects, N is less than 500, less than 400, less than 300, or less than 200. In some aspects, N ranges from about 40 to about 150. In exemplary embodiments, the microorganism exhibits a methane production efficiency per molecule of carbon dioxide (CO_2) that is at least or about 25 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material (e.g., at least or about 40, 50, 60, or 70 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material). In exemplary embodiments, the microorganism exhibits a methane production efficiency per molecule of carbon dioxide (CO_2) that is at least or about 25 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material (e.g., at least or about 40, 50, 60, or 70 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material) while exhibiting a doubling time of at least or about 72 hours (e.g., a doubling time of at least or about 80, 90, or 100 hours). Methods of determining the number of carbon dioxide molecules converted to methane per carbon dioxide molecule converted to cellular material are known in the art and include the method described in Example 3.

[0242] In exemplary embodiments, the microorganism of the present disclosures is capable of continuously maintaining for at least 30 days (e.g., for at least or about 6 months, at least or about 12 months) a methane production efficiency per molecule of carbon dioxide (CO_2) that is at least or about 25 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material (e.g., at least or about 40 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material, at least or about 70 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material). In exemplary embodiments, the microorganism of the present disclosures is capable of continuously maintaining for at least or about 12 months a methane production efficiency per molecule of carbon dioxide (CO_2) that is at least or about 70 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material. In exemplary embodiments, the microorganisms of the present disclosures are capable of continuously maintaining such a methane production efficiency, while in a stationary phase or a nearly stationary phase having a doubling time of at least or about 36, 72 hours (e.g., a doubling time of at least or about 80, 90, 100, 240 hours).

[0243] Operating States. The microorganisms of the present disclosures may exist at any point in time in a dormant state or an operating state. As used herein, the term "dormant state" refers to a state in which the presently disclosed microorganisms are not producing methane (e.g., not producing methane at a detectable level). In exemplary aspects, the dormant state is induced by interrupting or ceasing hydrogen supply or electricity to the microorganism. As used herein, the term "operating state" refers to a state in which the presently disclosed microorganisms are producing methane (e.g., producing methane at a detectable level). In exemplary aspects, the operating state is induced by supplying (e.g., re-supplying) a hydrogen supply or electricity to the microorganism.

[0244] In exemplary aspects, the microorganisms of the present disclosures transition or cycle between an operating state and a dormant state. In exemplary aspects, the microorganisms of the present disclosures transition or cycle between an operating state and a dormant state without decreasing its methane productivity level. In exemplary aspects, the microorganisms of the present disclosures substantially maintain the methane productivity level of the operating state after transitioning out of a dormant state. As used herein, the term "substantially maintains the methane productivity level" refers to a methane productivity level which does not differ by more than 20% (e.g., within about 10% higher or lower) than a first methane productivity level. Accordingly, in exemplary aspects, the microorganisms of the present disclosures are substantially resilient to being placed in a dormant state for a relatively long period of time, inasmuch as the microorganisms return to the methane productivity level exhibited before being placed in the dormant state within a relatively short period of time.

[0245] In exemplary aspects, after being in a dormant state for at least 2 hours as induced by interrupting or ceasing hydrogen supply or electricity, the microorganism of the present disclosures is capable of returning to at least 80% (e.g., at least 85%, at least 90%, at least 95%, at least 98%, 100%) of the methane productivity in the operating state within 20 minutes of re-supplying hydrogen or electricity. In exemplary aspects, after being in a dormant state for at least 2 hours as induced by interrupting or ceasing hydrogen supply or electricity, the microorganism of the present disclosures is capable of returning to at least 80% (e.g., at least 85%, at least 90%, at least 95%, at least 98%, 100%) of the methane productivity in the operating state within 10 minutes of re-supplying hydrogen or electricity. In exemplary aspects, after being in a dormant state for at least 2 hours as induced by interrupting or ceasing hydrogen supply or electricity, the microorganism of the present disclosures is capable of returning to at least 80% (e.g., at least 85%, at least 90%, at least 95%, at least 98%, 100%) of the methane productivity in the operating state within 5 minutes or within 2 minutes of re-supplying hydrogen or electricity. In exemplary aspects, the microorganism is in a dormant state for at least 2 hours (e.g., at least 4 hours, 6 hours, 8 hours, 10 hours, 15 hours, 24 hours, 48 hours, 72 hours, or more) as induced by interrupting or ceasing hydrogen supply or electricity. In exemplary aspects, the microorganism is exposed to a condition in which the hydrogen supply or electricity is interrupted or ceased for a period of at least 2 hours (e.g., at least 4 hours, 6 hours, 8 hours, 10 hours, 15 hours, 24 hours, 48 hours, 72 hours, or more). In exemplary embodiments, the methane productivity level in the operating state is within a range of about 300 VVD to about 500 VVD.

[0246] Growth phases. When the microorganisms are in an operating state, the methanogenic microorganisms may be in one of a variety of growth phases, which differ with regard to the growth rate of the microorganisms (which can be expressed, e.g., as doubling time of microorganism number or cell mass). The phases of growth typically observed include a lag phase, an active growth phase (also known as exponential or logarithmic phase when microorganisms multiply rapidly), a stationary phase, and a death phase (exponential or logarithmic decline in cell numbers). In some aspects, the microorganisms of the present disclosures are in a lag phase, an active growth phase, a stationary phase, or a nearly stationary phase.

[0247] In some embodiments, the methanogenic microorganisms are in an active growth phase in which the methanogenic microorganisms are actively multiplying at a rapid rate. In some aspects, the doubling time of the microorganisms may be rapid or similar to that observed during the growth phase in its natural environment or in a nutrient-rich environment. For example, the doubling time of the methanogenic microorganisms in the active growth phase is about 15 minutes, about 20 minutes, about 30 minutes, about 45 minutes, about 60 minutes, about 75 minutes, about 80 minutes, about 90 minutes, or about 2 hours.

[0248] Stationary phase represents a growth phase in which, after the logarithmic or active growth phase, the rate of cell division and the rate of cell death are in equilibrium or near equilibrium, and thus a relatively constant concentration of microorganisms is maintained in the reactor. (See, Eugene W. Nester, Denise G. Anderson, C. Evans Roberts Jr., Nancy N. Pearsall, Martha T. Nester; Microbiology: A Human Perspective, 2004, Fourth Edition, Chapter 4, which is incorporated by reference herein in its entirety).

[0249] In exemplary embodiments, the methanogenic microorganisms are in an stationary growth phase or nearly stationary growth phase in which the methanogenic microorganisms are not rapidly growing or have a substantially reduced growth rate. In some aspects, the doubling time of the methanogenic microorganisms is about 1 day or greater, including about 30 hours, 36 hours, 48 hours, 72 hours, 80 hours, 90 hours, 100 hours, 110 hours, 120 hours, 200 hours, 240 hours, 2, 3, 4, 5, 6, days or greater or about 1, 2, 3, 4 weeks or greater, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 months or greater.

[0250] In exemplary embodiments, the methanogenic microorganisms are capable of surviving in a stationary phase or a nearly stationary phase having a doubling time of at least or about 72 hours (e.g., a doubling time of at least or about 80, 90, or 100 hours) for a period of time which is at least 30 days (e.g., for at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 months).

[0251] In exemplary embodiments, the microorganism of the present disclosures, while in a stationary phase or a nearly stationary phase having a doubling time of at least or about 36, 72 hours (e.g., a doubling time of at least or about 80, 90, 100, 240 hours), is capable of continuously maintaining for at least 30 days (e.g., for at least or about 6 months, at least or about 12 months) a methane production efficiency per molecule of carbon dioxide (CO_2) that is at least or about 25 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material (e.g., at least or about 40 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material, at least or about 70 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material). In exemplary embodiments, the microorganism of the present disclosures, while in a stationary phase or a nearly stationary phase having a doubling time of at least or about 100 hours, is capable of continuously maintaining for at least 12 months a methane production efficiency per molecule of carbon dioxide (CO_2) that is at least or about 70 CO_2 molecules converted to methane per CO_2 molecule converted to cellular material.

[0252] In exemplary embodiments, the methanogenic microorganisms are initially in an active growth phase and subsequently in a stationary or nearly stationary phase. In exemplary embodiments, when in an operating state, the methanogenic microorganisms cycle between an active growth phase and a stationary or nearly stationary phase. In exemplary aspects, the microorganisms of the present disclosures transition or cycle between an active growth phase and a stationary or nearly stationary phase without decreasing its methane production efficiency, as described above.

[0253] Combinations of Phenotypic Characteristic. With regard to the above listing of phenotypic characteristics, (1) and (2) may be considered as required features of the microorganisms of the present disclosures, while (3), (4), (5), and (6) may be considered as optional features of the microorganisms of the present disclosures. In exemplary embodiments, the microorganisms of the present disclosures exhibit (1), (2), (3), (4), (5), and (6). In exemplary aspects, the microorganism of the present disclosures exhibits, in addition to (1) and (2), a combination of phenotypic characteristics selected from the group consisting of: [(3), (4), and (5)], [(3) and (4)], [(3)], [(3) and (5)], [(3) and (6)], [(4) and (5)], [(4)], [(4) and (6)], [(5) and (6)], [(5)], and [(6)]. All combinations and sub-combinations thereof are contemplated herein.

[0254] Additional phenotypic characteristics. In exemplary embodiments, the microorganisms of the present disclosures exhibit additional phenotypic characteristics (in addition to the phenotypic characteristics set forth above as (1) to (6)).

[0255] In exemplary aspects, the microorganism is (i) capable of producing methane via hydrogenotrophic methanogenesis under the maximal hydrogen supply conditions and in a fermenter as described in Example 2 at (a volume of methane at standard temperature and pressure produced per day) divided by the liquid volume of the culture (VVD) of at least about 300 VVD; (ii) capable of producing methane via electrobiological methanogenesis under the conditions and in a cell as described in Example 2 at a VVD of at least about 300 VVD; or a both of (i) and (ii). In exemplary embodiments, the microorganisms of the present disclosures are capable of producing methane from carbon dioxide and hydrogen via hydrogenotrophic methanogenesis. In exemplary embodiments, the microorganism is capable of producing methane via hydrogenotrophic methanogenesis under the maximal hydrogen supply conditions and in a fermenter as described in Example 2 at a VVD of at least about 300 VVD (e.g., at least or about 500 VVD, at least or about 1000 VVD, at least or about 2000 VVD, at least or about 3000 VVD, at least or about 5000 VVD, at least or about 10,000 VVD. In exemplary aspects, the microorganism is capable of producing no more than 100,000 VVD under such conditions. In exemplary embodiments, the microorganisms of the present disclosures are capable of producing methane from carbon dioxide, electricity, and water, via a process known as electrobiological methanogenesis. In exemplary embodiments, the microorganism is capable of producing methane via electrobiological methanogenesis under the conditions and in a cell as described in Example 2 at a VVD of at least about 300 VVD (e.g., at least or about 500 VVD, at least or about 1000 VVD, at least or about 2000 VVD, at least or about 3000 VVD, at least or about 5000 VVD, at least or about 10,000 VVD. In exemplary aspects, the microorganism is capable of producing no more than 100,000 VVD under such conditions. Methods of determining methane productivity in units of VVD are set forth herein. See Example 2.

[0256] The specific catalytic activity of methanogenic microorganisms can be expressed as the ratio of moles of methane formed per hour to moles of carbon in the microbial biomass. Under some conditions, one of the necessary substrates may be limiting the reaction, in which case the specific catalytic capacity may exceed the measured specific catalytic activity. Thus, an increase in the limiting substrate would lead to an increase in the observed specific catalytic activity. Under other conditions, the observed specific catalytic activity may be saturated with substrate, in which case an increase in substrate concentration would not yield an increase in specific catalytic activity. Under substrate saturating conditions, the observed specific catalytic activity would equal the specific catalytic capacity. Methods of determining specific catalytic activity for methane production are described herein. See Example 5.

[0257] In exemplary embodiments, the microorganisms of the present disclosures growing under steady state conditions (e.g., conditions as described in Example 1) are capable of exhibiting a specific catalytic capacity that is in excess of the specific catalytic activity that supports its growth. In exemplary embodiments, the specific catalytic activity of the microorganisms of the present disclosures is at least 10 fold greater than observed during steady-state growth with doubling times in the range of 100 hours. In exemplary embodiments, the microorganism of the present disclosures is capable of producing methane at a rate or an amount which is consistent with the increase in hydrogen or electricity supplied to the microorganisms. For example, in exemplary aspects, the microorganisms are capable of producing an X-fold increase in methane production in response to an X-fold increase in the supply of hydrogen or electricity, wherein X is any number greater than 1, e.g., 2, 5, 10. In exemplary embodiments, when supplied with a 2-fold increase in hydrogen supply (e.g., from 0.2 L/min to 0.4 L/min), the microorganisms of the present disclosures are capable of exhibiting a 2-fold increase in methane productivity.

[0258] In exemplary aspects, the microorganism of the present disclosures exhibits additional resilience or resistance to exposure to contaminants other than oxygen or carbon monoxide, such as, for example, ethanol, sulfur oxides, and nitrogen oxides. In exemplary aspects, the microorganisms of the present disclosures are capable of substantially returning to the methane productivity level after exposure to a contaminant selected from the group consisting of: ethanol, sulfur oxides, and nitrogen oxides. In exemplary aspects, the microorganisms of the present disclosures are capable of returning to a methane productivity level which is at least 80% of the methane productivity level observed in the operating state within 20 minutes (e.g., within 10 minutes, within 5 minutes, within 2 minutes) after an exposure of at least 10 minutes to the contaminant.

[0259] Additionally, the microorganisms in exemplary embodiments exhibit phenotypic characteristics other than those described herein as (1) to (6) and (i) and (ii).

Kits

[0260] The present invention further provides kits comprising any one or a combination of: a culture comprising methanogenic microorganisms, a reactor, and a culture medium. The culture of the kit may be in accordance with any of the teachings on cultures described herein. In exemplary embodiments, the kit comprises a culture comprising an adapted strain of methanogenic microorganisms that are capable of growth and/or survival under high temperature conditions (e.g., above about 50° C., as further described herein), high salt or high conductivity conditions (as further described herein). In some embodiments, the kit comprises only the methanogenic microorganisms. The culture medium of the kits may be in accordance with any of the teachings on culture medium described herein. In some embodiments, the kit comprises a culture medium comprising the components of Medium 1 or comprising the components of Medium 2, as described herein. In some embodiments, the kit comprises only the culture medium. In certain of these aspects, the kit may comprise the reactor comprising an anode and cathode. The reactor may be in accordance with any of the teachings of reactors described herein.

III. Implementations and Applications of the System

[0261] The biological reactor according to any of the embodiments discussed above may be used in a variety of implementations or applications, such as are illustrated in FIGS. **13** and **14**.

[0262] For example, a biological reactor may be used as part of a stand-alone system **500**, as illustrated in FIG. **13**. The system **500** may be used to provide multiple energy sources (e.g., electricity and methane), or to store electrical energy produced during favorable conditions as other energy resources (e.g., methane) for use when electrical energy cannot be generated at required levels. Such a stand-alone system **500** may be particularly useful in processing spatially or temporally stranded electricity where or when this electricity does not have preferable markets.

[0263] The system **500** may include a biological reactor **502** coupled to one or more electricity sources, for example a carbon-based power plant (e.g., coal-fired power plant, natural gas-fired power plant, or biomass-fired power plant) **504**, a wind-powered turbine **506**, water-powered turbine **508**, a fuel cell **510**, solar thermal system **512** or photovoltaic system **514**, or a nuclear power plant **516**. It will be recognized that other sources of electricity (e.g., a geothermal power source, or a capacitor or super capacitor used for energy storage) may be used in addition to or in substitution for those illustrated. According to one embodiment, the biological reactor **502** may be coupled directly to carbon-based power plant **504**, nuclear power plant **516**, or other power plant that may not be able to ramp power production up or down without significant costs and/or delays, and in such a system the biological reactor **502** uses surplus electricity to convert carbon dioxide into methane that can be used in a generator to produce sufficient electricity to meet additional demands. According to another embodiment, the biological reactor **502** may use surplus electricity (electricity that is not needed for other purposes) generated by one or more of the sources **506**, **508**, **510**, **512**, **514** to convert carbon dioxide into methane to be used in a generator to produce electricity when wind, water, solar or other conditions are unfavorable to produce electricity or to produce sufficient electricity to meet demands.

[0264] As is also illustrated in FIG. **13**, the biological reactor **502** may be coupled to one or more carbon dioxide sources, for example one or more carbon-based power plants (e.g., coal-fired power plant, natural gas-fired power plant, biomass-fired power plant, or carbon-based fuel cells, which may be used as heating and power co-generation facilities or as dedicated factory power facilities) **520**, which plants may be the same as or different from the plant **504**. Alternatively, the stand-alone system **500** may be disposed in the vicinity of an industrial plant that provides carbon dioxide as an byproduct or a waste product, including ethanol manufacturing plants (e.g., fuel ethanol fermentation facilities) **522**, industrial manufacturing plants (e.g., cement manufacturing plants or chemical manufacturing facilities) **524**, commercial manufacturing plants (e.g., breweries) **526**, and petrochemical refineries **528**. While such significant point source emissions may serve well as a source of carbon dioxide for the biological reactor **502**, it may also be possible to use atmospheric sources **530** as well (by using a carbon dioxide adsorption/desorption systems to capture atmospheric carbon dioxide, for example). As a further alternative, the carbon dioxide may be stored for use in the biological reactor (e.g., a stored source **532**).

[0265] Where a significant point source of emissions is used as the carbon dioxide source (e.g., sources **520**, **522**, **524**, **526**, **528**), the carbon dioxide emissions may be diverted into the biological reactor **502** to produce methane when electric power is available at prices below a pre-determined threshold. When electric power is above the pre-determined threshold, the carbon dioxide emissions may instead be emitted to the atmosphere, or it may be stored (as represented by the source **532**) for later utilization in the biological reactor **502**.

[0266] According to certain embodiments, the carbon dioxide from a point emission source may be commingled with other gases, including carbon monoxide, hydrogen, hydrogen sulfide, nitrogen, or oxygen or other gases common to industrial processes, or it may be substantially pure. The mixture of gases can be delivered directly to the biological reactor **502**, or the carbon dioxide may be separated from the gaseous mixture before delivery to the biological reactor **502**. Such sources of mixed gases include landfills, trash-to-energy facilities, municipal or industrial solid waste facilities, anaerobic digesters, concentrated animal feeding operations, natural gas wells, and facilities for purifying natural gas, which sources may be considered along side the illustrated sources **520**, **522**, **524**, **526**, **528**, **530**, **532**.

[0267] In operation, electricity and carbon dioxide may be delivered to the biological reactor **502** continuously to maintain a desired output of methane. Alternatively, the delivery rate of the electrical current, the carbon dioxide, or water to the biological reactor **502** may be varied which may cause the rate of methane production to vary. The variations in electrical current, carbon dioxide, and water may vary according to design (to modulate the rate of methane production in response to greater or lesser demand) or as the availability of these inputs varies.

[0268] As is also illustrated in FIG. **13**, the system **500** may include certain post-processing equipment **540** associated with the biological reactor **502**. For example, depending on the nature of the biological reactor **502**, the flow of material exiting the first (cathode) chamber may be sent to a liquid-gas separator. Alternatively, it may be necessary to process the methane from a gaseous form into a liquid form, which may be more convenient for purposes of storage or transport. According to still further embodiments, the gas may need to be filtered to remove byproducts, which byproducts may be stored or transported separately or may be disposed of as waste material. In any event, the methane produced by the biological reactor may be sent to a storage site **550**, or optionally to a distribution or transportation system **552** such as is discussed in detail with reference to the system illustrated in FIG. **14**. The methane may also be used locally, for example to replace natural gas in local operations for heat, or in chemical production.

[0269] It will be recognized that while the discussion has focused on methane as the primary product of the reactor **502**, the reactor **502** also will produce oxygen, which may be referred to as a secondary product or as a byproduct. Oxygen may be stored or transported in the same fashion as methane, and as such a parallel storage site and/or distribution system may be established for the oxygen generated as well. As one such example, the oxygen may be used locally, for example to enhance the efficiency of combustion and/or fuel cell energy conversion.

[0270] In the alternative to a stand-alone implementation, an integrated system **600** may be provided wherein a reactor **602** is coupled to an electrical power distribution grid **604**, or power grid for short, as illustrated in FIG. **14**. The power grid **604** may connect to a source of electricity **606**, for example one or more power plants discussed above, such as a carbon-based power plant (e.g., coal-fired power plant, natural gas-fired power plant, or biomass-fired power plant), a wind-powered turbine, water-powered turbine, a fuel cell, solar thermal system or photovoltaic system, or a nuclear power plant. These plants **606** may be connected, via transmission substations **608** and high-voltage transmission lines **610**, to power substations **612** and associated local distribution grids **614**. A local distribution grid **614** may be connected to one or more biological reactors **602** according to the present disclosure via an induction circuit **616**.

[0271] As noted above, certain of these power plants, such as those combusting the carbon-based fuels, operate most efficiently at steady state (i.e., ramping power production up or down causes significant costs and/or delays). The power grid may also be connected to power plants that have a variable output, such as the wind-powered and water-powered turbines and the solar-thermal and photovoltaic systems. Additionally, power users have variable demand. As such, the electricity that power producers with the lowest marginal operating expenses desire to supply to the grid **604** can, and typically does, exceed demand during extended periods (so called off-peak periods). During those periods, the excess capacity can be used by one or more biological reactors **602** according to the present disclosure to produce methane.

[0272] As also noted above, the biological reactor **602** may be coupled to one or more carbon dioxide sources **620**, for example including carbon-based power plants (e.g., coal-fired power plant, natural gas-fired power plant, biomass-fired power plant, or carbon-based fuel cells). Alternatively, the system **600** may be disposed near an industrial plant that provides carbon dioxide as a byproduct or a waste product, or may use atmospheric sources of carbon dioxide or stored carbon dioxide. In fact, while it may be possible to have a readily available source of carbon dioxide for conversion into methane when off-peak electricity is also available, it might also be necessary to store carbon dioxide during non-off-peak (or peak) periods for later conversion when the electricity is available. For example, an industrial source of carbon dioxide may typically generate most of its carbon dioxide during daylight hours, which may coincide with the typical peak demand period for electricity, causing some manner of storage to be required so that sufficient carbon dioxide is available to be used in conjunction with off-peak electricity production. Simple and inexpensive, gas impermeable tanks may be sufficient for such storage for short periods of time, such as part of a day or for several days. As to such storage issues for longer periods or for larger volumes, considerable effort is presently being devoted to sequestration of carbon dioxide in underground storage sites, and it may be possible to utilize the sequestered carbon dioxide stored in such sites as the source **620** of carbon dioxide for use in the biological reactors **602** according to the present disclosure.

[0273] As was the case with the system **500**, the system **600** may include optional post-processing equipment **630** that is used to separate or treat the methane produced in the reactor **602** as required. The methane may be directed from the biological reactor **602** (with or without post-processing) into one or more containment vessels **640**. In fact, the methane may be stored in aboveground storage tanks, or transported via local or interstate natural gas pipelines to underground storage locations, or reservoirs, such as depleted gas reservoirs, aquifers, and salt caverns. Additionally, the methane may be liquefied for even more compact storage, in particular where the biological reactors **602** are located where a connection to a power grid and a source of carbon dioxide are readily available, but the connection to a natural gas pipeline is uneconomical.

[0274] It will be further noted from FIG. **14** that methane may be taken from storage **640** or sent directly from the reactor **602** (optionally via the post-processing equipment **630**) to a methane collection subsystem **650**. From the collection subsystem **650**, the methane may be introduced into a transport system **652**, which system **652** may be a system of local, interstate or international pipelines for the transportation of methane, or alternatively natural gas. In this regard, the methane produced by the reactor **602** may take advantage of existing infrastructure to transport the methane from its location of production to its location of consumption. The transportation system **652** may be coupled to a distribution subsystem **654** that further facilitates its transmission to the consumer **656**, which consumer may be located remote from the biological reactor **602**. It will be recognized that according to certain embodiments of the present disclosure, the consumer **656** may even be one of the sources of electricity **606** connected to the power grid **604**.

[0275] It will also be recognized that a biological reactor for producing methane may be useful in a closed atmospheric environment containing carbon dioxide or in which carbon dioxide is released by respiration, or other biological processes or by chemical reactions such as combustion or by a fuel cell. According to such an embodiment, the biological reactor may be operating as a stand-alone implementation (as in FIG. **13**) or as part of an integrated system (as in FIG. **14**). The carbon dioxide in such an environment can be combined in the biological reactor with electrical current and water to produce methane and oxygen. Production of methane by this process may occur in a building sealed for containment purposes, or underground compartment, mine or cave or in submersible vehicle such as a submarine, or any other device or compartment that has limited access to external molecular oxygen, but sufficient electrical power, water and carbon dioxide to support the production of methane and oxygen. Oxygen produced by the biological reactor may likewise be stored as a gas, or liquefied for future use, sale or distribution.

[0276] While the foregoing examples have discussed the potential uses for methane produced by the biological reactor in meeting industrial, commercial, transportation, or residential needs (e.g., conversion into electricity through combustion in a carbon-based fuel generator or other uses, such as heating or cooking, non-combustion based conversion of methane into electricity such as via fuel cells, or chemical conversion into other compounds such as via halogenation, or reaction with other reactive species), it is also possible to appreciate the use of the biological reactor according to the present disclosure, either in a stand-alone system or as connected to a power grid, as a mechanism for carbon capture. That is, separate and apart from its uses to provide an alternative energy resource, the biological reactors according to the present disclosure may be used to remove carbon dioxide from the atmosphere, where the carbon dioxide is produced by living microorganisms, by chemical oxidation of organic material or from combustion of carbon-based fossil fuels, in particular where the carbon dioxide may be produced by large point sources such as fossil fuel power plants, cement kilns or fermentation facilities. The conversion of carbon dioxide into methane thus may produce not only methane, which has multiple other uses, but the conversion of carbon dioxide according to the present disclosure may generate or earn carbon credits for the source of the carbon dioxide, in that the carbon dioxide production of the source is decreased. These carbon credits may then be used within a regulatory scheme to offset other activities undertaken by the carbon dioxide producer, or in the life cycle of the products used or sold by the carbon dioxide producer, such as for renewable fuels derived from biomass, or gasoline refined from crude petroleum or may be used within a trading scheme to produce a separate source of revenue. Credits or offsets may be sold or conveyed in association with the methane, or oxygen, or other secondary products generated by the biological reactor or through the use of the biological reactor, or the credits may be traded independently such as on an exchange or sold directly to customers. In cases where the biological reactor functions within a business, or as part of a business contract with an entity, that uses oxygen, natural gas or methane from fossil or geologic sources, the methane produced by the biological reactor can be delivered to, or sold into a natural gas distribution system at times or in locations different from the use of natural gas and the business may retain any credits or offsets associated with the oxygen or methane produced with the biological reactor and apply such credit or offsets to natural gas or oxygen purchased from other sources and not produced directly by the biological reactor.

