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Draft Taxonomic Outline of the *Bacteroidetes*, *Planctomycetes*, *Chlamydiae*, *Spirochaetes*, *Fibrobacteres*, *Fusobacteria*, *Acidobacteria*, *Verrucomicrobia*, *Dictyoglomi*, and *Gemmatimonadetes*

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This revised Taxonomic Outline seeks to reconcile that of Garrity et al. (2001) [Appendix 2 of Bergeys volume 2A] with the description of additional taxa and new phylogenetic analyses calculated by Wolfgang Ludwig (Figures 1 and 2). While the Outline seeks to be complete for all taxa validated prior to July 1, 2006, some taxa described after that date are included.

The new phylogenetic trees are strict **consensus trees** based on various **maximum likelihood** and **maximum parsimony** analysis and corrected according to results obtained when applying alternative treeing methods. **Multifurcations** indicate that a common branching order was not significantly supported after applying alternative treeing approaches. Detailed branching orders are shown if supported by at least 50% of the 'treeings' performed in addition to the maximum likelihood approach.

Important information for the authors: Given that the focus is on the higher (taxonomic) ranks rather restrictive variability filters were applied. Consequently, **resolution power is lost for lower levels**. Of special importance, relationships within genera are only based upon maximum likelihood analyses and lack the resolution that would be obtained with genus-family level analyses. Furthermore, the type strain tree is an extract of comprehensive trees comprising some thousand sequences. Thus, trees provided by the authors - based upon smaller data sets and including the variable sequence positions - for the respective groups may differ with respect to detailed topology especially at levels of closer relationship within and between genera. **Branch lengths** - in first instance - **indicate significance** (and only roughly reflect estimated number of changes).

This proposed outline is being offered ahead of publication for comments. While we have sought the opinions of experts on various lineages prior to releasing this draft, we would greatly appreciate further constructive comments. Please send your comments to: Barny Whitman at whitman@uga.edu.

Request for information: We have been unable to find 16S rRNA sequences for the taxa listed below (Table 1). If you know of a sequence for these organisms, can you send them to Barny Whitman (whitman@uga.edu) or Wolfgang Ludwig (ludwig@mikro.biologie.tu-muenchen.de).

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Figure Legends.

Figure 1. Consensus dendrogram reflecting the phylogenetic relationships of the phyla *Planctomycetes*, *Chlamydiae*, *Spirochaetes*, *Fibrobacteres*, *Fusobacteria*, *Acidobacteria*, *Verrucomicrobia*, *Dictyoglomi*, and *Gemmatimonadetes*. The tree is based on maximum likelihood analyses of a data set comprising about 5000 almost full-length high quality 16S rRNA sequences from representatives of the each phylum and another 1000 representing the major lines of descent of the three domains *Bacteria*, *Archaea* and *Eucarya*. The topology was evaluated by distance matrix and maximum parsimony analyses of the data set. In addition maximum parsimony analyses of all currently available almost complete small subunit rRNA sequences (137,400 of ARB-SILVA release 92, Prüsse et al., 2007) were performed. Only alignment positions invariant in at least 50% of the included primary structures were included for tree reconstruction. Multifurcations indicate that a common relative branching order was not significantly supported applying alternative treeing methods. The (horizontal) branch lengths indicate the significance of the respective node separation.

Figure 2. Consensus dendrogram reflecting the phylogenetic relationships of the phylum *Bacteroidetes*. Analyses were performed as described for Figure 1.

The proposed taxonomic outline

Phylum BXV. *Planctomycetes* phyl. nov.

- Class I. *Planctomycea*^{VP}
 - Order I. *Planctomycetales*^{VP}
 - Family I. *Planctomycetaceae*^{VP}
 - Genus I. *Planctomyces*^{AL(T)}
 - Genus II. *Blastopirellula*^{VP}
 - Genus III. *Gemmata*^{VP}
 - Genus IV. *Isosphaera*^{VP}
 - Genus V. *Pirellula*^{VP}
 - Genus VI. *Rhodopirellula*^{VP}
 - Genus VII. *Schlesneria*^{VP}
 - Genus VIII. *Singulisphaera*^{VP}
 - Order II. “*Brocadiales*”
 - Family I. “*Brocadiaceae*”
 - Genus I. “*Candidatus Brocadia*”^(T)
 - Genus II. “*Candidatus Kuenenia*”
 - Genus III. “*Candidatus Scalindua*”
 - Genus IV. “*Candidatus Anammoxoglobus*”
 - Genus V. “*Candidatus Jettenia*”

Phylum BXVI. *Chlamydiae* phyl. nov.

