

# DPANN Archaea from Vázquez-Campos et al (2021)

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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
Order <i>Anstonellales</i>	[Ans.to.nel.la'les] <b>N.L. fem. dim. n.</b> <i>Anstonella</i> , referring to the type genus <i>Anstonella</i> ; <b>-ales</b> , ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Anstonellales</i> , the <i>Anstonella</i> order	The order <i>Anstonellales</i> is circumscribed based on two independent concatenated protein phylogenies of 122 and 93 markers, and supported by the rank normalisation approach as per Parks et al. (2018). It constitutes the most inclusive clade that includes the families <i>Anstonellaceae</i> , and <i>Bilamarchaeaceae</i> . The type genus is <i>Anstonella</i> . The order is equivalent to the lineage LFWA-IIIc in this manuscript, and o__UBA10214 in the GTDB r89/r202 (Parks et al., 2017).	<i>Microcaldia</i>	<i>Anstonella</i>	<a href="https://seqco.de/i:23471">seqco.de/i:23471</a>
Order <i>Burarchaeales</i>	[Bur.ar.chae.a'les] <b>N.L. neut. n.</b> <i>Burarchaeum</i> , referring to the type genus <i>Burarchaeum</i> ; <b>-ales</b> , ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Burarchaeales</i> , the <i>Burarchaeum</i> order	The order <i>Burarchaeales</i> is circumscribed based on two independent concatenated protein phylogenies of 122 and 93 markers, and supported by the rank normalisation approach as per Parks et al. (2018). The description is the same as that of its sole genus and species. The type genus is <i>Burarchaeum</i> . The order is equivalent to LFWA-IIIc in this manuscript and o__B9-G16 in GTDB r202 (Parks et al., 2017).	<i>Microcaldia</i>	<i>Burarchaeum</i>	<a href="https://seqco.de/i:23464">seqco.de/i:23464</a>
		The order <i>Gugararchaeales</i>			

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Order <i>Gugararchaeales</i>	[Gu.gar.ar.chae.a'les] <b>N.L. neut. n.</b> <i>Gugararchaeum</i> , referring to the type genus <i>Gugararchaeum</i> ; -ales, ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Gugararchaeales</i> , the <i>Gugararchaeum</i> order	is circumscribed based on two independent concatenated protein phylogenies of 122 and 93 markers, and supported by the rank normalisation approach as per Parks et al. (2018). The description is the same as that of its sole genus and species. The type genus is <i>Gugararchaeum</i> . The order is equivalent to LFWA-IIIa in this manuscript and appears as o_CABMDC01 in GTDB r202 (Parks et al., 2017).	<i>Microcaldia</i>	<i>Gugararchaeum</i>	<a href="https://seqco.de/i:23460">seqco.de/i:23460</a>
Order <i>Norongarragalinales</i>	[No.ron.gar.ra.ga.li.na'les] <b>N.L. fem. n.</b> <i>Norongarragalina</i> , referring to the type genus <i>Norongarragalina</i> ; -ales, ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Norongarragalinales</i> , the <i>Norongarragalina</i> order	The order <i>Norongarragalinales</i> is circumscribed based on two independent concatenated protein phylogenies of 122 and 93 markers, and supported by the rank normalisation approach as per Parks et al. (2018). The description is the same as that of its sole genus and species. The type genus is <i>Norongarragalina</i> . This order is equivalent to LFWA-II in this manuscript, and o_UBA8480 in GTDB r89/r202 (Parks et al., 2017).	<i>Microcaldia</i>	<i>Norongarragalina</i>	<a href="https://seqco.de/i:23477">seqco.de/i:23477</a>
Order <i>Tiddalikarchaeales</i>	[Tid.da.lik.ar.chae.a'les] <b>N.L. neut. n.</b> <i>Tiddalikarchaeum</i> , referring to the type genus <i>Tiddalikarchaeum</i> ; -ales, ending to denote an order; <b>N.L. fem. pl. n.</b> <i>Tiddalikarchaeales</i> , the <i>Tiddalikarchaeum</i> order	The order <i>Tiddalikarchaeales</i> is circumscribed based on two independent concatenated protein phylogenies of 122 and 93 markers, and supported by the rank normalisation approach as per Parks et al. (2018). The description is the same as that of its sole genus and species. The type genus is <i>Tiddalikarchaeum</i> .	<i>Nanobdellia</i>	<i>Tiddalikarchaeum</i>	<a href="https://seqco.de/i:23451">seqco.de/i:23451</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		The order is equivalent to CG07-land from Probst et al. (2018) or o__CG07-land in GTDB r89/r202 (Parks et al., 2017).			
