

Compilation of small ribosomal subunit RNA structures

Jean-Marc Neefs, Yves Van de Peer, Peter De Rijk, Sabine Chapelle and Rupert De Wachter*
Departement Biochemie, Universiteit Antwerpen (UIA), Universiteitsplein 1, B-2610 Antwerp, Belgium

ABSTRACT

The database on small ribosomal subunit RNA structure contained 1804 nucleotide sequences on April 23, 1993. This number comprises 365 eukaryotic, 65 archaeal, 1260 bacterial, 30 plastidial, and 84 mitochondrial sequences. These are stored in the form of an alignment in order to facilitate the use of the database as input for comparative studies on higher-order structure and for reconstruction of phylogenetic trees. The elements of the postulated secondary structure for each molecule are indicated by special symbols. The database is available on-line directly from the authors by ftp and can also be obtained from the EMBL nucleotide sequence library by electronic mail, ftp, and on CD ROM disk.

CONTENTS OF THE DATABASE

The database on small ribosomal subunit RNA (further abbreviated as SSU rRNA) currently contains 1804 nucleotide sequences, stored in the form of an alignment and containing the postulated secondary structure pattern in encoded form. This number comprises 365 eukaryotic cytoplasmic, 65 archaeal, 1260 bacterial, 30 plastidial, and 84 mitochondrial SSU rRNAs. Partial sequences are included if the combined length of the sequenced segments corresponds to homologous segments in *Escherichia coli* SSU rRNA amounting to at least 70% of the chain length of the latter molecule.

Previous compilations (1–5) included a table listing for each entry the species name, further specifications such as the strain, variety, or tissue used for isolation of the gene, taxonomic position of the species, length and completeness of the sequence, and accession number in nucleotide sequence libraries. Complete literature references were also included for each entry. Because the number of available structures has nearly doubled since publication of the preceding compilation (5), such a table and the accompanying references would now require an estimated 20 pages just to cover the additional structures entered in the database during the last year. Table 1 has therefore been restricted to a list of the names of species for which the SSU rRNA structure is recorded in the database. However, this list covers all the structures now filed, not just those added since the preceding compilation. Instructions for obtaining the complete table including further specifications and literature references, separately or together with the structural data, are given below.

TAXONOMIC CLASSIFICATION OF SPECIES

For the Eukarya, the taxonomic classification of the species listed in Table 1 is according to Brusca and Brusca (6) for the Animalia, according to Cronquist (7) for the higher plants, according to Ainsworth et al. (8) for the higher fungi, and according to Corliss (9) for the remaining eukaryotes.

For the Bacteria and the Archaea, the classification followed is based on the phylogeny described by Woese and coworkers (10–12). However, the assignment of a species to one of the taxa distinguished by these authors is often problematic. To our knowledge there does not exist a list assigning each bacterial or archaeal species to one of the divisions or subdivisions that they distinguish. Moreover, many sequences now become available through deposition in one of the nucleotide sequence libraries, which in many cases is not (yet) accompanied by publication in a journal. The bacterial and archaeal SSU rRNA sequences deposited in these libraries are accompanied by a taxonomic description which does not correspond to that of Woese et al. (10–12) but is based on Bergey's Manual of Systematic Bacteriology (13). Even the sequences described in the literature are not always accompanied by an assignment of the species to one of the taxa distinguished by Woese and coworkers. In order to obtain a more or less consistent classification, we have therefore constructed an evolutionary tree from the alignment of all archaeal, bacterial, and plastidial SSU rRNA sequences, 1355 in total. The method followed for constructing the tree has been described in detail elsewhere (14). In short, a dissimilarity matrix was computed, corrected for multiple mutation (15), and a tree derived by neighbour-joining (16). The outline of the resulting tree is shown in Fig. 1. Most of the clusters visible in the tree correspond to the archaeal and bacterial divisions and subdivisions distinguished by Woese and coworkers (10–12). However, in the bacterial subtree, the genera *Fibrobacter* and *Fusobacterium* do not integrate in any of the clusters. They are therefore listed separately in Table 1.

