

# Lineages of Omnitrophota described in Seymour et al., 2023

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Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Class <i>Omnitrophia</i>	[Om.ni.tro'phi.a] N.L. <b>masc. n.</b> <i>Omnitrophus</i> , referring to the type genus <i>Omnitrophus</i> ; <i>-ia</i> , ending to denote a class; N.L. <b>neut. pl. n.</b> <i>Omnitrophia</i> , the <i>Omnitrophus</i> class	This class belongs to the phylum <i>Omnitrophota</i> . The description for this class is currently the same as for the order <i>Omnitrophales</i> . The nomenclatural type of the class is the genus <i>Omnitrophus</i> .	<i>Omnitrophota</i>	<i>Omnitrophus</i>	<a href="https://seqco.de/i:23663">seqco.de/i:23663</a>
Class <i>Aquiviventia</i>	[A.qui.vi.ven'ti.a] N.L. <b>masc. n.</b> <i>Aquivivens</i> , referring to the type genus <i>Aquivivens</i> ; <i>-ia</i> , ending to denote a class; N.L. <b>neut. pl. n.</b> <i>Aquiviventia</i> , the <i>Aquivivens</i> class	This class belongs to the phylum <i>Omnitrophota</i> . The description for the class is currently the same as for the order <i>Aquiviventes</i> . The nomenclatural type for the class is the genus <i>Aquivivens</i> .	<i>Omnitrophota</i>	<i>Aquivivens</i>	<a href="https://seqco.de/i:23666">seqco.de/i:23666</a>
Order <i>Pluralincolimonadales</i>	[Plu.ra.l.in.co.li.mo.na.da'les] N.L. <b>fem. n.</b> <i>Pluralincolimonas</i> , referring to the type genus <i>Pluralincolimonas</i> ; <i>-ales</i> , ending to denote an order; N.L. <b>fem. pl. n.</b> <i>Pluralincolimonadales</i> , the <i>Pluralincolimonas</i> order	This order belongs to the class <i>Gorgyraia</i> , in the phylum <i>Omnitrophota</i> . As a monotypic order, the description for the order is currently the same as for the genus <i>Pluralincolimonas</i> , the nomenclatural type for the order.	<i>Gorgyraia</i>	<i>Pluralincolimonas</i>	<a href="https://seqco.de/i:23731">seqco.de/i:23731</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Order <i>Omnitrophales</i>	[Om.ni.tro.pha'les] <b>N.L. masc. n.</b> <i>Omnitrophus</i> , referring to the type genus <i>Omnitrophus</i> ; <i>-ales</i> , ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Omnitrophales</i> , the <i>Omnitrophus</i> order	This order belongs to the class <i>Omnitrophia</i> , in the phylum <i>Omnitrophota</i> . Cell sizes vary within the order, with most observed cells and DNA recovered from serial-filtration experiments associated with small cell size. Several members encode very large ORFs putatively involved in adhesion, and ADP/ATP translocases. Genomic predictions indicate respiratory pathways as predominantly conserved in the order for energy metabolism. Genomes of this order have been recovered from freshwater, groundwater, wastewater, geothermal springs, saline sediment, soil and engineered environments. Samples from which assemblies were derived were taken under aerobic conditions at circumneutral pH, where reported. The nomenclatural type of the order is the genus <i>Omnitrophus</i> .	<i>Omnitrophia</i>	<i>Omnitrophus</i>	<a href="https://seqco.de/i:23662">seqco.de/i:23662</a>
Order <i>Aquiviventes</i>	[A.qui.vi.ven.ta'les] <b>N.L. masc. n.</b> <i>Aquivivens</i> , referring to the type genus <i>Aquivivens</i> ; <i>-ales</i> , ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Aquiviventes</i> , the order whose nomenclatural type is the genus <i>Aquivivens</i>	This order belongs to the class <i>Aquivivencia</i> in the phylum <i>Omnitrophota</i> . The description for the order is currently the same as for the type for the order, the genus <i>Aquivivens</i> .	<i>Aquivivencia</i>	<i>Aquivivens</i>	<a href="https://seqco.de/i:23667">seqco.de/i:23667</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Order <i>Taenariocolales</i>	[Tae.na.ri.co.la'les] <b>N.L. fem. n.</b> <i>Taenaricola</i> , referring to the type genus <i>Taenaricola</i> ; <i>-ales</i> , ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Taenariocolales</i> , the <i>Taenaricola</i> order	This order belongs to the class <i>Gorgyraia</i> , in the phylum <i>Omnitrophota</i> . This is a monotypic order, and currently has the same description as the nomenclatural type for the order, the genus <i>Taenaricola</i> .	<i>Gorgyraia</i>	<i>Taenaricola</i>	<a href="https://seqco.de/i:23735">seqco.de/i:23735</a>
Order <i>Velesiimonadales</i>	[Ve.le.si.i.mo.na.da'les] <b>N.L. fem. n.</b> <i>Velesiimonas</i> , referring to the type genus <i>Velesiimonas</i> ; <i>-ales</i> , ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Velesiimonadales</i> , the <i>Velesiimonas</i> order	The taxonomic placement of this order is uncertain in the phylum <i>Omnitrophota</i> . This is a monotypic order and its description is currently the same as for its nomenclatural type, the genus <i>Velesiimonas</i> .	<b><i>Incertae sedis</i> (Bacteria):</b> This taxon can be confidently placed within the phylum <i>Omnitrophota</i> , however, placement within a class remains uncertain, as using different marker sets for phylogenomic analyses places this taxon in different taxonomic positions in the phylum. Thus, any phylogenetic relationships established without increased taxon sampling may suffer from tree reconstruction artefacts.	<i>Velesiimonas</i>	<a href="https://seqco.de/i:23739">seqco.de/i:23739</a>
Order <i>Aquitaenariimonadales</i>	[A.qui.tae.na.ri.i.mo.na.da'les] <b>N.L. fem. n.</b> <i>Aquitaenariimonas</i> , referring to the type genus <i>Aquitaenariimonas</i> ; <i>-ales</i> , ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Aquitaenariimonadales</i> , order of the genus <i>Aquitaenariimonas</i>	This order belongs to the class <i>Gorgyraia</i> , in the phylum <i>Omnitrophota</i> . The description of this order is currently the same as for the nomenclatural type of the order, the genus <i>Aquitaenariimonas</i> .	<i>Gorgyraia</i>	<i>Aquitaenariimonas</i>	<a href="https://seqco.de/i:23727">seqco.de/i:23727</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Order <i>Duberdicusellales</i>	[Du.ber.di.cu.sel.la'les] <b>N.L. fem. dim. n.</b> <i>Duberdicusella</i> , referring to the type genus <i>Duberdicusella</i> ; <i>-ales</i> , ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Duberdicusellales</i> , the <i>Duberdicusella</i> order	This order belongs to the class <i>Velamenicoccia</i> , phylum <i>Omnitrophota</i> . Genes encoding tight-adherence complexes, very large ORFs and those associated with energy metabolism are variably present. Assemblies belonging to this order originate predominantly from saline sediments, although several assemblies are derived from metagenomic samples from soil and geothermal springs. Although limited information associated with environmental conditions at time of sampling is available, the temperature range where reported is 28-41 °C, and a pH range from 5.9 to 10.1. The type for this order is the genus <i>Duberdicusella</i> .	<i>Velamenicoccia</i>	<i>Duberdicusella</i>	<a href="https://seqco.de/i:23745">seqco.de/i:23745</a>