IV. Other Exemplary Embodiments

[0277] According to one embodiment, a method of converting carbon dioxide to methane comprises a) preparing a culture of hydrogenotrophic methanogenic archaea, b) placing the culture of hydrogenotrophic methanogenic archaea in a cathode chamber of an electrolysis chamber, the electrolysis chamber having an anode and a cathode, the cathode situated in the cathode chamber, and the cathode and anode chambers separated by a selectively permeable barrier; c) supplying carbon dioxide to the cathode chamber of the electrolysis chamber; d) supplying water to the electrolysis chamber, and e) wherein the hydrogenotrophic methanogenic archaea utilize the electrons released by the cathode and convert the carbon dioxide to methane. Additionally, step e) of such a method may only result in the production of methane gas by the hydrogenotrophic methanogenic archaea and a separate stream of oxygen gas by the anode.

[0278] According to another embodiment, a method of converting carbon dioxide to methane comprises a) preparing a culture of hydrogenotrophic methanogenic archaea; b) placing the culture of hydrogenotrophic methanogenic archaea in a cathode chamber of an electrolysis chamber, the electrolysis chamber having an anode chamber and a cathode chamber wherein the anode chamber has an anode and the cathode chamber has a cathode; c) supplying carbon dioxide to the electrolysis chamber; d) supplying water to the electrolysis chamber; e) wherein an electric potential difference is maintained between the cathode and the anode; and f) wherein the hydrogenotrophic methanogenic archaea utilize the electric potential difference between the cathode and the anode to convert the carbon dioxide to methane. According to such a method, the anode chamber and the cathode chamber may be separated by a selectively permeable barrier.

EXAMPLE 1

[0279] This example describes an exemplary method of maintaining a *Methanothermobacter* microorganism of the present disclosures and an exemplary method of cryopreserving the microorganism.

[0280] The microorganisms of strain UC120910 are maintained in Medium 1, disclosed herein, at 60° C. under anaerobic conditions comprising 80% hydrogen, 20% carbon dioxide in a New Brunswick BioFlo 110 Fermenter with a 1.3 L nominal total volume glass vessel. The culture vessel contains four full-height baffles, extending 6 mm from the wall. Double bladed, 6-blade Rushton Impellers (52 mm diameter) are placed inside the culture vessel and are maintained at a typical stirring speed of about 1000 RPM. The hydrogen sparger is a perforated tube (10 perforations ~0.5 mm diameter) placed in a circle just below the bottom impeller. The primary bubbles released from the sparger are relatively large and are substantially broken up by the action of the impeller.

[0281] The culture vessel is maintained at a constant 60° C. and at a liquid volume within a range of about 0.3 L to about 1 L (e.g., 0.7 L). Because water is a by-product of methanogensis, liquid is constantly being removed from the reactor. The microorganisms are maintained in the culture vessel within a measured biomass range of about 0.005 to about 0.011 g dry solid/mL water (0.5-1% dry mass per unit volume).

[0282] Alternatively, the microorganisms of strain UC120910 are maintained in culture tubes or bottles comprising either Medium 1 or ATCC medium 2133:0SU967 at 60° C. under anaerobic conditions comprising a gas phase of 80% hydrogen, 20% carbon dioxide. As a further alternative, the microorganisms of strain UC120910 are maintained on the surface of solidified Medium 1 or ATCC medium 2133: 0SU967 at 60° C. under anaerobic conditions comprising a gas phase of 80% hydrogen, 20% carbon dioxide.

[0283] The microorganisms are cryopreserved by suspending microorganisms in a liquid growth medium containing 10% glycerol. The microorganism suspension is then placed into a −80° C. freezer. The cryopreserved organisms are returned to growth by inoculation into fresh liquid medium or onto solidified medium and incubation under anaerobic conditions at 60° C. as described above.

EXAMPLE 2

[0284] This example describes two exemplary methods of using the microorganisms of the present disclosures for producing methane.

Hydrogenotrophic Methanogensis

[0285] Microorganisms of strain UC120910 are cultured in a New Brunswick BioFlo 110 Fermenter in Medium 1 as essentially described in Example 1. Methane and hydrogen outflow rates from the batch culture are calculated as a function of the hydrogen and methane mass spectrometry signals (corrected for ionization probability) and the hydrogen inflow rate. The calculation assumes that all hydrogen that enters the batch culture is either converted to methane at a ratio of 4 H_2:1 CH_4 or exits the culture as unreacted hydrogen. Under steady state conditions with doubling times of 50 hours or greater, the small proportion of hydrogen that is consumed in the growth of the organisms is neglected in the calculation.

[0286] Calculation of VVD methane productivity. The volumetric flow of hydrogen entering the culture is controlled by a gas mass-flow controller and provides a primary reference for determination of the rate of methane production. The ratio of masses detected by the mass spectrometer at mass 15 to that at mass 2 is determined for a range of methane to hydrogen ratios in standard gas mixtures generated by gas mass-flow controllers to obtain correction constants. The ratio of mass 15 to mass 2 in experimental gas streams is then multiplied by the correction constant to obtain the ratio of methane to hydrogen gas in the fermenter/reactor exit gas stream. By assuming that hydrogen in the input gas stream is converted to methane at a 4:1 molar ratio, the absolute rate of methane and hydrogen flow out of the reactor is calculated from the input hydrogen flow rate and the observed gas ratio in the exit flow. Methane productivity in units of VVD are calculated as the volume of methane in the exit flow per day divided by the liquid volume of the fermenter/reactor.

[0287] In an exemplary method, microorganisms of strain UC120910 are cultured in a New Brunswick BioFlo 110 Fermenter in Medium 1 as essentially described in Example 1. Specifically, the Fermenter is maintained with impellers stirring at 1000 RPM and a culture volume of 400 mL and at a temperature of 60° C. Hydrogen gas is delivered to the system at a gas flow rate of 10 L/min H_2 and carbon dioxide is delivered at a gas flow rate of 2.5 L/min.

Electrobiological Methanogensis

[0288] An electrochemical cell was fabricated as shown in FIG. **16**. The frame was made from polyether ether ketone (PEEK) with an anode and cathode compartment separated by Nafion 115. The anode compartment contained a titanium mesh backed by solid graphite as current collector and gas diffusion layer, an anode made of woven graphite cloth, with a carbon black coating, containing 0.5% platinum, on the anode on the side adjacent to the Nafion membrane. The cathode compartment contained a woven graphite cloth with no platinum and a solid graphite current collector.

[0289] The geometry of the electrochemical cell was cylindrical with catholyte solution inserted into the middle of the cathode and flowing radially to a fluid collection channel near the outer edge of the cathode. The catholyte solution comprised Medium 1 or Medium 1 with added NaCl to increase conductivity. No reduced carbon feedstocks are provided by the medium, thereby demonstrating the autotrophic nature of the microorganisms of strain UC120910 when reducing power is provided by an electrode. The catholyte flow rate was approximately 1 ml/min and the active volume of the cathode was approximately 0.25 ml. Water supply to the anode is via diffusion across the membrane from the cathode and oxygen produced on the anode diffuses out of the cell through channels open to the air.

[0290] The electrochemical cell and a culture of microorganisms of strain UC120910 were held at a fixed temperature within a glass convection oven, while various electrical potentials were held across the cell as shown in FIG. **17**. A supply of Argon and CO_2 carrier gas was used to keep the catholyte solution saturated with CO_2 and also to carry methane product quickly to a mass spectrometer for analysis. A chilled vapor trap was used to keep excess water from entering the mass spectrometer.

[0291] FIGS. **18** and **19** show data collected at 60° C. with a catholyte culture of microorganisms of strain UC120910 having a biomass density of 8.4 mg dry mass per mL culture. FIG. **18** shows the methane and hydrogen production in the cathode as a function of time as the full cell voltage is varied linearly. Methane production begins at lower voltages than hydrogen production. Sodium chloride is added to increase the catholyte conductivity from 8 mS/cm to 25 mS/cm.

[0292] FIG. **19** shows methane and hydrogen production as a function of time for full cell voltages held at the fixed values indicated. As shown in FIG. **19**, the microorganisms produce methane nearly instantaneously upon the addition of power (voltage) and the maximum methane production level at each voltage level is reached within 10 minutes of voltage addition. As shown in FIG. **19**, the microorganisms stop producing methane nearly instantaneously upon the removal of power (voltage) and the baseline methane production level at each voltage level is reached within 10 minutes of voltage removal.

EXAMPLE 3

[0293] This example provides an exemplary comparative study of doubling time and carbon dioxide utilization efficiency among a microorganism of the present disclosures and an unadapted precursor microorganism.

[0294] At the time of deposit of strain UC120910, the dilution rate (reciprocal of the doubling time) of the continuous culture in the fermenter was determined by measuring the rate of culture fluid removal from the fermenter by the system that maintains a constant liquid volume in the chamber. The results of this analysis demonstrated that the culture had a doubling time of 110.8 hours. Samples from this culture were also used directly as catholyte (plus living methanogenesis catalyst) in the experiments presented in FIGS. **18** and **19**.

[0295] The sample of the continuous culture in the fermenter described above was also analyzed to determine carbon dioxide utilization efficiency as expressed by the ratio of (the number of carbon dioxide molecules converted to methane) to (the number of carbon dioxide molecules converted to cellular materials). Specifically, the dry mass of cells in a given volume was determined by drying pelleted cells to constant weight and found to be 8.4 g/L of culture. Based upon the determined doubling time, the biomass increases at a rate of 0.076 g/L/hour to maintain this steady-state biomass concentration. This molar content of carbon in the biomass was estimated using the empirical formula for cell composition provided by Schill et al., Biotech Bioeng 51(6): 645-658 (1996): $CH_{1.68}O_{0.39}N_{0.24}$, to obtain the moles of biomass carbon produced per unit time. The moles of methane produced in the same time was determined as described in Example 2. Following these procedures, it was determined that the yield of methane per molecule of carbon gained in biomass, $Y_{P/X}$, was 66.9 molecules of methane produced for every one molecule of carbon dioxide converted to cellular material. This result is also expressed as 98.5% of the fixed carbon being converted to methane and only 1.5% of the fixed carbon being diverted to biomass.

[0296] The microorganism of strain UC120910 is an adapted strain of DMSZ 3590, which is described in Schill et al., (1996), supra. According to Schill et al., the unadapted strain of DMSZ 3590 exhibited methane production rates as high as ~270 volumes of methane at standard temperature and pressure per volume of culture per day (VVD). At each of the tested rates, the doubling times were shown to be between 3 and 10 hours. This active growth phase is useful when biomass is the desired product. For the purposes of producing methane, any production of additional biomass is an unwanted byproduct. The highest $Y_{P/X}$ documented by Schill et al. (see Table IV) was 19.6, or about 5% of fixed carbon being diverted to biomass.

[0297] Based on the data reported in Schill et al. and the data reported herein, the efficiency of carbon dioxide conversion to methane of the microorganisms of strain UC120910 are superior to those of DSMZ 3590, since only 1.5% of the carbon dioxide is converted into cellular material or maintenance of the culture, in contrast to the ~5% of the supplied carbon dioxide converted into biomass and cellular maintenance by the microorganisms of Schill et al. Without being bound to a particular theory, the superior methane productivity of UC120910 may be due to the fact that the microorganisms of this strain exhibit a remarkably low doubling time.

EXAMPLE 4

[0298] This example describes an exemplary method of testing resilience to contaminants.

Recovery from Oxygen Exposure

[0299] Methanogenic organisms are regarded as extremely strict anaerobes. Oxygen is known as an inhibitor of the enzyme catalysts of both hydrogen uptake and methanogenesis. A low oxidation-reduction potential (ORP) in the growth medium is regarded as important to methanogenesis.

[0300] In some embodiments, the *Methanothermobacter* microorganism of the present disclosures is resilient to oxygen exposure, as the microorganism demonstrates a methane productivity level after oxygen exposure which is substantially the same as the methane productivity level exhibited before oxygen exposure.

[0301] Resilience to oxygen exposure may be analyzed by measuring the methane productivity before, during, and after oxygen exposure for various time periods. Specifically, resilience may be measured by maintaining the microorganism as essentially set forth in Example 1 and measuring the methane productivity level as essentially described in Example 2.

[0302] The culture vessel is exposed to 100% air for 10 minutes, 90 minutes, or 15 hours at a flow rate of 500 cc/min. Ambient air comprises approximately (by molar content/volume) 78% nitrogen, 21% oxygen, 1% argon, 0.04% carbon dioxide, trace amounts of other gases, and a variable amount (average around 1%) of water vapor.

[0303] During exposure to 100% air, methanogenesis is believed to be stopped and the ORP of the culture medium rises. The air used in the experiment also displaces CO_2 dissolved in the medium, causing the pH to rise. Following the 10 minute exposure to 100% air, gas flows of H_2 and CO_2 were restored (100 cc/min H_2, 25cc/min CO_2).

[0304] In a first experiment, 1.5 ml of a 2.5% solution of sulfide (Na_2SH_2O) is added within 4 minutes of terminating air feed and restoring the H_2/CO_2 gas feed. Sulfide is widely used to control the ORP of the cultures, control that is regarded as essential. In another experiment, no sulfide was added.

[0305] The presence of the hydrogen in the gas phase is sufficient to reduce the ORP of the culture to enable methanogenesis, no additional control of the ORP of the culture is required. The lack of necessity of sulfide is of note in that methanogenic cultures are typically maintained at 10,000 ppm hydrogen sulfide in the gas phase. Such high levels of sulfide are not tolerated in certain industrial process, for instance, natural gas pipeline tariffs in the United States set maximum levels of hydrogen sulfide content of natural gas ranging from 4-16 ppm, depending upon the pipeline system.

Recovery from Carbon Monoxide Exposure

[0306] Carbon monoxide (CO) is another known inhibitor of enzymes involved in both hydrogen uptake and methanogenesis. CO is a potential contaminant of CO_2 and hydrogen streams derived from gasification of coal or biomass resources. The effect CO on methane formation by methanogen cultures is examined. Resilience to CO exposure may be analyzed by measuring the methane productivity before, during, and after oxygen exposure for various time periods. Specifically, resilience to carbon monoxide may be measured by maintaining the microorganism as essentially set forth in Example 1 and measuring the methane productivity level as essentially described in Example 2.

[0307] The pH of the culture is maintained constant by keeping CO_2 at 20% of the gas mix and changing only the composition of the other 80% of the gas. The culture is exposed to a mixture of 8% CO and 72% hydrogen at a flow rate of 100 cc/min and CO_2 at 25 cc/min for a period of 1.7 hours. Then the culture is restored to a flow of 80% hydrogen at a flow rate of 100 cc/min and CO_2 at 25 cc/min.

[0308] The culture is optionally subsequently exposed to a mixture of 16% CO and 64% hydrogen at a flow rate of 100 cc/min and CO_2 at 25 cc/min for a period of 1 hour. The culture is then restored to a flow of 80% hydrogen at a flow rate of 100 cc/min and CO_2 at 25 cc/min.

[0309] The culture is optionally exposed to a mixture of 40% CO and 40% hydrogen at a flow rate of 100 cc/min and CO_2 at 25 cc/min for a period of 20 minutes. The culture is then restored to a flow of 80% hydrogen at a flow rate of 100 cc/min and CO_2 at 25 cc/min.

[0310] The culture is optionally exposed to a mixture of 60% CO and 20% hydrogen at a flow rate of 100 cc/min and CO_2 at 25 cc/min.

[0311] During each exposure, methane production is measured as essentially described in Example 2.

EXAMPLE 5

[0312] This example demonstrates that the *Methanothermobacter* microorganism of the present disclosures demonstrates an excess of specific catalytic capacity when grown under steady-state, nearly stationary conditions in a continuous culture fermentor.

[0313] The specific catalytic activity of methanogenic microorganisms can be expressed as the ratio of moles of methane formed per hour to moles of carbon in the microbial biomass. Under some conditions, one of the necessary substrates may be limiting the reaction, in which case the specific catalytic capacity may exceed the measured specific catalytic activity. Thus, an increase in the limiting substrate would lead to an increase in the observed specific catalytic activity. Under other conditions, the observed specific catalytic activity may be saturated with substrate, in which case an increase in substrate concentration would not yield an increase in specific catalytic activity. Under substrate saturating conditions, the observed specific catalytic activity would equal the specific catalytic capacity.

[0314] For strain UC120910 growing at steady state as described in Example 1 with a hydrogen feed rate of 0.2 L/min, the specific catalytic activity for methane production, qP, was observed to be 0.37 moles methane produced per mole biomass carbon per hour. When the hydrogen feed rate was doubled to 0.4 L/min, qP doubled as well to 0.72 moles methane produced per mole biomass carbon per hour. Thus, the steady-state culture of UC120910 contains specific catalytic capacity that is in excess of the specific catalytic activity that supports its growth. In other experiments with hydrogen feed rates of up to 5 L/min, specific catalytic activity of up to 4 moles methane per mole biomass carbon have been observed without signs of saturation of the rate. Thus, the specific catalytic activity of the strain is at least 10 fold greater than observed during steady-state growth with doubling times in the range of 100 hours.

EXAMPLE 6

[0315] Vertical electrolysis chamber/cell configuration. A cylindrical electrolysis cell, 1.2 cm in internal diameter, was constructed from polusulfone plastic and arranged with an air-exposed anode on the bottom, covered by a Nafion 117 PEM and the closed cathode chamber on the top (FIG. **3**). A Pt-carbon catalytic layer on a carbon mesh gas diffusion layer (GDE-LT) was used as the anode, with a titanium ring current collector around the circumference of the cell. The active area of the Nafion 117 PEM was 1.2 cm^2. The enclosed cathode chamber had a total internal volume of 3 ml and during operation the ~1.5 ml of gas phase above the liquid phase was swept with a continuous flow (20 ml/min) of inert carrier gas. The composition of the exit gas, including any gases emitted within the cathode chamber, was analyzed continuously by mass spectrometry. The cathode electrode was constructed from reticulated vitreous carbon foam (ERG Materials and Aerospace Corp.) in the form of a cylinder, 1.2 cm diameter, 1 cm tall, placed in contact with the PEM, filling approximately half of the chamber, and connected electrically to the outside via a titanium wire. The cathode chamber was filled with 1.5 ml concentrated cell suspension, which settled into and filled the foam electrode. The carbon foam provided a high surface area for close contact between the cathode and the microorganisms. Occasionally, gas was released from bubbles formed in the solution by the addition of 5-10 microliters of antifoam agent.

[0316] Preparation of the cell suspension. Initial culture growth. Cells were grown in a continuously stirred tank fermenter, BioFlo 110, with a total internal volume of 1.3 L and a typical liquid volume of 0.6 L. An initial inoculum of the autotrophic hydrogenotrophic thermophilic methanogen, Methanothermobacter thermautotrophicus, DSMZ 3590, was grown at 60° C. as a batch culture in a medium containing the following components: Na3nitrilotriacetate, 0.81 mM; nitrilotriacetic acid, 0.4 mM; $NiCl_2$-$6H_2O$, 0.005 mM; $CoCl_2$-$6H_2O$, 0.0025 mM; Na_2MoO_4-$2H_2O$, 0.0025 mM; $MgCl_2$-$6H_2O$, 1.0 mM; $FeSO_4$-$7H_2O$, 0.2 mM; Na_2SeO_3, 0.001 mM; Na_2WO_4, 0.01 mM; KH_2PO_4, 10 mM; NaCl, 10 mM; L-cystein 0.2 mM. This medium was sparged with a 4:1 H_2:CO_2 gas mixture generated with mass flow controllers at a total flow of 250 standard ml/minute. The pH of the medium was initially maintained at 6.85 via a pH stat that used 2M ammonium hydroxide to make adjustments. During the early growth phase of the culture when methane production was limited by cell concentration and increased at an exponential rate, a 0.5M sodium sulfide solution was added as needed to maintain the redox potential below −300 mV. Once the culture was grown and methane production reached a steady-state, the culture maintained the redox potential below −450 mV on its own, using hydrogen as the reducing agent. Sulfide addition was slowed to a minimal rate (<1 ppm of H_2S in the outflow gas, as determined by mass spectrometry) needed for maintaining steady methane productivity with this strain of methanogen. Under these conditions, steady state methane production corresponds to 96-98% conversion of the input hydrogen.

[0317] Selection of a strain adapted to nearly stationary growth conditions. After steady state conditions had been established, the culture was maintained for several weeks without the addition of fresh medium. Instead, the increased volume of the culture generated by water production during methanogenesis was continually removed. The inorganic nutrients removed along with the removed medium and microorganisms were replaced from a 100× concentrated stock formulated as follows: Na_3nitrilotriacetate, 81 mM; nitrilotriacetic acid, 40 mM; $NiCl_2$-$6H_2O$, 0.5 mM; $CoCl_2$-$6H_2O$, 0.25 mM; Na_2MoO_4-$2H_2O$, 0.25 mM; $MgCl_2$-$6H_2O$, 100 mM; $FeSO_4$-$7H_2O$, 20 mM; Na_2SeO_3, 0.1 mM; Na_2WO_4, 1.0 mM; KH_2PO_4, 1.0 M; NaCl, 1.0 M; L-cysteine, 20 mM. The goal of maintaining this extended culture under nearly stationary growth conditions was to select for a strain that could perform well and survive under conditions similar to those that are encountered in the electrolysis chamber.

[0318] Performance under electrolysis conditions. The adapted culture, at a cell concentration of 5-7g dry weight/L, was starved for energy by sparging at 250 ml/min with a 4:1 gas mixture of Ar:CO_2 for several hours until neither hydrogen nor methane appeared in the effluent gas stream. The cells in a sample from the culture were then concentrated three-fold by centrifugation under anaerobic conditions and resuspended at a final concentration of 15-21 g dry weight/L. One and one half milliliters of this concentrated suspension was placed into the chamber and impregnated into the carbon foam cathode (FIG. **3**). The cathode was polarized at a voltage of 3.0 to 4.0 V, relative to the anode, and the gasses emerging from the chamber were monitored in a 20 ml/min flow of He carrier gas. As can be seen in FIG. **15**, methane is the sole gas product at voltages less than 4.0V, but a minor proportion of hydrogen gas can also be produced at higher voltages. Other possible electrochemical reaction products, such as carbon monoxide, formic acid or methanol were not detected.

[0319] Various alternative improvements. Many modifications of this setup are anticipated and intended to be within the scope of this disclosure. Expanded graphite foam or particulate graphite or other high surface to volume electrically conductive materials may be suitable as cathode electrodes. A circulating cathode solution may allow for more rapid and complete gas exchange with the outside of the electrolysis chamber. Alternative temperatures may allow for more efficient charge transfer across the membrane separating the cathode and anode chamber. Alternative materials, including composite Nafion/PTFE, may be suitable for use as the selectively permeable membrane separating the cathode and anode chambers. Alternative geometries of the chambers may improve the charge and gas transport to and from the microbes. Alternative strains of methanogenic microbes may be more tolerant of the various mechanical strains, electrical demands, and metabolite exposure present in this invention.

[0320] All references, including publications, patent applications, and patents, cited herein are hereby incorporated by reference to the same extent as if each reference were individually and specifically indicated to be incorporated by reference and were set forth in its entirety herein.

[0321] The use of the terms "a" and "an" and "the" and similar referents in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. The terms "comprising," "having," "including," and "containing" are to be construed as open-ended terms (i.e., meaning "including, but not limited to,") unless otherwise noted.

[0322] Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range and each endpoint, unless otherwise indicated herein, and each separate value and endpoint is incorporated into the specification as if it were individually recited herein.

[0323] All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

[0324] Any combination of the above-described elements in all possible variations thereof is encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context.