It should be noted that the evolutionary distances between the branching points leading to the clusters visible in the tree of Fig. 1 are very small, especially for the major clusters of the Bacteria. Trees such as this one were constructed periodically as the SSU rRNA sequence alignment grew in size. Although the clusters indicated in Fig. 1 were reproducibly formed, the branching order of these clusters was not constant but changed as a function of the composition of the sequence collection. However, the tree can serve to assign bacterial species to a given division or subdivision because, although the relative position of the clusters

* To whom correspondence should be addressed

is variable, the appurtenance of each bacterial species to a particular cluster is stable.

In Table 1, for the Bacteria, no hierarchical distinction is made between divisions (e.g. the spirochetes) and subdivisions (e.g. the α , β , γ , δ , and ϵ subdivisions of the division Proteobacteria). This is because the subdivisions do not always form together a monophyletic cluster. As an example, in the tree of Fig. 1, the Proteobacteria ϵ group is separated from the monophyletic cluster formed by the Proteobacteria α , β , γ and δ groups. As for the division of Gram positive bacteria and relatives, its two subdivisions of high and low GC contents almost never form together a monophyletic cluster in the trees that we obtain. For the Archaea, on the contrary, a distinction is made between the divisions Crenarchaeota and Euryarchaeota (12). The latter division is subdivided into 8 subdivisions. Of these, the Methanobacterales, Methanococcales, Thermococcales and Methanopyrales correspond to lineages distinguished by Olsen and Woese (12). The Methanomicrobiales group of the latter authors comprises the Methanomicrobium group, the Halobacteria, and *Archaeoglobus fulgidus* in the tree of Fig. 1.

SECONDARY STRUCTURE MODEL

Prokaryotic and eukaryotic models, nucleotide variability

Fig. 2 shows the prokaryotic secondary structure model, applicable to SSU rRNAs from archaea, bacteria, plastids, and mitochondria. The model of Fig. 3 applies to eukaryotic cytoplasmic SSU rRNAs. In contrast to the corresponding figures in the preceding compilation (5), the models shown in Fig. 2 and 3 do not simply distinguish between conserved and variable areas, but give a more detailed description of the variability of each site. The latter is defined as the ratio of the substitution rate at the considered site to the average substitution rate for the entire molecule. The quantitative derivation of the variability of each site from the sequence alignment is described in detail elsewhere (17). Sites that are absolutely conserved, and those that are occupied only in a limited number of SSU rRNAs, are indicated by special symbols. The remaining ones were partitioned into five equally large categories of increasing variability. In Fig. 2 and 3, such sites are represented by dots with a diameter commensurate with their variability. Variable areas previously distinguished on a more intuitive basis and indicated on the general secondary structure models of the preceding compilation (5) are still shown on Figg. 2 and 3 as V1 to V9.

Helix numbering system and changes made to the models

Helices are given a different number if separated by a multibranched loop (e.g. helices 9 and 10), by a pseudoknot loop (e.g. helices 1 and 2), or by a single stranded area that does not form a loop (e.g. helices 2 and 32). A single number is attributed to 50 'universal' helices, which are present in all hitherto known SSU rRNAs from Archaea, Bacteria and plastids. They are also present in all known eukaryotic SSU rRNAs except in those of Microsporidia, where some of these helices are missing. The number of universal helices has risen from 48 in the preceding compilation (5) to 50 because the tertiary interaction described by Woese and Gutell (18) has been taken into account. This interaction effectively transforms the helix previously numbered 19 into three helices now numbered 19 to 21.