Family <i>Anstonellaceae</i>	[Ans.to.nel.la'ce.ae] <b>N.L. fem. dim. n.</b> <i>Anstonella</i> , referring to the type genus <i>Anstonella</i> ; - <i>aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Anstonellaceae</i> , the <i>Anstonella</i> family	The family <i>Anstonellaceae</i> is circumscribed based on two independent concatenated protein phylogenies of 122 and 93 markers, and supported by the rank normalisation approach as per Parks et al. (2018). The description is the same as that of its sole genus and species. The type genus is <i>Anstonella</i> . This family is equivalent to f__UBA10161 in the GTDB r89/r202 (Parks et al., 2017).	<i>Anstonellales</i>	<i>Anstonella</i>	<a href="https://seqco.de/i:23467">seqco.de/i:23467</a>
Family <i>Bilamarchaeaceae</i>	[Bi.lam.ar.chae.a'ce.ae] <b>N.L. neut. n.</b> <i>Bilamarchaeum</i> , referring to the type genus <i>Bilamarchaeum</i> ; - <i>aceae</i> , ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Bilamarchaeaceae</i> , the <i>Bilamarchaeum</i> family	The family <i>Bilamarchaeaceae</i> is circumscribed based on two independent concatenated protein phylogenies of 122 and 93 markers, and supported by the rank normalisation approach as per Parks et al. (2018). The description is the same as that of its sole genus and species. The type genus is <i>Bilamarchaeum</i> . This family is equivalent to f__UBA10214 in the GTDB r89/r202 (Parks et al., 2017).	<i>Anstonellales</i>	<i>Bilamarchaeum</i>	<a href="https://seqco.de/i:23470">seqco.de/i:23470</a>
Family	[Bur.ar.chae.a'ce.ae] <b>N.L. neut. n.</b> <i>Burarchaeum</i> , referring to the type genus <i>Burarchaeum</i> ; - <i>aceae</i> , ending to denote a	The family <i>Burarchaeaceae</i> is circumscribed based on two independent concatenated protein phylogenies of 122 and 93 markers, and supported by the rank normalisation approach as per Parks et al.	<i>Burarchaeales</i>	<i>Burarchaeum</i>	<a href="https://seqco.de/i:23463">seqco.de/i:23463</a>

<i>Burarchaeaceae</i> <b>Proposed Taxon</b>	family; <b>N.L. fem. pl. n.</b> <b>Etymology</b> <i>Burarchaeaceae</i> , the	(2018). The description is the same as that of its sole <b>Description</b>	<b>Parent Taxon</b>	<b>Type</b>	<b>Registry URL</b>
	<i>Burarchaeum</i> family	genus and species. The type genus is <i>Burarchaeum</i> . The family is equivalent to f__B9-G16 in GTDB r202 (Parks et al., 2017).			