Order <i>Ghiorseimicrobiales</i>	[Ghi.or.sei.mi.cro.bi.a'les] <b>N.L. neut. n.</b> <i>Ghiorseimicrobium</i> , referring to the type genus <i>Ghiorseimicrobium</i> ; <i>-ales</i> , ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Ghiorseimicrobiales</i> , the <i>Ghiorseimicrobium</i> order	This order belongs to the class <i>Velamenicoccia</i> , phylum <i>Omnitrophota</i> . As a monotypic order, the description is currently the same as for the genus <i>Ghiorseimicrobium</i> , the nomenclatural type for the order.	<i>Velamenicoccia</i>	<i>Ghiorseimicrobium</i>	<a href="https://seqco.de/i:23762">seqco.de/i:23762</a>
Family <i>Velesiimonadaceae</i>	[Ve.le.si.i.mo.na.da'ce.ae] <b>N.L. fem. n.</b> <i>Velesiimonas</i> , referring to the type genus <i>Velesiimonas</i> ; <i>-aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Velesiimonadaceae</i> , the <i>Velesiimonas</i> family	This family belongs to the order <i>Velesiimonadales</i> . As a monotypic family, the description of the family is currently the same as for the genus <i>Velesiimonas</i> , the nomenclatural type for the family.	<i>Velesiimonadales</i>	<i>Velesiimonas</i>	<a href="https://seqco.de/i:23738">seqco.de/i:23738</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Family <i>Aquitaenariimonadaceae</i>	[A.qui.tae.na.ri.i.mo.na.da'ce.ae] <b>N.L. fem. n.</b> <i>Aquitaenariimonas</i> , referring to the type genus <i>Aquitaenariimonas</i> ; - <i>aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Aquitaenariimonadaceae</i> , family of the genus <i>Aquitaenariimonas</i>	This family belongs to the order <i>Aquitaenariimonadales</i> , in the class <i>Gorgyraia</i> , phylum <i>Omnitrophota</i> . The description for this family is currently the same as for the genus <i>Aquitaenariimonas</i> , as no other representatives for this family is available. The type for the family is the genus <i>Aquitaenariimonas</i> .	<i>Aquitaenariimonadales</i>	<i>Aquitaenariimonas</i>	<a href="https://seqco.de/i:23726">seqco.de/i:23726</a>
Family <i>Danuiimicrobiaceae</i>	[Da.nu.i.i.mi.cro.bi.a'ce.ae] <b>N.L. neut. n.</b> <i>Danuiimicrobium</i> , referring to the type genus <i>Danuiimicrobium</i> ; - <i>aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Danuiimicrobiaceae</i> , the <i>Danuiimicrobium</i> family	This family belongs to the order <i>Omnitrophales</i> , class <i>Omnitrophia</i> , phylum <i>Omnitrophota</i> . As a monotypic family, the description of the family is currently the same as for the genus <i>Danuiimicrobium</i> , the nomenclatural type for the family.	<i>Omnitrophales</i>	<i>Danuiimicrobium</i>	<a href="https://seqco.de/i:23685">seqco.de/i:23685</a>
Family <i>Ghiorseimicrobiaceae</i>	[Ghi.or.sei.mi.cro.bi.a'ce.ae] <b>N.L. neut. n.</b> <i>Ghiorseimicrobium</i> , referring to the type genus <i>Ghiorseimicrobium</i> ; - <i>aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Ghiorseimicrobiaceae</i> , the <i>Ghiorseimicrobium</i> family	This family belongs to the order <i>Ghiorseimicrobiales</i> , class <i>Velamenicoccia</i> , phylum <i>Omnitrophota</i> . The description for this monotypic family is the same as for its nomenclatural type, the genus <i>Ghiorseimicrobium</i> .	<i>Ghiorseimicrobiales</i>	<i>Ghiorseimicrobium</i>	<a href="https://seqco.de/i:23761">seqco.de/i:23761</a>
Family <i>Omnitrophaceae</i>	[Om.ni.tro.pha'ce.ae] <b>N.L. masc. n.</b> <i>Omnitrophus</i> , referring to the type genus <i>Omnitrophus</i> ; - <i>aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Omnitrophaceae</i> , family of the genus <i>Omnitrophus</i>	This family belongs to the order <i>Omnitrophales</i> , in the class <i>Omnitrophia</i> , phylum <i>Omnitrophota</i> . The description of this monotypic family is currently the same as the genus <i>Omnitrophus</i> . The nomenclatural type of the family is the genus <i>Omnitrophus</i> .	<i>Omnitrophales</i>	<i>Omnitrophus</i>	<a href="https://seqco.de/i:23661">seqco.de/i:23661</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Family <i>Fredricksoniimonadaceae</i>	[Fred.rick.so.ni.i.mo.na.da'ce.ae] <b>N.L. fem. n.</b> <i>Fredricksoniimonas</i> , referring to the type genus <i>Fredricksoniimonas</i> ; <i>-aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Fredricksoniimonadaceae</i> , the <i>Fredricksoniimonas</i> family	This family belongs to the order <i>Zapsychores</i> , class <i>Velamenicoccia</i> , phylum <i>Omnitrophota</i> . Very large ORFs are pervasive within the family. Tight-adherence complexes are encoded by members of the order. Data regarding energy metabolism is uncertain. Assemblies assigned to the family have been derived from metagenomes from ground-, waste- and other freshwater, sediment, and soil. The nomenclatural type for the family is the genus <i>Fredricksoniimonas</i> .	<i>Zapsychores</i>	<i>Fredricksoniimonas</i>	<a href="https://seqco.de/i:23754">seqco.de/i:23754</a>
Family <i>Taenariiviventaceae</i>	[Tae.na.ri.i.vi.ven.ta'ce.ae] <b>N.L. fem. n.</b> <i>Taenariivivens</i> , referring to the type genus <i>Taenariivivens</i> ; <i>-aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Taenariiviventaceae</i> , the <i>Taenariivivens</i> family	The family belongs to the order <i>Omnitrophales</i> , class <i>Omnitrophia</i> , phylum <i>Omnitrophota</i> . Where known, cells are < 0.3 µm. Genomes encode ADP/ATP translocases, very large ORFs, and are consistent with predicted respiratory pathways. Assemblies assigned to the family have been recovered from ground water, wastewater, geothermal springs, soil, and saline sediments. Where data is available, assemblies originated from samples taken at circumneutral pH and temperatures close to 10 °C. The nomenclatural type for the family is the genus <i>Taenariivivens</i> .	<i>Omnitrophales</i>	<i>Taenariivivens</i>	<a href="https://seqco.de/i:23688">seqco.de/i:23688</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Family <i>Pluralincolimonadaceae</i>	[Plu.ra.li.n.co.li.mo.na.da'ce.ae] <b>N.L. fem. n.</b> <i>Pluralincolimonas</i> , referring to the type genus <i>Pluralincolimonas</i> ; <i>-aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Pluralincolimonadaceae</i> , the <i>Pluralincolimonas</i> family	This family belongs to the order <i>Pluralincolimonadales</i> , class <i>Gorgyraia</i> , phylum <i>Omnitrophota</i> . This family is currently a monotypic family, and has the same description as the nomenclatural type of the family, the genus <i>Pluralincolimonas</i> .	<i>Pluralincolimonadales</i>	<i>Pluralincolimonas</i>	<a href="https://seqco.de/i:23730">seqco.de/i:23730</a>
Family <i>Abzuiibacteriaceae</i>	[Ab.zu.i.i.bac.te.ri.a'ce.ae] <b>N.L. neut. n.</b> <i>Abzuiibacterium</i> , referring to the type genus <i>Abzuiibacterium</i> ; <i>-aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Abzuiibacteriaceae</i> , the <i>Abzuiibacterium</i> family	This family belongs to the order <i>Omnitrophales</i> , in the class <i>Omnitrophia</i> , phylum <i>Omnitrophota</i> . The description of this monotypic family is currently the same as the genus <i>Abzuiibacterium</i> . The nomenclatural type of the family is the genus <i>Abzuiibacterium</i> .	<i>Omnitrophales</i>	<i>Abzuiibacterium</i>	<a href="https://seqco.de/i:23673">seqco.de/i:23673</a>