Helices specific to the prokaryotic model (Fig. 2) are given composite numbers of the form Pa-b, where a is the number of

the preceding universal helix and b sequentially numbers all helices inserted between universal helices a and a+1. Helices specific to the eukaryotic model (Fig. 3) are similarly numbered Ea-b. In Figg. 2 and 3, not all eukaryote- and prokaryote-specific helices that are encountered in various species are indicated, because these models in fact have the shape of the *Escherichia coli* and *Saccharomyces cerevisiae* SSU rRNA secondary structure models, respectively. As an example, in *Drosophila melanogaster* SSU rRNA, the loop separating helices E23-2 and E23-5 is a multifurcation bearing two more helices numbered E23-3 and E23-4 (5). These and other supernumerary helices that are present in a minority of SSU rRNAs are not indicated in Figg. 2 and 3, one of the reasons being that the variability of the sites composing such helices cannot be computed in a dependable manner. However, in Table 2 the presence or absence of eukaryote specific helices in SSU rRNAs of different taxa is summarized.

Mitochondrial SSU rRNAs, though they can be described by the prokaryotic model, show extreme variability in length, ranging from about 600 nucleotides in flagellates to about 2000 nucleotides in plants. This coincides with the absence of several universal helices in the smaller molecules and with the presence of extra helices of the P-series in the larger ones. A tentative helix occupancy table for mitochondrial SSU rRNAs and examples of secondary structure models can be found in a previous compilation (4). The alignment of, and transposition of secondary structure models to, mitochondrial SSU rRNAs is less dependable than for other SSU rRNAs, not only because of the variability in length, but also because some of the mitochondrial sequences are very monotonous due to their high AU contents.

Examples of secondary structure models

Figg. 4 to 7 are examples of secondary structure models applied to specific SSU rRNA sequences. Fig. 4 represents the SSU rRNA of the bacterium *Escherichia coli*, whereas the SSU rRNA of the halophilic archaebacterium *Halobacterium halobium* is shown in Fig. 5. The eukarya are represented by the structure of SSU rRNAs of the red alga *Palmaria palmata* in Fig. 6, and of the polymastigote *Giardia duodenalis* in Fig. 7. The latter model is shown as an example of a molecule possessing a restricted number of helices in variable areas V2 (helices 9 to 11) and V4 (helices E23-n). Finally, an example of a model for an animal mitochondrial SSU rRNA is shown in Fig. 8.

COMPLETENESS, ACCURACY, AND AVAILABILITY OF THE DATA

SSU rRNA sequences deposited in the GenBank and EMBL nucleotide sequence libraries are obtained weekly from the EMBL file server by electronic mail. By means of an appropriate set of programs, each new sequence is aligned with the most closely related one already present in the alignment, the secondary structure pattern is transposed to the newly aligned sequence, and the complementarity of the postulated secondary structure elements is checked. Manual corrections are made if necessary by means of a specially developed editor. Finally, the newly aligned sequence is automatically compared with the original record in order to eliminate any errors that might have been introduced during editing of the alignment.

Files containing all the SSU rRNA sequences present in our database are available in the following three formats.

- 1) The sequences, listed one by one, written continuously without the gaps needed for alignment and without indication of secondary structure elements.
- 2) The sequences, listed one by one, but with nucleotide symbols interspersed with the gaps necessary for alignment. In this file, each sequence covers 4807 positions, which is the present length of the complete alignment of all eukaryotic, archaeal, bacterial, and organellar sequences.
- 3) The sequences, listed in the form of an alignment with indication of the secondary elements. The alignment is divided into 49 pages each comprising 100 positions containing a nucleotide or a gap. These positions alternate with an equal number of positions that are either blank or contain a symbol indicating the beginning or end of a secondary structure element. The secondary structure model adopted for each SSU rRNA sequence is completely defined in this file.

In addition, there are files containing a taxonomic list of species for which the SSU rRNA sequence is known, plus further data as listed in Table 1 of the previous compilation (5) and literature references, and a file containing general documentation on the database.

These files will be made available through 'anonymous ftp' on host uiam3.uia.ac.be (143.169.8.1). The files, as well as later updates, will also be made available to the EMBL nucleotide sequence library at Heidelberg for distribution on their file server and on their CD-ROM disk. Due to the increasing volume of the database, copying it onto diskettes is getting cumbersome. However, researchers who do not have access to the aforementioned distribution channels can address requests for obtaining specific parts of the database on magnetic media to the authors in writing or by sending an electronic mail message to dwachter@reks.uia.ac.be or to rrna@reks.uia.ac.be.