Family <i>Gugararchaeaceae</i>	[Gu.gar.ar.chae.a'ce.ae] <b>N.L. neut. n.</b> <i>Gugararchaeum</i> , referring to the type genus <i>Gugararchaeum</i> ; -aceae, ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Gugararchaeaceae</i> , the <i>Gugararchaeum</i> family	The family <i>Gugararchaeaceae</i> is circumscribed based on two independent concatenated protein phylogenies of 122 and 93 markers, and supported by the rank normalisation approach as per Parks et al. (2018). The description is the same as that of its sole genus and species. The type genus is <i>Gugararchaeum</i> . The family appears in GTDB r202 (Parks et al., 2017) as f__CABMDC01.	<i>Gugararchaeales</i>	<i>Gugararchaeum</i>	<a href="https://seqco.de/i:23459">seqco.de/i:23459</a>
Family <i>Norongarralinaceae</i>	[No.ron.gar.ra.ga.li.na'ce.ae] <b>N.L. fem. n.</b> <i>Norongarralina</i> , referring to the type genus <i>Norongarralina</i> ; -aceae, ending to denote a family; <b>N.L. fem. pl. n.</b> <i>Norongarralinaceae</i> , the <i>Norongarralina</i> family	The family <i>Norongarralinaceae</i> is circumscribed based on two independent concatenated protein phylogenies of 122 and 93 markers, and supported by the rank normalisation approach as per Parks et al. (2018). The description is the same as that of its sole genus and species. The type genus is <i>Norongarralina</i> . This family is equivalent to f__0-14-0-20-59-11 in the GTDB r89/r202 (Parks et al., 2017).	<i>Norongarralinales</i>	<i>Norongarralina</i>	<a href="https://seqco.de/i:23476">seqco.de/i:23476</a>
		The family <i>Tiddalikarchaeaceae</i> is circumscribed based on two independent concatenated			

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Family <i>Tiddalikarchaeaceae</i>	[Tid.da.lik.ar.chae.a'ce.ae] <b>N.L. neut. n. <i>Tiddalikarchaeum</i>,</b> referring to the type genus <i>Tiddalikarchaeum</i> ; -aceae, ending to denote a family; <b>N.L. fem. pl. n. <i>Tiddalikarchaeaceae</i>,</b> the <i>Tiddalikarchaeum</i> family	protein phylogenies of 122 and 93 markers, and supported by the rank normalisation approach as per Parks et al. (2018). The description is the same as that of its sole genus and species. The type genus is <i>Tiddalikarchaeum</i> . The family is equivalent to f__CG07-land in GTDB r89/r202 (Parks et al., 2017).	<i>Tiddalikarchaeales</i>	<i>Tiddalikarchaeum</i>	<a href="https://seqco.de/i:23456">seqco.de/i:23456</a>
Genus <i>Anstonella</i>	[Ans.to.nel'la] <b>N.L. fem. dim. n. <i>Anstonella</i>,</b> archaeon named after ANSTO, Australian Nuclear Science and Technology Organisation, institution managing the Little Forest Legacy Site	The type species is <i>Anstonella stagnisolia</i> . The genus appears as g__CABMCJ01 in GTDB r202 (Parks et al., 2017).	<i>Anstonellaceae</i>	<i>Anstonella stagnisolia</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23465">seqco.de/i:23465</a>
Genus <i>Bilamarchaeum</i>	[Bi.lam.ar.chae'um] <b>N.L. n. <i>bilama</i>,</b> freshwater turtle in Dharawal language, in reference to their presence still nowadays in the creeks and rivers associated with the Little Forest Legacy Site; <b>N.L. neut. n. <i>archaeum</i>,</b> archaeon; <b>N.L. neut. n. <i>Bilamarchaeum</i>,</b> an archaeon from the turtle lands	The type species is <i>Bilamarchaeum dharawalense</i> . The genus appears as g__CAILMU01 in GTDB r202 (Parks et al., 2017).	<i>Bilamarchaeaceae</i>	<i>Bilamarchaeum dharawalense</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23468">seqco.de/i:23468</a>