- Class I. *Chlamydiae*^{VP}
 - Order I. *Chlamydiales*^{AL(T)}
 - Family I. *Chlamydiaceae*^{AL}
 - Genus I. *Chlamydia*^{AL(T)}
 - Family II. *Parachlamydiaceae*^{VP}
 - Genus I. *Parachlamydia*^{VP(T)}
 - Genus II. *Neochlamydia*^{VP}
 - Family III. *Simkaniaceae*^{VP}
 - Genus I. *Simkania*^{VP(T)}
 - Genus II. “*Candidatus Rhabdochlamydia*”
 - Family IV. *Waddliaceae*^{VP}
 - Genus I. *Waddlia*^{VP(T)}

Note:

- 1) Although many species of the *Chlamydia* (*C. abortus*, *C. caviae*, *C. psittaci*, *C. felis*, *C. pecorum*, and *C. pneumoniae*) have been reclassified to *Chlamydophila*, this reorganization is not universally accepted. The original classification is retained for the present.

Phylum BXVII. *Spirochaetes* phyl. nov.

- Class I. *Spirochaetes*^{VP}
 - Order I. *Spirochaetales*^{AL}
 - Family I. *Spirochaetaceae*^{AL}
 - Genus I. *Spirochaeta*^{AL(T)}
 - Genus II. *Borrelia*^{AL}
 - Genus III. *Cristispira*^{AL}
 - Genus IV. *Treponema*^{AL}
 - Family II “*Brachyspiraceae*”
 - Genus I. *Brachyspira*^{VP(T)}
 - Family III “*Brevinemaceae*”
 - Genus I. *Brevinema*^{VP(T)}
 - Family IV. *Leptospiraceae*^{AL}
 - Genus I. *Leptospira*^{AL(T)}
 - Genus II. *Leptonema*^{VP}
 - Genus III. *Turneriella*^{VP}
 - Family V. *Incertae sedis*
 - Genus I. *Clevelandina*^{VP}
 - Genus II. *Diplocalyx*^{VP}
 - Genus III. *Hollandina*^{VP}
 - Genus IV. *Pillotina*^{VP}

Notes:

- 1) *Serpulina*^{VP} reclassified as *Brachyspira*, replacement of family “*Serpulinaceae*” with “*Brachyspiraceae*”
- 2) No sequences available for the symbionts *Clevelandina*, *Diplocalyx*, *Hollandina*, *Pillotina*, hence placement in Family *Incertae Sedis*.
- 3) Based upon the 16SrRNA sequence analysis, the family *Spirochaetaceae* is not clearly monophyletic.

Phylum BXVIII. *Fibrobacteres* phyl. nov.

- Class I. “*Fibrobacteria*”
 - Order I. “*Fibrobacterales*”
 - Family I. “*Fibrobacteraceae*”
 - Genus I. *Fibrobacter*^{VP(T)}

Phylum BXIX. *Acidobacteria* phyl. nov.

- Class I. *Acidobacteria*^{VP}
- Order I. *Acidobacteriales*^{VP(T)}
- Family I “*Acidobacteriaceae*”
- Genus I. *Acidobacterium*^{VP(T)}
- Genus II. *Geothrix*^{VP}
- Genus III. *Holophaga*^{VP}

Note:

- 1) *Terriglobus* validated in 2007 and not included

Phylum BXX. *Bacteroidetes* phyl. nov.

- Class I. “*Bacteroidia*”
- Order I. “*Bacteroidales*”
- Family I. *Bacteroidaceae*^{AL}
- Genus I. *Bacteroides*^{AL(T)}
- Genus II. *Acetofilamentum*^{VP}
- Genus III. *Acetomicrobium*^{VP}
- Genus IV. *Acetothermus*^{VP}
- Genus V. *Anaerorhabdus*^{VP}

Note:

- 1) The following genera are not in the tree- *Acetofilamentum*, *Acetomicrobium*, *Acetothermus*, *Anaerorhabdus*. A partial sequence is available for *Acetomicrobium*, but no sequences are available for the others.
- 2) *Megamonas*^{VP} transferred to Firmicutes as recommended by Morotomi et al. (2007) IJSEM 57:1673-1674.

- Family II “*Marinilabiliaceae*”
- Genus I. *Marinilabilia*^{VP(T)}
- Genus II. *Anaerophaga*^{VP}
- Genus III. *Alkaliflexus*^{VP}

Note:

- 1) There is only weak support for including *Cytophaga fermentans* in this family. In any case, it could be a new genus.