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REFERENCES

1. Huysmans,E., De Wachter,R. (1986), *Nucleic Acids Res.* **14**, r73–r117.
2. Dams,E., Hendriks,L., Van de Peer,Y., Neefs,J.M., Smits,G., Vandebemt,I., De Wachter,R. (1988), *Nucleic Acids Res.* **16**, r87–r173.
3. Neefs,J.-M., Van de Peer,Y., Hendriks,L., De Wachter,R. (1990), *Nucleic Acids Res.* **18**, 2237–2317.
4. Neefs,J.-M., Van de Peer,Y., De Rijk,P., Goris,A., De Wachter,R. (1991), *Nucleic Acids Res.* **19**, 1987–2015.
5. De Rijk,P., Neefs,J.-M., Van de Peer,Y., De Wachter,R. (1992), *Nucleic Acids Res.* **20**, 2075–2089.
6. Brusca,R.C., Brusca,G.J. (1990), *Invertebrates*, Sinauer Associates, Inc., Sunderland.
7. Cronquist,A. (1971), *Introductory Botany*, Harper & Row, New York.
8. Ainsworth,G.C., Sparrow,F.K., Sussman,A.S. (1973), *The Fungi: an Advanced Treatise*, Academic Press, New York, Vol. 4A.
9. Corliss,J.O. (1984), *BioSystems* **17**, 8–126.
10. Woese,C.R. (1987), *Microbiol. Rev.* **51**, 221–271.
11. Woese,C.R. (1991), in Selander,R.K., Clark,A.G., Whittam,T.S. (eds.), *Evolution at the Molecular Level*. Sinauer Associates, Inc., Sunderland, pp. 1–24.
12. Olsen,G.J., Woese,C.R. (1993), *FASEB J.* **7**, 113–123.
13. Holt,J.G. (1984, 1986, 1989) *Bergey's Manual of Systematic Bacteriology*, Williams & Wilkins, Baltimore, Vol. 1–4.
14. Van de Peer,Y., Neefs,J.-M., De Wachter,R. (1990), *J. Mol. Evol.* **30**, 463–476.
15. Jukes,T.H., Cantor,C.R. (1969) in Munro,H.N. (ed.), *Mammalian Protein Metabolism*. Academic Press, New York, pp. 21–132.
16. Saitou,N., Nei,M. (1987), *Mol. Biol. Evol.* **4**, 406–425.
17. Van de Peer,Y., Neefs,J.-M., De Rijk,P., De Wachter,R. (1993), *J. Mol. Evol.*, in press.
18. Woese,C.R., Gutell,R.R. (1989), *Proc. Natl. Acad. Sci. USA* **86**, 3119–3122.

Table 1. List of species for which the SSU rRNA structure is recorded in the database^a.

| | |
|----------------------------|----------------------------|
| EUKARYA | Discoglossus pictus |
| ANIMALIA | Eleutherodactylus cuneatus |
| CHORDATA | Gastrophryne carolinensis |
| VERTEBRATA | Grandisonia alternans |
| MAMMALIA | Hyla cinerea |
| Homo sapiens 1 | Ichthyophis bannanicus |
| Homo sapiens 2 | Nesomantis thomasseti |
| Homo sapiens 3 | Plethodon yonhalossee |
| Mus musculus | Scaphiopus holbrookii |
| Oryctolagus cuniculus | Siren intermedia |
| Rattus norvegicus 1 | Typhlonectes natans |
| Rattus norvegicus 2 | Xenopus borealis |
| | Xenopus laevis |
| AVES | |
| Gallus gallus | |
| Turdus migratorius | |
| REPTILIA | |
| Alligator mississippiensis | |
| Heterodon platyrhinos | |
| Pseudemys scripta | |
| Sceloporus undulatus | |
| AMPHIBIA | |
| Ambystoma mexicanum | |
| Amphiuma tridactylum | |
| Bufo valliceps | |
| osteichthyes | |
| Fundulus heteroclitus | |
| Latimeria chalumnae | |
| Sebastolobus altivelis | |
| CHONDRICHTYES | |
| Echinorhinus cookei | |
| Rhinobatos lentiginosus | |
| Squalus acanthias | |
| AGNATHA | |
| Eptatretus stouti | |
| Lampetra aepyptera | |