TABLE 1

Class	Order	Family	Genus	Species	Taxonomy ID
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	*fulgidus*	224325
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	*infectus*	403219
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	*lithotrophicus*	138903
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	*profundus*	572546
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	*veneficus*	58290
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	sp. Arc22	403220
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	sp. Fe70_19	669409
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	sp. Fe70_20	669410
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	sp. NI85-A	269231
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	sp. NS-tSRB-2	330389
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	sp. NS70-A	269230

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	sp. PM70-1	387631
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Archaeoglobus*	Unclassified	269247
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Ferroglobus*	*placidus*	589924
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Ferroglobus*	Unclassified	269249
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Geoglobus*	*ahangari*	113653
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Geoglobus*	sp. AF1T1440	568410
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Geoglobus*	sp. AF1T2020	568411
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Geoglobus*	sp. AF2T1421	568413
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Geoglobus*	sp. AF2T819	568412
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Geoglobus*	sp. SBH6	565033
Archaeoglobi	Archaeoglobales	Archaeoglobaceae	*Geoglobus*	sp. SN4	685720
Archaeoglobi	Archaeoglobales	Unclassified	Unclassified	Unclassified	309173
Archaeoglobi	Unclassified	Unclassified	Unclassified	Unclassified	763499
Halobateria	Halobacteriales	Halobacteriaceae	*Haladaptatus*	*cibarius*	453847
Halobateria	Halobacteriales	Halobacteriaceae	*Haladaptatus*	*litoreus*	553468
Halobateria	Halobacteriales	Halobacteriaceae	*Haladaptatus*	*paucihalophilus*	797209
Halobateria	Halobacteriales	Halobacteriaceae	*Halalkalicoccus*	*jeotgali*	413810
Halobateria	Halobacteriales	Halobacteriaceae	*Halalkalicoccus*	*tibetensis*	175632
Halobateria	Halobacteriales	Halobacteriaceae	*Halalkalicoccus*	sp. C15	370968
Halobateria	Halobacteriales	Halobacteriaceae	*Halalkalicoccus*	Unclassified	663941
Halobateria	Halobacteriales	Halobacteriaceae	*Halarchaeum*	*acidiphilum*	489138
Halobateria	Halobacteriales	Halobacteriaceae	*Halarchaeum*	sp. HY-204-1	744725
Halobateria	Halobacteriales	Halobacteriaceae	*Haloalcalophilium*	*atacamensis*	119862
Halobateria	Halobacteriales	Halobacteriaceae	*Haloalcalophilium*	Unclassified	260475
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*aidinensis*	56545
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*algeriensis*	337689
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*amylolytica*	396317
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*argentinensis*	43776
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*californiae*	662475
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*hispanica*	634497
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*japonica*	29282
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*marismortui*	272569
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*quadrata*	182779
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*siamensis*	456446
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*sinaiiensis*	662476
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	*vallismortis*	662477
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	Unclassified	44098
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 113	536043
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 12B-U	584967
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 2KYS1	367810
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 2Sb1	329271
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 2TK2	251319
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 2TK3	251320
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 3TK1	251317
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 3TL4	367812
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 3TL6	367809
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 4TK1	251318
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 4TK3	251321
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 5Mm10	329272
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. 9D-U	584968
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. A283	362893
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. A337	362892
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. A43	362894
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. AB19	367757
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. AJ4	222985
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. AJ7	229734
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. Arch325ppt-a	682724
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. ARG-2	69009
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. AS7094	262078
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. aus-5	464028
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. B19-RDX	589455
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. B22-GYDX	589454
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. B44A	370972
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. C205090908-1R	593534
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. CH7	596417
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. CHA1	596418
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. CHB-U	584969
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. D1	242927
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. D21	520558
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. Ez1.2	655453
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC130__30	493028
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC134__14	493029
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC134__15	493030

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__1	493031
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__10	493032
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__11	493033
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__12	493034
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__13	493035
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__2	493036
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__3	493037
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__4	493038
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__5	493039
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__6	493040
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__7	493041
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__8	493042
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC137__9	493043
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC167__2	493044
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__1	493045
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__10	493046
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__11	493047
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__12	493048
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__13	493049
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__14	493050
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__15	493051
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__16	493052
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__17	493053
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__18	493054
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__19	493055
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__20	493056
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__21	493057
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__22	493058
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__23	493059
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__24	493060
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__25	493061
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__26	493062
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__27	493063
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__28	493064
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__29	493065
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__3	493066
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__31	493067
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__32	493068
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__33	493069
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__34	493070
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__35	493071
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__36	493072
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__37	493073
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__38	493074
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__39	493075
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__4	493076
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__40	493077
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__41	493078
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__5	493079
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__6	493080
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__7	493081
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__8	493082
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. FC168__9	493083
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. GR3	574570
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. GSP101	614216
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. GSP108	614217
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. HST01-2R	575195
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. HST03	575194
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. I.B14	564675
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. I.B17	564677
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. I.B27	564684
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. I.B29	564686
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. I.C3	564689
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. I.C4	564690
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. I.C5	564691
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. I.C6	564692
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. I.C7	564693
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. LCKW-Isolate15A	338959
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. LCKW-Isolate20A	338960
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. LCKW-Isolate20N	338961
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. LK1	796337
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. M4r1	323740
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. MGG2	717750

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. MGG3	717751
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. OHF-1	217171
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. OHF-2	217024
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. Q6	323742
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. RBCA-10^2	584970
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. SP2(1)	402992
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. SP2(2)	402870
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. SP4	402871
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	sp. YW016	340950
Halobateria	Halobacteriales	Halobacteriaceae	*Haloarcula*	Unclassified	376544
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	*jilantaiense*	355548
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	*noricense*	223182
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	*piscisalsi*	413968
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	*salinarum* (strain Mex)	33003
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	*salinarum* (strain Port)	33004
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	*salinarum* (strain Shark)	33005
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	*salinarum* R1	478009
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	*salinarum* sp. NRC-1	64091
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	Unclassified	2243
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 0Cb11	639868
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 0Cb21	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 0Cb22	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 0Cb23	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 15C0	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 15C11	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 15C21	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 15C23	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 15C31	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 1TK1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 1TK2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 1TK3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 2-24-2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 2-24-3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 2-24-4	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 2-24-5	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 2-24-6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 2-24-7	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 2Ma3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 3KYS1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 5Mm6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 7Sb5	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. 9R	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. AS133	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. AS28	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. AS7092	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. AUS-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. AUS-2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. BCCS 030	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. BCCS 039	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. BIHGY150/14	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. BIHSTY150/18	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. CH11	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. EL 001	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. EL 002	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. EL 003	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. Ez21	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. EzA	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. FIC145_1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. FIC145_2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. FIC146_1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. FIC146_2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. FIC146_3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. FIC146_4	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. GN101	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. GRB	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. HA3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. halo-3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. HM01	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. HM02	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. HM11	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. HM13	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. HM3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. HP-R1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. HSC3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. I.B12	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. I.C16	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. I.C17	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. I.C2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. I.C24	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. I.C26	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. I.C29	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. I.C30	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. I.C31	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. JCM 9447	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. JP-6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. LCKS000-Isolate10	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. LCKS000-Isolate39	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. LCKS200-Isolate33	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. MO51	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. MVBDU1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. MVBDU2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. NCIMB 714	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. NCIMB 718	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. NCIMB 720	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. NCIMB 733	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. NCIMB 734	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. NCIMB 741	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. NCIMB 765	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. P102070208-3O	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. P102070208-3R	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. P92A090908-6O	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. P92A090908-6P	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. SG1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. SP3(2)	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. TG1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. IJ-EY1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. XH3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	sp. Y12	
Halobateria	Halobacteriales	Halobacteriaceae	*Halobacterium*	Unclassified	260463
Halobateria	Halobacteriales	Halobacteriaceae	*Halobaculum*	*gomorrense*	43928
Halobateria	Halobacteriales	Halobacteriaceae	*Halobiforma*	*haloterrestris*	148448
Halobateria	Halobacteriales	Halobacteriaceae	*Halobiforma*	*lacisalsi*	358396
Halobateria	Halobacteriales	Halobacteriaceae	*Halobiforma*	*nitratireducens*	130048
Halobateria	Halobacteriales	Halobacteriaceae	*Halobiforma*	Unclassified	417359
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	*dombroskii*	179637
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	*hamelinensis*	332168
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	*morrhuae*	2250
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	*qingdaonensis*	224402
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	*saccharolyticus*	62319
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	*salifodinae*	36738
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	*thailandensis*	335952
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	Unclassified	29286
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. 001/2	481737
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. 004/1-2	481736
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. BIGigoW09	481735
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. BIHTY10/11	481734
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. CH8B	596420
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. CH8K	596421
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. FC211	493090
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HA4	723882
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HP-R5	701664
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HPA-86	436977
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HPA-87	436978
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HSA18	436979
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HSA19	436980
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HSA20	436981
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HSt 2.0	557878
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HSt 2.2	557879
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HSt 3.0	557880
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HSt 3.1	557881
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HSt 4.0	557882
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HSt 4.1	557883
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. HSt 5.0	557884

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. IS10-2	335951
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	sp. JCM 8979	228414
Halobateria	Halobacteriales	Halobacteriaceae	*Halococcus*	Unclassified	260465
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*alexandrines*	114529
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*antrum*	381855
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*berberensis*	340952
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*denitrificans*	662478
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*elongans*	403191
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*gibbonsii*	35746
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*larsenii*	302484
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*lucentense*	523840
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*mediterranei*	523841
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*mucosum*	662479
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*opilio*	381854
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*prahovense*	381852
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*rutilus*	381853
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*sulfurifontis*	662480
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*viridis*	381851
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	*volcanii*	309800
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	Unclassified	2253
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. 25H4_1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. 25H4_2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. 25H4_3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. 25H4_4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. 50C21_1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. 50C21_2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. 50C21_3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. 50C21_4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. 50C21_5	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. 50C21_6	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. A317	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. A440	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. Aa2.2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. B-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. B-3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. B-4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. Bej51	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. BejS3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. BS1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. BS2a	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. BS2b	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. BV2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CIBAARC2BR	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CS1-10	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CS1-3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CS1-4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CS1-5	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CS1-7	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CS1-8	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CS1-9	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CS2-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CS3-01	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CS3-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CT2-4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CT3-3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CT3-7	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CT4-2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CT4-3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. CT4-7	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. D107	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. D1227	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_10	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_11	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_12	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_13	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_14	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_5	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_6	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_7	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_8	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB247_9	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB25_1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB25_2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB25_3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB25_4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB25_5	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB25_6	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB25_7	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB25_8	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FB25_9	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_10	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_11	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_12	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_13	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_14	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_15	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_16	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_17	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_18	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_19	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_20	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_21	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_5	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_6	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_7	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_8	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FC28_9	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FIB210_1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FIB210_2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FIB210_3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FIB210_4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FIB210_5	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FIB210_6	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FIB210_7	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FIB210_8	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. FIB210_9	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. GSP103	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. GSP104	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. GSP105	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. GSP106	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. GSP107	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. H4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. HA1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. HA2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. HSC4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. LSC3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. LWp2.1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. M14	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. M16	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. M5	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. M6	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. M7	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. M8	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. MO20	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. MO25	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. MO52	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. MO55	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. N5	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. PA13	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. PA14	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. PA15	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. PA16	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. PA17	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. SA1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. SA2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. SA3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. SA4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. SA6	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. SA7	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. Set21	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. SOP	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. SP1(2a)	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. SP2(3)	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. SP3(1)	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. VKMM004	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. VKMM006	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. VKMM009	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. VKMM01	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. VKMM010	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. VKMM011	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. VKMM015	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. YT216	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. YT226	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. YT228	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. YT236	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. YT247	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	sp. ZJ203	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloferax*	Unclassified	260473
Halobateria	Halobacteriales	Halobacteriaceae	*Halogeometricum*	*borinquense*	469382
Halobateria	Halobacteriales	Halobacteriaceae	*Halogeometricum*	sp. 50C25	493144
Halobateria	Halobacteriales	Halobacteriaceae	*Halogeometricum*	sp. 5Sa3	329275
Halobateria	Halobacteriales	Halobacteriaceae	*Halogeometricum*	sp. KL	627706
Halobateria	Halobacteriales	Halobacteriaceae	*Halogeometricum*	sp. P29B070208-1P	593539
Halobateria	Halobacteriales	Halobacteriaceae	*Halogeometricum*	sp. SS1	484017
Halobateria	Halobacteriales	Halobacteriaceae	*Halogeometricum*	Unclassified	436947
Halobateria	Halobacteriales	Halobacteriaceae	*Halogranum*	*rubrum*	553466
Halobateria	Halobacteriales	Halobacteriaceae	*Halomicrobium*	*katesii*	437163
Halobateria	Halobacteriales	Halobacteriaceae	*Halomicrobium*	*mukohataei*	485914
Halobateria	Halobacteriales	Halobacteriaceae	*Halomicrobium*	sp. A191	362891
Halobateria	Halobacteriales	Halobacteriaceae	*Halomicrobium*	sp. Bet58	643748
Halobateria	Halobacteriales	Halobacteriaceae	*Halomicrobium*	sp. KM	627707
Halobateria	Halobacteriales	Halobacteriaceae	*Halopiger*	*xanaduensis*	797210
Halobateria	Halobacteriales	Halobacteriaceae	*Haloplanus*	*natans*	376171
Halobateria	Halobacteriales	Halobacteriaceae	*Haloplanus*	sp. RO5-8	555874
Halobateria	Halobacteriales	Halobacteriaceae	*Haloplanus*	Unclassified	682717
Halobateria	Halobacteriales	Halobacteriaceae	*Haloquadratum*	*walsbyi* - C23	768065
Halobateria	Halobacteriales	Halobacteriaceae	*Haloquadratum*	*walsbyi* - DSM 16790	362976
Halobateria	Halobacteriales	Halobacteriaceae	*Haloquadratum*	Unclassified	329270
Halobateria	Halobacteriales	Halobacteriaceae	*Halorhabdus*	*tiamatea*	430914
Halobateria	Halobacteriales	Halobacteriaceae	*Halorhabdus*	*utahensis*	519442
Halobateria	Halobacteriales	Halobacteriaceae	*Halorhabdus*	Unclassified	643678
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*africanae*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*aidingense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*alkaliphilum*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*arcis*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*californiense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*cibarium*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*cibi*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*constantinense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*coriense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*distributum*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*ejinorense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*ezzemoulense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*halophilum*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*jeotgali*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*lacusprofundi*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*lipolyticum*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*litoreum*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*luteum*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*orientale*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*saccharovorum*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*sodomense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*tebenquichense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*terrestre*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*tibetense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*trapanicum*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*vacuolatum*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	*xinjiangense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. 106	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. 11-10^6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. 11GM-10^3	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. 12-10^3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. 2TL9	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. 5TL6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. 9B-U	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. A29	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. A33	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. A407	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. A87B	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. AC 1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Arch265ppt-f	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Arch270ppt-f	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Arch325ppt-b	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. AS2-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. AS2-11	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. AS2-14	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. AS2-17	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. AS2-2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. AS2-3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. AS2-5	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. AS2-6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. AS2-7	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. B10-MWDX	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. B12-RDX	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. B13-MW	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. B20-RDX	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. B23	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. B36	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. B43	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. B6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. B6-RDX	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Beja5	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Bet217	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Bet25	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Bet512	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. BG-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Bitterns-10^3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. C35	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. CGSA-14	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. CGSA-42	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. CH2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. CH3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. CHA-MPN-10^6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. CHC	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. CHC-U	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Crystal-Bi-White-U	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Crystal-Bii-Red-U	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. CS1-2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. CS4-4	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. CT4-02	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. CY	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. D1A	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. D24	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. DS10	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. DV427	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. DW6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. E4	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. EN-2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. ETD6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Ez228	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Ez24	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Ez26	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Ez5-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Ez5-2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Ez522	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Ez526	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Ez59	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Ez5RB	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. EzA1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Eza4	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. EzB1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. EzS2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. EzS6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. F100	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. F23A	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. F42A	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. FIC145	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. FIC234	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. GS1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. GSL5.48	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. GSP100	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. HALO-G*	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. HBCC-2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. HEN2-25	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. HEN2-39	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B11	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B15	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B18	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B19	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B20	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B21	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B23	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B26	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B28	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B30	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B4	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B5	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B8	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.B9	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.C11	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.C12	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.C28	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.C8	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. I.C9	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. IMCC2547A	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. IMCC2607	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. IMCC8195	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. L56	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. MG215	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. MG23	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. MG25	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. MG525	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. MG526	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. PV6	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. RBC-10^4	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. RBCA-10^3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. RBCB-10^2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. RBCB-10^3	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. s1-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. SC1.2	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. SH4	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. Slt1	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. SYM	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. T1/2S95	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP001	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP003	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP004	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP008	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP009	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP015	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP017	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP018	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP019	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP020	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP023	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP024	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP025	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP026	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP028	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP029	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP033	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP034	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP036	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP037	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP041	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP042	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP044	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP045	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP046	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP048	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP050	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP051	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP053	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP054	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP055	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP056	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP057	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP058	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP059	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP060	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP062	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP063	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP071	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP074	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP081	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP082	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP084	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP085	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP086	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP094	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP099	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP101	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP103	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP105	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP109	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP115	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP116	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP117	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP118	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP121	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP124	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP125	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP126	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP132	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP133	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP135	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP143	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP145	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP146	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP148	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP149	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP150	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP151	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP152	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP153	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP154	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP158	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP159	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP160	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP162	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP163	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP165	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP167	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP168	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP169	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP172	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP173	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP175	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP176	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP177	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP178	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP179	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP181	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP182	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP183	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP188	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP189	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP192	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP196	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP197	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP198	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP201	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP202	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP203	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP205	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP207	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP208	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP209	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP210	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP212	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP214	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP215	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP217	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP218	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP219	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP220	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP222	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP224	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP225	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP226	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP227	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP228	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP229	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP230	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP231	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP233	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP235	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP240	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP244	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP245	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP246	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP247	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP249	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP250	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP252	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP254	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP260	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP261	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP263	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP265	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP267	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP269	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP271	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP272	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP273	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP277	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP300	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP302	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP303	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP306	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP309	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP312	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP313	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP315	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP317	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP318	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP319	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP320	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP329	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. TP341	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. VKMM017	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. VKMM019	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. VKMM033	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. YT245	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. YW059	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. YYJ	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	sp. YYJ21	
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	archaeon DEEP-1	97928
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	archaeon ORGANIC1__A	98847
Halobateria	Halobacteriales	Halobacteriaceae	*Halorubrum*	Unclassified	399555

