

# Register list proposing 16 new names including *Wolframiiaptor gerlachensis* sp. nov.

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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
Family <i>Wolframiiaptoraceae</i>	[Wolf.ra.mi.i.rap.to.ra.ce'ae] <b>N.L. masc. n.</b> <i>Wolframiiaptor</i> , type genus of the family; - <i>aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Wolframiiaptoraceae</i> , family of the genus <i>Wolframiiaptor</i>	Members of this family are associated with thermal aquatic environments, and have been identified from geothermal springs in China, New Zealand and the USA, and a marine hydrothermal vent in the Western Pacific. Phylogenomic inference robustly recovers the genomes of these organisms as a well-supported monophyletic lineage within the order <i>Caldarchaeales</i> , and delineation of these taxa as a family is supported by Relative Evolutionary Divergence (RED) and Average Amino Acid Identity (AAI). AAI values among designated type genomes for species in this family range between 65 and 85 % within proposed genera, and between 49 and 57 % among members of different genera. The distribution of genes required for oxidative phosphorylation indicate that members of the family may either be strict or facultative anaerobes. Sulfide-dependent respiration may also occur in some members of the family, but this trait is not conserved for all genera. Several putative tungsten-dependent ferredoxin oxidoreductases, specifically aldehyde ferredoxin oxidoreductases (AORs), formaldehyde ferredoxin oxidoreductases (FORs) and glyceraldehyde-3-phosphate ferredoxin oxidoreductases (GAPORs) are encoded by genomes belonging to this family.	<i>Caldarchaeales</i>	<i>Wolframiiaptor</i>	<a href="https://seqco.de/i:22818">seqco.de/i:22818</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Wolframiiraptor</i>	[Wolf.ra.mi.i.rap'tor] <b>N.L. neut. n.</b> <i>wolframium</i> , tungsten; <b>L. masc. n.</b> <i>raptor</i> , snatcher or thief; <b>N.L. masc. n.</b> <i>Wolframiiraptor</i> , snatcher of tungsten	Members of this genus have been identified from geothermal springs from the U.S. Great Basin, Yellowstone National Park, USA, and the Rehai and Ruidian geothermal fields, Tengchong, China. AAI values among genomes representing separate species within the genus range between 81 and 90 %. Based on ancestral state reconstruction analysis, likely losses of the genes encoding cytochrome C oxidase subunits, the aerobic carbon-monoxide dehydrogenase large subunit, and sulfide:quinone oxidoreductase ( <i>Sqr</i> ), indicate that members of this genus are likely strict anaerobes, and are also incapable of sulfide-dependent respiration. Genomes of this genus encode a <i>tupA</i> subunit of the tungstate (Tup) ABC transporter, and contain several genes encoding for tungsten-dependent oxidoreductases, including three putative AOR-like, one FOR-like and one GAPOR-like proteins. This taxon is supported as a genus-level group by phylogenomics, AAI and RED.	<i>Wolframiiraptoraceae</i>	<i>Wolframiiraptor gerlachensis</i> <sup>TS</sup>	<a href="https://seqco.de/i:22817">seqco.de/i:22817</a>
Genus <i>Terraquivivens</i>	[Ter.ra.qui'vi.vens] <b>L. fem. n.</b> <i>terra</i> , the earth; <b>L. fem. n.</b> <i>aqua</i> , water; <b>L. pres. part.</b> <i>vivens</i> , living; <b>N.L. fem. n.</b> <i>Terraquivivens</i> , living in water from the earth	Genomes of members of this genus were recovered from metagenomic sequencing of samples obtained from geothermal springs from China, New Zealand and USA. AAI values among members of different species within the genus range between 78 and 86 %. Based on ancestral state reconstruction analysis, likely losses of cytochrome C oxidase and aerobic carbon monoxide dehydrogenase subunit encoding genes occurred in an ancestral population to the genus, indicating that members of this genus are likely anaerobes. Although no <i>in vitro</i> evidence of tungsten utilization or dependence for this organism is available, the presence of genes encoding the tungstate ABC transporter ( <i>tupABC</i> ) is conserved within the genus, which suggest the ability to take up tungstate from the environment. Of the tungsten-dependent AORs investigated in this study, several are conserved within the genus, but the type of aldehydes oxidized by these enzymes remain unclear. Sulfide-dependent respiration is likely in these organisms as sulfide:quinone oxidoreductase ( <i>sqr</i> )-encoding genes are mostly present in the genomes of these organisms. Delineation of this taxon as a genus-level group is supported by phylogenomics, AAI and RED values.	