Family <i>Taenaricolaceae</i>	[Tae.na.ri.co.la'ce.ae] <b>N.L. fem. n.</b> <i>Taenaricola</i> , referring to the type genus <i>Taenaricola</i> ; <i>-aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Taenaricolaceae</i> , the <i>Taenaricola</i> family	This family belongs to the order <i>Taenaricolales</i> , class <i>Gorgyraia</i> , phylum <i>Omnitrophota</i> . As a monotypic family, the description of the family is currently the same as for the genus <i>Taenaricola</i> , the nomenclatural type for the family.	<i>Taenaricolales</i>	<i>Taenaricola</i>	<a href="https://seqco.de/i:23734">seqco.de/i:23734</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Family <i>Aquiviventaceae</i>	[A.qui.vi.ven.ta'ce.ae] <b>N.L. masc. n.</b> <i>Aquivivens</i> , referring to the type genus <i>Aquivivens</i> ; <i>-aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Aquiviventaceae</i> , family of the genus <i>Aquivivens</i>	This family belongs to the order <i>Aquivinentales</i> , class <i>Aquiviventia</i> , phylum <i>Omnitrophota</i> . Observed cell sizes of organisms in this family were predominantly small (0.2 µm), but some variation in cell size has been observed. Members differ in the presence of genes encoding tight-adherence complexes, ADP/ATP translocases, and very large ORFs. Most members of this family encode diverse respiratory pathways and electron transport chain components. Genomes belonging to this family originate from groundwater, wastewater, lake and river water, geothermal springs and soil. Metagenomic samples from which assemblies were recovered largely originated from microaerobic environments with circumneutral pH. The nomenclatural type for the family is the genus <i>Aquivivens</i> .	<i>Aquivinentales</i>	<i>Aquivivens</i>	<a href="https://seqco.de/i:23668">seqco.de/i:23668</a>
Family <i>Aquinolibacteriaceae</i>	[A.quin.co.li.bac.te.ri.a'ce.ae] <b>N.L. neut. n.</b> <i>Aquinolibacterium</i> , referring to the type genus <i>Aquinolibacterium</i> ; <i>-aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Aquinolibacteriaceae</i> , the <i>Aquinolibacterium</i> family	This family belongs to the order <i>Omnitrophales</i> , in the class <i>Omnitrophia</i> , phylum <i>Omnitrophota</i> . The presence of ADP/ATP translocase is variable within the family, but very large ORFs are frequently encoded by members of the family. High rates of carbon assimilation was observed for members of the family on root exudates and leaf litter. The nomenclatural type for the family is the genus <i>Aquinolibacterium</i> .	<i>Omnitrophales</i>	<i>Aquinolibacterium</i>	<a href="https://seqco.de/i:23677">seqco.de/i:23677</a>



Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Family <i>Duberdicusellaceae</i>	[Du.ber.di.cu.sel.la'ce.ae] <b>N.L. fem. dim. n.</b> <i>Duberdicusella</i> , referring to the type genus <i>Duberdicusella</i> ; <i>-aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Duberdicusellaceae</i> , the <i>Duberdicusella</i> family	This family belongs to the order <i>Duberdicusellales</i> , class <i>Velamenicoccia</i> , phylum <i>Omnitrophota</i> . As a monotypic family, the description of the family is currently the same as for the genus <i>Duberdicusella</i> , the nomenclatural type for the family.	<i>Duberdicusellales</i>	<i>Duberdicusella</i>	<a href="https://seqco.de/i:23744">seqco.de/i:23744</a>
Genus <i>Taenaricola</i>	[Tae.na.ri'co.la] <b>L. masc. adj.</b> <i>taenarius</i> , of or belonging to the underground; <b>N.L. fem. suff. -cola</b> , inhabitant; <b>N.L. fem. n.</b> <i>Taenaricola</i> , inhabitant of the underground	This genus belongs to the family <i>Taenaricolaceae</i> , order <i>Taenaricolales</i> , class <i>Gorgyraia</i> , phylum <i>Omnitrophota</i> . This monotypic genus currently has the same description that the type species for the genus, <i>Taenaricola geysiris</i> .	<i>Taenaricolaceae</i>	<i>Taenaricola geysiri</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23733">seqco.de/i:23733</a>
Genus <i>Multiplicimicrobium</i>	[Mul.ti.pli.ci.mi.cro'bi.um] <b>L. fem. adj.</b> <i>multiplex</i> , manifold; <b>L. neut. n.</b> <i>microbium</i> , a microbe; <b>N.L. neut. n.</b> <i>Multiplicimicrobium</i> , a microbe from many different environments	This genus belongs to the family <i>Aquincolibacteriaceae</i> , order <i>Omnitrophales</i> , class <i>Omnitrophia</i> , phylum <i>Omnitrophota</i> . Assemblies assigned to this genus were recovered from samples of groundwater and engineered environments. The nomenclatural type for the genus is the species <i>Multiplicimicrobium inquinatum</i> .	<i>Aquincolibacteriaceae</i>	<i>Multiplicimicrobium inquinatum</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23680">seqco.de/i:23680</a>
Genus <i>Pluralincolimonas</i>	[Plu.ra.l.in.co.li.mo'nas] <b>L. adj.</b> <i>pluralis</i> , belonging or relating to more than one, relating to many; <b>L. fem. n.</b> <i>incola</i> , inhabitant; <b>L. fem. n.</b> <i>monas</i> , a monad; <b>N.L. fem. n.</b> <i>Pluralincolimonas</i> , a monad that inhabits many places	This genus belong the to family <i>Pluralincolimonadaceae</i> , order <i>Pluralincolimonadales</i> , class <i>Gorgyraia</i> , phylum <i>Omnitrophota</i> . Some genes associated with respiration are encoded by genomes assigned to this genus, with no genes for acetogenesis. Assemblies assigned to this genus originate from ground water, freshwater ponds, soil, and permafrost. The type for the genus is the species <i>Pluralincolimonas frigidipaludosa</i> .	<i>Pluralincolimonadaceae</i>	<i>Pluralincolimonas frigidipaludosa</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23729">seqco.de/i:23729</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Ghiorseimicrobium</i>	[Ghi.or.sei.mi.cro'bi.um] L. <b>neut. n.</b> <i>microbium</i> , a microbe; N.L. <b>neut. n.</b> <i>Ghiorseimicrobium</i> , a microbe named for William Ghiorse, for his contributions in geomicrobiology and biogeochemistry, particularly in the deep biosphere	This monotypic genus belongs to the family <i>Ghiorseimicrobiaceae</i> , order <i>Ghiorseimicrobiales</i> , class <i>Velamenicoccia</i> , phylum <i>Omnitrophota</i> . Currently, the description for this genus is the same as for its nomenclatural type <i>Ghiorseimicrobium undicola</i> .	<i>Ghiorseimicrobiaceae</i>	<i>Ghiorseimicrobium undicola</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23760">seqco.de/i:23760</a>
Genus <i>Abzuiibacterium</i>	[Ab.zu.i.i.bac.te'ri.um] N.L. <b>n.</b> <i>Abzu</i> , the Mesopotamian god of fresh water; L. <b>neut. n.</b> <i>bacterium</i> , a bacterium; N.L. <b>neut. n.</b> <i>Abzuiibacterium</i> , a bacterium named after the Mesopotamian god of fresh water, Abzu	This monotypic genus belongs to the family <i>Abzuiibacteriaceae</i> , order <i>Omnitrophales</i> , class <i>Omnitrophia</i> , phylum <i>Omnitrophota</i> . The description of this monotypic genus is currently the same as that of the species <i>Abzuiibacterium crystallinum</i> , the type species for the genus.	<i>Abzuiibacteriaceae</i>	<i>Abzuiibacterium crystallinum</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23674">seqco.de/i:23674</a>