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Halosarcina*	*pallida*	411361
Halobateria	Halobacteriales	Halobacteriaceae	*Halosarcina*	sp. RO1-4	553469
Halobateria	Halobacteriales	Halobacteriaceae	*Halosarcina*	sp. RO1-64	671107
Halobateria	Halobacteriales	Halobacteriaceae	*Halosimplex*	*carlsbadense*	797114
Halobateria	Halobacteriales	Halobacteriaceae	*Halosimplex*	Unclassified	260471
Halobateria	Halobacteriales	Halobacteriaceae	*Halostagnicola*	*larsenii*	353800
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	*daqingensis*	588898
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	*hispanica*	392421
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	*jeotgali*	413811
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	*limicola*	370323
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	*longa*	370324
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	*saccharevitans*	301967
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	*salina*	504937
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	*thermotolerans*	121872
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	*turkmenica*	543526
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	*turpansis*	239108
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. A206A	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. A82	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. AB30	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. arg-4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. D113	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. D83A	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. DV582A-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. DV582B-3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. DV582c2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. DV582c4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. E49	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. E57B	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. EzB3	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. EzSm	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. FIC147	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. FIC148__1	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. FIC148__2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. GSL-11	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. L52	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. LPNTC	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. MO19	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. MO23	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. MO24	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. XJNU-19	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. XJNU-45	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. XJNU-45-4	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. XJNU-86-2	
Halobateria	Halobacteriales	Halobacteriaceae	*Haloterrigena*	sp. XJNU-97	
Halobateria	Halobacteriales	Halobacteriaceae	*Halovivax*	*asiaticus*	332953
Halobateria	Halobacteriales	Halobacteriaceae	*Halovivax*	*ruber*	387341
Halobateria	Halobacteriales	Halobacteriaceae	*Halovivax*	sp. A21	520557
Halobateria	Halobacteriales	Halobacteriaceae	*Halovivax*	sp. B45	596429
Halobateria	Halobacteriales	Halobacteriaceae	*Halovivax*	sp. E107	596430
Halobateria	Halobacteriales	Halobacteriaceae	*Halovivax*	sp. EN-4	388350
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	*aegyptia*	129789
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	*aibiensis*	248371
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	*asiatica*	64602
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	*chahannaoensis*	68911
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	*hulunbeirensis*	123783
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	*magadii*	547559
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	*taiwanensis*	160846
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	*wudunaoensis*	70318
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	sp. A137	362883
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	sp. ATCC 43988	63741
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	sp. B49	370966
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	sp. F4A	362882
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	sp. F5	359307
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	sp. Tunisia HMg-25	138615
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	sp. Tunisia HMg-27	138616
Halobateria	Halobacteriales	Halobacteriaceae	*Natrialba*	Unclassified	549377
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	*aidingensis*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	*altunense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	*ejinorense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	*gari*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	*pallidum*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	*pellirubrum*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	*versiforme*	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	*xinjiang*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. 2TK1	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. 5TK1	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. A85	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. ABDH11	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. ABDH17	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. B19	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. B5-RDX	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. B77A	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. CX2021	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. CY21	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. D74	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. E92B	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. FP1R	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. GSP102	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. GSP109	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. HA33DX	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. HDS1-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. HM06	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. J7	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. LPN89	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. XA3-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. XJNU-10	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. XJBU-49	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. XJNU-57	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. enrichment culture clone ABDH17	630201
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. enrichment culture clone ABDH2	630202
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. enrichment culture clone ABDH34	630203
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	sp. enrichment culture clone ABDH37	630204
Halobateria	Halobacteriales	Halobacteriaceae	*Natrinema*	Unclassified	261026
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	*gregoryi*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrionobacterium*	*innermongoliae*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. 2-24-1	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. 2-24-8	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrionobacterium*	sp. AS-7091	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. B-MWDX	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. SSL-6	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrionobacterium*	sp. SSL6	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. XJNU-101	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. XJNU-12	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrionobacterium*	sp. XJNU-13	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. XJNU-22	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. XJNU-36	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrionobacterium*	sp. XJNU-39	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. XJNU-43	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. XJNU-46	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrionobacterium*	sp. XJNU-62	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. XJNU-74	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. XJNU-75	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrionobacterium*	sp. XJNU-77	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. XJNU-96	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronobacterium*	sp. XJNU-99	
Halobateria	Halobacteriales	Halobacteriaceae	*Natrionobacterium*	Unclassified	523723
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	*aibiensis*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	*amylolyticus*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	*jeotgali*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	*occultus*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	*occultus SP4*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	*xinjiangense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	*yunnanense*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	*zabuyensis*	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp.	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. Ah-36	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. D50	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. D58A	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. E7	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. F30AI	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. GS3	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. M13	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. Sua-E41	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. Sua-E43	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. TC6	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. XH4	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. XJNU-111	
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	sp. enrichment culture clone ABDH12	630205
Halobateria	Halobacteriales	Halobacteriaceae	*Natronococcus*	Unclassified	236503
Halobateria	Halobacteriales	Halobacteriaceae	*Natronolimnobius*	*baerhuensis*	253108
Halobateria	Halobacteriales	Halobacteriaceae	*Natronolimnobius*	*innermongolicus*	253107
Halobateria	Halobacteriales	Halobacteriaceae	*Natronolimnobius*	Unclassified	549379
Halobateria	Halobacteriales	Halobacteriaceae	*Natronomonas*	*pharaonis*	348780
Halobateria	Halobacteriales	Halobacteriaceae	*Natronomonas*	sp. DV462A	585976
Halobateria	Halobacteriales	Halobacteriaceae	*Natronomonas*	Unclassified	436949
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	*aibiense*	348826
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	*bangense*	61858
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	*sulfidifaciens*	388259
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	*thiooxidans*	308853
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	*tibetense*	63128
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	sp. CG-4	640944
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	sp. CG-6	640943
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	sp. Sua-E01	549372
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	sp. Tenzan-10	134815
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	sp. Wadi Natrun-19	134814
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	sp. XJNU-14	642520
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	sp. XJNU-92	642521
Halobateria	Halobacteriales	Halobacteriaceae	*Natronorubum*	Unclassified	260478
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon 10AH	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon 14AHG	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon 30AH	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon 82M4	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon 86M4	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon 89M4	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon 8AHG	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon 93dLM4	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon 93lLM4	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon 98NT4	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon 9AH	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon B13-RDX	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon CSW1.15.5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon CSW2.24.4	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon CSW2.25.5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon CSW2.27.5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon CSW4.03.5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon CSW4.05.5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon CSW4.11.5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon CSW4.22.4	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon CSW5.28.5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon CSW6.14.5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon CSW8.8.11	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon HA15	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon HA25	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon S8a	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon SC4	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon SC7	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon SC8	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon SC9	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon sech10	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon sech14	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon sech4	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon sech6	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon sech7a	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon sech8	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon sech9	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon W1	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	haloarchaeon YNPASCul	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon 309	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GLYP1	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GX1	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GX10	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GX21	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GX26	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GX3	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GX31	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GX48	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GX60	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GX7	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GX71	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon GX74	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon HO2-1	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon IMCC2586B	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon IMCC8204	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon KeC-11	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon L1	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon RO1-6	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon RO3-11	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon RO5-14	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon RO5-2	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon Ston11	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon Ston12	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon Ston16	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon Ston2	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon Ston28	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon Ston3	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon Ston5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon Ston6	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TBN12	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TBN19	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TBN21	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TBN37	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TBN4	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TBN49	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TBN5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TBN51	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TBN53	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TNN10	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TNN18	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TNN28	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TNN44	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TNN50	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	archaeon TNN58	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	halophilic archaeon 194-10	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	halophilic archaeon 1DH38	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	halophilic archaeon 1SC5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	halophilic archaeon 2DH35	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	halophilic archaeon DH34	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	halophilic archaeon HS47	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	halophilic archaeon MK13-1	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	halophilic archaeon NaxosII	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	halophilic archaeon PalaeII	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	halophilic archaeon SC3	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	halophilic archaeon SC6	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	mixed culture haloarchaeon CDI-271	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	mixed culture haloarchaeon CDI-276	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	mixed culture haloarchaeon CDII-272	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	mixed culture haloarchaeon CDIII-273	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	mixed culture haloarchaeon CLI-248	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	mixed culture haloarchaeon CLI-250	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	mixed culture haloarchaeon CLI-257	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	mixed culture haloarchaeon CLI-265	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	mixed culture haloarchaeon YE.LI-230	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	Sambhar Salt Lake archaeon HA1	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	Sambhar Salt Lake archaeon HA6	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	*Halobacterium* sp. NCIMB 763	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	gen. sp.	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	gen. sp. 524	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	gen. sp. 56	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	gen. sp. 600	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	gen. sp. H1	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	gen. sp. SR1.5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	gen. sp. T5.7	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	enrichment culture clone SLAb1__archaeon	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured archaeon DEEP-10	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured archaeon DEEP-2	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured archaeon DEEP-5	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured archaeon DEEP-6	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured archaeon DEEP-7	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured archaeon DEEP-8	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured archaeon DEEP-9	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon CDI-271	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon CDII-272	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon CDIII-273	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon CLI-248	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon CLI-250	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon CLI-257	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon Envl-181	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon Envl-182	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon Envl-184	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon FLAS10H9	
Halobateria	Halobacteriales	Halobacteriaceae	Unclassified	uncultured haloarchaeon YE.LI-230	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*aarhusense*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*alcaliphilum*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*beijingense*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*bryantii*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*congolense*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*curvum*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*espanolae*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*formicicum*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*ivanovii*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*oryzae*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*palustre*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*subterraneum*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*thermaggregans*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	*uliginosum*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp.	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. 0372-D1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. 169	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. 25	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. 28	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. 8-1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. AH1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. BRM9	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. C5/51	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. Ch	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. F	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. GH	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. HD-1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. IM1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. M03	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. M2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. MB4	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. Mg38	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. Mic5c12	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. Mic6c05	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. MK4	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. OM15	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. Ps21	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. SA-12	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. T01	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. T11	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. Tc3	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. TM-8	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. TS2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. XJ-3a	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	sp. YCM1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobacterium*	Unclassified	176306
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*acididurans*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*arboriphilus*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*curvatus*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*cuticularis*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*filiformis*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*gottschalkii*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*millerae*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*olleyae*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*oralis*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*ruminantium*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*smithii* ATCC 35061	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*smithii* DSM 11975	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*smithii* DSM 2374	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*smithii* DSM 2375	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*thaueri*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*woesei*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	*wolinii*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	Unclassified	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. 110	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. 1Y	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. 30Y	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. 62	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. 87.7	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. AbM4	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. AK-87	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. CIRG-GMbb01	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. CIRG-GMbb02	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. FM1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. FMB1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. FMB2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. FMB3	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. FMBK1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. FMBK2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. FMBK3	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. FMBK4	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. FMBK5	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. FMBK6	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. FMBK7	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. HW23	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. LRsD4	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. Mc30	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. MCTS 1-B	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. MCTS 2-G	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. MD101	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. MD102	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. MD103	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. MD104	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. MD105	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. OCP	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. RsI3	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. RsW3	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. SM9	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. WBY1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. XT106	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. XT108	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. XT109	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. YE286	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. YE287	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. YE288	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. YE300	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. YE301	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. YE302	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. YE303	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. YE304	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. YLM1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. Z4	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. Z6	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. Z8	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	endosymbiont 'TS1' of Trimyema compressum	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	methanogenic endosymbiont of Nyctotherus cordiformis	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	methanogenic endosymbiont of Nyctotherus ovalis	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	methanogenic endosymbiont of Nyctotherus velox	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	methanogenic symbiont RS104	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	methanogenic symbiont RS105	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	methanogenic symbiont RS208	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	methanogenic symbiont RS301	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	methanogenic symbiont RS404	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	methanogenic symbiont RS801	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	methanogenic symbiont RS802	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. HI1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. HI26	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. HI28	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. HW1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. HW2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. HW3	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. LHD12	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. LHD2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. LHM8	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. LRsD2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. LRsD3	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. LRsM1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. R1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. R2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. R3	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. R4	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. R5	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. RsI12	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. RsI17	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. RsI4	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. RsW10	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	sp. RsW2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	uncultured archaeon Ar40	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	uncultured *Methanobrevibacter* sp.	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	uncultured termite gut bacterium Cd30	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC12	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC13	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC15	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC19	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC20	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC23	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC24	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC25	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC26	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC27	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC28	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC32	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC33	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC40	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC41	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC44	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC50	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC51	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC52	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC53	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC61	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC65	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanobrevibacter*	unidentified methanogen ARC66	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	*Stadtmanae*	339860
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	sp. R6	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	Uncultured *Methanosphaera* sp.	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	unidentified methanogen ARC14	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	unidentified methanogen ARC17	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	unidentified methanogen ARC18	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	unidentified methanogen ARC21	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	unidentified methanogen ARC29	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	unidentified methanogen ARC30	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	unidentified methanogen ARC39	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	unidentified methanogen ARC43	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	unidentified methanogen ARC49	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	unidentified methanogen ARC62	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanosphaera*	Unidentified methanogen ARC8	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	*defluvii*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	*marburgensis*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	*thermautotrophicus* str. Delta H	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	*thermautotrophicus* str. Winter	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	*thermoflexus*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	*thermophilus*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	*wolfeii*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	sp. RY3	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	sp. THUT3	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	sp. enrichment clone M2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	sp. enrichment clone PY1	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	sp. enrichment clone PY2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	sp. enrichment clone SA11	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermobacter*	sp. enrichment clone SA2	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon A2.95.53	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon A8.96.15	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon A9.96.64	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 12aF	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 14aZ	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 15aZ	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 1aR	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 1aZ	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 25aG	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 26aM	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 2aG	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 36aR	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 37aM	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 3aG	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 40aM	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 55aZ	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 58aZ	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon 77aZ	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon RMAS	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	methanogen 5c	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	methanogen MEm1 associated with *Eudiplodinium maggii*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	methanogen MEm2 associated with *Eudiplodinium maggii*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	methanogen MEm3 associated with *Eudiplodinium maggii*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	methanogen MIp1 associated with *Isotricha prostoma*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	methanogen MIp2 associated with *Isotricha prostoma*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	methanogen MPm1 associated with *Polyplastron multivesiculatum*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	methanogen MPm2 associated with *Polyplastron multivesiculatum*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	methanogen MPm3 associated with *Polyplastron multivesiculatum*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	*Methanobacteriaceae archaeon* enrichment clone M13	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	*Methanobacteriaceae archaeon* enrichment culture clone MBT-13	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured Methanobacteriaceae *archaeon*	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen MRE08	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR07	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR09	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR11	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR12	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR16	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR18	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR21	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR23	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR26	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR27	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR29	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR37	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR44	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-MCR45	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME01	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME05	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME07	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME09	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME10	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME15	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME29	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME31	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME36	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME38	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME44	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME45	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME47	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured methanogen RS-ME50	
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermus*	*fervidus*	523846
Methanobacteria	Methanobacteriales	Methanobacteriaceae	*Methanothermus*	*sociabilis*	2181
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	enrichment culture E21A2	114581
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	archaeon enrichment clone M65	388592
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	uncultured Methanobacteriales archaeon	194842
Methanobacteria	Methanobacteriales	Methanobacteriaceae	Unclassified	Unidentified Methanobacteriales	58668
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	*fervens*	573064
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	*indicus*	213231
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	*infernus*	573063
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	*jannaschii*	243232
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	*vulcanius*	579137
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	sp. 70-8-3	345590
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	sp. E1885-M	269226
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	sp. FS406-22	644281
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	sp. KIN24-T80	667126
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	sp. Mc-1-85	213203
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	sp. Mc-2-70	213204
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	sp. Mc-2-85	213203
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	sp. Mc-365-70	213206
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	sp. Mc-365-85	213207
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	sp. Mc-I-85	213208
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	sp. Mc-S-85	213209
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanocaldococcus*	Unclassified	328406
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanotorris*	*formicicus*	213185
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanotorris*	*igneus*	2189
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanotorris*	sp. Mc-I-70	213186
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanotorris*	sp. Mc-S-70	213187
Methanococci	Methanococcales	Methanocaldococcaceae	*Methanotorris*	Unclassified	549381
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	*aeolicus*	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	*maripaludis*	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	*vannielii*	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	*voltae*	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	sp. Mc55_19	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	sp. Mc55_2	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	sp. Mc55_20	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	sp. Mc70_1	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	sp. Mc70_2	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	sp. Mc85_2	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	sp. Ms33_19	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	sp. Ms33_20	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	sp. Ms55_19	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	sp. Ms55_20	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	sp. P2F9701a	
Methanococci	Methanococcales	Methanococcaceae	*Methanococcus*	Unclassified	262498
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	*okinawensis*	
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	*thermolithotrophicus*	
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	sp. E1855-M	
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	sp. Ep55	
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	sp. Ep70	
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	sp. Mc-1-55	
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	sp. Mc37	
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	sp. Mc55	
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	sp. Mc70	
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	sp. Mc70_19	
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	sp. Pal55-Mc	
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	sp. enrichment clone M11	388596
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	sp. enrichment clone M37	388597
Methanococci	Methanococcales	Methanococcaceae	*Methanothermococcus*	Unclassified	269251
Methanococci	Methanococcales	Unclassified	Unclassified	archaeal str. vp183	114585
Methanococci	Methanococcales	Unclassified	Unclassified	archaeal str. vp21	114587
Methanococci	Methanococcales	Unclassified	Unclassified	hyperthermophilic methanogen FS406-22	412882
Methanococci	Methanococcales	Unclassified	Unclassified	Unclassified	345627
Methanomicrobia	Methanocellales	Methanocellaceae	*Methanocella*	*paludicola*	304371
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	*aggregans*	176294
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	*bavaricum*	
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	*labreanum*	
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	*parvum*	
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	*sinense*	
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	sp. MSP	
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	sp. T07	
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	sp. T08	
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	*Metopus contortus* archaeal symbiont	
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	*Metopus palaeformis* endosymbiont	
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	*Trimyema* sp. archaeal symbiont	
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	Unclassified	176309
Methanomicrobia	Methanomicrobiales	Methanocorpusculaceae	*Methanocorpusculum*	uncultured archaeon Ar37	97121
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	*bourgensis*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	*chikugoensis*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	*marisnigri*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	*marisnigri* JR1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	*palmolei*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	*receptaculi*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	*submarinus*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	*thermophilus*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	Unclassified	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. 10	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. 20	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. 22	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. BA1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. dm2	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. HC	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. HC-1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. IIE1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. LH	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. LH2	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. M06	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. M07	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. M11	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. MAB1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. MAB2	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. MAB3	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. MQ-4	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. RPS4	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. T02	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. T03	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. T05	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. T10	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. T14	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. enrichment culture clone BAMC-1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	sp. enrichment culture clone BAMC-2	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoculleus*	uncultured sp.	183762
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanofollis*	*aquaemaris*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanofollis*	*ethanolicus*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanofollis*	*formosanus*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanofollis*	*liminatans*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanofollis*	*tationis*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanofollis*	sp. YCM2	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanofollis*	sp. YCM3	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanofollis*	sp. YCM4	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanofollis*	Unclassified	262500
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanogenium*	*boonei*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanogenium*	*cariaci*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanogenium*	*frigidum*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanogenium*	*marinum*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanogenium*	*organophilum*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanogenium*	sp. AK-8	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanogenium*	*archaeon* ACE1_A	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanogenium*	*archaeon* SCALE-14	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanogenium*	Unclassified	292409
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoplanus*	*endosymbiosus*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoplanus*	*limicola*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoplanus*	*petrolearius*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoplanus*	sp. MobH	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanoplanus*	Unclassified	404323
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	*archaeon* 11aR	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	*archaeon* 22aZ	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	*archaeon* 29aM	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	*archaeon* 34aM	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	*archaeon* 56aR	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	*archaeon* 66aM	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	*archaeon* 6aM	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	strain EBac	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	*Nasutitermes takasagoensis* symbiont MNt1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	*Nasutitermes takasagoensis* symbiont MNt2	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	*Pericapritermes nitobei* symbiont MPn1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	*Plagiopyla nasuta* symbiont	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	methanogenic endosymbiont of *Brachonella* sp.	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	methanogenic endosymbiont of *Caenomorpha* sp.	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	methanogenic endosymbiont of *Caenomorpha* sp. 10	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	methanogenic endosymbiont of *Caenomorpha* sp. 2	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	methanogenic endosymbiont of *Caenomorpha*-like sp. 1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	methanogenic endosymbiont of *Caenomorpha*-like sp. 4	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	methanogenic endosymbiont of *Caenomorpha*-like sp. 8	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured *archaeon* ACE4_A	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured *archaeon* Ar27	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured *archaeon* Ar32	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured *archaeon* BURTON24_A	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured *Methanomicrobiaceae archaeon*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 10	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 12	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 19	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 20	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 22	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 31	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 34	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 36	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 38	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 41	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 46	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 47	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 48	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 49	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 52	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 55	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 57	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 58	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 60	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	Unclassified	uncultured sheep rumen methanogen clone 9	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanospirillum*	*hungatei*	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanospirillum*	Unclassified	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanospirillum*	sp. K18-1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanospirillum*	sp. TM20-1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanospirillum*	sp. enrichment culture clone D2CL__Arch__16S__clone2A	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanospirillum*	sp. enrichment culture clone D2CL__Arch__16S__clone2B	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanospirillum*	sp. enrichment culture clone D2CL__mvrD__Clone1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanospirillum*	Unclassified	262503
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanospirillum*	Unclassified	346907
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanomicrobium* mobile	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanobacterium* sp. enrichment culture clone MBT-1	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanobacterium* sp. enrichment culture clone MBT-10	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanobacterium* sp. enrichment culture clone MBT-12	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanobacterium* sp. enrichment culture clone MBT-2	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanobacterium* sp. enrichment culture clone MBT-3	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanobacterium* sp. enrichment culture clone MBT-5	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanobacterium* sp. enrichment culture clone MBT-6	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanobacterium* sp. enrichment culture clone MBT-7	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanobacterium* sp. enrichment culture clone MBT-8	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanobacterium* sp. enrichment culture clone MBT-9	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	*Methanomicrobium* sp. enrichment culture clone MBT-4	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanomicrobium*	uncultured Methanomicrobium sp.	
Methanomicrobia	Methanomicrobiales	Methanomicrobiaceae	*Methanolacinia*	*Methanolacinia paynteri*	
Methanopyri	Methanopyrales	Methanopyraceae		uncultured *Methanopyrales archaeon*	345629

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Thermococci	Thermococcales	Thermococcaceae	*Palaeococcus*	*ferrophilus*	
Thermococci	Thermococcales	Thermococcaceae	*Palaeococcus*	*Helgesonii*	
Thermococci	Thermococcales	Thermococcaceae	*Palaeococcus*	Sp. Ax00-33	
Thermococci	Thermococcales	Thermococcaceae	*Pyrococcus*	*abyssi*	
Thermococci	Thermococcales	Thermococcaceae	*Pyrococcus*	*Furiosus*	
Thermococci	Thermococcales	Thermococcaceae	*Pyrococcus*	*Glycovorans*	
Thermococci	Thermococcales	Thermococcaceae	*Pyrococcus*	*Horikoshii*	
Thermococci	Thermococcales	Thermococcaceae	*Pyrococcus*	*Pyrococcus woesei*	
				Pyrococcus sp.	
				Pyrococcus sp. 12/1	
				Pyrococcus sp. 121	
				Pyrococcus sp. 303	
				Pyrococcus sp. 304	
				Pyrococcus sp. 312	
				Pyrococcus sp. 32-4	
				Pyrococcus sp. 321	
				Pyrococcus sp. 322	
				Pyrococcus sp. 323	
				Pyrococcus sp. 324	
				Pyrococcus sp. 95-12-1	
				Pyrococcus sp. AV5	
				Pyrococcus sp. Ax99-7	
				Pyrococcus sp. C2	
				Pyrococcus sp. CH1	
				Pyrococcus sp. ES4	
				Pyrococcus sp. EX2	
				Pyrococcus sp. Fla95-Pc	
				Pyrococcus sp. GB-3A	
				Pyrococcus sp. GB-D	
				Pyrococcus sp. GBD	
				Pyrococcus sp. GI-H	
				Pyrococcus sp. GI-J	
				Pyrococcus sp. GIL	
				Pyrococcus sp. HT3	
				Pyrococcus sp. JT1	
				Pyrococcus sp. MA2.31	
				Pyrococcus sp. MA2.32	
				Pyrococcus sp. MA2.34	
				Pyrococcus sp. MV1019	
				Pyrococcus sp. MV4	
				Pyrococcus sp. MV7	
				Pyrococcus sp. MZ14	
				Pyrococcus sp. MZ4	
				Pyrococcus sp. NA2	
				Pyrococcus sp. NS102-T	
				Pyrococcus sp. Pikanate 5017	
				Pyrococcus sp. ST700	
				Pyrococcus sp. Tc-2-70	
				Pyrococcus sp. Tc95-7C-I	
				Pyrococcus sp. TC95-7C-S	
				Pyrococcus sp. Tc95_6	
				Pyrococcus sp. V211	
				Pyrococcus sp. V212	
				Pyrococcus sp. V221	
				Pyrococcus sp. V222	
				Pyrococcus sp. V231	
				Pyrococcus sp. V232	
				Pyrococcus sp. V61	
				Pyrococcus sp. V62	
				Pyrococcus sp. V63	
				Pyrococcus sp. V72	
				Pyrococcus sp. V73	
				Pyrococcus sp. VB112	
				Pyrococcus sp. VB113	
				Pyrococcus sp. VB81	
				Pyrococcus sp. VB82	
				Pyrococcus sp. VB83	
				Pyrococcus sp. VB85	
				Pyrococcus sp. VB86	
				Pyrococcus sp. VB93	
			Thermococcus	*Thermococcus acidaminovorans*	
				Thermococcus aegaeus	
				Thermococcus aggregans	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
				Thermococcus alcaliphilus	
				Thermococcus atlanticus	
				Thermococcus barophilus	
				Thermococcus barophilus MP	
				Thermococcus barossii	
				Thermococcus celer	
				Thermococcus celericrescens	
				Thermococcus chitonophagus	
				Thermococcus coalescens	
				Thermococcus fumicolans	
				Thermococcus gammatolerans	
				Thermococcus gammatolerans EJ3	
				Thermococcus gorgonarius	
				Thermococcus guaymasensis	
				Thermococcus hydrothermalis	
				Thermococcus kodakarensis	
				Thermococcus kodakarensis KOD1	
				Thermococcus litoralis	
				Thermococcus litoralis DSM 5473	
				Thermococcus marinus	
				Thermococcus mexicalis	
				Thermococcus nautilus	
				Thermococcus onnurineus	
				Thermococcus onnurineus NA1	
				Thermococcus pacificus	
				Thermococcus peptonophilus	
				Thermococcus peptonophilus JCM 9653	
				Thermococcus profundus	
				Thermococcus radiotolerans	
				Thermococcus sibiricus	
				Thermococcus sibiricus MM 739	
				Thermococcus siculi	
				Thermococcus stetteri	
				Thermococcus thioreducens	
				Thermococcus waimanguensis	
				Thermococcus waiotapuensis	
				Thermococcus zilligii	
				Thermococcus sp.	
				Thermococcus sp. 'AEPII 1a'	
				Thermococcus sp. 'Bio pl 0405IT2'	
				Thermococcus sp. 11N.A5	
				Thermococcus sp. 12-4	
				Thermococcus sp. 13-2	
				Thermococcus sp. 13-3	
				Thermococcus sp. 1519	
				Thermococcus sp. 21-1	
				Thermococcus sp. 23-1	
				Thermococcus sp. 23-2	
				Thermococcus sp. 26-2	
				Thermococcus sp. 26-3	
				Thermococcus sp. 26/2	
				Thermococcus sp. 28-1	
				Thermococcus sp. 29-1	
				Thermococcus sp. 300-Tc	
				Thermococcus sp. 31-1	
				Thermococcus sp. 31-3	
				Thermococcus sp. 5-1	
				Thermococcus sp. 70-4-2	
				Thermococcus sp. 83-5-2	
				Thermococcus sp. 9N2	
				Thermococcus sp. 9N2.20	
				Thermococcus sp. 9N2.21	
				Thermococcus sp. 9N3	
				Thermococcus sp. 9oN-7	
				Thermococcus sp. A4	
				Thermococcus sp. AF1T14.13	
				Thermococcus sp. AF1T1423	
				Thermococcus sp. AF1T20.11	
				Thermococcus sp. AF1T6.10	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
				Thermococcus sp. AF1T6.12	
				Thermococcus sp. AF1T6.63	
				Thermococcus sp. AF2T511	
				Thermococcus sp. Ag85-vw	
				Thermococcus sp. AM4	
				Thermococcus sp. AMT11	
				Thermococcus sp. Anhete70-I78	
				Thermococcus sp. Anhete70-SCI	
				Thermococcus sp. Anhete85-I78	
				Thermococcus sp. Anhete85-SCI	
				Thermococcus sp. AT1273	
				Thermococcus sp. Ax00-17	
				Thermococcus sp. Ax00-27	
				Thermococcus sp. Ax00-39	
				Thermococcus sp. Ax00-45	
				Thermococcus sp. Ax01-2	
				Thermococcus sp. Ax01-3	
				Thermococcus sp. Ax01-37	
				Thermococcus sp. Ax01-39	
				Thermococcus sp. Ax01-61	
				Thermococcus sp. Ax01-62	
				Thermococcus sp. Ax01-65	
				Thermococcus sp. Ax98-43	
				Thermococcus sp. Ax98-46	
				Thermococcus sp. Ax98-48	
				Thermococcus sp. Ax99-47	
				Thermococcus sp. Ax99-57	
				Thermococcus sp. Ax99-67	
				Thermococcus sp. B1	
				Thermococcus sp. B1001	
				Thermococcus sp. B4	
				Thermococcus sp. BHI60a21	
				Thermococcus sp. BHI80a28	
				Thermococcus sp. BHI80a40	
				Thermococcus sp. CAR-80	
				Thermococcus sp. CKU-1	
				Thermococcus sp. CKU-199	
				Thermococcus sp. CL1	
				Thermococcus sp. CL2	
				Thermococcus sp. CMI	
				Thermococcus sp. CNR-5	
				Thermococcus sp. CX1	
				Thermococcus sp. CX2	
				Thermococcus sp. CX3	
				Thermococcus sp. CX4	
				Thermococcus sp. CYA	
				Thermococcus sp. Dex80a71	
				Thermococcus sp. Dex80a75	
				Thermococcus sp. ES1	
				Thermococcus sp. Fe85_1_2	
				Thermococcus sp. GB18	
				Thermococcus sp. GB20	
				Thermococcus sp. GE8	
				Thermococcus sp. Gorda2	
				Thermococcus sp. Gorda3	
				Thermococcus sp. Gorda4	
				Thermococcus sp. Gorda5	
				Thermococcus sp. Gorda6	
				Thermococcus sp. GT	
				Thermococcus sp. GU5L5	
				Thermococcus sp. HJ21	
				Thermococcus sp. JDF-3	
				Thermococcus sp. KI	
				Thermococcus sp. KS-1	
				Thermococcus sp. KS-8	
				Thermococcus sp. MA2.27	
				Thermococcus sp. MA2.28	
				Thermococcus sp. MA2.29	
				Thermococcus sp. MA2.33	
				Thermococcus sp. MV1031	
				Thermococcus sp. MV1049	
				Thermococcus sp. MV1083	
				Thermococcus sp. MV1092	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
				Thermococcus sp. MV1099	
				Thermococcus sp. MZ1	
				Thermococcus sp. MZ10	
				Thermococcus sp. MZ11	
				Thermococcus sp. MZ12	
				Thermococcus sp. MZ13	
				Thermococcus sp. MZ2	
				Thermococcus sp. MZ3	
				Thermococcus sp. MZ5	
				Thermococcus sp. MZ6	
				Thermococcus sp. MZ8	
				Thermococcus sp. MZ9	
				Thermococcus sp. NS85-T	
				Thermococcus sp. P6	
				Thermococcus sp. Pd70	
				Thermococcus sp. Pd85	
				Thermococcus sp. Rt3	
				Thermococcus sp. SB611	
				Thermococcus sp. SN531	
				Thermococcus sp. SRB55_1	
				Thermococcus sp. SRB70_1	
				Thermococcus sp. SRB70_10	
				Thermococcus sp. Tc-1-70	
				Thermococcus sp. Tc-1-85	
				Thermococcus sp. Tc-1-95	
				Thermococcus sp. Tc-2-85	
				Thermococcus sp. Tc-2-95	
				Thermococcus sp. Tc-365-70	
				Thermococcus sp. Tc-365-85	
				Thermococcus sp. Tc-365-95	
				Thermococcus sp. Tc-4-70	
				Thermococcus sp. Tc-4-85	
				Thermococcus sp. Tc-I-70	
				Thermococcus sp. Tc-I-85	
				Thermococcus sp. Tc-S-70	
				Thermococcus sp. Tc-S-85	
				Thermococcus sp. Tc55_1	
				Thermococcus sp. Tc55_12	
				Thermococcus sp. Tc70-4C-I	
				Thermococcus sp. Tc70-4C-S	
				Thermococcus sp. Tc70-7C-I	
				Thermococcus sp. Tc70-7C-S	
				Thermococcus sp. Tc70-CRC-I	
				Thermococcus sp. Tc70-CRC-S	
				Thermococcus sp. Tc70-MC-S	
				Thermococcus sp. Tc70-SC-I	
				Thermococcus sp. Tc70-SC-S	
				Thermococcus sp. Tc70-vw	
				Thermococcus sp. Tc70_1	
				Thermococcus sp. Tc70_10	
				Thermococcus sp. Tc70_11	
				Thermococcus sp. Tc70_12	
				Thermococcus sp. Tc70_20	
				Thermococcus sp. Tc70_6	
				Thermococcus sp. Tc70_9	
				Thermococcus sp. Tc85-0 age SC	
				Thermococcus sp. Tc85-4C-I	
				Thermococcus sp. Tc85-4C-S	
				Thermococcus sp. Tc85-7C-S	
				Thermococcus sp. Tc85-CRC-I	
				Thermococcus sp. Tc85-CRC-S	
				Thermococcus sp. Tc85-MC-I	
				Thermococcus sp. Tc85-MC-S	
				Thermococcus sp. Tc85-SC-I	
				Thermococcus sp. Tc85-SC-ISCS	
				Thermococcus sp. Tc85-SC-S	
				Thermococcus sp. Tc85_1	
				Thermococcus sp. Tc85_10	
				Thermococcus sp. Tc85_11	
				Thermococcus sp. Tc85_12	
				Thermococcus sp. Tc85_13	
				Thermococcus sp. Tc85_19	
				Thermococcus sp. Tc85_2	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
				Thermococcus sp. Tc85__20	
				Thermococcus sp. Tc85__9	
				Thermococcus sp. Tc95-CRC-I	
				Thermococcus sp. Tc95-CRC-S	
				Thermococcus sp. Tc95-MC-I	
				Thermococcus sp. Tc95-MC-S	
				Thermococcus sp. Tc95-SC-S	
				Thermococcus sp. TK1	
				Thermococcus sp. TM1	
				Thermococcus sp. TS3	
				Thermococcus sp. vp197	
				environmental samples	
				Thermococcus sp. enrichment clone SA3	
				uncultured *Thermococcus* sp.	
Thermoplasmata	Thermoplasmatales	Ferroplasmaceae	*Acidiplasma*	*aeolicum*	507754
		Ferroplasmaceae	*Ferroplasma*	*acidarmanus*	
		Ferroplasmaceae	*Ferroplasma*	*acidiphilum*	
		Ferroplasmaceae	*Ferroplasma*	*Cupricumulans*	
		Ferroplasmaceae	*Ferroplasma*	*Thermophilum*	
		Ferroplasmaceae	*Ferroplasma*	Sp. JTC3	
		Ferroplasmaceae	*Ferroplasma*	Sp. clone E8A015	
		Ferroplasmaceae	*Ferroplasma*	Sp. Type II	
		Ferroplasmaceae	*Ferroplasma*	Uncultured *Ferroplasma* sp.	
		Picrophilaceae	*Picrophilus*	*Oshimae*	
		Picrophilaceae	*Picrophilus*	*torridus*	
		Thermoplasmataceae	Thermoplasmataceae	*Acidophilum*	
		Thermoplasmataceae	Thermoplasmataceae	*Volcanium*	
		Thermoplasmataceae	Thermoplasmataceae	Sp. 67.1	
		Thermoplasmataceae	Thermoplasmataceae	Sp. P61	
		Thermoplasmataceae	Thermoplasmataceae	Sp. S01	
		Thermoplasmataceae	Thermoplasmataceae	Sp. S02	
		Thermoplasmataceae	Thermoplasmataceae	Sp. Xt101	
		Thermoplasmataceae	Thermoplasmataceae	Xt102	
		Thermoplasmataceae	Thermoplasmataceae	XT103	
		Thermoplasmataceae	Thermoplasmataceae	XT107	
		Thermoplasmataceae	*Thermogymnomonas*	*acidicola*	
unclassified	unclassified	unclassified	Unclassified	uncultured SA2 group euryarchaeote	
				uncultured SA1 group euryarchaeote	
				uncultured marine euryarchaeote DH148-Y15	
				uncultured marine euryarchaeote DH148-Y16	
				uncultured marine euryarchaeote DH148-Y19	
				uncultured marine euryarchaeote DH148-Y2	
				uncultured marine euryarchaeote DH148-Y4	
				uncultured marine euryarchaeote DH148-Z1	
				uncultured marine group IV euryarchaeote	
				uncultured marine group III euryarchaeote	
				uncultured marine group III euryarchaeote AD1000-40-D7	
				uncultured marine group III euryarchaeote HF10__21C05	
				uncultured marine group III euryarchaeote HF130__43E12	
				uncultured marine group III euryarchaeote HF130__95B02	
				uncultured marine group III euryarchaeote HF200__25B11	
				uncultured marine group III euryarchaeote HF500__17G02	
				uncultured marine group III euryarchaeote KM3-28-E8	
				uncultured marine group III euryarchaeote SAT1000-53-B3	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
				uncultured marine group II euryarchaeote	
				uncultured marine group II euryarchaeote 37F11	
				uncultured marine group II euryarchaeote AD1000-18-D2	
				uncultured marine group II euryarchaeote DeepAnt-15E7	
				uncultured marine group II euryarchaeote DeepAnt-JyKC7	
				uncultured marine group II euryarchaeote EF100_57A08	
				uncultured marine group II euryarchaeote HF10_15F03	
				uncultured marine group II euryarchaeote HF10_15F05	
				uncultured marine group II euryarchaeote HF10_15G04	
				uncultured marine group II euryarchaeote HF10_20F02	
				uncultured marine group II euryarchaeote HF10_24E03	
				uncultured marine group II euryarchaeote HF10_25H10	
				uncultured marine group II euryarchaeote HF10_27F06	
				uncultured marine group II euryarchaeote HF10_28B09	
				uncultured marine group II euryarchaeote HF10_29E05	
				uncultured marine group II euryarchaeote HF10_30E08	
				uncultured marine group II euryarchaeote HF10_30F11	
				uncultured marine group II euryarchaeote HF10_35F06	
				uncultured marine group II euryarchaeote HF10_36B02	
				uncultured marine group II euryarchaeote HF10_39E10	
				uncultured marine group II euryarchaeote HF10_43A09	
				uncultured marine group II euryarchaeote HF10_48G07	
				uncultured marine group II euryarchaeote HF10_53B05	
				uncultured marine group II euryarchaeote HF10_61D03	
				uncultured marine group II euryarchaeote HF10_65D04	
				uncultured marine group II euryarchaeote HF10_73E12	
				uncultured marine group II euryarchaeote HF10_8H07	
				uncultured marine group II euryarchaeote HF10_90C09	
				uncultured marine group II euryarchaeote HF130_17B12	
				uncultured marine group II euryarchaeote HF130_17D07	
				uncultured marine group II euryarchaeote HF130_21B04	
				uncultured marine group II euryarchaeote HF130_26G06	
				uncultured marine group II euryarchaeote HF130_27A09	
				uncultured marine group II euryarchaeote HF130_28F07	
				uncultured marine group II euryarchaeote HF130_29F10	
				uncultured marine group II euryarchaeote HF130_30F08	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
				uncultured marine group II euryarchaeote HF130_31B11	
				uncultured marine group II euryarchaeote HF130_32D03	
				uncultured marine group II euryarchaeote HF130_33C02	
				uncultured marine group II euryarchaeote HF130_34E01	
				uncultured marine group II euryarchaeote HF130_35A10	
				uncultured marine group II euryarchaeote HF130_37H07	
				uncultured marine group II euryarchaeote HF130_40B01	
				uncultured marine group II euryarchaeote HF130_40B02	
				uncultured marine group II euryarchaeote HF130_40G07	
				uncultured marine group II euryarchaeote HF130_40G09	
				uncultured marine group II euryarchaeote HF130_44A02	
				uncultured marine group II euryarchaeote HF130_49F04	
				uncultured marine group II euryarchaeote HF130_4G08	
				uncultured marine group II euryarchaeote HF130_56E12	
				uncultured marine group II euryarchaeote HF130_67F08	
				uncultured marine group II euryarchaeote HF130_6E07	
				uncultured marine group II euryarchaeote HF130_71B05	
				uncultured marine group II euryarchaeote HF130_73G01	
				uncultured marine group II euryarchaeote HF130_75B06	
				uncultured marine group II euryarchaeote HF130_76G06	
				uncultured marine group II euryarchaeote HF130_83E02	
				uncultured marine group II euryarchaeote HF130_88G10	
				uncultured marine group II euryarchaeote HF130_90E09	
				uncultured marine group II euryarchaeote HF130_94A03	
				uncultured marine group II euryarchaeote HF200_101H01	
				uncultured marine group II euryarchaeote HF200_102F03	
				uncultured marine group II euryarchaeote HF200_103E03	
				uncultured marine group II euryarchaeote HF200_15F06	
				uncultured marine group II euryarchaeote HF200_25F07	
				uncultured marine group II euryarchaeote HF200_35B05	
				uncultured marine group II euryarchaeote HF200_35E02	
				uncultured marine group II euryarchaeote HF200_43D02	
				uncultured marine group II euryarchaeote HF200_44E05	
				uncultured marine group II euryarchaeote HF200_49H12	
				uncultured marine group II euryarchaeote HF200_50D06	
				uncultured marine group II euryarchaeote HF200_63E02	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
				uncultured marine group II euryarchaeote HF200_64G08	
				uncultured marine group II euryarchaeote HF200_65H08	
				uncultured marine group II euryarchaeote HF200_66A10	
				uncultured marine group II euryarchaeote HF200_70E08	
				uncultured marine group II euryarchaeote HF200_71A04	
				uncultured marine group II euryarchaeote HF200_72A06	
				uncultured marine group II euryarchaeote HF200_78D05	
				uncultured marine group II euryarchaeote HF200_84A01	
				uncultured marine group II euryarchaeote HF200_89A11	
				uncultured marine group II euryarchaeote HF200_97B09	
				uncultured marine group II euryarchaeote HF500_100E05	
				uncultured marine group II euryarchaeote HF500_11G07	
				uncultured marine group II euryarchaeote HF500_22F05	
				uncultured marine group II euryarchaeote HF500_24F01	
				uncultured marine group II euryarchaeote HF500_25E08	
				uncultured marine group II euryarchaeote HF500_26A05	
				uncultured marine group II euryarchaeote HF500_30A08	
				uncultured marine group II euryarchaeote HF500_47D04	
				uncultured marine group II euryarchaeote HF500_56B09	
				uncultured marine group II euryarchaeote HF500_58A11	
				uncultured marine group II euryarchaeote HF500_67F10	
				uncultured marine group II euryarchaeote HF70_105F02	
				uncultured marine group II euryarchaeote HF70_106D07	
				uncultured marine group II euryarchaeote HF70_14F12	
				uncultured marine group II euryarchaeote HF70_25A12	
				uncultured marine group II euryarchaeote HF70_39H11	
				uncultured marine group II euryarchaeote HF70_41E01	
				uncultured marine group II euryarchaeote HF70_48A05	
				uncultured marine group II euryarchaeote HF70_48G03	
				uncultured marine group II euryarchaeote HF70_51B02	
				uncultured marine group II euryarchaeote HF70_53G11	
				uncultured marine group II euryarchaeote HF70_59C08	
				uncultured marine group II euryarchaeote HF70_89B11	
				uncultured marine group II euryarchaeote HF70_91G08	
				uncultured marine group II euryarchaeote HF70_95E04	
				uncultured marine group II euryarchaeote HF70_97E04	