- Family III. “*Rikenellaceae*”
- Genus I. *Rikenella*^{VP(T)}
- Genus II. *Alistipes*^{VP}
- Family IV. “*Porphyromonadaceae*”
- Genus I. *Porphyromonas*^{VP(T)}
- Genus II. *Barnesiella*^{VP}
- Genus III. *Dysgonomonas*^{VP}

Genus IV. *Paludibacter*^{VP}
Genus V. *Parabacteroides*^{VP}
Genus VI. *Petrimonas*^{VP}
Genus VII. *Proteiniphilum*^{VP}
Genus VIII. *Tannerella*^{VP}

Family V. “*Prevotellaceae*”

Genus I. *Prevotella*^{VP(T)}
Genus II. *Xylanibacter*^{VP}

Notes:

- 1) Added *Xylanibacter* to “*Prevotellaceae*”. *Xylanibacter* appears to be supported by Ueki et al. (IJSEM56:2215).
- 2) *Hallella* appears to be nearly identical to *Prevotella dentalis*- for that reason, this genus is not used.

Class II. *Flavobacteria*^{VP}

Order I. “*Flavobacteriales*”

Family I. *Flavobacteriaceae*^{VP}

Genus I. *Flavobacterium*^{AL(T)}
Genus II. *Aequorivita*^{VP}
Genus III. *Algibacter*^{VP}
Genus IV. *Aquimarina*^{VP}
Genus V. *Arenibacter*^{VP}
Genus VI. *Bergeyella*^{VP}
Genus VII. *Bizionia*^{VP}
Genus VIII. *Capnocytophaga*^{VP}
Genus IX. *Cellulophaga*^{VP}
Genus X. *Chryseobacterium*^{VP}
Genus XI. *Cloacibacterium*^{VP}
Genus XII. *Coenonia*^{VP}
Genus XIII. *Costertonia*^{VP}
Genus XIV. *Croceibacter*^{VP}
Genus XV. *Dokdonia*^{VP}
Genus XVI. *Donghaeana*^{VP}
Genus XVII. *Elizabethkingia*^{VP}
Genus XVIII. *Empedobacter*^{VP}
Genus XIX. *Epilithonimonas*^{VP}
Genus XX. *Flaviramulus*^{VP}
Genus XXI. *Formosa*^{VP}
Genus XXII. *Gaetbulibacter*^{VP}
Genus XXIII. *Gelidibacter*^{VP}
Genus XXIV. *Gillisia*^{VP}
Genus XXV. *Gramella*^{VP}
Genus XXVI. *Kaistella*^{VP}

Genus XXVII. *Kordia*^{VP}
 Genus XXVIII. *Krokinobacter*^{VP}
 Genus XXIX. *Lacinutrix*^{VP}
 Genus XXX. *Leeuwenhoekella*^{VP}
 Genus XXXI. *Lutibacter*^{VP}
 Genus XXXII. *Maribacter*^{VP}
 Genus XXXIII. *Mariniflexile*^{VP}
 Genus XXXIV. *Mesonia*^{VP}
 Genus XXXV. *Muricauda*^{VP}
 Genus XXXVI. *Myroides*^{VP}
 Genus XXXVII. *Nonlabens*^{VP}
 Genus XXXVIII. *Olleya*^{VP}
 Genus XXXIX. *Ornithobacterium*^{VP}
 Genus XL. *Persicivirga*^{VP}
 Genus XLI. *Polaribacter*^{VP}
 Genus XLII. *Psychroflexus*^{VP}
 Genus XLIII. *Psychroserpens*^{VP}
 Genus XLIV. *Riemerella*^{VP}
 Genus XLV. *Robiginitalea*^{VP}
 Genus XLVI. *Salegentibacter*^{VP}
 Genus XLVII. *Sandarakinotalea*^{VP}
 Genus XLVIII. *Sediminicola*^{VP}
 Genus XLIX. *Sejongia*^{VP}
 Genus L. *Stenothermobacter*^{VP}
 Genus LI. *Subsaxibacter*^{VP}
 Genus LII. *Subsaximicrobium*^{VP}
 Genus LIII. *Tenacibaculum*^{VP}
 Genus LIV. *Ulvibacter*^{VP}
 Genus LV. *Vitellibacter*^{VP}
 Genus LVI. *Wautersiella*^{VP}
 Genus LVII. *Weeksella*^{VP}
 Genus LVIII. *Winogradskyella*^{VP}
 Genus LIX. *Yeosuana*^{VP}
 Genus LX. *Zhouia*^{VP}
 Genus LXI. *Zobellia*^{VP}