Genus <i>Burarchaeum</i>	[Bur.ar.chae'um] <b>N.L. n. <i>burus</i>,</b> from buru, meaning kangaroo in the Dharawal language; <b>N.L. neut. n. <i>archaeum</i>,</b> archaeon; <b>N.L. neut. n. <i>Burarchaeum</i>,</b> an archaeon from the land of the kangaroos	The type species is <i>Burarchaeum australiense</i> . The genus appears as g__CABMJK01 in GTDB r202 (Parks et al., 2017).	<i>Burarchaeaceae</i>	<i>Burarchaeum australiense</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23461">seqco.de/i:23461</a>
Genus <i>Gugararchaeum</i>	[Gu.gar.ar.chae'um] <b>N.L. n. <i>gugara</i>,</b> meaning kookaburra in Dharawal language - bird endemic to Australia; <b>N.L. neut. n. <i>archaeum</i>,</b> archaeon; <b>N.L. neut. n. <i>Gugararchaeum</i>,</b> archaeon named after the	The type species is <i>Gugararchaeum adminiculabundum</i> . The genus appears as g__CABMDC01 in GTDB r202 (Parks et al., 2017).	<i>Gugararchaeaceae</i>	<i>Gugararchaeum adminiculabundum</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23457">seqco.de/i:23457</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Genus <i>Norongarragalina</i>	aboriginal name of the kookaburra [No.ron.gar.ra.ga.li'na] <b>N.L. n.</b> <i>Norongarragalus</i> , Norongarragal, Dharawal clan group who traditionally occupied the Menai/Lucas Heights area where the present study took place; <b>L. fem. adj. suff.</b> <i>-ina</i> , pertaining or belonging to; <b>N.L. fem. n.</b> <i>Norongarragalina</i> , organism named after the Norongarragal clan in Australia	The type species is <i>Norongarragalina meridionalis</i> . This genus is equivalent to g__0-14-0-20-59-11 in GTDB r89/r202 (Parks et al., 2017).	<i>Norongarragalinaceae</i>	<i>Norongarragalina meridionalis</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23474">seqco.de/i:23474</a>
Genus <i>Tiddalikarchaeum</i>	[Tid.da.lik.ar.chae'um] <b>N.L. masc. n.</b> <i>Tiddalikus</i> , named after the frog from the Australian Aboriginal mythology; <b>N.L. neut. n.</b> <i>archaeum</i> , archaeon; <b>N.L. neut. n.</b> <i>Tiddalikarchaeum</i> , the archaeon named after the greedy Aboriginal mythological Australian frog that burst with water, referring to the bathtub effect exhibited by the disposal trenches at the Little Forest Legacy Site	The type species is <i>Tiddalikarchaeum anstoanum</i> . The genus appears as g__CABMEV01 in GTDB r202 (Parks et al., 2017).	<i>Tiddalikarchaeaceae</i>	<i>Tiddalikarchaeum anstoanum</i> <sup>Ts</sup>	<a href="https://seqco.de/i:23454">seqco.de/i:23454</a>
Species <i>Anstonella stagnisolia</i> <sup>Ts</sup>	[stag.ni.so'lia] <b>L. v.</b> <i>stagno</i> , to overflow; <b>L. neut. n.</b> <i>solium</i> , tub, bathtub; <b>N.L. neut. pl. n.</b> <i>stagnisolia</i> , overflowing bathtubs, in reference to the phenomenon described during heavy rainfalls at the Little Forest Legacy Site trenches	The type material is the metagenome assembled genome (MAG) LFW-35 (ERS2655287) recovered from the groundwater of the Little Forest Legacy Site (NSW, Australia). The MAG consists of 1.33 Mbp in 68 contigs with an estimated completeness of 97.8%, redundancy of 2.2%, 16S, 23S and 5S rRNA gene, and 21 tRNAs. The GC content of this MAG is 50.3%. The type material appears in GTDB r202 (Parks et al., 2017) as reference for s__CABMCJ01 sp902384585.	<i>Anstonella</i>	NCBI Assembly: GCA_902384585.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23466">seqco.de/i:23466</a>

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Bilamarchaeum dharawalense</i> <sup>Ts</sup>	[dha.ra.wa.len'se] <b>N.L. neut. adj.</b> <i>dharawalense</i> , pertaining to the Dharawal country, traditional name of the lands where the Little Forest Legacy Site is located	The type material is the metagenome assembled genome (MAG) LFW-283_2 (ERS2655319) recovered from the groundwater of the Little Forest Legacy Site (NSW, Australia). The MAG consists of 1.27 Mbp in 63 contigs with an estimated completeness of 95.7%, redundancy of 0%, 16S, 23S and 5S rRNA gene, and 20 tRNAs. The GC content of this MAG is 40.0%. The type material appears in GTDB r202 (Parks et al., 2017) as reference for s_CAILMU01 sp902386555.	<i>Bilamarchaeum</i>	NCBI Assembly: GCA_902386555.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23469">seqco.de/i:23469</a>