TABLE 1-continued

Class	Order	Family	Genus	Species	Taxonomy ID
				uncultured marine group II euryarchaeote KM3-130-D10	
				uncultured marine group II euryarchaeote KM3-136-D10	
				uncultured marine group II euryarchaeote KM3-72-G3	
				uncultured marine group II euryarchaeote KM3-85-F5	
				uncultured marine group II euryarchaeote SAT1000-15-B12	
				uncultured archaeon ACE-6	
				uncultured archaeon BURTON-41	
				uncultured archaeon BURTON-47	
				uncultured archaeon CLEAR-15	
				uncultured archaeon CLEAR-24	
				uncultured archaeon PENDANT-17	
				uncultured archaeon PENDANT-33	
				euryarchaeote J3.25-8	
				euryarchaeote D4.75-18 115532	
				euryarchaeote D4.75-4	
				euryarchaeote DJ3.25-13	
				euryarchaeote J4.75-12	
				euryarchaeote J4.75-15	
				euryarchaeote J4.75-24	
				euryarchaeote SvA99MeOH	
				euryarchaeote SvA99TMA	
				methanogenic archaeon CH1270	
				methanogenic archaeon F1/B-1	
				methanogenic archaeon F1/B-2	
				methanogenic archaeon F1/B-3	
				methanogenic archaeon F1/P-1	
				methanogenic archaeon F1/P-2	
				methanogenic archaeon F1/P-3	
				methanogenic archaeon F4/B-1	
				methanogenic archaeon F4/B-2	
				methanogenic archaeon F4/B-3	
				methanogenic archaeon F4/P-1	
				methanogenic archaeon F4/P-2	
				methanogenic archaeon F4/P-3	
				methanogenic archaeon U3/B-1	
				methanogenic archaeon U3/P-1	
				methanogen sp.	

TABLE 2

Name of Unclassified Species	Taxonomy ID No.
euryarchaeote enrichment culture clone BAMC-3	679265
euryarchaeote enrichment culture clone MST-5	645575
euryarchaeote enrichment culture clone T-RF243d	670234
euryarchaeote enrichment culture clone T-RF243e	670235
euryarchaeote enrichment culture clone T-RF259	670236
planktonic euryarchaeote	110443
uncultured archaeon BA1a1	92881
uncultured archaeon BA1a2	92882
uncultured archaeon BA1b1	92883
uncultured archaeon BA2e8	92884
uncultured archaeon BA2F4fin	92893
uncultured archaeon BA2H11fin	92894
uncultured archaeon O23F7	114539
uncultured archaeon TA1a4	92885
uncultured archaeon TA1a6	92890
uncultured archaeon TA1a9	92888
uncultured archaeon TA1b12	92886
uncultured archaeon TA1c9	92889
uncultured archaeon TA1e6	92890
uncultured archaeon TA1f2	92891
uncultured archaeon TA2e12	92892
uncultured archaeon WCHA1-57	74278
uncultured archaeon WCHA2-08	74279
uncultured archaeon WCHD3-02	74273
uncultured archaeon WCHD3-07	74274
uncultured archaeon WCHD3-16	74275
uncultured archaeon WCHD3-30	74263
uncultured archaeon WCHD3-33	74276
uncultured archaeon WCHD3-34	74277
uncultured euryarchaeote	114243
uncultured euryarchaeote a118ev	117334
uncultured euryarchaeote a50ev	117335
uncultured euryarchaeote a60ev	117333
uncultured euryarchaeote Alv-FOS1	337892
uncultured euryarchaeote Alv-FOS4	337893
uncultured euryarchaeote Alv-FOS5	337891

TABLE 2-continued

Name of Unclassified Species	Taxonomy ID No.
uncultured euryarchaeote AM-20A__122	115055
uncultured euryarchaeote AM-20A__123	115056
uncultured euryarchaeote ARMAN-1	425594
uncultured euryarchaeote AT-200__29	115057
uncultured euryarchaeote AT-200__P25	115058
uncultured euryarchaeote AT-5__21	115059
uncultured euryarchaeote AT-5__P24	115060
uncultured euryarchaeote CA-15__22	115061
uncultured euryarchaeote CA-15__23	115062
uncultured euryarchaeote CA-15__27	115063
uncultured euryarchaeote CA-15__32	115064
uncultured euryarchaeote CA-15__P4	115065
uncultured euryarchaeote DF-5__21	115066
uncultured euryarchaeote June4.75-16	134989
uncultured euryarchaeote ME-450__21	115067
uncultured euryarchaeote ME-450__30	115068
uncultured euryarchaeote ME-450__38	115069
uncultured euryarchaeote ME-450__P14	115070
uncultured euryarchaeote ME-450__P9	115071
uncultured euryarchaeote pBRKC101	91308
uncultured euryarchaeote pBRKC112	91309
uncultured euryarchaeote pBRKC128	91310
uncultured euryarchaeote pBRKC134	91312
uncultured euryarchaeote pBRKC22	91306
uncultured euryarchaeote pBRKC84	91307
uncultured euryarchaeote pBRKC91	91311
uncultured euryarchaeote SB95-35	115072
uncultured euryarchaeote SB95-48	115073
uncultured euryarchaeote SB95-87	115074
uncultured euryarchaeote VAL1	85383
uncultured euryarchaeote VAL112	85386
uncultured euryarchaeote VAL125	85387
uncultured euryarchaeote VAL147	85395
uncultured euryarchaeote VAL2	85384
uncultured euryarchaeote VAL28	85394
uncultured euryarchaeote VAL31-1	85396
uncultured euryarchaeote VAL33-1	85397
uncultured euryarchaeote VAL35-1	85398
uncultured euryarchaeote VAL40	85392
uncultured euryarchaeote VAL47	85388
uncultured euryarchaeote VAL68	85385
uncultured euryarchaeote VAL78	85389
uncultured euryarchaeote VAL84	85390
uncultured euryarchaeote VAL9	85393
uncultured euryarchaeote VAL90	85391
uncultured Green Bay ferromanganous micronodule archaeon ARB5	140616
uncultured Green Bay ferromanganous micronodule archaeon ARC3	140617
uncultured Green Bay ferromanganous micronodule archaeon ARF3	140614
uncultured Green Bay ferromanganous micronodule archaeon ARG4	140615
uncultured haloarchaeon MSP1	75449
uncultured haloarchaeon MSP11	75452
uncultured haloarchaeon MSP12	75453
uncultured haloarchaeon MSP14	75454
uncultured haloarchaeon MSP16	75455
uncultured haloarchaeon MSP17	75456
uncultured haloarchaeon MSP22	75457
uncultured haloarchaeon MSP23	75458
uncultured haloarchaeon MSP41	75459
uncultured haloarchaeon MSP8	75450
uncultured haloarchaeon MSP9	75451
uncultured marine archaeon AEGEAN__50	147164
uncultured marine archaeon AEGEAN__51	147166
uncultured marine archaeon AEGEAN__52	147167
uncultured marine archaeon AEGEAN__53	147168
uncultured marine archaeon AEGEAN__54	147174
uncultured marine archaeon AEGEAN__55	147169
uncultured marine archaeon AEGEAN__57	147175
uncultured marine archaeon AEGEAN__58	147176
uncultured marine archaeon AEGEAN__59	147177

TABLE 2-continued

Name of Unclassified Species	Taxonomy ID No.
uncultured marine archaeon AEGEAN__60	147178
uncultured marine archaeon AEGEAN__62	147170
uncultured marine archaeon AEGEAN__63	147171
uncultured marine archaeon AEGEAN__64	147172
uncultured marine archaeon AEGEAN__65	147173
uncultured marine archaeon AEGEAN__66	147181
uncultured marine archaeon AEGEAN__68	147179
uncultured marine archaeon AEGEAN__71	147180
uncultured marine archaeon AEGEAN__73	147182
uncultured marine archaeon AEGEAN__74	147183
uncultured marine euryarchaeote	257466
uncultured marine euryarchaeote dh148-A14	149701
uncultured marine euryarchaeote dh148-A18	149702
uncultured marine euryarchaeote dh148-A7	149700
uncultured marine euryarchaeote DH148-W1	123945
uncultured marine euryarchaeote dh148-W10	149705
uncultured marine euryarchaeote dh148-W15	149706
uncultured marine euryarchaeote dh148-W16	149707
uncultured marine euryarchaeote dh148-W17	149708
uncultured marine euryarchaeote dh148-W23	149709
uncultured marine euryarchaeote DH148-W24	123946
uncultured marine euryarchaeote dh148-W3	149703
uncultured marine euryarchaeote dh148-W9	149704
uncultured methanogen CIBARC-1	153143
uncultured methanogen CRARC-3	153144
uncultured methanogen MRE-MCR1	143132
uncultured methanogen MRE-MCR2	143133
uncultured methanogen MRE-MCR3	143134
uncultured methanogen MRE-MCR4	143135
uncultured methanogen MRE-MCR5	143136
uncultured methanogen MRE-MCR6	143137
uncultured methanogen MRE-ME1	143138
uncultured methanogen MRE-ME3	143139
uncultured methanogen MRE-ME4	143140
uncultured methanogen MRE-ME5	143141
uncultured methanogen MRE01	143138
uncultured methanogen MRE02	143139
uncultured methanogen MRE03	143144
uncultured methanogen MRE04	143145
uncultured methanogen MRE05	143146
uncultured methanogen MRE06	143147
uncultured methanogen MRE07	143148
uncultured methanogen MRE09	143149
uncultured methanogen MRE10	143150
uncultured methanogen MRE11	143151
uncultured methanogen MRE12	143152
uncultured methanogen RS-MCR01	143109
uncultured methanogen RS-MCR04	143110
uncultured methanogen RS-MCR06	143111
uncultured methanogen RS-MCR08	143112
uncultured methanogen RS-MCR10	143113
uncultured methanogen RS-MCR15	143114
uncultured methanogen RS-MCR22	143115
uncultured methanogen RS-MCR25	143116
uncultured methanogen RS-MCR40	143117
uncultured methanogen RS-MCR41	143118
uncultured methanogen RS-MCR43	143119
uncultured methanogen RS-MCR46	143120
uncultured methanogen RS-ME11	143121
uncultured methanogen RS-ME19	143122
uncultured methanogen RS-ME22	143123
uncultured methanogen RS-ME24	143124
uncultured methanogen RS-ME26	143125
uncultured methanogen RS-ME30	143126
uncultured methanogen RS-ME32	143127
uncultured methanogen RS-ME33	143128
uncultured methanogen RS-ME34	143129
uncultured methanogen RS-ME39	143130
uncultured methanogen RS-ME49	143131
uncultured methanogen VIARC-0	153145
uncultured methanogen VIARC-4	153146
uncultured methanogenic archaeon	198240

TABLE 2-continued

Name of Unclassified Species	Taxonomy ID No.
uncultured methanogenic archaeon 'South African gold mine'	260753
uncultured methanogenic archaeon RC-I	351160
uncultured methanogenic symbiont PA101	161327
uncultured methanogenic symbiont PA102	161319
uncultured methanogenic symbiont PA103	161318
uncultured methanogenic symbiont PA104	161306
uncultured methanogenic symbiont PA105	161336
uncultured methanogenic symbiont PA112	161305
uncultured methanogenic symbiont PA114	161320
uncultured methanogenic symbiont PA119	161303
uncultured methanogenic symbiont PA123	161302
uncultured methanogenic symbiont PA124	161329
uncultured methanogenic symbiont PA127	161299
uncultured methanogenic symbiont PJ101	161314
uncultured methanogenic symbiont PJ102	161335
uncultured methanogenic symbiont PJ109	161315
uncultured methanogenic symbiont PJ118	161330
uncultured methanogenic symbiont ST102	161337
uncultured methanogenic symbiont ST103	161322
uncultured methanogenic symbiont ST104	161300
uncultured methanogenic symbiont ST105	161323
uncultured methanogenic symbiont ST107	161308
uncultured methanogenic symbiont ST109	161317
uncultured methanogenic symbiont ST111	161325
uncultured methanogenic symbiont ST113	161328
uncultured methanogenic symbiont ST117	161326
uncultured methanogenic symbiont ST126	161324
uncultured methanogenic symbiont ST129	161334
uncultured methanogenic symbiont ST131	161298
uncultured methanogenic symbiont ST140	161313
uncultured methanogenic symbiont ST143	161333
uncultured methanogenic symbiont ST144	161307
uncultured methanogenic symbiont ST152	161301
uncultured methanogenic symbiont ST153	161311
uncultured methanogenic symbiont ST154	161321
uncultured methanogenic symbiont ST155	161296
uncultured methanogenic symbiont ST157	161297
uncultured methanogenic symbiont ST158	161310
uncultured methanogenic symbiont ST159	161316
uncultured methanogenic symbiont ST162	161309
uncultured methanogenic symbiont ST164	161304
uncultured methanogenic symbiont ST165	161312
uncultured methanogenic symbiont ST167	161332
uncultured methanogenic symbiont ST168	161331
unidentified euryarchaeote	29293
unidentified methanogen ARC31	68396
unidentified methanogen ARC45	68397
unidentified methanogen ARC46	68398
unidentified methanogen ARC63	68399
unidentified methanogen ARC64	68400
unidentified methanogen ARC9	68395

TABLE 3

Name of Unclassified Species	Taxonomy ID
anaerobic methanogenic archaeon E15-1	93517
anaerobic methanogenic archaeon E15-10	93526
anaerobic methanogenic archaeon E15-2	93518
anaerobic methanogenic archaeon E15-3	93519
anaerobic methanogenic archaeon E15-4	93520
anaerobic methanogenic archaeon E15-5	93521
anaerobic methanogenic archaeon E15-6	93522
anaerobic methanogenic archaeon E15-7	93523
anaerobic methanogenic archaeon E15-8	93524
anaerobic methanogenic archaeon E15-9	93525
anaerobic methanogenic archaeon E30-1	93527
anaerobic methanogenic archaeon E30-10	93536
anaerobic methanogenic archaeon E30-2	93528
anaerobic methanogenic archaeon E30-3	93529