Genus <i>Aquincolibacterium</i>	[A.quin.co.li.bac.te'ri.um] L. <b>fem. n.</b> <i>aqua</i> , water; L. <b>masc. / fem. n.</b> <i>incola</i> , inhabitant; L. <b>neut. n.</b> <i>bacterium</i> , a bacterium; N.L. <b>neut. n.</b> <i>Aquincolibacterium</i> , bacterial inhabitant of water	This genus belongs to the family <i>Aquincolibacteriaceae</i> , order <i>Omnitrophales</i> , class <i>Omnitrophia</i> , phylum <i>Omnitrophota</i> . Very large ORFs, respiratory pathways, and sugar and peptide transporters are encoded by the genomes belonging to this genus. Species in this genus encode a cytoplasmic Group A3 [FeFe] hydrogenase, and a reversible acetyl-CoA synthetase that may be used for acetate utilization and/or acetogenesis. Assemblies assigned to this genus originate from lakes, groundwater and soil. The nomenclatural type for the genus is <i>Aquincolibacterium aerophilum</i> .	<i>Aquincolibacteriaceae</i>	<i>Aquincolibacterium aerophilum</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23676">seqco.de/i:23676</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Phelpsiimicrobium</i>	[Phelp.si.i.mi.cro'bi.um] <b>L. neut. n. <i>microbium</i></b> , a microbe; <b>N.L. neut. n. <i>Phelpsiimicrobium</i></b> , a microbe named for Tommy J. Phelps, an American environmental scientist, for his contributions to subsurface science	This monotypic genus belongs to the family <i>Velamenicoccaceae</i> , order <i>Velamenicoccales</i> , class <i>Velamenicoccia</i> , phylum <i>Omnitrophota</i> . The genus description is currently the same as for the species <i>Phelpsiimicrobium noxiivivens</i> , the nomenclatural type for the genus.	<i>Velamenicoccaceae</i>	<i>Phelpsiimicrobium noxiivivens</i> <sup>TS</sup>	<a href="https://seqco.de/i:23741">seqco.de/i:23741</a>
Genus <i>Undivivens</i>	[Un.di.vi'vens] <b>L. fem. n. <i>unda</i></b> , water; <b>L. pres. part. <i>vivens</i></b> , living; <b>N.L. masc. n. <i>Undivivens</i></b> , living in water	This genus belongs to the family <i>Profunditerraquicolaceae</i> , order <i>Gygaellales</i> , class <i>Velamenicoccia</i> , phylum <i>Omnitrophota</i> . Assemblies for the genus originate from industrial wastewater and soil. The nomenclatural type for the genus is <i>Undivivens industriae</i> .	<i>Profunditerraquicolaceae</i>	<i>Undivivens industriae</i> <sup>TS</sup>	<a href="https://seqco.de/i:23779">seqco.de/i:23779</a>
Genus <i>Pegaeibacterium</i>	[Pe.gae.i.bac.te'ri.um] <b>N.L. fem. n. <i>Pegaeae</i></b> , Greek freshwater nymphs of springs; <b>L. neut. n. <i>bacterium</i></b> , a bacterium; <b>N.L. neut. n. <i>Pegaeibacterium</i></b> , a bacterium named for Greek freshwater nymphs of springs	This genus belongs to the family <i>Aquincolibacteriaceae</i> , in the order <i>Omnitrophales</i> , class <i>Omnitrophia</i> , phylum <i>Omnitrophota</i> . Assemblies belonging to this genus originated from lake water and sediment. Some genes associated with respiration are encoded by members of the genus. Very large ORFs are predicted to be encoded by members of this genus. The nomenclatural type for this genus is the species <i>Pegaeibacterium caenilacustre</i> .	<i>Aquincolibacteriaceae</i>	<i>Pegaeibacterium caenilacustre</i> <sup>TS</sup>	<a href="https://seqco.de/i:23682">seqco.de/i:23682</a>
Genus <i>Makaraimicrobium</i>	[Ma.ka.ra.i.mi.cro'bi.um] <b>N.L. n. <i>Makara</i></b> , a mystical creature of the waters in Hindu mythology; <b>L. neut. n. <i>microbium</i></b> , a microbe; <b>N.L. neut. n. <i>Makaraimicrobium</i></b> , a microbe named for Makara	This genus belongs to the family <i>Tantalellaceae</i> , order <i>Tantalellales</i> , class <i>Gorgyraia</i> , phylum <i>Omnitrophota</i> . All known assemblies originate from water. The nomenclatural type for the genus is the species <i>Makaraimicrobium thalassicum</i> .	<i>Tantalellaceae</i>	<i>Makaraimicrobium thalassicum</i> <sup>TS</sup>	<a href="https://seqco.de/i:23711">seqco.de/i:23711</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Velesiimonas</i>	[Ve.le.si.i.mo'nas] <b>N.L. n.</b> <i>Veles</i> , the Slavic god of earth, waters and the underworld; <b>L. fem. n.</b> <i>monas</i> , a monad; <b>N.L. fem. n.</b> <i>Velesiimonas</i> , a monad named for Veles, the Slavic god of earth, waters and the underworld	This monotypic genus belongs to the family <i>Velesiimonadaceae</i> , and currently has the same description as its nomenclatural type, the species <i>Velesiimonas alkalicola</i> .	<i>Velesiimonadaceae</i>	<i>Velesiimonas alkalicola</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23737">seqco.de/i:23737</a>
Genus <i>Aquitaenariimonas</i>	[A.qui.tae.na.ri.i.mo'nas] <b>L. fem. n.</b> <i>aqua</i> , water; <b>L. masc. adj.</b> <i>taenarius</i> , of or belonging to underground; <b>L. fem. n.</b> <i>monas</i> , a monad; <b>N.L. fem. n.</b> <i>Aquitaenariimonas</i> , a monad from water from underground	This genus belongs to the family <i>Aquitaenariimonadaceae</i> , order <i>Aquitaenariimonadales</i> , class <i>Gorgyraia</i> , phylum <i>Omnitrophota</i> . The description for this monotypic genus is currently the same as for the species <i>Aquitaenariimonas noxiae</i> . The type species for the genus is <i>Aquitaenariimonas noxiae</i> .	<i>Aquitaenariimonadaceae</i>	<i>Aquitaenariimonas noxiae</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23725">seqco.de/i:23725</a>
Genus <i>Taenariivivens</i>	[Tae.na.ri.i.vi'vens] <b>L. masc. adj.</b> <i>taenarius</i> , belowground; <b>L. pres. part.</b> <i>vivens</i> , living; <b>N.L. fem. n.</b> <i>Taenariivivens</i> , living belowground	This genus belongs to the family <i>Taenariiviventaceae</i> , order <i>Omnitrophales</i> , phylum <i>Omnitrophota</i> . As a monotypic genus, the description is currently the same as for the nomenclatural type for the genus, <i>Taenariivivens baikalensis</i> .	<i>Taenariiviventaceae</i>	<i>Taenariivivens baikalensis</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23687">seqco.de/i:23687</a>
Genus <i>Aquivivens</i>	[A.qui.vi'vens] <b>L. fem. n.</b> <i>aqua</i> , water; <b>L. pres. part.</b> <i>vivens</i> , living; <b>N.L. masc. n.</b> <i>Aquivivens</i> , living in water	This genus belongs to the family <i>Aquiviventaceae</i> , order <i>Aquiviventales</i> , class <i>Aquiviventia</i> , <i>Omnitrophota</i> . As the genus is currently monotypic, the description is the same as for the species <i>Aquivivens invisus</i> .	<i>Aquiviventaceae</i>	<i>Aquivivens invisus</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23669">seqco.de/i:23669</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Duberdicusella</i>	[Du.ber.di.cu'sel.la] <b>N.L. fem. dim. n.</b> <i>Duberdicusella</i> , named for Duberdicus, the Lusitanian god of the sea and rivers	This genus belongs to the family <i>Duberdicusellaceae</i> , in the order <i>Duberdicusellales</i> , class <i>Velamenicoccia</i> , phylum <i>Omnitrophota</i> . The description of this monotypic genus is currently the same as that of the nomenclatural type for the genus <i>Duberdicusella sinuisediminis</i> .	<i>Duberdicusellaceae</i>	<i>Duberdicusella sinuisediminis</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23743">seqco.de/i:23743</a>