Species <i>Burarchaeum australiense</i> <sup>Ts</sup>	[aus.tra.lien'se] <b>N.L. neut. adj.</b> <i>australiense</i> , referring to Australia	The type material is the metagenome assembled genome (MAG) LFW-281_7 (ERS2655318) recovered from the groundwater of the Little Forest Legacy Site (NSW, Australia). The MAG consists of 1.20 Mbp in 76 contigs with an estimated completeness of 96.8%, redundancy of 5.4%, 16S and 5S rRNA gene, and 18 tRNAs. The GC content of this MAG is 57.6%. The type material appears in GTDB r202 (Parks et al., 2017) as reference for s_CABMJK01 sp902386535.	<i>Burarchaeum</i>	NCBI Assembly: GCA_902386535.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23462">seqco.de/i:23462</a>
	[ad.mi.ni.cu.la.bun'dum] <b>L. neut. adj.</b> <i>adminiculabundum</i> , self-supporting, in reference to the limited external	The type material is the metagenome assembled genome (MAG) LFW-121_3 (ERS2655302) recovered from the groundwater of the Little Forest Legacy Site (NSW, Australia). The MAG consists of 1.47 Mbp in 76			

Species <b>Proposed Taxon</b> <i>Gugararchaeum</i>	<b>Etymology</b> requirements and its suggested independence from a	<b>Description</b> contigs with an estimated completeness of 96.8%,	<b>Parent Taxon</b> <i>Gugararchaeum</i>	<b>Type</b> NCBI Assembly: GCA_902384795.1 <sup>Ts</sup>	<b>Registry URL</b> <a href="https://seqco.de/i:23458">seqco.de/i:23458</a>
<i>adminiculabundum</i> <sup>Ts</sup>	host/symbiote, due to the predicted presence of pathways for the biosynthesis of amino acids, purines, pyrimidines, thiamine, and riboflavin	redundancy of 2.2%, 16S, 23S, and 5S rRNA gene, and 21 tRNAs. The GC content of this MAG is 49.8%. The type material appears in GTDB r202 (Parks et al., 2017) as reference for s__CABMDC01 sp902384795.			
Species <i>Norongarragalina meridionalis</i> <sup>Ts</sup>	[me.ri.dio.na'lis] <b>L. fem. adj.</b> <i>meridionalis</i> , southern, referring to the Southern hemisphere, where its first genome was reconstructed	The type material is the metagenome assembled genome (MAG) LFW-144_1 (ERS2655293) recovered from the groundwater of the Little Forest Legacy Site (NSW, Australia). The MAG consists of 0.93 Mbp in 49 contigs with an estimated completeness of 93.5%, redundancy of 1.1%, 16S and 5S rRNA gene, and 20 tRNAs. The GC content of this MAG is 57.5%. The type material appears in GTDB r202 (Parks et al., 2017) as reference for s__0-14-0-20-59-11 sp902384935.	<i>Norongarragalina</i>	NCBI Assembly: GCA_902384935.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23475">seqco.de/i:23475</a>
Species <i>Tiddalikarchaeum anstoanum</i> <sup>Ts</sup>	[ans.to.a'num] <b>N.L. neut. adj.</b> <i>anstoonum</i> , from ANSTO, Australian Nuclear Science and Technology Organisation, institution managing the Little Forest Legacy Site	The type material is the metagenome assembled genome (MAG) LFW-252_1 (ERS2655302) recovered from the groundwater of the Little Forest Legacy Site (NSW, Australia). The MAG consists of 1.16 Mbp in 56 contigs with an estimated completeness of 95.7%, redundancy of 1.1%, 16S, 23S, and 5S rRNA gene, and 21 tRNAs. The GC content of this MAG is 36.5%.	<i>Tiddalikarchaeum</i>	NCBI Assembly: GCA_902385255.1 <sup>Ts</sup>	<a href="https://seqco.de/i:23455">seqco.de/i:23455</a>



Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		The type material appears in GTDB r202 (Parks et al., 2017) as reference for s_CABMEV01 sp902385255.			