Table 1. continued

| | |
|----------------------------|----------------------------|
| Myxine glutinosa | CNIDARIA |
| Petromyzon marinus | ANTHOZOA |
| | Anemonia sulcata |
| UROCHORDATA | |
| Herdmania momus | PLANTAE |
| Styela plicata | MAGNOLIOPHYTA |
| CEPHALOCHORDATA | LILIOPSIDA |
| Branchiostoma floridae | Oryza sativa |
| CHAETOGNATHA | Zea mays |
| Sagitta elegans | |
| ARTHROPODA | MAGNOLIOPSIDA |
| INSECTA | Alnus glutinosa |
| Acyrtosiphon pisum | Arabidopsis thaliana |
| Aedes albopictus | Buckleya distichophylla |
| Drosophila melanogaster | Buxus sempervirens |
| Tenebrio molitor | Clematis rehderiana |
| CHELICERATA | Cornus florida |
| Amblyomma americanum | Cornus racemosa |
| Eurytelma californica | Dendrophthora domingensis |
| MALACOSTRACA | Euonymus alatus |
| Argulus nobilis | Fragaria ananassa |
| Artemia salina | Glycine max |
| Callinectes sapidus | Hedera helix |
| Oedignathus inermis | Hydrocotyle sibthorpioides |
| Palaemonetes kadiakensis | Lycopersicon esculentum |
| Penaeus aztecus | Macadamia ternifolia |
| Procambarus leonensis | Nyssa sylvatica |
| Raninoides louisianensis | Phoradendron serotinum |
| Stenopus hispidus | Schoepfia arenaria |
| PENTASTOMIDA | Sinapis alba 1 |
| Porocephalus crotali | Sinapis alba 2 |
| NEMATODA | |
| SECERNENTEA | PINOPHYTA |
| Caenorhabditis elegans | CYCADOPSIDA |
| Haemonchus contortus | Podocarpus falcatus |
| Haemonchus placei | Podocarpus henkellii |
| Haemonchus similis | Zamia pumila |
| Strongyloides stercoralis | |
| PLATYHELMINTHES | FUNGI |
| TREMATODA | ZYgomycotina |
| Opisthorchis viverrini | Endogone pisiformis |
| Schistosoma haematobium | Gigaspora margarita |
| Schistosoma japonicum | Glomus intraradices |
| Schistosoma mansoni 1 | Mucor racemosus |
| Schistosoma mansoni 2 | |
| Schistosoma spindale | ASCOMYCOTINA |
| | HEMIASCOMYCETES |
| TURBELLARIA | Candida albicans 1 |
| Bothromesostoma personatum | Candida albicans 2 |
| Crenobia alpina | Candida glabrata 1 |
| Dendrocoelum lacteum | Candida glabrata 2 |
| Dugesia mediterranea | Candida parapsilosis |
| MOLLUSCA | Candida tropicalis 1 |
| BIVALVIA | Candida tropicalis 2 |
| Crassostrea virginica | Candida viswanathii |
| Placoplecten magellanicus | Clavispora lusitaniae 1 |
| GASTROPODA | Clavispora lusitaniae 2 |
| Limicolaria kambeul | Debaryomyces hansenii 1 |
| POLYPLACOPHORA | Debaryomyces hansenii 2 |
| Acanthopleura japonica | Dekkera bruxellensis |
| ACANTHOCEPHALA | Dipodascus albidus |
| ARCHIACANTHOCEPHALA | Endomyces fibuliger |
| Moliniformis moliniformis | Galactomyces geotrichum |