Genus <i>Danuiimicrobium</i>	[Da.nu.i.i.mi.cro'bi.um] <b>N.L. n.</b> <i>Danu</i> , Hindu goddess of primordial waters; <b>L. neut. n.</b> <i>microbium</i> , a microbe; <b>N.L. neut. n.</b> <i>Danuiimicrobium</i> , a microbe named after the Hindu goddess of primordial water, Danu	This genus belongs to the family <i>Danuiimicrobiaceae</i> , in the order <i>Omnitrophales</i> , class <i>Omnitrophia</i> , phylum <i>Omnitrophota</i> . As a monotypic genus, the description is currently the same as for the type species of the genus, <i>Danuiimicrobium aquiferis</i> .	<i>Danuiimicrobiaceae</i>	<i>Danuiimicrobium aquiferis</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23684">seqco.de/i:23684</a>
Genus <i>Sherwoodlollariibacterium</i>	[Sher.wood.lo.l.la.ri.i.bac.te'ri.um] <b>L. neut. n.</b> <i>bacterium</i> , a bacterium; <b>N.L. neut. n.</b> <i>Sherwoodlollariibacterium</i> , a bacterium named for Barbara Sherwood Lollar, for her contributions to subsurface science	This genus belongs to the family <i>Profunditerraquicolaceae</i> , order <i>Gygaellales</i> , class <i>Velamenicoccia</i> , phylum <i>Omnitrophota</i> . Presence of genes encoding the tight-adherence complex is variable, and large ORFs are absent from genomes assigned to the genus. Assemblies originate from lake and groundwater. The nomenclatural type for the genus is <i>Sherwoodlollariibacterium unditelluris</i> .	<i>Profunditerraquicolaceae</i>	<i>Sherwoodlollariibacterium unditelluris</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23777">seqco.de/i:23777</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Fredricksoniimonas</i>	[Fred.rick.so.ni.i.mo'nas] L. fem. n. <i>monas</i> , a monad; N.L. fem. n. <i>Fredricksoniimonas</i> , a monad named for James K. Fredrickson, for his contributions in the field of deep subsurface microbiology	This genus belongs to the family <i>Fredricksoniimonadaceae</i> , order <i>Zapsychoales</i> , class <i>Velamnicoccia</i> , phylum <i>Omnitrophota</i> . Members of this genus encode very large ORFs, and genes for the tight-adherence complex and respiratory pathways. All assemblies assigned to this genus originate from freshwater or sediment. The nomenclatural type for the genus is the species <i>Fredricksoniimonas aquilentivivens</i> .	<i>Fredricksoniimonadaceae</i>	<i>Fredricksoniimonas aquilentivivens</i> <sup>TS</sup>	<a href="https://seqco.de/i:23753">seqco.de/i:23753</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Duberdicusella sinuisediminis</i> <sup>Ts</sup>	[si.nu.i.se.di.mi'nis] L. <b>masc. n.</b> <i>sinus</i> , a bay; L. <b>gen. n.</b> <i>sediminis</i> , of sediment; N.L. <b>gen. n.</b> <i>sinuisediminis</i> , of sediment from a bay	This species is the nomenclatural type for the genus <i>Duberdicusella</i> . Estimated genome size for this species ranges between 1.3 to 1.8 Mb. GC content for this species is 34.9-35.9 %. No large ORFs are predicted for members of this species. Genes associated mainly with an acetogenic metabolic scheme, along with an Rnf complex, and respiratory complex V (F-type ATPase) are encoded by the genomes of the species. A conductive pilin, a membrane-bound Group 4g [NiFe] and cytoplasmic Group A3 [FeFe] hydrogenases, and all components for the tight-adherence complex (Tad) and Type-4a pili are encoded by the genomes. Additionally, a "symbiotic" F-type ATPase is also encoded by the genomes. All assemblies assigned to this species originated from deep-sea hydrothermal vent sediment samples from Guaymas Basin, Gulf of California, Mexico, with some derived from samples with a reported temperature of 28 °C. The type for the species is the genome GCA_003644525.1.	<i>Duberdicusella</i>	NCBI Assembly: GCA_003644445.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23742">seqco.de/i:23742</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Makaraimicrobium thalassicum</i> <sup>Ts</sup>	[tha.las'si.cum] <b>Gr. fem. n.</b> <i>thalassa</i> , the sea; <b>Gr. neut. adj. suff. -icum</b> , suffix used with the sense of pertaining to; <b>N.L. neut. adj. thalassicum</b> , of the sea	This species is the type for the genus <i>Makaraimicrobium</i> . Estimated genome size for this species is 2 Mb. %GC content for this genome is 48.46%. No large ORF is encoded by this species. A basic acetogenic pathway for fermentation of sugars is encoded by the genome of this species. This may couple the oxidative ATP-yielding reactions of the EMP pathway, with an Rnf complex for redox balancing and a horse-shoe type TCA cycle. Of the respiratory complexes, only a respiratory F-type ATPase is encoded by this genome. Additionally, a "symbiotic" F-type ATPase and components for a Type-4 a pilus is encoded by the genome. The assembly for this species was recovered from a metagenomic sediment sample from a deep-sea hydrothermal vent from Guaymas Basin, Gulf of California, Mexico, where a temperature of 10 °C has been reported. The nomenclatural type for the species is the genome GCA_003644505.1.	<i>Makaraimicrobium</i>	NCBI Assembly: GCA_003644505.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23710">seqco.de/i:23710</a>



Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Fredricksoniimonas aquilentivivens</i> <sup>Ts</sup>	[a.qui.len.ti.vi'vens] L. <b>fem. n.</b> <i>aqua</i> , water; L. <b>masc. adj.</b> <i>lentus</i> , slow; L. <b>pres. part.</b> <i>vivens</i> , living; N.L. <b>part. adj.</b> <i>aquilentivivens</i> , living in slow water	This species is the type for the genus <i>Fredricksoniimonas</i> . In addition to genus characteristics, the estimated genome size for this species is 2 Mb. The %GC for the genome is 50.78 %. Coupled with a Group A3 [FeFe] hydrogenase encoded by the genome of this species, a reversible acetyl-CoA synthetase indicates likely acetogenesis in this species, through the production of acetate from acetyl-CoA by the fermentation of glucose and nucleotides. Respiratory complex I is present in the genome of this species, and can provide oxidized NAD <sup>+</sup> and maintain a proton gradient across the membrane. A respiratory F-type ATPase (complex V) is also present in the genome, and can produce ATP. A metal-reducing cytochrome is present in the genome. Additionally, a "symbiotic" F-type ATPase is also encoded by this genome, along with all genes required for the tight-adherence complex and a Type-4a pilus. A very large ORF is also encoded by this genome. The assembly was recovered from a metagenomic sample of lake water from Nästjärnen, Sweden. The nomenclatural type for the species is the genome GCA_903860135.1.	<i>Fredricksoniimonas</i>	NCBI Assembly: GCA_903860135.