<i>Wolframiiraptoraceae</i>	<i>Terraquivivens tikiterensis</i> <sup>TS</sup>	<a href="https://seqco.de/i:22827">seqco.de/i:22827</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Benthortus</i>	[Benth'or.tus] Gr. n. <i>benthos</i> , deep water; L. masc. perf. part. <i>ortus</i> , risen; N.L. masc. n. <i>Benthortus</i> , risen from deep water	<p>The genome of the current sole member of this genus was recovered from metagenomic sequencing data of hydrothermal vent communities present in the Lau Basin in the Western Pacific ocean. AAI values among this genus and closely related genera range between 50 and 57 %. Ancestral state reconstruction analysis indicated likely acquisitions of multiple copies of genes encoding methylmalonyl-CoA mutase (McmA1/2), NO-forming nitrite reductase (NirK), and cytochrome C oxidase subunit III (CoxC), and one copy of genes encoding nitrous-oxide reductase (NosZ) and aerobic carbon-monoxide dehydrogenase large subunit (CoxL), each. The tungsten (Tup) transporter substrate-binding subunit A, is encoded by the genome representative of this genus, and the AOR- and FOR-like encoding genes conserved within the family are also present in this genus. The presence of several cytochrome C oxidase subunits and the aerobic carbon-monoxide dehydrogenase large subunit indicate likely capacity for aerobic respiration within the genus. A sulfide:quinone oxidoreductase (<i>sqr</i>) gene is present in the genome and also indicates likely sulfide-dependent respiration within the genus. This genus is supported as distinct and exclusive based on phylogenomics, AAI and RED, and is part of the family <i>Wolframiiaptoraceae</i>.</p>	<i>Wolframiiaptoraceae</i>	<i>Benthortus lauensis</i> <sup>TS</sup>	<a href="https://seqco.de/i:22821">seqco.de/i:22821</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Geocrenenecus</i>	[Ge.o.cren.en.e'cus] Gr. <b>fem. n.</b> <i>ge</i> , the earth; Gr. <b>fem. n.</b> <i>krene</i> , a spring; <b>N.L. masc. n.</b> <i>enecus</i> , inhabitant; <b>N.L. masc. n.</b> <i>Geocrenenecus</i> , inhabitant of a spring of the earth	<p>Genomes of members of this genus have been recovered from metagenomic sequencing of samples from thermal springs in Yellowstone National Park, USA, and the Rehai and Ruidian geothermal fields, Tengchong, China. AAI values among different species in the genus range between 67 and 78 %. Ancestral reconstruction of character states indicated likely losses of the tungstate (Tup) transporter system, along with loss of the tungsten-dependent AOR-like encoding gene found in other members of the family. Likely gains within the genus were genes encoding dissimilatory sulfite reductase subunits (<i>dsrA/B</i>) along with sulfide:quinone oxidoreductase (<i>sqi</i>), which suggest pathways involved in sulfur metabolism and sulfide-dependent respiration within the genus. No homologs to known tungstate or molybdate transporters were identified from any of the MAGs belonging to the genus. Several putative tungsten-dependent ferredoxin oxidoreductases were identified as conserved within the genus, which included one AOR-like and one FOR-like encoding gene, respectively, conserved within the family, one AOR-like encoding gene conserved within this genus and its closest phylogenetic relative, <i>Wolframiiiraptor</i>, and an unknown protein shared with members of <i>Terraquivivens</i>. Based on the presence of cytochrome C oxidase subunits, some members of this genus may be capable of aerobic respiration. Phylogenomics, AAI and RED values, support the delineation of this taxon as a genus.</p>	<i>Wolframiiiraptoraceae</i>	<i>Geocrenenecus dongiae</i> <sup>TS</sup>	<a href="https://seqco.de/i:22822">seqco.de/i:22822</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