Saccharomyces capsularis
Torulaspora delbrueckii
Waltomyces lipofer
Yamadazyma guilliermondii
Yarrowia lipolytica
Zygosaccharomyces rouxii

EUASCOMYCETES

Ascospaera apis 1
Ascospaera apis 2
Aspergillus fumigatus 1
Aspergillus fumigatus 2
Aspergillus fumigatus 3
Aureobasidium pullulans
Byssochlamys nivea
Chaetomium elatum
Coccidioides immitis 1
Coccidioides immitis 2
Emmonsella capsulata
Eremascus albus
Exophiala dermatidis 1
Exophiala dermatidis 2
Exophiala dermatidis 3
Glomerella cingulata
Hypomyces chrysospermus
Leucostoma persoonii
Monascus purpureus
Neurospora crassa
Ophiostoma schenckii
Ophiostoma stenoceras
Ophiostoma ulmi
Penicillum notatum
Podospora anserina
Pseudallescheria boydii
Sclerotinia sclerotiorum
Sordaria fimicola
Talaromyces flavus
Taphrina deformans
Thermoascus crustaceus
Trichophyton rubrum

UNCERTAIN AFFILIATION

Pneumocystis carinii
Schizosaccharomyces pombe 1
Schizosaccharomyces pombe 2

BASIDIOMYCOTINA**USTOMYCETES**

Leucosporidium scottii
Rhodosporidium toruloides 1
Rhodosporidium toruloides 2
Sporobolomyces roseus
Ustilago maydis

TRUE BASIDIOMYCETES

Athelia bombacina
Boletus satanas
Bulleromyces albus
Coprinus cinereus
Cronartium ribicola
Filibasidiella neoformans 1
Filibasidiella neoformans 2
Filibasidiella neoformans 3
Microascus cirrosus
Spongipellis unicolor
Thanatephorus praticola
Trichosporon cutaneum
Xerocomus chrysenteron

PROTISTA**ASSEMBLAGE CHLOROBIONTS****CHLOROPHYTA**

Ankistrodesmus stipitatus
Asteromonas gracilis
Characium hindakii
Characium perforatum
Characium saccatum

Characium vacuolatum
Chlamydomonas reinhardtii
Chlorella ellipsoidea
Chlorella fusca
Chlorella kessleri
Chlorella lobophora
Chlorella minutissima
Chlorella protothecoides
Chlorella saccharophila
Chlorella sorokiniana
Chlorella vulgaris
Chlorococcopsis minuta
Coleochaete scutata
Coleochaete orbicularis
Dunaliella parva
Dunaliella salina
Friedmannia israelensis
Hydrodictyon reticulatum
Klebsormidium flaccidum
Nanochlorum eucaryotum
Neochloris aquatica
Neochloris vigenis
Parietochloris pseudoalveolaris
Pediastrum duplex
Prototheca wickerhamii
Prototheca zoppii
Scenedesmus obliquus
Spermatozopsis similis
Tetraselmis striata
Trebouxia impressa
Trebouxia magna
Trebouxia asymmetrica
Volvox carteri

CHAROPHYTA

Chlorokybus atmophyticus
Nitella sp.

ASSEMBLAGE CHROMOBIONTS**CHRYSOPHYTA**

Hibberdia magna
Mallomonas papillosa
Mallomonas striata
Ochromonas danica
Synura spinosa

DINOPHYTA

Alexandrium tamarense
Emiliania huxleyi 1
Emiliania huxleyi 2
Symbiodinium microadriaticum
Symbiodinium pilosum
Symbiodinium sp.
Tribonema aequale

PHAEOPHYTA

Costaria costata
Fucus gardneri
Bacillaria paxillifer
Cylindrotheca closterium
Nannochloropsis salina
Nitzschia apiculata
Rhizosolenia setigera
Skeletonema costatum
Stephanopyxis broschii