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23752">seqco.de/i:23752</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Aquitaenariimonas noxiae</i> <sup>Ts</sup>	[nox.i'ae] N.L. fem. gen. n. <i>noxiae</i> , of Nox, named for the Roman primordial goddess and personification of the night	This species is the type for the genus <i>Aquitaenariimonas</i> . The estimated genome size for members of this species is approximately 2 Mb. Two unique assemblies are available for this species, and range in % GC content from 42.05-42.75 %. The highest quality genome available for the species encodes a very large ORF, and genes associated with acetogenesis and the Wood-Ljungdahl pathway, but an Rnf complex is absent. A respiratory F-type ATPase, membrane-bound Group 4g [NiFe] hydrogenase and all components for a Type-4a pilus investigated are encoded in the genomes. This species has been recovered from metagenomic samples of groundwater from Crystal Geyser, near Green River, Utah, USA, with temperature measurements at sampling recorded at 17 °C. The nomenclatural type for the species is the genome GCA_002780005.1.	<i>Aquitaenariimonas</i>	NCBI Assembly: GCA_002780005.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23724">seqco.de/i:23724</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Aquincolibacterium</i> <i>lacustre</i>	[la.cus'tre] <b>N.L. neut. adj.</b> <i>lacustre</i> , belonging to the lake	<p>Estimated genome sizes for the species are 2.27-2.36 Mb, with %GC content of 50.32-50.59 %. Sugar and amino acid transporters are encoded by genomes in this species. Only respiratory complexes I and V are encoded by genomes of the species, and no terminal electron acceptors can confidently be identified. A cytoplasmic group A3 [FeFe] electron bifurcating hydrogenase is encoded by genomes of the species. Due to the incompleteness of respiratory pathways in this species and no terminal electron acceptors being predicted from the genomes, a reversible acetyl-CoA synthetase encoded by genomes of this species coupled with the Group A3 [FeFe] hydrogenase may be indicative of acetogenesis in this species. Respiratory complex I may be providing oxidized NAD<sup>+</sup> and maintain a proton gradient across the membrane, while the respiratory F-type ATPase (complex V) produces ATP. Genes for the production of a Type-4a pilus is also present, as well as the "symbiotic" F-type ATPase. Very large ORFs are encoded by members of this species. The nomenclatural type for the species is the genome GCA_903856085.1.</p>	<i>Aquincolibacterium</i>	NCBI Assembly: GCA_903856085.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23675">seqco.de/i:23675</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Multiplicimicrobium inquinatum</i> <sup>Ts</sup>	[in.qui.na'tum] L. <b>neut. adj.</b> <i>inquinatum</i> , polluted or defiled, referring to the recovery of this organism from wastewater	This species is the type for the genus <i>Multiplicimicrobium</i> . Estimated genome size for this species is between 2 and 2.25 Mb with a %GC content of 46.35-46.78 %. Very large ORFs or partial homologs to very large ORFs, containing domains associated with cellular adhesion, an ADP/ATP translocase, and genes associated with respiratory complex I, II, IV and V are encoded by genomes of this species. The presence of cytochrome c oxidase in the genome indicates that this species is likely aerobic, and nitric oxide is predicted as an alternative terminal electron acceptor. A reversible acetyl-CoA synthetase is also encoded by genomes of this species, and may be indicative of acetate utilization, or fermentation of sugars to acetate. All genes required for the production of the Type-4a pilus are present in genomes of this species. Assemblies for this species originated from activated sludge bioreactor samples. The nomenclatural type for the species is the genome GCA_002344825.1.	<i>Multiplicimicrobium</i>	NCBI Assembly: GCA_002344825.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23679">seqco.de/i:23679</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Pegaeibacterium caenilacustre</i> <sup>Ts</sup>	[cae.ni.la.cus'tre] L. <b>neut. n.</b> <i>caenum</i> , mud; <b>N.L. neut. adj.</b> <i>lacustre</i> , of or from a lake; <b>N.L. neut. adj.</b> <i>caenilacustre</i> , from mud from a lake	This species is the nomenclatural type for the genus <i>Pegaeibacterium</i> . Estimated genome sizes for the species range between 2.1 and 2.2 Mb with GC% of 54.27-54.30 %. Some components of the respiratory chain, particularly complex I and V, are encoded by genomes of this species. Cytoplasmic Group A3 [FeFe] and Group 4f [NiFe] hydrogenases are encoded by genomes of this species. As incomplete respiratory pathways are present in this species and no terminal electron acceptors are predicted from the genomes, the presence of a reversible acetyl-CoA synthetase coupled with the Group A3 [FeFe] hydrogenase may be indicative that this species is acetogenic, with respiratory complex I providing oxidized NAD <sup>+</sup> and maintaining a proton gradient across the membrane, and complex V (respiratory F-type ATPase) producing ATP. Both assemblies for the species originate from freshwater sediment from Lake Alinen Mustajärvi, Finland. The nomenclatural type for the species is the genome GCA_903820505.1.	<i>Pegaeibacterium</i>	NCBI Assembly: GCA_903820505.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23681">seqco.de/i:23681</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Taenariivivens baikalensis</i> <sup>Ts</sup>	[bai.ka.len'sis] N.L. fem. adj. <i>baikalensis</i> , of Baikal, referring to Lake Baikal, where this organism was identified	This species is the type for the genus <i>Taenariivivens</i> . The %GC content for this genome is 46.97%. Estimated genome size for the species is 2.6 Mb. Genes associated with respiratory complex I, II and V are encoded by the genome of this species. All genes required for the production of the Type-4a pilus are present in the genome. The genome also encodes genes for the tight adherence complex, the "symbiotic" F-type ATPase, and a very large ORF. The genome representing this species was recovered from a water sample from Lake Baikal, Russia. The nomenclatural type for the species is the genome GCA_009691445.1.	<i>Taenariivivens</i>	NCBI Assembly: GCA_009691445.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23686">seqco.de/i:23686</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Fredricksoniimonas borealis</i>	[bo.re.a'lis] L. <b>fem. adj.</b> <i>borealis</i> , pertaining to the North, boreal	In addition to characteristics provided for the genus, the estimated genome size for members of this species is 2.2-2.4 Mb with a GC content of 54.57-55.10 %. Genes associated with respiratory complexes, specifically complex I, II, III and V, and cytochrome bd ubiquinol are encoded by genomes of this species. A Group A3 [FeFe] hydrogenase is encoded by this species. A reversible acetyl-CoA synthetase may be indicative of acetate utilization, and/or acetogenesis coupled with the Group A3 [FeFe] hydrogenase. All genes required for the production of a Type-4a pilus and the tight-adherence complex are encoded by the genomes of the species, as well as very large ORFs. All assemblies originate from methane-rich freshwater lakes in Finland. The type for the species is the genome GCA_903901225.1.	