Notes:

- 1) *Stanierella* and *Gaetbulimicrobium* reclassified as *Aquimarina*
- 2) The 16SrRNA sequences of the following pairs of genera possess >97% sequence similarity and should be combined: *Sandarakinotalea-Nonlabens*; *Dokdonia-Krokinobacter*; and *Donghaeana-Persicivirga*.
- 3) The genus pairs possess 94 and 95% sequence similarity, respectively: *Lacinutrix-Olleya*; *Gramella-Salegentibacter*. On this basis, there is no clear indication that they should be combined
- 4) Two genera are not monophyletic and should be subdivided: *Bizionia*, *Cellulophaga*

- 5) The type strain of *Pibocella ponti* has been lost. If available, this strain would be reclassified within *Maribacter*. For that reason, it is not included in the outline.
- 6) This large family should be split up.
- 7) Taxa described after the July 1 (2006) deadline are: *Actibacter*, *Flagellimonas*, *Galbibacter*, *Gilvibacter*, *Lutimonas*, *Marixanthomonas*, *Sediminibacter*, *Tamlana*, *Zeaxanthinibacter*, *Zunongwangia*

Family II. “*Blattabacteriaceae*”
Genus I. *Blattabacterium*^{AL(T)}

Family III *Cryomorphaceae*^{VP}
Genus I. *Cryomorpha*^{VP(T)}
Genus II. *Brumimicrobium*^{VP}
Genus III. *Crocinitomix*^{VP}
Genus IV. *Fluviicola*^{VP}
Genus V. *Lishizhenia*^{VP}
Genus VI. *Owenweeksia*^{VP}

Notes:

- 1) Based upon the 16SrRNA sequence analysis, this family is not clearly monophyletic. Are there other criteria that would justify separating them?

Class III. “*Sphingobacteria*”
Order I. “*Sphingobacteriales*”
Family I. *Sphingobacteriaceae*^{VP}
Genus I. *Sphingobacterium*^{VP(T)}
Genus II. *Pedobacter*^{VP}

Note:

- 1) Other genera (*Mucilagibacter*, *Olivibacter*, *Parapedobacter*, *Pseudospingobacterium*) described after the deadline

Family III. “*Chitinophagaceae*”
Genus I. *Chitinophaga*^{VP(T)}
Genus II. *Terrimonas*^{VP}

Note:

- 1) Some of these genera were formerly classified in *Crenotrichaceae*. *Crenothrix* itself is a Proteobacteria (PNAS103:2363) so this family is not used. Therefore a novel family was created for the earliest described genus, “*Chitinophagaceae*”.
- 2) *Niastella*, which appears in the tree, was described after the deadline

- Family II. “*Saprospiraceae*”
 Genus I. *Saprospira*^{AL(T)}
 Genus II. *Aureispira*^{VP}
 Genus III. *Haliscomenobacter*^{AL}
 Genus IV. *Lewinella*^{VP}

Class IV. “*Cytophagia*”

Note:

- 1) This class seems to be justified by the tree, which suggests that the following taxa are not closely related to the *Sphingobacteria*. Because *Cytophagales* has priority over “*Flexibacterales*”, this name was chosen.

Order I. *Cytophagales*

- Family I. *Cytophagaceae*^{AL}
 Genus I. *Cytophaga*^{AL(T)}
 Genus II. *Adhaeribacter*^{VP}
 Genus III. *Arcicella*^{VP}
 Genus IV. *Dyadobacter*^{VP}
 Genus V. *Effluviibacter*^{VP}
 Genus VI. *Emticicia*^{VP}
 Genus VII. *Flectobacillus*^{AL}
 Genus VIII. *Flexibacter*^{AL}
 Genus IX. *Hymenobacter*^{VP}
 Genus X. *Larkinella*^{VP}
 Genus XI. *Leadbetterella*^{VP}
 Genus XII. *Meniscus*^{AL}
 Genus XIII. *Microscilla*^{AL}
 Genus XIV. *Pontibacter*^{VP}
 Genus XV. *Rhodonellum*^{VP}
 Genus XVI. *Runella*^{AL}
 Genus XVII. *Spirosoma*^{AL}
 Genus XVIII. *Sporocytophaga*^{AL}

Notes:

- 1) *Cytophaga* replaces *Flexibacter* as the type genus, use *Cytophagaceae* because it has priority and “*Flexibacteraceae*”, which is not validly published;
- 2) move *Algoriphagus*, *Aquiflexum*, *Cyclobacterium* to new family (“*Cyclobacteriaceae*”);
- 3) move *Chitinophaga*, *Niastella* to new family (“*Chitinophagaceae*”);
- 4) move *Fabibacter*, *Reichenbachiella*, *Roseivirga* to “*Flammeovirgaceae*”;
- 5) *Hongiella* reclassified to *Algoriphagus*.
- 6) No sequences for *Meniscus*. Described after deadline: *Persicitalea*,

- Family II. “*Cyclobacteriaceae*”
 Genus I. *Cyclobacterium*^{VP(T)}
 Genus II. *Algoriphagus*^{VP}
 Genus III. *Aquiflexum*^{VP}
 Genus IV. *Belliella*^{VP}
 Genus V. *Echinicola*^{VP}

Notes:

- 1) *Rhodonellum* was described after the deadline.
- 2) *Chimaericella* spp. reclassified as *Algoriphagus*

- Family III. “*Flammeovirgaceae*”
 Genus I. *Flammeovirga*^{VP(T)}
 Genus II. *Fabibacter*^{VP}
 Genus III. *Flexithrix*^{AL}
 Genus IV. *Persicobacter*^{VP}
 Genus V. *Reichenbachiella*^{VP}
 Genus VI. *Roseivirga*^{VP}

Notes:

- 1) *Marinicola* transferred to *Roseovirga* (IJSEM 56,1059).
- 2) rRNA gene analysis does not provide evidence that this family is monophyletic.
- 3) *Flexibacter* appears to be paraphyletic

Order II. Incertae sedis

- Family I. “*Rhodothermaceae*”
 Genus I. *Rhodothermus*^{VP(T)}
 Genus II. *Salinibacter*^{VP}

Notes:

- 1) Some of these were formerly classified in *Crenotrichaceae*. *Crenothrix* itself is a Proteobacteria (PNAS103:2363) so this family is not used. The new taxon is named the family “*Rhodothermaceae*” after the first described genus.
- 2) These genera as well as *Balneola* and *Thermonema* (see below) appear to be deep taxa, possibly novel orders or classes.

Order III. Incertae sedis

- Genus I. *Balneola*^{VP}

Order IV. Incertae sedis

- Genus I. *Thermonema*^{VP}

Order V. Incertae sedis

- Genus I. *Toxothrix*^{AL}

Note:

- 1) A sequence is not available for this organism, so its assignment is ambiguous.

Phylum BXXI. *Fusobacteria* phyl. nov.

Class I. "*Fusobacteria*"

Order I. "*Fusobacteriales*"

Family I. "*Fusobacteriaceae*"

Genus I. *Fusobacterium*^{AL(T)}

Genus II. *Cetobacterium*^{VP}

Genus III. *Ilyobacter*^{VP}

Genus IV. *Propionigenium*^{VP}

Family II. "*Leptotrichiaceae*"

Genus I. *Leptotrichia*^{AL(T)}

Genus II. *Sebaldella*^{VP}

Genus III. *Streptobacillus*^{AL}

Genus IV. *Sneathia*^{VP}

Notes:

1) formed new family „*Leptotrichiaceae*"

2) united *Cetobacterium* (incertae sedis) with "*Fusobacteriaceae*"

3) Should *Ilyobacter* and *Propionigenium* be united into one genus (as *Propionigenium*)?

Phylum BXXII. *Verrucomicrobia* phyl. nov.

Class I. *Verrucomicrobiae*^{VP}

Order I. *Verrucomicrobiales*^{VP(T)}

Family I. *Verrucomicrobiaceae*^{VP}

Genus I. *Verrucomicrobium*^{VP(T)}

Genus II. *Prostheco bacter*^{VP}

Family II. "*Akkermansiaceae*"

Genus I. *Akkermansia*^{VP(T)}

Family III. "*Rubritaleaceae*"

Genus I. *Rubritalea*^{VP(T)}

Class II. *Opitutae*^{VP}

Order I. *Opitiales*^{VP}

Family I. *Opitutaceae*^{VP}

Genus I. *Opitutus*^{VP(T)}

Genus II. *Alterococcus*^{VP}

Order II. *Puniceicoccales*^{VP}

Family I. *Puniceicoccaceae*^{VP}

Genus I. *Puniceicoccus*^{VP(T)}

Genus II. *Pelagicoccus*^{VP}

Genus III. *Coraliomargarita*^{VP}

Genus IV. *Cerasicoccus*^{VP}

Class III. "*Spartobacteria*"
Order I. "*Chthoniobacterales*"
Family I. "*Chthoniobacteraceae*"
Genus I. "*Chthoniobacter*"^(T)
Family II. "*Xiphinematobacteraceae*"
Genus I. "*Candidatus Xiphinematobacter*"

Notes:

1) Moved *Victivallis* to "*Lentisphaerae*"

Phylum BXXIII. *Dictyoglomi* phyl. nov.