ASSEMBLAGE CILIATES**CILIOPHORA**

Blepharisma americanum
Colpidium campylum
Colpoda inflata
Euplotes aediculatus
Glaucomea chattoni
Metopus palaeformis
Onychodromus quadricornutus
Opisthonecta henneguyi
Oxytricha granulifera

Table 1. continued

| | |
|---|--------------------|
| Oxytricha nova | Giardia duodenalis |
| Paramecium tetraurelia | Giardia muris |
| ASSEMBLAGE CRYPTOMONADS | |
| CRYPTOPHYTA | |
| Cryptomonas phi 1 | |
| Cryptomonas phi 2 | |
| Pyrenomonas salina 1 | |
| Pyrenomonas salina 2 | |
| ASSEMBLAGE DINOFLAGELLATES | |
| PERIDINEA | |
| Cryptocodinium cohnii | |
| Cryptosporidium muris 1 | |
| Cryptosporidium muris 2 | |
| Cryptosporidium parvum 1 | |
| Cryptosporidium parvum 2 | |
| Prorocentrum micans | |
| ASSEMBLAGE EUGLENOZOA | |
| EUGLENOPHYTA | |
| Euglena gracilis | |
| KINETOPLASTIDEA | |
| Bodo caudatus | |
| Critchidia fasciculata | |
| Endotrypanum monterogei | |
| Leishmania amazonensis | |
| Leishmania brasiliensis | |
| Leishmania donovani | |
| Leishmania major | |
| Leishmania tarentolae 1 | |
| Leishmania tarentolae 2 | |
| Leptomonas sp. | |
| Tritrichomonas foetus | |
| Trypanosoma brucei | |
| Trypanosoma cruzi 1 | |
| Trypanosoma cruzi 2 | |
| ASSEMBLAGE MASTIGOMYCETES | |
| CHYTRIDIOMYCOTA | |
| Blastocladiella emersonii | |
| Chytridium confervae | |
| Neocallimastix frontalis | |
| Neocallimastix joyonii | |
| Neocallimastix sp. | |
| Piromonas communis | |
| Spizellomyces acuminatus | |
| Achlya bisexualis | |
| Lagenidium giganteum | |
| Phytophthora megasperma 1 | |
| Phytophthora megasperma 2 | |
| ASSEMBLAGE MICROSPORIDIA | |
| MICROSPORIDIA | |
| Encephalitozoon cuniculi | |
| Vairimorpha necatrix | |
| ASSEMBLAGE POLYMASTIGOTES | |
| Giardia ardeae | |
| Giardia intestinalis | |
| ASSEMBLAGE RHIZOPODS | |
| AMOEBOZOA | |
| Acanthamoeba castellanii 1 | |
| Acanthamoeba castellanii 2 | |
| Acanthamoeba palestinensis | |
| Entamoeba histolytica | |
| Hartmannella vermiformis 1 | |
| Hartmannella vermiformis 2 | |
| Naegleria gruberi | |
| Paratetramitus jugosus | |
| Tetramitus rostratus | |
| Vahlkampfia lobospinosa | |
| EUMYCETOZOA | |
| Dictyostelium discoideum | |
| Physarum polycephalum | |
| ASSEMBLAGE RHODOPHYTES | |
| RHODOPHYTA | |
| Gracilaria lemaneiformis | |
| Gracilaria tikvahiae | |
| Gracilaria verrucosa | |
| Gracilaropsis sp. | |
| Palmaria palmata | |
| ASSEMBLAGE SPOROZOA | |
| APICOMPLEXA | |
| Babesia bigemina 1 | |
| Babesia bigemina 2 | |
| Babesia bigemina 3 | |
| Babesia bovis | |
| Babesia caballi | |
| Babesia equi | |
| Babesia rodhaini | |
| Plasmodium berghei 1 | |
| Plasmodium berghei 2 | |
| Plasmodium cynomolgi 1 | |
| Plasmodium cynomolgi 2 | |
| Plasmodium falciparum 1 | |
| Plasmodium falciparum 2 | |
| Plasmodium fragile | |
| Plasmodium gallinaceum | |
| Plasmodium lophurae | |
| Plasmodium malariae | |
| Plasmodium vivax | |
| Sarcocystis muris | |
| Theileria annulata | |
| Theileria buffeli | |
| Theileria parva | |
| Toxoplasma gondii | |
| ARCHAEA | |
| EURYARCHAEOTA | |
| HALOBACTERIA | |
| Halobacterium cutirubrum | |
| Halobacterium halobium | |
| Halobacterium marismortui 1 | |
| Halobacterium marismortui 2 | |
| Halobacterium volcanii | |
| Halobacterium sp. | |
| Halococcus morrhuae 1 ATCC 17082 | |
| Halococcus morrhuae 2 NRC 16008, NCMB 746 | |
| Haloferax mediterranei ATCC 33500 | |
| Natronobacterium magadii NCMB 2190 | |
| METHANOBACTERIALES | |
| Methanobacterium bryantii | |
| Methanobacterium formicicum DSM 1312 | |
| Methanobacterium thermoautotrophicum 1 | |
| Methanobacterium thermoautotrophicum 2 | |
| Methanobacterium thermoformicium 1 | |
| Methanobacterium thermoformicium 2 | |