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
anaerobic methanogenic archaeon E30-4	93530
anaerobic methanogenic archaeon E30-5	93531
anaerobic methanogenic archaeon E30-6	93532
anaerobic methanogenic archaeon E30-7	93533
anaerobic methanogenic archaeon E30-8	93534
anaerobic methanogenic archaeon E30-9	93535
anaerobic methanogenic archaeon ET1-1	93507
anaerobic methanogenic archaeon ET1-10	93516
anaerobic methanogenic archaeon ET1-2	93508
anaerobic methanogenic archaeon ET1-3	93509
anaerobic methanogenic archaeon ET1-4	93510
anaerobic methanogenic archaeon ET1-5	93511
anaerobic methanogenic archaeon ET1-6	93512
anaerobic methanogenic archaeon ET1-7	93513
anaerobic methanogenic archaeon ET1-8	93514
anaerobic methanogenic archaeon ET1-9	93515
anaerobic methanogenic archaeon SN15	548434
anaerobic methanogenic archaeon SN20	548432
anaerobic methanogenic archaeon SN22	548433
archaeon #33-9	328513
archaeon 'A215-UMH 22% pond'	199002
archaeon 'A311-UMH 31% pond'	199004
archaeon 'A315-UMH 31% pond'	199005
archaeon 'A319-UMH 31% pond'	199006
archaeon 'A356-UMH 31% pond'	199007
archaeon 'A363-UMH 31% pond'	199008
archaeon 'AN201-UMH 22% pond'	199003
archaeon 26-4a1	210392
archaeon 26-4a6	210393
archaeon 26-5a1	210394
archaeon 26-a101	210395
archaeon 26-a134	210396
archaeon 4R	323739
archaeon A1	631354
archaeon Bitterns-U	584993
archaeon CP.B3	413980
archaeon D3.5-B	115530
archaeon G70	288910
archaeon G76.1	378395
archaeon G76.3	378397
archaeon G76.4	378396
archaeon G80	288911
archaeon GSL1A	378398
archaeon GSL1C	378400
archaeon GSL1D	378399
archaeon HR3812-Enrichment-017	
archaeon HR3812-Enrichment-018	
archaeon HR3812-Enrichment-019	
archaeon HR3812-Enrichment-020	
archaeon HR3812-Enrichment-021	
archaeon HR3812-Enrichment-022	
archaeon K-4a2archaeon K-5a2	
archaeon LL25A1archaeon LL25A10	
archaeon LL25A2archaeon LL25A3	
archaeon LL25A4archaeon LL25A6	
archaeon LL25A7archaeon LL25A8	
archaeon LL37A1archaeon LL37A19	
archaeon LL37A2archaeon LL37A20	
archaeon LL37A29	
archaeon LL37A3	
archaeonLL37A33	
archaeon LL37A35	
archaeon SL1.19	
archaeon SL1.60	
archaeon SL1.61	
archaeon SL2.43	
archaeon SL2.45	
archaeon SVAL2.51	
archaeon SVAL2.52	
archaeon SVAL2.53	
archaeon SVAL2.54	
archaeon SVAL2.55	
archaeon SVAL2.56	
archaeon enrichment clone M21	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
archaeon enrichment clone M33	
archaeon enrichment culture clone 10P	
Aarchaeon enrichment culture clone 1TP	
Aarchaeon enrichment culture clone 2TP	
Aarchaeon enrichment culture clone AOM-Clone-A11	
archaeon enrichment culture clone AOM-Clone-A2	
archaeon enrichment culture clone AOM-Clone-B2	
archaeon enrichment culture clone AOM-Clone-B6	
archaeon enrichment culture clone AOM-Clone-C3	
archaeon enrichment culture clone AOM-Clone-C9	
archaeon enrichment culture clone AOM-Clone-D10	
archaeon enrichment culture clone AOM-Clone-E10	
archaeon enrichment culture clone AOM-Clone-E7	
archaeon enrichment culture clone AOM-Clone-E9	
archaeon enrichment culture clone AOM-Clone-F5	
archaeon enrichment culture clone AOM-Clone-F9	
archaeon enrichment culture clone AOM-Clone-G10	
archaeon enrichment culture clone AOM-Clone-H9	
archaeon enrichment culture clone Arch10	
archaeon enrichment culture clone ARQ17-JL	
archaeon enrichment culture clone ARQ19-JL	
archaeon enrichment culture clone ARQ2-JL	
archaeon enrichment culture clone ARQ9-JL	
archaeon enrichment culture clone C1-10C-A	
archaeon enrichment culture clone C1-11C-A	
archaeon enrichment culture clone C1-13C-A	
archaeon enrichment culture clone C1-16C-A	
archaeon enrichment culture clone C1-18C-A	
archaeon enrichment culture clone C1-19C-A	
archaeon enrichment culture clone C1-1C-A	
archaeon enrichment culture clone C1-20C-A	
archaeon enrichment culture clone C1-24C-A	
archaeon enrichment culture clone C1-26C-A	
archaeon enrichment culture clone C1-29C-A	
archaeon enrichment culture clone C1-2C-A	
archaeon enrichment culture clone C1-30C-A	
archaeon enrichment culture clone C1-31C-A	
archaeon enrichment culture clone C1-32C-A	
archaeon enrichment culture clone C1-34C-A	
archaeon enrichment culture clone C1-38C-A	
archaeon enrichment culture clone C1-3C-A	
archaeon enrichment culture clone C1-42C-A	
archaeon enrichment culture clone C1-44C-A	
archaeon enrichment culture clone C1-46C-A	
archaeon enrichment culture clone C1-47C-A	
archaeon enrichment culture clone C1-48C-A	
archaeon enrichment culture clone C1-4C-A	
archaeon enrichment culture clone C1-52C-A	
archaeon enrichment culture clone C1-5C-A	
archaeon enrichment culture clone C1-8C-A	
archaeon enrichment culture clone C3-15C-A	
archaeon enrichment culture clone C3-18C-A	
archaeon enrichment culture clone C3-1C-A	
archaeon enrichment culture clone C3-20C-A	
archaeon enrichment culture clone C3-22C-A	
archaeon enrichment culture clone C3-26C-A	
archaeon enrichment culture clone C3-33C-A	
archaeon enrichment culture clone C3-37C-A	
archaeon enrichment culture clone C3-41C-A	
archaeon enrichment culture clone C3-42C-A	
archaeon enrichment culture clone C3-47C-A	
archaeon enrichment culture clone C3-54C-A	
archaeon enrichment culture clone C3-56C-A	
archaeon enrichment culture clone C3-5C-A	
archaeon enrichment culture clone C3-7C-A	
archaeon enrichment culture clone C4-10C-A	
archaeon enrichment culture clone C4-11C-A	
archaeon enrichment culture clone C4-12C-A	
archaeon enrichment culture clone C4-14C-A	
archaeon enrichment culture clone C4-15C-A	
archaeon enrichment culture clone C4-16C-A	
archaeon enrichment culture clone C4-17C-A	
archaeon enrichment culture clone C4-18C-A	
archaeon enrichment culture clone C4-20C-A	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
archaeon enrichment culture clone C4-21C-A	
archaeon enrichment culture clone C4-22C-A	
archaeon enrichment culture clone C4-23C-A	
archaeon enrichment culture clone C4-24C-A	
archaeon enrichment culture clone C4-26C-A	
archaeon enrichment culture clone C4-27C-A	
archaeon enrichment culture clone C4-28C-A	
archaeon enrichment culture clone C4-29C-A	
archaeon enrichment culture clone C4-2C-A	
archaeon enrichment culture clone C4-30C-A	
archaeon enrichment culture clone C4-32C-A	
archaeon enrichment culture clone C4-34C-A	
archaeon enrichment culture clone C4-35C-A	
archaeon enrichment culture clone C4-37C-A	
archaeon enrichment culture clone C4-38C-A	
archaeon enrichment culture clone C4-3C-A	
archaeon enrichment culture clone C4-40C-A	
archaeon enrichment culture clone C4-41C-A	
archaeon enrichment culture clone C4-42C-A	
archaeon enrichment culture clone C4-43C-A	
archaeon enrichment culture clone C4-45C-A	
archaeon enrichment culture clone C4-46C-A	
archaeon enrichment culture clone C4-47C-A	
archaeon enrichment culture clone C4-48C-A	
archaeon enrichment culture clone C4-49C-A	
archaeon enrichment culture clone C4-4C-A	
archaeon enrichment culture clone C4-50C-A	
archaeon enrichment culture clone C4-51C-A	
archaeon enrichment culture clone C4-52C-A	
archaeon enrichment culture clone C4-54C-A	
archaeon enrichment culture clone C4-6C-A	
archaeon enrichment culture clone C4-8C-A	
archaeon enrichment culture clone C4-9C-A	
archaeon enrichment culture clone Dan60__A10E	
archaeon enrichment culture clone Dan60__A11E	
archaeon enrichment culture clone Dan60__A12E	
archaeon enrichment culture clone Dan60__A13E	
archaeon enrichment culture clone Dan60__A14E	
archaeon enrichment culture clone Dan60__A15E	
archaeon enrichment culture clone Dan60__A16E	
archaeon enrichment culture clone Dan60__A17E	
archaeon enrichment culture clone Dan60__A18E	
archaeon enrichment culture clone Dan60__A19E	
archaeon enrichment culture clone Dan60__A1E	
archaeon enrichment culture clone Dan60__A20E	
archaeon enrichment culture clone Dan60__A2E	
archaeon enrichment culture clone Dan60__A3E	
archaeon enrichment culture clone Dan60__A4E	
archaeon enrichment culture clone Dan60__A5E	
archaeon enrichment culture clone Dan60__A6E	
archaeon enrichment culture clone Dan60__A7E	
archaeon enrichment culture clone Dan60__A8E	
archaeon enrichment culture clone Dan60__A9E	
archaeon enrichment culture clone Dan60S__A10E	
archaeon enrichment culture clone Dan60S__A11E	
archaeon enrichment culture clone Dan60S__A12E	
archaeon enrichment culture clone Dan60S__A13E	
archaeon enrichment culture clone Dan60S__A14E	
archaeon enrichment culture clone Dan60S__A15E	
archaeon enrichment culture clone Dan60S__A16E	
archaeon enrichment culture clone Dan60S__A17E	
archaeon enrichment culture clone Dan60S__A18E	
archaeon enrichment culture clone Dan60S__A19E	
archaeon enrichment culture clone Dan60S__A1E	
archaeon enrichment culture clone Dan60S__A20E	
archaeon enrichment culture clone Dan60S__A2E	
archaeon enrichment culture clone Dan60S__A3E	
archaeon enrichment culture clone Dan60S__A4E	
archaeon enrichment culture clone Dan60S__A5E	
archaeon enrichment culture clone Dan60S__A6E	
archaeon enrichment culture clone Dan60S__A7E	
archaeon enrichment culture clone Dan60S__A8E	
archaeon enrichment culture clone Dan60S__A9E	
archaeon enrichment culture clone DGGE-1A	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
archaeon enrichment culture clone DGGE-2A	
archaeon enrichment culture clone DGGE-4A	
archaeon enrichment culture clone EA17.1	
archaeon enrichment culture clone EA29.3	
archaeon enrichment culture clone EA29.6	
archaeon enrichment culture clone EA3.11	
archaeon enrichment culture clone EA3.3	
archaeon enrichment culture clone EA3.5	
archaeon enrichment culture clone EA8.1	
archaeon enrichment culture clone EA8.8	
archaeon enrichment culture clone EA8.9	
archaeon enrichment culture clone HS25__1	
archaeon enrichment culture clone HS7__1	
archaeon enrichment culture clone LCB__A1C7	
archaeon enrichment culture clone LCB__A1C9	
archaeon enrichment culture clone MBT-11	
archaeon enrichment culture clone McrA2	
archaeon enrichment culture clone MST-4	
archaeon enrichment culture clone Nye-0__2-enr40	
archaeon enrichment culture clone PW15.4A	
archaeon enrichment culture clone PW15.6	
archaeon enrichment culture clone PW15.7A	
archaeon enrichment culture clone PW20.4A	
archaeon enrichment culture clone PW25.2A	
archaeon enrichment culture clone PW25.9	
archaeon enrichment culture clone PW30.6A	
archaeon enrichment culture clone PW32.12A	
archaeon enrichment culture clone PW32.5A	
archaeon enrichment culture clone PW45.1	
archaeon enrichment culture clone PW45.7A	
archaeon enrichment culture clone PW45.9A	
archaeon enrichment culture clone PW5.2A	
archaeon enrichment culture clone PW54.3A	
archaeon enrichment culture clone PW54.4	
archaeon enrichment culture clone PW68.8A	
archaeon enrichment culture clone R3-1a11	
archaeon enrichment culture clone R3-1a2	
archaeon enrichment culture clone R3-1a3	
archaeon enrichment culture clone R3-1a6	
archaeon enrichment culture clone R3-1b6	
archaeon enrichment culture clone R3-1d10	
archaeon enrichment culture clone R3-1e5	
archaeon enrichment culture clone R3-1e8	
archaeon enrichment culture clone R3-1f5	
archaeon enrichment culture clone R3-1g4	
archaeon enrichment culture clone R3-1h9	
archaeon enrichment culture clone T-RF321	
archaeon enrichment culture clone VNC3A001	
archaeon enrichment culture clone VNC3A005	
archaeon enrichment culture clone YE25__1	
archaeon enrichment culture clone YE7__1	
archaeon enrichment culture clone YE7__5	
archaeon enrichment culture DGGE band 1507ag 1	
archaeon enrichment culture DGGE band 1507cas 1	
archaeon enrichment culture DGGE band 1507cas 2	
archaeon enrichment culture DGGE band 1510b-ker 1	
archaeon enrichment culture DGGE band 1510b-ker 2	
archaeon enrichment culture DGGE band 1521cmc 1	
archaeon enrichment culture DGGE band 1521cmc 2	
archaeon enrichment culture DGGE band 1523rope 1	
archaeon enrichment culture DGGE band 1523rope 2	
archaeon enrichment culture DGGE band DS13	
archaeon enrichment culture DGGE band DS18	
archaeon enrichment culture DGGE band DS19	
methanogenic archaeon enrichment culture clone 4.17a Arc Band 1	
methanogenic archaeon enrichment culture clone 4.17b Arc Band 1	
methanogenic archaeon enrichment culture clone BAMC-4	
methanogenic archaeon enrichment culture clone BAMC-5	
methanogenic archaeon enrichment culture clone NapK-0__20-enr35	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
methanogenic archaeon enrichment culture clone NapK-0__20-enr36	
methanogenic archaeon enrichment culture clone Napk-0__20-enr74	
methanogenic archaeon enrichment culture clone NapK-80__100-enr37	
toluene-degrading methanogenic consortium archaeon	
uncultured ammonia-oxidizing archaeon	
uncultured archaeal symbiont PA110	
uncultured archaeal symbiont PA111	
uncultured archaeal symbiont PA115	
uncultured archaeal symbiont PA120	
uncultured archaeal symbiont PA121	
uncultured archaeal symbiont PA122	
uncultured archaeal symbiont PA201	
uncultured archaeal symbiont PA202	
uncultured archaeal symbiont PA203	
uncultured archaeal symbiont PA204	
uncultured archaeal symbiont ST101	
uncultured archaeal symbiont ST119	
uncultured archaeal symbiont ST120	
uncultured archaeal symbiont ST123	
uncultured archaeal symbiont ST124	
uncultured archaeal symbiont ST141	
uncultured archaeal symbiont ST150	
uncultured archaeon	
uncultured archaeon MedDCM-OCT-S02-C115	
uncultured archaeon MedDCM-OCT-S04-C14	
uncultured archaeon MedDCM-OCT-S04-C140	
uncultured archaeon MedDCM-OCT-S04-C163	
uncultured archaeon MedDCM-OCT-S04-C246	
uncultured archaeon MedDCM-OCT-S05-C10	
uncultured archaeon MedDCM-OCT-S05-C205	
uncultured archaeon MedDCM-OCT-S05-C32	
uncultured archaeon MedDCM-OCT-S05-C418	
uncultured archaeon MedDCM-OCT-S05-C57	
uncultured archaeon MedDCM-OCT-S05-C724	
uncultured archaeon MedDCM-OCT-S06-C18	
uncultured archaeon MedDCM-OCT-S08-C16	
uncultured archaeon MedDCM-OCT-S08-C282	
uncultured archaeon MedDCM-OCT-S08-C37	
uncultured archaeon MedDCM-OCT-S08-C54	
uncultured archaeon MedDCM-OCT-S08-C82	
uncultured archaeon MedDCM-OCT-S08-C92	
uncultured archaeon MedDCM-OCT-S09-C13	
uncultured archaeon MedDCM-OCT-S09-C50	
uncultured archaeon MedDCM-OCT-S11-C441	
uncultured archaeon MedDCM-OCT-S11-C473	
uncultured archaeon 'Antarctica #17'	
uncultured archaeon 'Norris Geyer Basin #1'	
uncultured archaeon 'Norris Geyer Basin #13'	
uncultured archaeon 'Norris Geyer Basin #14'	
uncultured archaeon 'Norris Geyer Basin #16'	
uncultured archaeon 'Norris Geyer Basin #4'	
uncultured archaeon 'Norris Geyer Basin #6'	
uncultured archaeon 'Norris Geyer Basin #8'	
uncultured archaeon 'Norris Geyer Basin #9'	
uncultured archaeon 'Obsidian Pool #1'	
uncultured archaeon 'Obsidian Pool #10'	
uncultured archaeon 'Obsidian Pool #3'	
uncultured archaeon 'Obsidian Pool #4'	
uncultured archaeon 'Obsidian Pool #6'	
uncultured archaeon 'Obsidian Pool #9'	
uncultured archaeon 'Queen's Laundry #28'	
uncultured archaeon 101B	
uncultured archaeon 102A	
uncultured archaeon 103D	
uncultured archaeon 112D	
uncultured archaeon 113C	
uncultured archaeon 130D	
uncultured archaeon 142C	
uncultured archaeon 145B	
uncultured archaeon 15A	
uncultured archaeon 17B	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
uncultured archaeon 19a-1	
uncultured archaeon 19a-14	
uncultured archaeon 19a-18	
uncultured archaeon 19a-19	
uncultured archaeon 19a-23	
uncultured archaeon 19a-27	
uncultured archaeon 19a-29	
uncultured archaeon 19a-4	
uncultured archaeon 19a-5	
uncultured archaeon 19b-1	
uncultured archaeon 19b-16	
uncultured archaeon 19b-17	
uncultured archaeon 19b-2	
uncultured archaeon 19b-23	
uncultured archaeon 19b-24	
uncultured archaeon 19b-26	
uncultured archaeon 19b-30	
uncultured archaeon 19b-31	
uncultured archaeon 19b-32	
uncultured archaeon 19b-34	
uncultured archaeon 19b-35	
uncultured archaeon 19b-37	
uncultured archaeon 19b-38	
uncultured archaeon 19b-39	
uncultured archaeon 19b-41	
uncultured archaeon 19b-42	
uncultured archaeon 19b-46	
uncultured archaeon 19b-5	
uncultured archaeon 19b-52	
uncultured archaeon 19b-7	
uncultured archaeon 19b-8	
uncultured archaeon 19b-9	
uncultured archaeon 19c-1	
uncultured archaeon 19c-10	
uncultured archaeon 19c-12	
uncultured archaeon 19c-17	
uncultured archaeon 19c-18	
uncultured archaeon 19c-27	
uncultured archaeon 19c-31	
uncultured archaeon 19c-33	
uncultured archaeon 19c-35	
uncultured archaeon 19c-36	
uncultured archaeon 19c-45	
uncultured archaeon 19c-49	
uncultured archaeon 19c-5	
uncultured archaeon 19c-50	
uncultured archaeon 19c-51	
uncultured archaeon 19c-52	
uncultured archaeon 19c-53	
uncultured archaeon 19c-54	
uncultured archaeon 1MT315	
uncultured archaeon 1MT325	
uncultured archaeon 20a-1	
uncultured archaeon 20a-10	
uncultured archaeon 20a-12	
uncultured archaeon 20a-15	
uncultured archaeon 20a-17	
uncultured archaeon 20a-2	
uncultured archaeon 20a-25	
uncultured archaeon 20a-28	
uncultured archaeon 20a-3	
uncultured archaeon 20a-6	
uncultured archaeon 20a-7	
uncultured archaeon 20a-9	
uncultured archaeon 20B	
uncultured archaeon 20b-1	
uncultured archaeon 20b-10	
uncultured archaeon 20b-14	
uncultured archaeon 20b-15	
uncultured archaeon 20b-16	
uncultured archaeon 20b-18	
uncultured archaeon 20b-22	
uncultured archaeon 20b-25	
uncultured archaeon 20b-26	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
uncultured archaeon 20b-27	
uncultured archaeon 20b-28	
uncultured archaeon 20b-30	
uncultured archaeon 20b-31	
uncultured archaeon 20b-37	
uncultured archaeon 20b-39	
uncultured archaeon 20b-4	
uncultured archaeon 20b-40	
uncultured archaeon 20b-47	
uncultured archaeon 20b-53	
uncultured archaeon 20b-54	
uncultured archaeon 20b-7	
uncultured archaeon 20b-9	
uncultured archaeon 20c-10	
uncultured archaeon 20c-12	
uncultured archaeon 20c-16	
uncultured archaeon 20c-17	
uncultured archaeon 20c-18	
uncultured archaeon 20c-19	
uncultured archaeon 20c-20	
uncultured archaeon 20c-22	
uncultured archaeon 20c-23	
uncultured archaeon 20c-25	
uncultured archaeon 20c-29	
uncultured archaeon 20c-3	
uncultured archaeon 20c-37	
uncultured archaeon 20c-39	
uncultured archaeon 20c-4	
uncultured archaeon 20c-42	
uncultured archaeon 20c-43	
uncultured archaeon 20c-47	
uncultured archaeon 20c-52	
uncultured archaeon 20c-54	
uncultured archaeon 20c-8	
uncultured archaeon 20D	
uncultured archaeon 22C	
uncultured archaeon 26A	
uncultured archaeon 27	
uncultured archaeon 27A	
uncultured archaeon 27D	
uncultured archaeon 2C100	
uncultured archaeon 2C129	
uncultured archaeon 2C130	
uncultured archaeon 2C169	
uncultured archaeon 2C174	
uncultured archaeon 2C25	
uncultured archaeon 2C30	
uncultured archaeon 2C300X	
uncultured archaeon 2C46	
uncultured archaeon 2C8	
uncultured archaeon 2C82	
uncultured archaeon 2C83	
uncultured archaeon 2C84	
uncultured archaeon 2C87	
uncultured archaeon 2C9	
uncultured archaeon 2MT1	
uncultured archaeon 2MT103	
uncultured archaeon 2MT120	
uncultured archaeon 2MT16	
uncultured archaeon 2MT196	
uncultured archaeon 2MT198	
uncultured archaeon 2MT22	
uncultured archaeon 2MT310	
uncultured archaeon 2MT320	
uncultured archaeon 2MT53	
uncultured archaeon 2MT7	
uncultured archaeon 2MT8	
uncultured archaeon 2MT98	
uncultured archaeon 60B	
uncultured archaeon 61B	
uncultured archaeon 61D	
uncultured archaeon 63-A1	
uncultured archaeon 63-A10	
uncultured archaeon 63-A11	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
uncultured archaeon 63-A12	
uncultured archaeon 63-A14	
uncultured archaeon 63-A15	
uncultured archaeon 63-A16	
uncultured archaeon 63-A17	
uncultured archaeon 63-A18	
uncultured archaeon 63-A19	
uncultured archaeon 63-A20	
uncultured archaeon 63-A21	
uncultured archaeon 63-A22	
uncultured archaeon 63-A23	
uncultured archaeon 63-A24	
uncultured archaeon 63-A3	
uncultured archaeon 63-A4	
uncultured archaeon 63-A5	
uncultured archaeon 63-A6	
uncultured archaeon 63-A7	
uncultured archaeon 63-A8	
uncultured archaeon 63-A9	
uncultured archaeon 63D	
uncultured archaeon 64D	
uncultured archaeon 65B	
uncultured archaeon 65C	
uncultured archaeon 66D	
uncultured archaeon 70A	
uncultured archaeon 71A	
uncultured archaeon 71C	
uncultured archaeon 73A	
uncultured archaeon 73D	
uncultured archaeon 76A	
uncultured archaeon 80B	
uncultured archaeon 82D	
uncultured archaeon 83D	
uncultured archaeon 84C	
uncultured archaeon 85A	
uncultured archaeon 90C	
uncultured archaeon 91B	
uncultured archaeon 93A	
uncultured archaeon 94B	
uncultured archaeon 94D	
uncultured archaeon 95A	
uncultured archaeon A016	
uncultured archaeon A140	
uncultured archaeon A145	
uncultured archaeon A148	
uncultured archaeon A151	
uncultured archaeon A153	
uncultured archaeon A154	
uncultured archaeon A157	
uncultured archaeon A174	
uncultured archaeon A175	
uncultured archaeon A177	
uncultured archaeon A178	
uncultured archaeon ACA1-0cm	
uncultured archaeon ACA1-9cm	
uncultured archaeon ACA10-0cm	
uncultured archaeon ACA16-9cm	
uncultured archaeon ACA17-9cm	
uncultured archaeon ACA3-0cm	
uncultured archaeon ACA4-0cm	
uncultured archaeon AM-1	
uncultured archaeon AM-10	
uncultured archaeon AM-11	
uncultured archaeon AM-12	
uncultured archaeon AM-13	
uncultured archaeon AM-14	
uncultured archaeon AM-15	
uncultured archaeon AM-16	
uncultured archaeon AM-17	
uncultured archaeon AM-18	
uncultured archaeon AM-19	
uncultured archaeon AM-2	
uncultured archaeon AM-20	
uncultured archaeon AM-21	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
uncultured archaeon AM-22	
uncultured archaeon AM-3	
uncultured archaeon AM-4	
uncultured archaeon AM-5	
uncultured archaeon AM-6	
uncultured archaeon AM-7	
uncultured archaeon AM-8	
uncultured archaeon AM-9	
uncultured archaeon APA1-0cm	
uncultured archaeon APA2-17cm	
uncultured archaeon APA3-0cm	
uncultured archaeon APA3-11cm	
uncultured archaeon APA4-0cm	
uncultured archaeon APA6-17cm	
uncultured archaeon APA7-17cm	
uncultured archaeon Ar21	
uncultured archaeon Ar26	
uncultured archaeon Ar28	
uncultured archaeon Arc.1	
uncultured archaeon Arc.118	
uncultured archaeon Arc.119	
uncultured archaeon Arc.148	
uncultured archaeon Arc.168	
uncultured archaeon Arc.171	
uncultured archaeon Arc.2	
uncultured archaeon Arc.201	
uncultured archaeon Arc.212	
uncultured archaeon Arc.22	
uncultured archaeon Arc.3	
uncultured archaeon Arc.4	
uncultured archaeon Arc.43	
uncultured archaeon Arc.75	
uncultured archaeon Arc.9	
uncultured archaeon Arc.98	
uncultured archaeon Cas14#1	
uncultured archaeon Cas14#2	
uncultured archaeon Cas14#3	
uncultured archaeon Cas14#4	
uncultured archaeon Cas14#5	
uncultured archaeon Cas14#6	
uncultured archaeon Cas18#1	
uncultured archaeon Cas18#2	
uncultured archaeon Cas18#3	
uncultured archaeon Cas18#4	
uncultured archaeon Cas19#1	
uncultured archaeon Cas19#2	
uncultured archaeon Cas19#3	
uncultured archaeon Cas19#4	
uncultured archaeon Cas19#5	
uncultured archaeon Cas19#6	
uncultured archaeon Cas20#1	
uncultured archaeon Cas20#2	
uncultured archaeon Cas20#3	
uncultured archaeon Cas20#4	
uncultured archaeon Cas20#5	
uncultured archaeon CR-PA10a	
uncultured archaeon CR-PA12a	
uncultured archaeon CR-PA13a	
uncultured archaeon CR-PA15a	
uncultured archaeon CR-PA16a	
uncultured archaeon CR-PA1a	
uncultured archaeon CR-PA2a	
uncultured archaeon CR-PA4a	
uncultured archaeon CR-PA6a	
uncultured archaeon CR-PA7a	
uncultured archaeon CR-PA8a	
uncultured archaeon CRA12-27cm	
uncultured archaeon CRA13-11cm	
uncultured archaeon CRA20-0cm	
uncultured archaeon CRA36-0cm	
uncultured archaeon CRA4-23cm	
uncultured archaeon CRA7-0cm	
uncultured archaeon CRA7-11cm	
uncultured archaeon CRA8-11cm	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
uncultured archaeon CRA8-23cm	
uncultured archaeon CRA8-27cm	
uncultured archaeon CRA9-27cm	
uncultured archaeon CRE-FL10a	
uncultured archaeon CRE-FL11a	
uncultured archaeon CRE-FL1a	
uncultured archaeon CRE-FL2a	
uncultured archaeon CRE-FL3a	
uncultured archaeon CRE-FL4a	
uncultured archaeon CRE-FL5a	
uncultured archaeon CRE-FL6a	
uncultured archaeon CRE-FL7a	
uncultured archaeon CRE-FL8a	
uncultured archaeon CRE-FL9a	
uncultured archaeon CRE-PA10a	
uncultured archaeon CRE-PA11a	
uncultured archaeon CRE-PA2a	
uncultured archaeon CRE-PA3a	
uncultured archaeon CRE-PA4a	
uncultured archaeon CRE-PA5a	
uncultured archaeon CRE-PA6a	
uncultured archaeon CRE-PA7a	
uncultured archaeon CRE-PA8a	
uncultured archaeon CRE-PA9a	
uncultured archaeon CRO-11a	
uncultured archaeon CRO-12a	
uncultured archaeon CRO-14a	
uncultured archaeon CRO-1a	
uncultured archaeon CRO-2a	
uncultured archaeon CRO-3a	
uncultured archaeon CRO-4a	
uncultured archaeon CRO-5a	
uncultured archaeon CRO-6a	
uncultured archaeon CRO-7a	
uncultured archaeon CRO-8a	
uncultured archaeon DGGE band PSARC-1	
uncultured archaeon DGGE band PSARC-2	
uncultured archaeon E1b	
uncultured archaeon ER-E	
uncultured archaeon ER-H	
uncultured archaeon GA01	
uncultured archaeon GA02	
uncultured archaeon GA04	
uncultured archaeon GA10	
uncultured archaeon GA32	
uncultured archaeon GA42	
uncultured archaeon GA54	
uncultured archaeon GA55	
uncultured archaeon GA67	
uncultured archaeon GA77	
uncultured archaeon GZfos10C7	
uncultured archaeon GZfos11A10	
uncultured archaeon GZfos11H11	
uncultured archaeon GZfos12E1	
uncultured archaeon GZfos12E2	
uncultured archaeon GZfos13E1	
uncultured archaeon GZfos14B8	
uncultured archaeon GZfos17A3	
uncultured archaeon GZfos17C7	
uncultured archaeon GZfos17F1	
uncultured archaeon GZfos17G11	
uncultured archaeon GZfos18B6	
uncultured archaeon GZfos18C8	
uncultured archaeon GZfos18F2	
uncultured archaeon GZfos18H11	
uncultured archaeon GZfos19A5	
uncultured archaeon GZfos19C7	
uncultured archaeon GZfos19C8	
uncultured archaeon GZfos1C11	
uncultured archaeon GZfos1D1	
uncultured archaeon GZfos21B5	
uncultured archaeon GZfos22D9	
uncultured archaeon GZfos23H7	
uncultured archaeon GZfos23H9	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
uncultured archaeon GZfos24D9	
uncultured archaeon GZfos26B2	
uncultured archaeon GZfos26D6	
uncultured archaeon GZfos26D8	
uncultured archaeon GZfos26E7	
uncultured archaeon GZfos26F9	
uncultured archaeon GZfos26G2	
uncultured archaeon GZfos27A8	
uncultured archaeon GZfos27B6	
uncultured archaeon GZfos27E6	
uncultured archaeon GZfos27E7	
uncultured archaeon GZfos27G5	
uncultured archaeon GZfos28B8	
uncultured archaeon GZfos28G7	
uncultured archaeon GZfos29E12	
uncultured archaeon GZfos30H9	
uncultured archaeon GZfos31B6	
uncultured archaeon GZfos32E4	
uncultured archaeon GZfos32E7	
uncultured archaeon GZfos32G12	
uncultured archaeon GZfos33E1	
uncultured archaeon GZfos33H6	
uncultured archaeon GZfos34A6	
uncultured archaeon GZfos34G5	
uncultured archaeon GZfos34H10	
uncultured archaeon GZfos34H9	
uncultured archaeon GZfos35A2	
uncultured archaeon GZfos35B7	
uncultured archaeon GZfos35D7	
uncultured archaeon GZfos36D8	
uncultured archaeon GZfos37B2	
uncultured archaeon GZfos37D1	
uncultured archaeon GZfos3D4	
uncultured archaeon GZfos9C4	
uncultured archaeon GZfos9D1	
uncultured archaeon GZfos9D8	
uncultured archaeon GZfos9E5	
uncultured archaeon HA01	
uncultured archaeon HA03	
uncultured archaeon HA04	
uncultured archaeon HA05	
uncultured archaeon HA06	
uncultured archaeon HA08	
uncultured archaeon HA09	
uncultured archaeon HA10	
uncultured archaeon HA11	
uncultured archaeon HA19	
uncultured archaeon HA25	
uncultured archaeon HA48	
uncultured archaeon HA55	
uncultured archaeon KNIA11	
uncultured archaeon KNIA12	
uncultured archaeon KNIA13	
uncultured archaeon KNIA14	
uncultured archaeon KNIA15	
uncultured archaeon n1d	
uncultured archaeon n41r	
uncultured archaeon OS-1	
uncultured archaeon OS-10	
uncultured archaeon OS-11	
uncultured archaeon OS-12	
uncultured archaeon OS-13	
uncultured archaeon OS-14	
uncultured archaeon OS-15	
uncultured archaeon OS-16	
uncultured archaeon OS-17	
uncultured archaeon OS-18	
uncultured archaeon OS-19	
uncultured archaeon OS-2	
uncultured archaeon OS-20	
uncultured archaeon OS-21	
uncultured archaeon OS-22	
uncultured archaeon OS-23	
uncultured archaeon OS-24	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
uncultured archaeon OS-25	
uncultured archaeon OS-26	
uncultured archaeon OS-27	
uncultured archaeon OS-28	
uncultured archaeon OS-29	
uncultured archaeon OS-3	
uncultured archaeon OS-30	
uncultured archaeon OS-31	
uncultured archaeon OS-32	
uncultured archaeon OS-33	
uncultured archaeon OS-4	
uncultured archaeon OS-5	
uncultured archaeon OS-6	
uncultured archaeon OS-7	
uncultured archaeon OS-8	
uncultured archaeon OS-9	
uncultured archaeon pHGPA1	
uncultured archaeon pHGPA13	
uncultured archaeon pPACMA-A	
uncultured archaeon pPACMA-B	
uncultured archaeon pPACMA-C	
uncultured archaeon pPACMA-E	
uncultured archaeon pPACMA-F	
uncultured archaeon pPACMA-G	
uncultured archaeon pPACMA-H	
uncultured archaeon pPACMA-I	
uncultured archaeon pPACMA-J	
uncultured archaeon pPACMA-K	
uncultured archaeon pPACMA-L	
uncultured archaeon pPACMA-M	
uncultured archaeon pPACMA-N	
uncultured archaeon pPACMA-P	
uncultured archaeon pPACMA-Q	
uncultured archaeon pPACMA-S	
uncultured archaeon pPACMA-T	
uncultured archaeon pPACMA-U	
uncultured archaeon pPACMA-V	
uncultured archaeon pPACMA-W	
uncultured archaeon pPACMA-X	
uncultured archaeon pPACMA-Y	
uncultured archaeon pPCA10.1	
uncultured archaeon pPCA12.14	
uncultured archaeon pPCA12.6	
uncultured archaeon pPCA13.4	
uncultured archaeon pPCA13.5	
uncultured archaeon pPCA14.16	
uncultured archaeon pPCA14.17	
uncultured archaeon pPCA14.18	
uncultured archaeon pPCA14.41	
uncultured archaeon pPCA15.21	
uncultured archaeon pPCA17.1	
uncultured archaeon pPCA19.6	
uncultured archaeon pPCA2.4	
uncultured archaeon pPCA4.21	
uncultured archaeon pPCA4.4	
uncultured archaeon pPCA4.9	
uncultured archaeon pPCA7.13	
uncultured archaeon pPCA7.17	
uncultured archaeon pPCA7.21	
uncultured archaeon pPCA7.30	
uncultured archaeon pPCA7.34	
uncultured archaeon pPCA7.6	
uncultured archaeon pPCA7.8	
uncultured archaeon pPCA8.3	
uncultured archaeon RSS50-1	
uncultured archaeon RSS50-10	
uncultured archaeon RSS50-11	
uncultured archaeon RSS50-2	
uncultured archaeon RSS50-3	
uncultured archaeon RSS50-4	
uncultured archaeon RSS50-5	
uncultured archaeon RSS50-6	
uncultured archaeon RSS50-7	
uncultured archaeon RSS50-8	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
uncultured archaeon RSS50-9	
uncultured archaeon S15-1	
uncultured archaeon S15-10	
uncultured archaeon S15-11	
uncultured archaeon S15-12	
uncultured archaeon S15-13	
uncultured archaeon S15-14	
uncultured archaeon S15-15	
uncultured archaeon S15-16	
uncultured archaeon S15-17	
uncultured archaeon S15-18	
uncultured archaeon S15-19	
uncultured archaeon S15-2	
uncultured archaeon S15-20	
uncultured archaeon S15-21	
uncultured archaeon S15-22	
uncultured archaeon S15-23	
uncultured archaeon S15-24	
uncultured archaeon S15-25	
uncultured archaeon S15-26	
uncultured archaeon S15-27	
uncultured archaeon S15-28	
uncultured archaeon S15-29	
uncultured archaeon S15-3	
uncultured archaeon S15-30	
uncultured archaeon S15-4	
uncultured archaeon S15-5	
uncultured archaeon S15-6	
uncultured archaeon S15-7	
uncultured archaeon S15-8	
uncultured archaeon S15-9	
uncultured archaeon S30-1	
uncultured archaeon S30-10	
uncultured archaeon S30-11	
uncultured archaeon S30-12	
uncultured archaeon S30-13	
uncultured archaeon S30-14	
uncultured archaeon S30-15	
uncultured archaeon S30-16	
uncultured archaeon S30-17	
uncultured archaeon S30-18	
uncultured archaeon S30-19	
uncultured archaeon S30-2	
uncultured archaeon S30-20	
uncultured archaeon S30-21	
uncultured archaeon S30-22	
uncultured archaeon S30-23	
uncultured archaeon S30-24	
uncultured archaeon S30-25	
uncultured archaeon S30-26	
uncultured archaeon S30-27	
uncultured archaeon S30-28	
uncultured archaeon S30-29	
uncultured archaeon S30-3	
uncultured archaeon S30-30	
uncultured archaeon S30-4	
uncultured archaeon S30-5	
uncultured archaeon S30-6	
uncultured archaeon S30-7	
uncultured archaeon S30-8	
uncultured archaeon S30-9	
uncultured archaeon SAGMA-1	
uncultured archaeon SAGMA-10	
uncultured archaeon SAGMA-11	
uncultured archaeon SAGMA-12	
uncultured archaeon SAGMA-13	
uncultured archaeon SAGMA-14	
uncultured archaeon SAGMA-15	
uncultured archaeon SAGMA-16	
uncultured archaeon SAGMA-17	
uncultured archaeon SAGMA-2	
uncultured archaeon SAGMA-3	
uncultured archaeon SAGMA-4	
uncultured archaeon SAGMA-6	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
uncultured archaeon SAGMA-7	
uncultured archaeon SAGMA-8	
uncultured archaeon SAGMA-9	
uncultured archaeon SAGMA-A	
uncultured archaeon SAGMA-B	
uncultured archaeon SAGMA-C	
uncultured archaeon SAGMA-D	
uncultured archaeon SAGMA-E	
uncultured archaeon SAGMA-F	
uncultured archaeon SAGMA-G	
uncultured archaeon SAGMA-H	
uncultured archaeon SAGMA-I	
uncultured archaeon SAGMA-J	
uncultured archaeon SAGMA-J2	
uncultured archaeon SAGMA-K	
uncultured archaeon SAGMA-L	
uncultured archaeon SAGMA-M	
uncultured archaeon SAGMA-N	
uncultured archaeon SAGMA-O	
uncultured archaeon SAGMA-P	
uncultured archaeon SAGMA-Q	
uncultured archaeon SAGMA-R	
uncultured archaeon SAGMA-S	
uncultured archaeon SAGMA-T	
uncultured archaeon SAGMA-U	
uncultured archaeon SAGMA-V	
uncultured archaeon SAGMA-W	
uncultured archaeon SAGMA-X	
uncultured archaeon SAGMA-Y	
uncultured archaeon SAGMA-Z	
uncultured archaeon SC1	
uncultured archaeon SC2	
uncultured archaeon SC4	
uncultured archaeon SC6	
uncultured archaeon SC7	
uncultured archaeon SJC-11b	
uncultured archaeon SJC-125a	
uncultured archaeon SJD-102	
uncultured archaeon SJD-103	
uncultured archaeon SJD-105	
uncultured archaeon SJD-107	
uncultured archaeon SJD-111	
uncultured archaeon SJD-114	
uncultured archaeon SL-C	
uncultured archaeon SL1-1	
uncultured archaeon SL2-d	
uncultured archaeon SM1	
uncultured archaeon SM1K20	
uncultured archaeon ST1-1	
uncultured archaeon ST1-10	
uncultured archaeon ST1-11	
uncultured archaeon ST1-12	
uncultured archaeon ST1-13	
uncultured archaeon ST1-14	
uncultured archaeon ST1-15	
uncultured archaeon ST1-16	
uncultured archaeon ST1-17	
uncultured archaeon ST1-18	
uncultured archaeon ST1-19	
uncultured archaeon ST1-2	
uncultured archaeon ST1-20	
uncultured archaeon ST1-21	
uncultured archaeon ST1-22	
uncultured archaeon ST1-23	
uncultured archaeon ST1-24	
uncultured archaeon ST1-25	
uncultured archaeon ST1-26	
uncultured archaeon ST1-27	
uncultured archaeon ST1-28	
uncultured archaeon ST1-29	
uncultured archaeon ST1-3	
uncultured archaeon ST1-30	
uncultured archaeon ST1-4	
uncultured archaeon ST1-5	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
uncultured archaeon ST1-6	
uncultured archaeon ST1-7	
uncultured archaeon ST1-8	
uncultured archaeon ST1-9	
uncultured archaeon SW1	
uncultured archaeon SW14	
uncultured archaeon SW3	
uncultured archaeon SW9	
uncultured archaeon SWY	
uncultured archaeon SYA-1	
uncultured archaeon SYA-106	
uncultured archaeon SYA-112	
uncultured archaeon SYA-12	
uncultured archaeon SYA-122	
uncultured archaeon SYA-125	
uncultured archaeon SYA-127	
uncultured archaeon SYA-13	
uncultured archaeon SYA-130	
uncultured archaeon SYA-133	
uncultured archaeon SYA-136	
uncultured archaeon SYA-141	
uncultured archaeon SYA-20	
uncultured archaeon SYA-26	
uncultured archaeon SYA-30	
uncultured archaeon SYA-32	
uncultured archaeon SYA-39	
uncultured archaeon SYA-45	
uncultured archaeon SYA-5	
uncultured archaeon SYA-50	
uncultured archaeon SYA-62	
uncultured archaeon SYA-7	
uncultured archaeon SYA-70	
uncultured archaeon SYA-74	
uncultured archaeon SYA-75	
uncultured archaeon SYA-77	
uncultured archaeon SYA-78	
uncultured archaeon SYA-8	
uncultured archaeon SYA-80	
uncultured archaeon SYA-81	
uncultured archaeon SYA-94	
uncultured archaeon SYA__2000__10	
uncultured archaeon SYA__2000__11	
uncultured archaeon SYA__2000__12	
uncultured archaeon SYA__2000__13	
uncultured archaeon SYA__2000__14	
uncultured archaeon SYA__2000__15	
uncultured archaeon SYA__2000__16	
uncultured archaeon SYA__2000__17	
uncultured archaeon SYA__2000__18	
uncultured archaeon SYA__2000__19	
uncultured archaeon SYA__2000__2	
uncultured archaeon SYA__2000__20	
uncultured archaeon SYA__2000__21	
uncultured archaeon SYA__2000__24	
uncultured archaeon SYA__2000__26	
uncultured archaeon SYA__2000__27	
uncultured archaeon SYA__2000__28	
uncultured archaeon SYA__2000__30	
uncultured archaeon SYA__2000__31	
uncultured archaeon SYA__2000__32	
uncultured archaeon SYA__2000__35	
uncultured archaeon SYA__2000__36	
uncultured archaeon SYA__2000__37	
uncultured archaeon SYA__2000__39	
uncultured archaeon SYA__2000__40	
uncultured archaeon SYA__2000__41	
uncultured archaeon SYA__2000__43	
uncultured archaeon SYA__2000__44	
uncultured archaeon SYA__2000__45	
uncultured archaeon SYA__2000__46	
uncultured archaeon SYA__2000__47	
uncultured archaeon SYA__2000__5	
uncultured archaeon SYA__2000__51	
uncultured archaeon SYA__2000__52	