<p>Species <i>Terraquivivens</i> <i>tengchongensis</i></p>	<p>[teng.chong.en'sis] <b>N.L. fem. adj.</b> <i>tengchongensis</i>, of Tengchong, referring to Tengchong, China, where these organisms were identified from</p>	<p>Fifteen MAGs for this organism were recovered from several sampling locations in Diretiyanqu, Gumingquan, Jinze and Shuirebaozha thermal springs in the Rehai and Ruidian geothermal fields, Tengchong. Binned genomes for this species ranged between 1,094,328 bp and 1,283,151 bp, in 2 to 160 contigs, and ranged in G+C content from 44.8 to 45.3 %. Completeness estimates for these genomes were between 90.3 and 97.1 %, with contamination estimated at 0-2.91 %, based on CheckM. This species is placed in <i>Terraquivivens</i>, in the family <i>Wolframiiiraptoraceae</i>, based on phylogenomic analysis using 122 archaeal marker genes. ANI values within the species range between 98 and 100 %, with all other values to the closest relatives being below species guidelines (79-85 %). In addition to the tungstate (Tup) ABC transporter detected in all members of the genus, the majority of the genomes for this species also encode a <i>wtpA/modA</i>-like protein that is homologous to <i>modA</i>-like sequences previously reported in <i>Pyrobaculum</i>. Most members of this species contain the gene <i>cydA</i> that encodes cytochrome bd ubiquinol oxidase subunit I, which appears to have been gained in only this species in the genus. Also, an unknown ferredoxin oxidoreductase, shared only by the sister species <i>Terraquivivens yellowstonensis</i>, is present in all genomes of this species studied here.</p>	<p><i>Terraquivivens</i></p>	<p>NCBI Assembly: GCA_023261845.1 <small>Ts</small></p>	<p><a href="https://seqco.de/i:22829">seqco.de/i:22829</a></p>

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Species <i>Terraquivivens tikiterensis</i> <sup>Ts</sup>	[ti.ki.ter.en'sis] N.L. fem. adj. <i>tikiterensis</i> , of Tikitere, Rotorua, New Zealand, where this organism was identified from	<p>The MAG of this organism was recovered from environmental sequencing of samples from Tikitere, Rotorua, New Zealand. The binned genome totals 1,536,389 bp and has a G+C content of 51.3 %. The genome completeness is estimated at 99.0 %, with very low (0.49 %) contamination based on CheckM. Comprehensive phylogenomic analysis of 120 archaeal marker genes places this taxon in the proposed candidate genus, <i>Terraquivivens</i>, in the proposed candidate family <i>Wolframiiiraptoraceae</i>. ANI values between this taxon and other members of the genus fall well below species delineation guidelines (76-78 %), and along with geographic isolation of this taxon from close relatives, delineation as a novel species is supported. Along with the tungstate (Tup) ABC transporter subunits, the molybdate transporter (<i>modABC</i>) and an additional putative <i>wtpA/modA</i>-like gene, homologous to <i>modA</i>-like sequences in <i>Pyrobaculum</i> species, suggest versatility in uptake of either molybdate or tungstate by this species. Two gene fragments encoding 4-hydroxybutyryl-CoA dehydratase (<i>abfD</i>) together, have been identified from the genome, indicating potential autotrophic CO<sub>2</sub> fixation through the oxygen-tolerant hydroxypropionate/hydroxybutyrate (HP/HB) cycle, while no other members of the family were found to possess these genes.</p>	<i>Terraquivivens</i>	NCBI Assembly: GCA_003056285.1 <sup>Ts</sup>	<a href="https://seqco.de/i:22826">seqco.de/i:22826</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
<p>Species <i>Geocrenenecus dongiae</i><sup>Ts</sup></p>	<p>[dong'i.