<i>Fredricksoniimonas</i>	NCBI Assembly: GCA_903901225.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23756">seqco.de/i:23756</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Aquivivens invisus</i> <sup>Ts</sup>	[in.vi'sus] L. <b>masc. adj.</b> <i>invisus</i> , unseen, referring to them being hidden or unseen as they occur in the subsurface	This species is the nomenclatural type for the genus <i>Aquivivens</i> . Genomes belonging to this species are predicted to range between 1.7 Mb and 2 Mb. %GC content for the species range between 62.83-63.50 %. Genomes of this species encode respiratory complexes I through V, with aerobic respiration being likely due to the presence of cytochrome c oxidase in the genomes. Nitrite is predicted as alternative terminal electron acceptor, while a metal-reducing cytochrome is also encoded by genomes belonging to this species. ADP/ATP translocase, components of the tight-adherence complex, genes for the production of a Type-4a pilus, and at least two very large ORFs are encoded by genomes of this species. Assemblies for this species originated from soil and groundwater samples from Rifle, Colorado, USA, with a pH of 7.28 and oxygen concentrations of 0.29 mM. The nomenclatural type for the species is the genome GCA_001804415.1.	<i>Aquivivens</i>	NCBI Assembly: GCA_001804415.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23665">seqco.de/i:23665</a>



Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Taenaricola geysiri</i> <sup>†s</sup>	[gey.si'ri] N.L. gen. n. <i>geysiri</i> , of or from a geyser, derived from the Icelandic Geysir	This species is the type for the genus <i>Taenaricola</i> . The genomes of this species is predicted to be 1.2 to 1.4 Mb, with % GC content of 42.51 to 42.8%. Genes related to acetogenesis and an Rnf complex are present. No components for respiratory complexes are present in the genomes. A conductive pilin and components involved in the production of a Type-4a pilus are encoded by the genomes. A membrane-bound Group 4g [NiFe] hydrogenase is encoded by the genomes belonging to this species. All genome assemblies available for this species originate from Crystal Geyser, near Green River, Utah, USA, where a temperature of 17.4 °C was recorded. The nomenclatural type for the species is the genome GCA_002781985.1.	<i>Taenaricola</i>	NCBI Assembly: GCA_002781985.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23732">seqco.de/i:23732</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Velesiimonas alkalicola</i> <sup>Ts</sup>	[a.l.ka.li'co.la] <b>N.L. neut. n.</b> <i>alkali</i> , alkaline; <b>N.L. fem. suff.</b> <i>-cola</i> , an inhabitant of; <b>N.L. fem. n.</b> <i>alkalicola</i> , inhabitant of alkaline environments	This species is the nomenclatural type for the genus <i>Velesiimonas</i> . The predicted genome size of this species is quite small in comparison to other <i>Omnitrophota</i> , at approximately 1.3 Mb. The % GC content of the genome is 37.82 %. No parasitism- or predation-associated genes are encoded by the genome for this species, and limited genes for energy metabolism are predicted for this genome, although, like other members in the phylum, the Type-4a pilus machinery is encoded. An Rnf complex, along with a respiratory F-type ATPase (complex V) are encoded by the genome of this species. The anaerobic sample from which the genome was derived was taken from serpentinized groundwater from an alkaline spring, in the Cedars, California, USA. The nomenclatural type for the species is GCA_013626165.1.	<i>Velesiimonas</i>	NCBI Assembly: GCA_013626165.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23736">seqco.de/i:23736</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Abzuiibacterium crystallinum</i> <sup>Ts</sup>	[crys.ta.li'num] L. <b>neut. adj.</b> <i>crystallinum</i> , crystalline, referring to Crystal Geyser where organism was detected	<p>This species is the nomenclatural type for the genus <i>Abzuiibacterium</i>. Two unique assemblies are available for the species and range in estimated genome size between 2.4 and 2.6 Mb, with a %GC content of 45.25-45.27 %.</p> <p>Respiratory pathways, including genes associated with respiratory complexes I through V, are present in this species. This species is likely able to respire aerobically, as a cytochrome bd ubiquinol oxidase is encoded by genomes of this species. Predicted alternative electron acceptors include nitrite, and nitric oxide, while metal-reducing cytochromes and a conductive pilin are also encoded by genomes of this species. Additionally, a reversible acetyl-CoA synthetase is also encoded by the genomes, and may be indicative of acetate utilization by this species. A complete set of the genes for the production of a Type 4a-pilus is encoded by genomes of this species. Genomes of this species also encode the "symbiotic" F-type ATPase, an ADP/ATP translocase, and a very large ORF. The genomes originated from metagenomic samples from Crystal Geyser, Utah, USA, with samples taken at a reported temperature of 17.4 °C. The nomenclatural type of the species is the genome GCA_002787155.1.</p>	<i>Abzuiibacterium</i>	NCBI Assembly: GCA_002787155.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23672">seqco.de/i:23672</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Pluralincolimonas frigidipaludosa</i> <sup>Ts</sup>	[fri.gi.di.pa.lu.do'sa] L. <b>masc. adj.</b> <i>frigidus</i> , cold; L. <b>fem. adj.</b> <i>paludosa</i> , boggy or marshy; N.L. <b>fem. adj.</b> <i>frigidipaludosa</i> , of a cold marsh or bog	This species is the type for the genus <i>Pluralincolimonas</i> . Estimate genome size for the species is 1.6 Mb, with a %GC of 51.75 %. This species encode an ADP/ATP translocase, and respiratory complexes I and V. All components investigated for the production of a Type-4a pilus is encoded by genomes of this species, as well as a cytoplasmic Group A3 [FeFe] hydrogenase. Coupled with the Group A3 [FeFe] hydrogenase, a reversible acetyl-CoA synthetase may indicate acetogenesis in this species, through the production of acetate from acetyl-CoA by the fermentation of glucose and nucleotides. Through the use of respiratory complex I, oxidized NAD <sup>+</sup> is provided and a proton gradient across the membrane is maintained, while the respiratory F-type ATPase (complex V) produces ATP. Genome data for this species originate from a permafrost sample from Stordalen Mire, Sweden, where a pH of 4.8 was reported. The nomenclatural type for the species is the genome GCA_003141835.1.	<i>Pluralincolimonas</i>	NCBI Assembly: GCA_003141835.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23728">seqco.de/i:23728</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Sherwoodlollaribacterium unditelluris</i> <sup>Ts</sup>	[un.di.tel.lu'ris] L. <b>fem. n.</b> <i>unda</i> , water; L. <b>gen. n.</b> <i>telluris</i> , from the earth; N.L. <b>gen. n.</b> <i>unditelluris</i> , of the water from the earth	This species is the nomenclatural type of the genus <i>Sherwoodlollaribacterium</i> . Estimated genome sizes for the species are 1.35-1.4 Mb, with %GC content of 41.02%. This species encodes several genes associated with acetogenesis, including an Rnf complex. A Group 4g [NiFe] hydrogenase is present in the genomes of this species, and all genes for the tight-adherence complex and for the production of a Type-4a pilus are present in the genome. The assemblies for this species is derived from metagenomes of groundwater from Crystal Geyser, near Green River, Utah. The nomenclatural type for the species is GCA_002771995.1.	<i>Sherwoodlollaribacterium</i>	NCBI Assembly: GCA_002771995.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23776">seqco.de/i:23776</a>