TABLE 3-continued

Name of Unclassified Species	Taxonomy ID
uncultured archaeon SYA__2000__54	
uncultured archaeon SYA__2000__55	
uncultured archaeon SYA__2000__57	
uncultured archaeon SYA__2000__58	
uncultured archaeon SYA__2000__59	
uncultured archaeon SYA__2000__6	
uncultured archaeon SYA__2000__60	
uncultured archaeon SYA__2000__61	
uncultured archaeon SYA__2000__62	
uncultured archaeon SYA__2000__63	
uncultured archaeon SYA__2000__66	
uncultured archaeon SYA__2000__67	
uncultured archaeon SYA__2000__68	
uncultured archaeon SYA__2000__7	
uncultured archaeon SYA__2000__70	
uncultured archaeon SYA__2000__8	
uncultured archaeon SYA__2000__9	
uncultured archaeon TA01	
uncultured archaeon TA02	
uncultured archaeon TA03	
uncultured archaeon TA04	
uncultured archaeon TA05	
uncultured archaeon VC2.1 Arc1	
uncultured archaeon VC2.1 Arc13	
uncultured archaeon VC2.1 Arc16	
uncultured archaeon VC2.1 Arc2	
uncultured archaeon VC2.1 Arc31	
uncultured archaeon VC2.1 Arc35	
uncultured archaeon VC2.1 Arc36	
uncultured archaeon VC2.1 Arc4	
uncultured archaeon VC2.1 Arc5	
uncultured archaeon VC2.1 Arc6	
uncultured archaeon VC2.1 Arc7	
uncultured archaeon VC2.1 Arc8	
uncultured archaeon WSB-1	
uncultured archaeon WSB-10	
uncultured archaeon WSB-11	
uncultured archaeon WSB-12	
uncultured archaeon WSB-13	
uncultured archaeon WSB-14	
uncultured archaeon WSB-15	
uncultured archaeon WSB-16	
uncultured archaeon WSB-17	
uncultured archaeon WSB-18	
uncultured archaeon WSB-19	
uncultured archaeon WSB-2	
uncultured archaeon WSB-20	
uncultured archaeon WSB-21	
uncultured archaeon WSB-3	
uncultured archaeon WSB-4	
uncultured archaeon WSB-5	
uncultured archaeon WSB-6	
uncultured archaeon WSB-7	
uncultured archaeon WSB-8	
uncultured archaeon WSB-9	
uncultured archeon 'KTK 18A'	
uncultured archeon 'KTK 28A'	
uncultured archeon 'KTK 31A'	
uncultured archeon 'KTK 4A'	
uncultured archeon 'KTK 9A'	
uncultured Banisveld landfill archaeon BVlowarchb2	
uncultured Banisveld landfill archaeon BVupparchb1	
uncultured compost archaeon	
uncultured deep-sea archaeon	
uncultured endolithic archaeon	
uncultured equine intestinal archaeal sp. DL11	
uncultured maize rhizosphere archaeon c9__45(Cr)	
uncultured maize root archaeon ZmrA1	
uncultured maize root archaeon ZmrA19	
uncultured maize root archaeon ZmrA30	
uncultured maize root archaeon ZmrA38	
uncultured maize root archaeon ZmrA4	
uncultured maize root archaeon ZmrA42	
uncultured marine archaeon	
uncultured marine archaeon DCM3921	
uncultured marine archaeon DCM6515	
uncultured marine archaeon DCM65231	
uncultured marine archaeon DCM74159	
uncultured marine archaeon DCM74161	
uncultured marine archaeon DCM858	
uncultured marine archaeon DCM860	
uncultured marine archaeon DCM861	
uncultured marine archaeon DCM862	
uncultured marine archaeon DCM863	
uncultured marine archaeon DCM865	
uncultured marine archaeon DCM866	
uncultured marine archaeon DCM867	
uncultured marine archaeon DCM871	
uncultured marine archaeon DCM873	
uncultured marine archaeon DCM874	
uncultured marine archaeon DCM875	
uncultured marine archaeon FF619	
uncultured marine archaeon FF620	
uncultured marine archaeon FIN625	
uncultured marine archaeon FIN654	
uncultured marine archaeon GIN492	
uncultured marine archaeon TS10C286	
uncultured marine archaeon TS10C294	
uncultured marine archaeon TS10C298	
uncultured marine archaeon TS10C299	
uncultured marine archaeon TS235C302	
uncultured marine archaeon TS235C306	
uncultured marine archaeon TS235C310	
uncultured methane-oxidizing archaeon	
uncultured methanogen R5	
uncultured methanogen R8	
uncultured methanogen R9	
uncultured rumen archaeon	
uncultured rumen archaeon M1	
uncultured rumen archaeon M2	
uncultured rumen archaeon M7	
uncultured rumen methanogen	
uncultured rumen methanogen 15	
uncultured rumen methanogen 2	
uncultured rumen methanogen 956	
uncultured rumen methanogen Hole9	
uncultured rumen methanogen M6	
uncultured soil archaeon	
uncultured sponge symbiont PAAR2	
uncultured sponge symbiont PAAR4	
uncultured sponge symbiont PAAR8	
uncultured sponge symbiont PAAR9	
uncultured thermal soil archaeon	
uncultured vent archaeon	
unidentified archaeon	
unidentified archaeon H1-B1	
unidentified archaeon H1-K16	
unidentified archaeon H1-K19	
unidentified archaeon H1-K2	
unidentified archaeon H1-K9	
unidentified archaeon H6-B1	
unidentified archaeon H6-K5	
unidentified archaeon H6-K6	
unidentified archaeon HB3-1	
unidentified archaeon S3-K14	
unidentified archaeon S3-K15	
unidentified archaeon S3-K25	
unidentified archaeon S3-K5	
unidentified archaeon S3-K9	
unidentified hydrothermal vent archaeon PVA__OTU__1	
unidentified hydrothermal vent archaeon PVA__OTU__3	
unidentified marine archaeon p712-12	
unidentified marine archaeon p712-13	
unidentified marine archaeon p712-24	
unidentified marine archaeon p712-3	
unidentified marine archaeon p712-37	
unidentified marine archaeon p712-63	

TABLE 4

Class	Order	Family	Genus	Species	Taxonomy ID
Thermoprotei	Caldisphaerales	Caldisphaeraceae	*Caldisphaera*	*draconis*	671066
Thermoprotei	Caldisphaerales	Caldisphaeraceae	*Caldisphaera*	*lagunensis*	200415
Thermoprotei	Caldisphaerales	Caldisphaeraceae	*Caldisphaera*		282527
Thermoprotei	Desulfurococcales	Desulfurococcaceae	*Acidilobus*	*aceticus*	105851
Thermoprotei	Desulfurococcales	Desulfurococcaceae	*Acidilobus*	*saccharovorans*	666510
Thermoprotei	Desulfurococcales	Desulfurococcaceae	*Acidilobus*	*sulfurireducens*	411357
Thermoprotei	Desulfurococcales	Desulfurococcaceae	*Acidilobus*	sp. 124-87	242702
Thermoprotei	Desulfurococcales	Desulfurococcaceae	*Acidilobus*	sp. 405-16	242704
Thermoprotei	Desulfurococcales	Desulfurococcaceae	*Acidilobus*	sp. 722-67	242705
Thermoprotei	Desulfurococcales	Desulfurococcaceae	*Acidilobus*		242694
Thermoprotei	Fervidicoccales	Fervidicoccaceae	*Fervidicoccus*	*fontis*	683846
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	*ambivalens*	2283
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	*brierleyi*	41673
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	*convivator*	269667
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	*hospitalis*	563177
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	*infernus*	12915
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	*manzaensis*	282676
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	*pozzuoliensis*	314564
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	*sulfidivorans*	619593
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	*tengchongensis*	146920
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	sp. Acii18	315459
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	sp. Acii19	315462
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	sp. Acii25	315461
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	sp. Acii26	315460
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	sp. BT	513519
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*	sp. F28	315458
Thermoprotei	Sulfolobales	Sulfolobaceae	*Acidianus*		310069
Thermoprotei	Thermoproteales	Thermofilaceae	*Thermofilum*	*librum*	54255
Thermoprotei	Thermoproteales	Thermofilaceae	*Thermofilum*	*pendens*	368408
Thermoprotei	Thermoproteales	Thermofilaceae	*Thermofilum*	sp. 1505	697581
Thermoprotei	Thermoproteales	Thermofilaceae	*Thermofilum*		310083
Thermoprotei	Unclassified	Unclassified	Unclassified	Unclassified	476105
Unclassified	Unclassified	Unclassified	*Candidatus Nitrosocaldus*	*yellowstonii*	498375
Unclassified	Unclassified	Unclassified	*Candidatus Nitrosocaldus*	Unclassified	766501
Unclassified	Unclassified	Unclassified	*Candidatus Nitrososphaera*	*gargensis*	497727
Unclassified	Unclassified	Unclassified	*Candidatus Nitrososphaera*	Unclassified	759874
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote 768-28	242701
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote OIA-40	161243
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote OIA-444	161244
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote OIA-592	161245
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote OIA-6	161242
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote SRI-298	132570
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote symbiont of *Axinella damicornis*	171717
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote symbiont of *Axinella verrucosa*	171716
Unclassified	Unclassified	Unclassified	Unclassified	marine crenarchaeote RS.Sph.032	340702
Unclassified	Unclassified	Unclassified	Unclassified	marine crenarchaeote RS.Sph.033	340703
Unclassified	Unclassified	Unclassified	Unclassified	Octopus Spring nitrifying crenarchaeote OS70	498372
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote symbiont of *Axinella sp.*	173517
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1196a	442104
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1196b	442105
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1198a	442106
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1219a	442107
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1224a	442108
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1225a	442109
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1231a	442112
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1233a	442110

TABLE 4-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1537a	442111
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1537b	442113
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1539a	442114
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1572a	442115
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1580a	442116
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1581a	442117
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1587a	442119
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone CULT1592a	442118
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment clone F81	485627
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-A01	550545
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-A02	550546
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-A03	550547
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-B01	550548
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-B02	550549
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-B03	550550
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-C01	550551
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-C02	550552
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-C03	550553
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-D01	550554
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-D02	550555
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-D03	550556
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-E01	550557
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-E02	550558
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-E03	550559
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-F01	550560
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-F02	550561
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-F03	550562

TABLE 4-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-G01	550563
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-G02	550564
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-G03	550565
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-H01	550566
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-H02	550567
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA10-H03	550568
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-A01	550569
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-A02	550570
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-B01	550572
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-B02	550573
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-C01	550575
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-C02	550576
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-D01	550578
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-D02	550579
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-E01	550581
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-F01	550584
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-F02	550585
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-G01	550587
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-G02	550588
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-H01	550590
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BA41-H02	550591
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-A01	550593
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-A02	550594
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-B01	550596