æ] N.L. gen. n. <i>dongiae</i>, named for the Chinese microbiologist, Prof. Xiuzhu Dong (1958-), for her contributions to the study of ecology and taxonomic classification of extremophiles</p>	<p>Fifteen MAGs representing this species were recovered from metagenomic sequencing efforts of thermal springs in the Rehai and Ruidian geothermal fields, Tengchong, China. The genomes ranged in size from 1,322,968 bp to 1,558,478 bp, in 21 to 188 contigs, and ranged in G+C content between 37.4 and 37.6 %. The genomes were estimated to be between 90.9 and 99.1 % complete, with limited contamination (0-0.97 %) based on CheckM. Phylogenomic analysis of 122 conserved archaeal markers robustly placed this taxon in the novel genus <i>Geocrenenecus</i>, in the family <i>Wolframiraptoraceae</i>. ANI comparisons within the species resulted in values above 99 %, while all comparisons to closest relatives were below 90 %. Similar to other members of the genus, no homologs to known tungstate or molybdate transporters were identified from members of this species, although one genome contained genes that were identified as <i>tupA</i>-like, as well as a homolog to the proposed <i>wtpA/modA</i>-like genes identified in <i>Pyrobaculum</i> species previously. This genome also encoded <i>nirK</i>, <i>nosZ</i> and <i>coxAC</i>, while <i>mcmA1</i> and <i>mcmA2</i> were identified in two genomes, however, all other members identified in this study belonging to this species lacked these genes. In addition to the several tungsten-dependent ferredoxin oxidoreductases conserved within the genus, all members of this species encode a GAPOR-like enzyme. The genomes of most members in the species encode the genes for cytochrome C oxidase subunits (<i>coxA/B</i>), cytochrome bd ubiquinol oxidase subunit I (<i>cydA</i>), and the aerobic carbon-monoxide dehydrogenase large subunit (<i>coxL</i>), which may indicate that members of this species can perform aerobic respiration.</p>	<p><i>Geocrenenecus</i></p>	<p>NCBI Assembly: GCA_023267855.1 <sup>Ts</sup></p>	<p><a href="https://seqco.de/i:22823">seqco.de/i:22823</a></p>

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Species <i>Terraquivivens yellowstonensis</i>	[yel.low.ston.en'sis] N.L. fem. adj. <i>yellowstonensis</i> , of Yellowstone, referring to Yellowstone National Park, USA, where this organism was identified from	Seven MAGs for this species were identified from four different springs in Yellowstone National Park, USA. The genomes are between 1,073,374 bp and 1,275,530 bp, in 19 to 35 contigs, and have a G+C content between 45.9 and 46.1 %. Completeness and contamination estimates based on CheckM are between 94.17 and 97.08 %, and 0 to 1.94 %, respectively. Phylogenomics with the ar122 markers robustly place this species in the genus <i>Terraquivivens</i> , in the family <i>Wolframiiaptoraceae</i> . ANI values among genomes for this species are 98-100 %, with all other pairwise values compared to members of the genus below 85 %. The gene encoding Sqr (sulfide:quinone oxidoreductase) is present in some members of the species, however, most of the genomes lack this gene. All genomes belonging to the species lack an AOR-like encoding gene that is conserved within the rest of the family, and possess an unknown oxidoreductase that is shared with <i>Terraquivivens tengchongensis</i> , however, the substrates for these enzymes are still unclear.	<i>Terraquivivens</i>	NCBI Assembly: GCA_023539445.1 Ts	<a href="https://seqco.de/i:22830">seqco.de/i:22830</a>
Species <i>Wolframiiaptor sinensis</i>	[sin.en'sis] N.L. masc. adj. <i>sinensis</i> , of or pertaining to China, where the organisms were identified from	Sixteen MAGs representing this species were identified from thermal springs in the Rehai and Ruidian geothermal fields, Tengchong, China. These genomes ranged in size from 990,328 bp to 1,230,238 bp, in 10 to 90 contigs, with G+C content of 53.7-55.6 %. Genome completeness was estimated at 92-98.1 %, with 0-2 % contamination, as determined with CheckM. This species is placed in the genus <i>Wolframiiaptor</i> , in the family <i>Wolframiiaptoraceae</i> , based on phylogenomic analysis of 122 conserved archaeal marker sequences. ANI values among members of the species range between 97 and 100 %, with comparisons with other members of the genus resulting in values below 80 %.	<i>Wolframiiaptor</i>	NCBI Assembly: GCA_023261815.1 Ts	<a href="https://seqco.de/i:22832">seqco.de/i:22832</a>