Class I. "*Dictyoglomia*"
Order I. "*Dictyoglomales*"
Family I. "*Dictyoglomaceae*"
Genus I. *Dictyoglomus*^{VP(T)}

Phylum BXXIV. *Gemmatimonadetes*

Class I. *Gemmatimonadetes*^{VP}
Order I. *Gemmatimonadales*^{VP(T)}
Family I. *Gemmatimonadaceae*^{VP}
Genus I. *Gemmatimonas*^{VP(T)}

Phylum BXXV. *Lentisphaerae* phyl. nov.

Class I. "*Lentisphaeria*"
Order I. *Lentisphaerales*^{VP}
Family I. "*Lentisphaeraceae*"
Genus I. *Lentisphaera*^{VP(T)}
Order II. *Victivallales*^{VP}
Family II. "*Victivallaceae*"
Genus I *Victivallis*^{VP(T)}

Note: Moved in *Victivallis* to the phylum *Lentisphaerae* from the phylum *Verrucomicrobia*.

Table 1. Taxa without 16S rRNA sequences

Phylum Bacteroidetes

Acetofilamentum rigidum dsm20769

Acetomicrobium

faecale dsm20678

flavium atcc43122 dsm20664 lmg 6941

Anaerorhabdus furcosa atcc 25662

Bacteroides

coagulans atcc29798 ccug48292 dsm20705 jcm12528 lmg8206

galacturonicus atcc43244 dsm3978

pectinophilus atcc43243

polypragmatus nrc2288

suis atcc35419 dsm20612 ccug15420 jcm6292

ureolyticus 104321 atcc33287 ccug7319 dsm20703 lmg6451 nctc10941

xylanolyticus atcc48289 dsm3808

Blattabacterium cuenoti

Chitinophaga pinensis

Crenothrix polyspora no culture

Cytophaga xylanolytica atcc51429 dsm6779

Flavobacterium

acidificum atcc8366 lmg8364 ncimb9891

acidurans atcc27383 ccug33441 lmg8388

devorans atcc10829 dsm30198 lmg4017

oceanosedimentum atcc31317

thermophilum bkm1325 ccm3496 ccug22401 nctc11526

Flexibacter filiformis

Galbibacter ab253567

Meniscus glaucopis atcc29398

Pedobacter heparinus atcc13125 ccug12810

Polaribacter irgensii atcc700398

Porphyromonas salivosa atcc49407 nctc116

Sphingobacterium antarcticum atcc51969

Thermonema lapsum atcc43542 dsm5718

Toxothrix trichogenes no culture

Weeksella zoohelcum ATCC 43767

Phylum Spirochaetes

Borrelia afzelii
Borrelia anserina no culture
Borrelia baltazardii
Borrelia brasiliensis
Borrelia caucasica no culture
Borrelia crociduræ no culture
Borrelia digesii no culture
Borrelia duttonii no culture
Borrelia graingeri no culture
Borrelia harveyi no culture
Borrelia hermsii no culture
Borrelia hispanica no culture
Borrelia latyschewii no culture
Borrelia mazzottii no culture
Borrelia parkeri no culture
Borrelia persica no culture
Borrelia recurrentis no culture
Borrelia theileri no culture
Borrelia tillæ no culture
Borrelia turicatae no culture
Borrelia venezuelensis no culture

Clevelandina reticulitermitidis

Diplocalyx calotermitidis

Hollandina pterotermitidis

Pillotina calotermitidis

Spirochaeta caldaria
Spirochaeta plicatilis no culture
Spirochaeta stenostrepta no strain info embl
Spirochaeta thermophila no type
Spirochaeta zuelzeræ no strain info embl

Treponema minutum
Treponema paraluisuniculi no culture
Treponema pectinovorum
Treponema pertenue no culture

Other phyla:

Dictyoglomus turgidum

Fusobacterium naviforme
Fusobacterium necrophorum subsp. funduliforme

Planctomyces bekefii
Planctomyces guttaeformis
Planctomyces stranskae