TABLE 4-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-B02	550597
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-C01	550599
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-C02	550600
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-D01	550601
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-D02	550602
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-E01	550603
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-E02	550604
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-F01	550606
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-F02	550607
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-G01	550609
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-G02	550610
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-H01	550612
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BC11-H02	550613
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-A01	550615
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-A02	550616
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-B01	550618
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-B02	550619
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-C01	550621
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-C02	550622
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-D01	550624
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-D02	550625
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-E01	550627
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-E02	550628
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-F01	550630

TABLE 4-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-F02	550631
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-G01	550633
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-G02	550634
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-H01	550636
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BD31-H02	550637
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-A01	550639
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-A02	550640
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-A03	550641
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-B01	550642
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-B02	550643
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-C01	550644
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-C02	550645
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-C03	550646
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-D01	550647
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-D02	550648
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-E01	550649
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-E02	550650
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-F01	550651
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-F02	550652
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-F03	550653
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-G01	550654
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-G02	550655
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-G03	550656
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-H01	550657

TABLE 4-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Unclassified	Unclassified	Unclassified	Unclassified	crenarchaeote enrichment culture clone SF06E-BG30-H02	550658
Unclassified	Unclassified	Unclassified	Unclassified	planktonic crenarchaeote	110442
Unclassified	Unclassified	Unclassified	Unclassified	unculturable Mariana archaeon no. 1	73126
Unclassified	Unclassified	Unclassified	Unclassified	unculturable Mariana archaeon no. 11	73127
Unclassified	Unclassified	Unclassified	Unclassified	unculturable Mariana archaeon no. 15	73128
Unclassified	Unclassified	Unclassified	Unclassified	uncultured ammonia-oxidizing crenarchaeote	666997
Unclassified	Unclassified	Unclassified	Unclassified	uncultured archaeon WCHA1-38	74272
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Crater Lake archaeon CL500-AR1	148262
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Crater Lake archaeon CL500-AR12	148263
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote	29281
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote 10-H-08	311458
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote 29d5	684057
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote 57a5	684058
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote 76h13	684059
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote AM-20A__101	115035
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote AM-20A__102	115036
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote AM-20A__103	115037
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote AM-20A__104	115038
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote AM-20A__117	115039
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote AT-200__1	115040
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote AT-200__7	115041
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote AT-5__1	115042
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote CA-15__P18	115043
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote DeepAnt-EC39	247023
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote DN-200__1	115044
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote DN-5__1	115045
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote DS-5__1	115046
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote DS-5__P21	115047
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote FFSC1	78160
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote FFSC2	77776
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote FFSC3	78161
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote FFSC4	78162
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote FRD0	88890
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSCul1	75613
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSCul13	75618
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSCul4	75614
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSCul5	75615

TABLE 4-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSCul7	75616
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSCul9	75617
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSNat1	75619
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSNat11	75622
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSNat12	75623
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSNat2	75620
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSNat20	75624
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote KBSNat4	75621
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote MCG	529375
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ME-450__20	115048
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ME-450__5	115049
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ME-450__9	115050
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ME-450__P3	115051
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ME-450__P5	115052
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ODPB-A12	95929
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ODPB-A18	95930
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ODPB-A2	95924
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ODPB-A3	95925
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ODPB-A6	95926
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ODPB-A7	95927
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote ODPB-A9	95928
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote pBRKC108	91318
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote pBRKC125	91319
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote pBRKC129	91315
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote pBRKC135	91314
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote pBRKC82	91316
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote pBRKC86	91313
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote pBRKC88	91317
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote SB95__1	115053
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote SB95__20	115054
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TRC132-3	115020
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TRC132-6	115021
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TRC132-7	115022
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TRC132-8	115023
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TRC132-9	115024
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TRC23-10	115025
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TRC23-28	115026

TABLE 4-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TRC23-30	115027
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TRC23-31	115028
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TRC23-38	115029
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC16-1	258888
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC16-10	258884
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC16-12	258883
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC16-14	258882
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC16-16	258880
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC16-18	258881
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC16-3	258887
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC16-6	258886
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC16-9	258885
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC89-10	258879
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC89-11	258878
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC89-136	258870
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC89-17	258874
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC89-20	258877
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC89-24	258876
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC89-30	258875
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC89-34	258873
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC89-36	258872
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote TREC89-44	258871
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL11	85495
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL114	85494
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL151	85499
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL159	85504
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL18	85496
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL20	85500
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL29	85503
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL42	85501
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL48	85502
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL76	85505
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL81	85498
Unclassified	Unclassified	Unclassified	Unclassified	uncultured crenarchaeote VAL96	85497
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRA0	147499
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRA1	147500
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRA27	147501

TABLE 4-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRA27x2	147502
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRA31B	147503
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRA32	147504
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRA33	147505
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRA9	147506
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRB1	147507
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRB15	147508
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRB25	147509
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRB27	147510
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRB31	147512
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRB32B	147511
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRB32x2	147513
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRB33	147514
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRB38	147515
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRB9A	147516
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRC0	147517
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRC15	147518
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRC1B	147519
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRC1x2	147520
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRC27	147521
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRC32	147522
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRC33A	147523
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRC33B	147524
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRC38	147525
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRC9	147526
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRD0	147527
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRD15	147528
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRD25B	147529
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRD25x2	147530
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRD31	147531
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRD32	147532
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRD33	147533
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRD38	147534
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRD9	147535
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Front Range soil crenarchaeote FRD9x2	147536
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Green Bay ferromanganous micronodule archaeon ARA7	140618

TABLE 4-continued

Class	Order	Family	Genus	Species	Taxonomy ID
Unclassified	Unclassified	Unclassified	Unclassified	uncultured Green Bay ferromanganous micronodule archaeon ARC12	140619
Unclassified	Unclassified	Unclassified	Unclassified	uncultured marine archaeon AEGEAN__56	147159
Unclassified	Unclassified	Unclassified	Unclassified	uncultured marine archaeon AEGEAN__67	147162
Unclassified	Unclassified	Unclassified	Unclassified	uncultured marine archaeon AEGEAN__69	147160
Unclassified	Unclassified	Unclassified	Unclassified	uncultured marine archaeon AEGEAN__70	147161
Unclassified	Unclassified	Unclassified	Unclassified	uncultured marine crenarchaeote	115413
Unclassified	Unclassified	Unclassified	Unclassified	uncultured marine group I crenarchaeote	360837
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon Antarctic12	33863
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon Antarctic5	33864
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon C11	52260
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon C20	52261
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon C33	52262
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon C35	52263
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon C46	52264
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon C48	52265
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon C6	52266
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon ICHT	43688
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon LMA137	57672
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon LMA226	57674
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon LMA229	57673
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon LMA238	57671
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon OARB	33862
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon PM23	52267
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon PM7	52268
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon PM8	52269
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon SCA11	50858
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon SCA1145	50793
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon SCA1150	50850
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon SCA1151	50851
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon SCA1154	50852
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon SCA1158	50853
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon SCA1166	50854
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon SCA1170	50855
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon SCA1173	50856
Unclassified	Unclassified	Unclassified	Unclassified	unidentified archaeon SCA1175	50857
Unclassified	Unclassified	Unclassified	Unclassified	unidentified hydrothermal vent archaeon PVA__OTU__2	45967
Unclassified	Unclassified	Unclassified	Unclassified	unidentified hydrothermal vent archaeon PVA__OTU__4	45969

TABLE 5

Name of Unclassified Species	Taxonomy ID
crenarchaeote 768-28	(242701)
crenarchaeote OIA-40	(161243)
crenarchaeote OIA-444	(161244)
crenarchaeote OIA-592	(161245)
crenarchaeote OIA-6	(161242)
crenarchaeote SRI-298	(132570)

TABLE 5-continued

Name of Unclassified Species	Taxonomy ID
crenarchaeote symbiont of *Axinella damicornis*	(171717)
crenarchaeote symbiont of *Axinella verrucosa*	(171716)
marine crenarchaeote RS.Sph.032	(340702)
marine crenarchaeote RS.Sph.033	(340703)
Octopus Spring nitrifying crenarchaeote OS70	(498372)
crenarchaeote symbiont of *Axinella* sp.	(173517)

TABLE 5-continued

Name of Unclassified Species	Taxonomy ID
crenarchaeote enrichment clone CULT1196a	(442104)
crenarchaeote enrichment clone CULT1196b	(442105)
crenarchaeote enrichment clone CULT1198a	(442106)
crenarchaeote enrichment clone CULT1219a	(442107)
crenarchaeote enrichment clone CULT1224a	(442108)
crenarchaeote enrichment clone CULT1225a	(442109)
crenarchaeote enrichment clone CULT1231a	(442112)
crenarchaeote enrichment clone CULT1233a	(442110)
crenarchaeote enrichment clone CULT1537a	(442111)
crenarchaeote enrichment clone CULT1537b	(442113)
crenarchaeote enrichment clone CULT1539a	(442114)
crenarchaeote enrichment clone CULT1572a	(442115)
crenarchaeote enrichment clone CULT1580a	(442116)
crenarchaeote enrichment clone CULT1581a	(442117)
crenarchaeote enrichment clone CULT1587a	(442119)
crenarchaeote enrichment clone CULT1592a	442118)
crenarchaeote enrichment clone F81	485627
crenarchaeote enrichment culture clone SF06E-BA10-A01	550545
crenarchaeote enrichment culture clone SF06E-BA10-A02	550546
crenarchaeote enrichment culture clone SF06E-BA10-A03	550547
crenarchaeote enrichment culture clone SF06E-BA10-B01	550548)
crenarchaeote enrichment culture clone SF06E-BA10-B02	550549)
crenarchaeote enrichment culture clone SF06E-BA10-B03	550550)
crenarchaeote enrichment culture clone SF06E-BA10-C01	550551)
crenarchaeote enrichment culture clone SF06E-BA10-C02	550552)
crenarchaeote enrichment culture clone SF06E-BA10-C03	550553)
crenarchaeote enrichment culture clone SF06E-BA10-D01	550554)
crenarchaeote enrichment culture clone SF06E-BA10-D02	550555)
crenarchaeote enrichment culture clone SF06E-BA10-D03	550556)
crenarchaeote enrichment culture clone SF06E-BA10-E01	550557)
crenarchaeote enrichment culture clone SF06E-BA10-E02	550558)
crenarchaeote enrichment culture clone SF06E-BA10-E03	550559)
crenarchaeote enrichment culture clone SF06E-BA10-F01	550560)
crenarchaeote enrichment culture clone SF06E-BA10-F02	550561)
crenarchaeote enrichment culture clone SF06E-BA10-F03	550562)
crenarchaeote enrichment culture clone SF06E-BA10-G01	550563)
crenarchaeote enrichment culture clone SF06E-BA10-G02	550564)
crenarchaeote enrichment culture clone SF06E-BA10-G03	550565)
crenarchaeote enrichment culture clone SF06E-BA10-H01	550566)
crenarchaeote enrichment culture clone SF06E-BA10-H02	550567)
crenarchaeote enrichment culture clone SF06E-BA10-H03	550568)
crenarchaeote enrichment culture clone SF06E-BA41-A01	550569)
crenarchaeote enrichment culture clone SF06E-BA41-A02	550570)
crenarchaeote enrichment culture clone SF06E-BA41-B01	550572)
crenarchaeote enrichment culture clone SF06E-BA41-B02	550573)
crenarchaeote enrichment culture clone SF06E-BA41-C01	550575)
crenarchaeote enrichment culture clone SF06E-BA41-C02	550576)
crenarchaeote enrichment culture clone SF06E-BA41-D01	550578)
crenarchaeote enrichment culture clone SF06E-BA41-D02	550579)
crenarchaeote enrichment culture clone SF06E-BA41-E01	550581)
crenarchaeote enrichment culture clone SF06E-BA41-F01	550584)
crenarchaeote enrichment culture clone SF06E-BA41-F02	550585)
crenarchaeote enrichment culture clone SF06E-BA41-G01	550587)
crenarchaeote enrichment culture clone SF06E-BA41-G02	550588)
crenarchaeote enrichment culture clone SF06E-BA41-H01	550590)
crenarchaeote enrichment culture clone SF06E-BA41-H02	550591)
crenarchaeote enrichment culture clone SF06E-BC11-A01	550593)
crenarchaeote enrichment culture clone SF06E-BC11-A02	550594)
crenarchaeote enrichment culture clone SF06E-BC11-B01	550596)
crenarchaeote enrichment culture clone SF06E-BC11-B02	550597)
crenarchaeote enrichment culture clone SF06E-BC11-C01	550599)
crenarchaeote enrichment culture clone SF06E-BC11-C02	550600)
crenarchaeote enrichment culture clone SF06E-BC11-D01	550601)
crenarchaeote enrichment culture clone SF06E-BC11-D02	550602)
crenarchaeote enrichment culture clone SF06E-BC11-E01	550603)
crenarchaeote enrichment culture clone SF06E-BC11-E02	550604)
crenarchaeote enrichment culture clone SF06E-BC11-F01	550606)
crenarchaeote enrichment culture clone SF06E-BC11-F02	550607)
crenarchaeote enrichment culture clone SF06E-BC11-G01	550609)
crenarchaeote enrichment culture clone SF06E-BC11-G02	550610)
crenarchaeote enrichment culture clone SF06E-BC11-H01	550612)
crenarchaeote enrichment culture clone SF06E-BC11-H02	550613)

TABLE 5-continued

Name of Unclassified Species	Taxonomy ID
crenarchaeote enrichment culture clone SF06E-BD31-A01	550615)
crenarchaeote enrichment culture clone SF06E-BD31-A02	550616)
crenarchaeote enrichment culture clone SF06E-BD31-B01	550618)
crenarchaeote enrichment culture clone SF06E-BD31-B02	550619)
crenarchaeote enrichment culture clone SF06E-BD31-C01	550621)
crenarchaeote enrichment culture clone SF06E-BD31-C02	550622)
crenarchaeote enrichment culture clone SF06E-BD31-D01	550624)
crenarchaeote enrichment culture clone SF06E-BD31-D02	550625)
crenarchaeote enrichment culture clone SF06E-BD31-E01	550627)
crenarchaeote enrichment culture clone SF06E-BD31-E02	550628)
crenarchaeote enrichment culture clone SF06E-BD31-F01	550630)
crenarchaeote enrichment culture clone SF06E-BD31-F02	550631)
crenarchaeote enrichment culture clone SF06E-BD31-G01	550633)
crenarchaeote enrichment culture clone SF06E-BD31-G02	550634)
crenarchaeote enrichment culture clone SF06E-BD31-H01	550636)
crenarchaeote enrichment culture clone SF06E-BD31-H02	550637)
crenarchaeote enrichment culture clone SF06E-BG30-A01	550639)
crenarchaeote enrichment culture clone SF06E-BG30-A02	550640
crenarchaeote enrichment culture clone SF06E-BG30-A03	550641
crenarchaeote enrichment culture clone SF06E-BG30-B01	550642
crenarchaeote enrichment culture clone SF06E-BG30-B02	550643
crenarchaeote enrichment culture clone SF06E-BG30-C01	550644
crenarchaeote enrichment culture clone SF06E-BG30-C02	550645
crenarchaeote enrichment culture clone SF06E-BG30-C03	550646
crenarchaeote enrichment culture clone SF06E-BG30-D01	550647
crenarchaeote enrichment culture clone SF06E-BG30-D02	550648
crenarchaeote enrichment culture clone SF06E-BG30-E01	550649
crenarchaeote enrichment culture clone SF06E-BG30-E02	550650
crenarchaeote enrichment culture clone SF06E-BG30-F01	550651
crenarchaeote enrichment culture clone SF06E-BG30-F02	550652
crenarchaeote enrichment culture clone SF06E-BG30-F03	550653
crenarchaeote enrichment culture clone SF06E-BG30-G01	550654
crenarchaeote enrichment culture clone SF06E-BG30-G02	550655
crenarchaeote enrichment culture clone SF06E-BG30-G03	550656
crenarchaeote enrichment culture clone SF06E-BG30-H01	550657
crenarchaeote enrichment culture clone SF06E-BG30-H02	550658
crenarchaeote enrichment culture clone SF06E-BG30-H03	550659
planktonic crenarchaeote	110442
unculturable Mariana archaeon no. 1	73126
unculturable Mariana archaeon no. 11	73127
unculturable Mariana archaeon no. 15	73128
uncultured ammonia-oxidizing crenarchaeote	666997
uncultured archaeon WCHA1-38	74272
uncultured Crater Lake archaeon CL500-AR1	148262
uncultured Crater Lake archaeon CL500-AR12	148263
uncultured crenarchaeote	29281
uncultured crenarchaeote 10-H-08	311458
uncultured crenarchaeote 29d5	684057
uncultured crenarchaeote 57a5	684058
uncultured crenarchaeote 76h13	684059
uncultured crenarchaeote AM-20A__101	115035
uncultured crenarchaeote AM-20A__102	115036
uncultured crenarchaeote AM-20A__103	115037
uncultured crenarchaeote AM-20A__104	115038
uncultured crenarchaeote AM-20A__117	115039
uncultured crenarchaeote AT-200__1	115040
uncultured crenarchaeote AT-200__7	115041
uncultured crenarchaeote AT-5__1	115042
uncultured crenarchaeote CA-15__P18	115043
uncultured crenarchaeote DeepAnt-EC39	247023
uncultured crenarchaeote DN-200__1	115044
uncultured crenarchaeote DN-5__1	115045
uncultured crenarchaeote DS-5__1	115046
uncultured crenarchaeote DS-5__P21	115047
uncultured crenarchaeote FFSC1	78160
uncultured crenarchaeote FFSC2	77776
uncultured crenarchaeote FFSC3	78161
uncultured crenarchaeote FFSC4	78162
uncultured crenarchaeote FRD0	88890
uncultured crenarchaeote KBSCul1	75613
uncultured crenarchaeote KBSCul13	75618
uncultured crenarchaeote KBSCul4	75614

TABLE 5-continued

Name of Unclassified Species	Taxonomy ID
uncultured crenarchaeote KBSCul5	75615
uncultured crenarchaeote KBSCul7	75616
uncultured crenarchaeote KBSCul9	75617
uncultured crenarchaeote KBSNat1	75619
uncultured crenarchaeote KBSNat11	75622
uncultured crenarchaeote KBSNat12	75623
uncultured crenarchaeote KBSNat2	75620
uncultured crenarchaeote KBSNat20	75624
uncultured crenarchaeote KBSNat4	75621
uncultured crenarchaeote MCG	529375
uncultured crenarchaeote ME-450__20	115048
uncultured crenarchaeote ME-450__5	115049
uncultured crenarchaeote ME-450__9	115050
uncultured crenarchaeote ME-450__P3	115051
uncultured crenarchaeote ME-450__P5	115052
uncultured crenarchaeote ODPB-A12	95929
uncultured crenarchaeote ODPB-A18	95930
uncultured crenarchaeote ODPB-A2	95924
uncultured crenarchaeote ODPB-A3	95925
uncultured crenarchaeote ODPB-A6	95926
uncultured crenarchaeote ODPB-A7	95927
uncultured crenarchaeote ODPB-A9	95928
uncultured crenarchaeote pBRKC108	91318
uncultured crenarchaeote pBRKC125	91319
uncultured crenarchaeote pBRKC129	91315
uncultured crenarchaeote pBRKC135	91314
uncultured crenarchaeote pBRKC82	91316
uncultured crenarchaeote pBRKC86	91313
uncultured crenarchaeote pBRKC88	91317
uncultured crenarchaeote SB95__1	115053
uncultured crenarchaeote SB95__20	115054
uncultured crenarchaeote TRC132-3	115020
uncultured crenarchaeote TRC132-6	115021
uncultured crenarchaeote TRC132-7	115022
uncultured crenarchaeote TRC132-8	115023
uncultured crenarchaeote TRC132-9	115024
uncultured crenarchaeote TRC23-10	115025
uncultured crenarchaeote TRC23-28	115026
uncultured crenarchaeote TRC23-30	115027
uncultured crenarchaeote TRC23-31	115028
uncultured crenarchaeote TRC23-38	115029
uncultured crenarchaeote TREC16-1	258888
uncultured crenarchaeote TREC16-10	258884
uncultured crenarchaeote TREC16-12	258883
uncultured crenarchaeote TREC16-14	258882
uncultured crenarchaeote TREC16-16	258881
uncultured crenarchaeote TREC16-18	258880
uncultured crenarchaeote TREC16-3	258887
uncultured crenarchaeote TREC16-6	258886
uncultured crenarchaeote TREC16-9	258885
uncultured crenarchaeote TREC89-10	258879
uncultured crenarchaeote TREC89-11	258878
uncultured crenarchaeote TREC89-136	258870
uncultured crenarchaeote TREC89-17	258874
uncultured crenarchaeote TREC89-20	258877
uncultured crenarchaeote TREC89-24	258876
uncultured crenarchaeote TREC89-30	258875
uncultured crenarchaeote TREC89-34	258873
uncultured crenarchaeote TREC89-36	258872
uncultured crenarchaeote TREC89-44	258871
uncultured crenarchaeote VAL11	85495
uncultured crenarchaeote VAL114	85494
uncultured crenarchaeote VAL151	85499
uncultured crenarchaeote VAL159	85496
uncultured crenarchaeote VAL18	85504
uncultured crenarchaeote VAL20	85500
uncultured crenarchaeote VAL29	85503
uncultured crenarchaeote VAL42	85501
uncultured crenarchaeote VAL48	85502
uncultured crenarchaeote VAL76	85505
uncultured crenarchaeote VAL81	85498
uncultured crenarchaeote VAL96	85497

TABLE 5-continued

Name of Unclassified Species	Taxonomy ID
uncultured Front Range soil crenarchaeote FRA0	147499
uncultured Front Range soil crenarchaeote FRA1	147500
uncultured Front Range soil crenarchaeote FRA27	147501
uncultured Front Range soil crenarchaeote FRA27x2	147502
uncultured Front Range soil crenarchaeote FRA31B	147503
uncultured Front Range soil crenarchaeote FRA32	147504
uncultured Front Range soil crenarchaeote FRA33	147505
uncultured Front Range soil crenarchaeote FRA9	147506
uncultured Front Range soil crenarchaeote FRB1	147507
uncultured Front Range soil crenarchaeote FRB15	147508
uncultured Front Range soil crenarchaeote FRB25	147509
uncultured Front Range soil crenarchaeote FRB27	147510
uncultured Front Range soil crenarchaeote FRB31	147511
uncultured Front Range soil crenarchaeote FRB32B	147512
uncultured Front Range soil crenarchaeote FRB32x2	147513
uncultured Front Range soil crenarchaeote FRB33	147514
uncultured Front Range soil crenarchaeote FRB38	147515
uncultured Front Range soil crenarchaeote FRB9A	147516
uncultured Front Range soil crenarchaeote FRC0	147517
uncultured Front Range soil crenarchaeote FRC15	147518
uncultured Front Range soil crenarchaeote FRC1B	147519
uncultured Front Range soil crenarchaeote FRC1x2	147520
uncultured Front Range soil crenarchaeote FRC27	147521
uncultured Front Range soil crenarchaeote FRC32	147522
uncultured Front Range soil crenarchaeote FRC33A	147523
uncultured Front Range soil crenarchaeote FRC33B	147524
uncultured Front Range soil crenarchaeote FRC38	147525
uncultured Front Range soil crenarchaeote FRC9	147526
uncultured Front Range soil crenarchaeote FRD0	147527
uncultured Front Range soil crenarchaeote FRD15	147528
uncultured Front Range soil crenarchaeote FRD25B	147529
uncultured Front Range soil crenarchaeote FRD25x2	147530
uncultured Front Range soil crenarchaeote FRD31	147531
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TABLE 5-continued

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What is claimed is:

1. A method of using electricity to produce methane, the method comprising:

maintaining a culture comprising living methanogenic microorganisms at a temperature above 50° C. in a reactor having a first chamber and a second chamber separated by a proton permeable barrier, the first chamber comprising a passage between an inlet and an outlet containing at least a porous electrically conductive cathode, the culture, and water, and the second chamber comprising at least an anode;

coupling electricity to the anode and the cathode;

supplying carbon dioxide to the culture in the first chamber; and

collecting methane from the culture at the outlet of the first chamber.

2. The method of claim **1**, comprising circulating an aqueous electrolytic medium through the passage and the cathode.

3. The method of claim **2**, wherein the passage is formed between the proton permeable barrier and a current collector.

4. The method of claim **2**, wherein the first chamber consists essentially of the porous electrically conductive cathode disposed in the passage between the inlet and the outlet, the culture comprising living methanogenic microorganisms, and the aqueous electrolytic medium circulating through the cathode.

5. The method of claim **5**, wherein the passage is formed between the proton permeable barrier and a current collector.

6. The method of claim **1**, wherein the proton permeable barrier comprises a solid polymer electrolyte membrane.

7. The method of claim **1**, wherein the porous electrically conductive cathode comprises a reticulated carbon foam.

8. The method of claim **1**, wherein the culture is maintained in the first chamber at a temperature above 55° C.

9. The method of claim **8**, wherein the culture is maintained in the first chamber at a temperature above 60° C.

10. The method of claim **1**, wherein the culture comprises Archaea adapted to nearly stationary growth conditions.

11. The method of claim **1**, wherein the culture comprises Archaea of the subkingdom Euryarcheaota.

12. The method of claim **11**, wherein the culture is a monoculture of Euryarcheaota.

13. The method of claim **12**, wherein the monoculture comprises *Methanothermobacter thermautotrophicus*.

14. The method of claim **1**, further comprising:

decoupling the electricity or terminating the carbon dioxide; and

subsequently recoupling the electricity or resupplying the carbon dioxide and returning to at least 80% of methane productivity within 20 minutes of the recoupling or the resupplying.

15. The method of claim **1**, wherein oxygen is a primary gaseous byproduct in the second chamber.

16. The method of claim **1**, wherein water is a primary net electron donor for the methanogenic microorganisms.

17. The method of claim **2**, wherein an organic carbon source is absent in the medium.

18. The method of claim **1**, comprising achieving an electrical current density above 6 mA/cm^2.

* * * * *