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Species <i>Geocrenenecus</i> <i>huangii</i>	[huang'i.i] N.L. gen. n. <i>huangii</i> , of Huang, named for the Chinese microbiologist, Prof. Li Huang (1958-), for his contributions to the study of virus ecology and taxonomic classification in hot springs	Twelve MAGs for this organism were recovered from metagenomes of thermal springs in the Rehai and Ruidian geothermal fields, Tengchong, Yunnan, China. The binned MAGs ranged between 1,361,286 bp and 1,697,407 bp, in 21 to 174 contigs, with a G+C content of 40.5 to 40.7 %. Genome completeness estimates were between 91.3 and 98.1 %, with contamination estimated at 0.97 to 1.46 % based on CheckM. Robust phylogenomic analysis based on 122 archaeal markers places this taxon in the genus <i>Geocrenenecus</i> , in the family <i>Wolframiraptoraceae</i> . Intraspecific ANI values all range between 99.3 and 100 %, while all other comparisons to other members within the genus range between 75 and 90 %. Like other members of the genus, several AORs were identified in the genomes of this species, with a GAPOR-like encoding gene in all members of the species. The presence of genes encoding some cytochrome C oxidase subunits ( <i>coxA/B</i> ), cytochrome bd ubiquinol oxidase subunit I ( <i>cydA</i> ), and the aerobic carbon-monoxide dehydrogenase large subunit ( <i>coxL</i> ), suggest that members of this species may be capable of aerobic respiration.	<i>Geocrenenecus</i>	NCBI Assembly: GCA_023254095.1 Ts	<a href="https://seqco.de/i:22825">seqco.de/i:22825</a>
Species <i>Terraquivivens</i> <i>ruidianensis</i>	[rui.di.an.en'sis] N.L. fem. adj. <i>ruidianensis</i> , of Ruidian, referring to the Ruidian geothermal fields, Yunnan, China, where these organisms were identified from	Two MAGs of this organism were recovered from environmental sequencing of samples from Jinze hot spring, in the Rehai geothermal field, Tengchong, Yunnan, China. The binned genomes are 1,273,812 bp in 8 contigs, and 1,298,744 bp in 50 contigs, respectively, and both genomes have a G+C content of 47.5 %. The genome completeness estimates for both are 98.5 %, with very low (0.97%) contamination based on CheckM. Phylogenomic analysis of the 120 archaeal marker genes in the ar122 dataset places this taxon in the proposed candidate genus, <i>Terraquivivens</i> , in the proposed candidate family <i>Wolframiraptoraceae</i> . ANI values between the two genomes are 99.9 %, while values between this taxon and other members of the genus fall below species delineation guidelines (80-82 %).	<i>Terraquivivens</i>	NCBI Assembly: GCA_023267885.1 Ts	<a href="https://seqco.de/i:22828">seqco.de/i:22828</a>

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<p>Species <i>Geocrenenecus arthurdayi</i></p>	<p>[ar.thur.day'i] <b>N.L. gen. n.</b> <i>arthurdayi</i>, of Arthur Day, named for the American geophysicist and volcanologist Dr. Arthur L. Day (1869-1960), for his seminal work in Earth sciences, particularly relating to the hot springs in Yellowstone National Park, USA</p>	<p>MAGs identified as belonging to this species were recovered from metagenomes sampled from two thermal springs in Yellowstone National Park, USA. The six MAGs for this species range between 1,530,521 bp and 1,985,835 bp, in 82-223 contigs, with a G+C content of 38.4-39.4 %. Completeness estimates were between 96.1 and 97.8 %, with 0 % contamination, based on CheckM. Phylogenomic inference based on the ar122 conserved archaeal marker set placed the species within the genus <i>Geocrenenecus</i>, in the family <i>Wolframiraptoraceae</i>. All genomes of this species were considered conspecific based on Average Nucleotide Identity (ANI), with pairwise values &gt;99 %. Comparisons against the closely related members of the genus resulted in pairwise values between 75 and 78 %. No homologs to known or putative tungstate or molybdate transporters were identified from any of the genomes belonging to this species. Unlike other members of the genus, no GAPOR-like tungsten-dependent ferredoxin oxidoreductase was identified in this species. One genome encoded an unknown oxidoreductase. All genomes belonging to this species encode methylmalonyl-CoA mutase (McmA1/2), indicative of potential propionate metabolism. Unlike other species in the genus, the genomes of this species lack genes encoding cytochrome c oxidase subunits, but contain genes encoding cytochrome bd ubiquinol oxidase subunit I (<i>cydA</i>), and the aerobic carbon-monoxide dehydrogenase large subunit (<i>coxL</i>). The genomes within this species does also encode a homolog of <i>arxA</i>, suggesting potential respiratory arsenate reduction.</p>	<p><i>Geocrenenecus</i></p>	<p>NCBI Assembly: GCA_023539395.1 Ts</p>	<p><a href="https://seqco.de/i:22824">seqco.de/i:22824</a></p>