Species <i>Undivivens industriae</i> <sup>Ts</sup>	[in.dus'tri.a.e] L. <b>gen. n.</b> <i>industriae</i> , of industry	This species is the type for the genus <i>Undivivens</i> . Estimated genome sizes range from 1.5-1.9 Mb with %GC content of 52.24-53.29%. Several genes for acetogenesis, along with an Rnf complex, and a respiratory F-type ATPase are present in the genomes of this species. A Group A3 [FeFe] hydrogenase is encoded by the species, and all genes associated with the production of a Type-4 pilus is present in the genome. Additionally, a "symbiotic" F-type ATPase is also encoded by genomes of this species. All assemblies were derived from samples of wastewater. The nomenclatural type for the species is the genome GCA_012514745.1.	<i>Undivivens</i>	NCBI Assembly: GCA_012514745.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23778">seqco.de/i:23778</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Aquincolibacterium</i> <i>aerophilum</i> <sup>Ts</sup>	[ae.ro'phi.lum] Gr. <b>masc. n.</b> <i>aer</i> , air; N.L. <b>masc. adj. suff.</b> <i>-philus</i> , loving; N.L. <b>neut. adj.</b> <i>aerophilum</i> , air-loving	This species is the nomenclatural type for the genus <i>Aquincolibacterium</i> . Estimated genome size of this species is 2.7 to 3 Mb. %GC content range between 52.58 to 53.08 %. Sugar and amino acid transport systems are encoded by genomes belonging to this species, and genes associated with Embden-Meyerhof glycolysis and the TCA cycle are present, although succinate dehydrogenase are absent from genomes. For respiration, a simplified system consisting of complex I, ubiquinone, and cytochrome bd ubiquinol is feasible, and would suggest a microaerophilic lifestyle. Genomes encode a cytoplasmic group A3 [FeFe] electron bifurcating hydrogenase and conductive pili, all genes analyzed for the production of a Type-4a pilus, as well as a respiratory F-type ATPase. Acetate utilization or acetogenesis may be possible as a reversible acetyl-CoA synthetase is present in this species, which, coupled with the Group A3 [FeFe] hydrogenase may produce acetate. Very large ORFs or partial homologs to very large ORFs are encoded by this species. All assemblies originated from water from the methane-rich boreal lake Lake Alinen-Mustajärvi, Finland. The nomenclatural type for the species is the genome GCA_903884815.1.	<i>Aquincolibacterium</i>	NCBI Assembly: GCA_903884815.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23678">seqco.de/i:23678</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Danuiimicrobium aquiferis</i> <sup>Ts</sup>	[a.qui.fe'ris] N.L. gen. n. <i>aquiferis</i> , of an aquifer	<p>This species is the nomenclatural type of the genus <i>Danuiimicrobium</i>. This species can likely respire, as the genomes encode respiratory complexes I, III and V. Alternative terminal electron acceptors are predicted to be nitrate and nitric oxide, and a metal-reducing cytochrome is also encoded by genomes of this species. Cytoplasmic Group A3 [FeFe], Group 4f [NiFe] and membrane-bound Group 4g [NiFe] hydrogenases are encoded by genomes of this species. Additionally, a reversible acetyl-CoA synthetase is encoded by genomes of this species, which may indicate acetate utilization, and/or alternatively, may indicate simplified acetogenesis through the fermentation of glucose or other sugars to acetate, together with the Group A3 [FeFe] hydrogenase encoded by this species. All genes associated with the production of a Type-4a pilus are present in this species, and a "symbiotic" F-type ATPase, ADP/ATP translocase, and very large ORFs are encoded by genomes of this species. Genome assemblies for this species were recovered from soil and groundwater from Rifle, Colorado, USA, with measurements for samples being reported with an oxygen concentration of 0.29 mM and a pH of 7.28. The type for the species is the genome GCA_001804285.1.</p>	<i>Danuiimicrobium</i>	NCBI Assembly: GCA_001804285.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23683">seqco.de/i:23683</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Ghiorseimicrobium undicola</i> <sup>Ts</sup>	[un.di'co.la] L. fem. n. <i>unda</i> , water; N.L. fem. suff. <i>-cola</i> , an inhabitant; N.L. fem. n. <i>undicola</i> , an inhabitant of water	This species is the type for the genus <i>Ghiorseimicrobium</i> . Predicted genome size estimates are 1.9-2 Mb with a GC content of 41.89%. Genes for acetogenesis through the Wood-Ljungdahl pathway is present in this species, along with an Rnf complex. Additionally, a respiratory F-type ATPase for ATP synthesis is also encoded by this genome. Metal-reducing cytochromes and a conductive pilin is present in this species, along with very large ORFs, some genes for the tight-adherence complex, and all genes for the production of a Type-4a pilus. The assembly for the species originate from groundwater from Crystal Geyser, Utah, USA, where the temperature at the time of sampling was reported as 17.4 °C. The nomenclatural type for the species is the genome GCA_002796125.1.	<i>Ghiorseimicrobium</i>	NCBI Assembly: GCA_002796125.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23759">seqco.de/i:23759</a>



Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Phelpsiimicrobium</i> <i>noxiivivens</i> <sup>Ts</sup>	[nox.i.i.vi'vens] <b>N.L. fem. n.</b> <i>Nox</i> , from the Roman primordial goddess and personification of the night, Nox; <b>L. pres. part.</b> <i>vivens</i> , living; <b>N.L. part. adj.</b> <i>noxiivivens</i> , living in darkness	This species is the type for the genus <i>Phelpsiimicrobium</i> . The estimated genome size for the species is between 1.5 to 1.8 Mb, with %GC for genomes ranging between 43.80-44.08 %. Genes for acetogenic pathways, and an Rnf complex is present in the genomes of this species. Genes for respiratory complexes I and V (respiratory F-type ATPase) are also present in the genomes, and are likely involved in redox balancing and ATP synthesis. All genes associated with the tight-adherence (Tad) complex, and the production of a Type-4a pilus is present in the genomes. A "symbiotic" F-type ATPase and very large ORFs are encoded by the genomes. All assemblies assigned to this species originate from Crystal Geyser, near Green River, Utah, USA. The nomenclatural type for the species is the genome GCA_001873995.1.	<i>Phelpsiimicrobium</i>	NCBI Assembly: GCA_001873995.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23740">seqco.de/i:23740</a>