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Species <i>Benthortus lauensis</i> <sup>Ts</sup>	[lau.en'sis] N.L. masc. adj. <i>lauensis</i> , of Lau, referring to the Lau Basin in the Western Pacific, where this organism was identified from	The MAG of this organism was recovered from metagenomic sequencing data of a deep-water hydrothermal sulfide deposit sample taken from the Lau Basin, in the Western Pacific. The binned genome of this organism is 1,470,116 bp in size, and consists of 112 contigs, with a G+C content of 54.8 %. CheckM-based quality assessment indicates a completeness of 94.0 % and a contamination estimate of 2.91 %. Phylogenomic reconstruction based on 122 conserved archaeal genes place this taxon in the family <i>Wolframiraptoraceae</i> . Only two putative tungsten-dependent AORs were predicted within the genome of this organism	<i>Benthortus</i>	NCBI Assembly: GCA_021650775.1 <sup>Ts</sup>	<a href="https://seqco.de/i:22820">seqco.de/i:22820</a>
Species <i>Wolframiraptor allenii</i>	[al.len'i.i] N.L. gen. n. <i>allenii</i> , of Allen, named for Dr. Eugene T. Allen (1864-1964), an American geochemist, for his pioneering work on the geochemistry of Yellowstone National Park, USA	Two MAGs representing this species were assembled from metagenomic sequence data determined from samples taken from thermal springs in Geyser Creek, Geyser Basin and the Lower Geyser Basin, Yellowstone National Park, USA. These genomes are 1,104,807 bp and 1,315,737 bp in size, 151 and 95 contigs, respectively, with a G+C content of 51.6 to 52.4 %. Completeness estimates for both genomes, as determined by CheckM, are 91.58 and 92.23 %, with 0 % contamination estimated. Phylogenomic analysis of 122 archaeal marker sequences places this species in the genus <i>Wolframiraptor</i> , in the family <i>Wolframiraptoraceae</i> . ANI values between these genomes are 99.0 %, while all other pairwise comparisons to closely related taxa are below 87 %.	<i>Wolframiraptor</i>	NCBI Assembly: GCA_023539495.1 <sup>Ts</sup>	<a href="https://seqco.de/i:22831">seqco.de/i:22831</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
<p>Species <i>Wolframiiaptor gerlachensis</i><sup>Ts</sup></p>	<p>[ger.lach.en'sis] N.L. masc. adj. <i>gerlachensis</i>, of Gerlach, the region where Great Boiling Spring is located in Nevada, and this organism was obtained from</p>	<p>A MAG representing this species was recovered from metagenomic sequencing of a stable enrichment culture, established from an <i>in situ</i> corn stover enrichment from Great Boiling Spring, Nevada, USA. Enrichment and maintenance of this species within the mixed-culture community was optimal at an incubation temperature of 80 °C with lignocellulose and sugars, at circumneutral pH. This species is dependent on tungsten for growth, with significant decline in its abundance within the community without tungsten added to the growth medium. Additionally, several tungstoenzymes conserved within the genus were expressed at a higher rate during growth on corn stover, suggesting direct involvement of tungstoenzymes in complex carbohydrate metabolism. Cells of this organism showed significant isotope enrichment when grown on isotopically labeled xylose-amended medium, with limited isotope enrichment during growth on medium amended with amino acids, glucose, ribose, and starch, indicating preferential assimilation of xylose. The genome sequence for this organism is 1,277,965 bp in size, and consists of 27 contigs and has a G+C content of 52 %. Completeness is estimated at 98.06 % with 0.49 % contamination, as estimated with CheckM. ANI comparisons among this genome and those of closely related species were below 86 %, supporting the delineation of this taxon as unique and distinct to other species in the genus.</p>	<p><i>Wolframiiaptor</i></p>	<p>NCBI Assembly: GCA_021323375.2 <sup>Ts</sup></p>	<p><a href="https://seqco.de/i:22816">seqco.de/i:22816</a></p>