Methanobacterium thermoformicum 3
 Methanobacterium thermoformicum 4
 Methanobacterium thermoformicum 5
 Methanobacterium thermoformicum 6
 Methanobacterium thermoformicum 7
 Methanobacterium thermoformicum 8
 Methanobacterium thermoformicum 9
 Methanobrevibacter arboriphilus
 Methanospaera stadtmanii
 Methanothermus fervidus 1
 Methanothermus fervidus 2

METHANOCOCCALES

Methanococcus igneus DSM 5666
 Methanococcus jannaschii
 Methanococcus thermolithotrophicus
 Methanococcus voltae
 Methanococcus vannielii

METHANOMICROBIUM GROUP

Methanocorpusculum parvum DSM 3823
 Methanogenium cariaci DSM 1497
 Methanogenium marisnigri DSM 1498
 Methanogenium organophilum DSM 3596
 Methanogenium thermophilum DSM 3915
 Methanohalophilus mahii DSM 5219
 Methanohalophilus zhilinae
 Methanohalophilus sp. 1
 Methanohalophilus sp. 2 DSM 3243
 Methanolobus tindarius DSM 2278
 Methanomicrobium mobile DSM 1539
 Methanoplanus limicola DSM 2279
 Methanosaeta concilii DSM 3013
 Methanosaeta thermoacetophila DSM 3870
 Methanosarcina acidivorans DSM 2834
 Methanosarcina barkeri DSM 1538
 Methanosarcina frisia DSM 3318
 Methanosarcina frisius
 Methanosarcina thermophila DSM 1825
 Methanosarcina sp. DSM 4659
 Methanospirillum hungatei
 Methanothrix soehngenii
 Methylcoccoides methylutens DSM 2657

THERMOCOCCALES

Thermococcus celer DSM 2476

THERMOPLASMA

Thermoplasma acidophilum

ARCHAEGLOBALES

Archaeoglobus fulgidus

METHANOPYRALES

Methanopyrus kandleri DSM 6324

CRENARACHAEOTA

Desulfurococcus mobilis
 Pyrodictium occultum DSM 2709
 Sulfolobus shibatae DSM 5389
 Sulfolobus solfataricus
 Thermofilum pendens DSM 2475
 Thermoproteus tenax

BACTERIA

PROTEOBACTERIA ALPHA

Afipia clevelandensis
 Afipia felis ATCC 53690
 Agrobacterium tumefaciens DSM 30105
 Anaplasma marginale
 Ancylobacter aquaticus ATCC 25396
 Azospirillum lipoferum
 Bangasternus orientalis endosymbiont
 Bartonella bacilliformis 1 ATCC 35685
 Bartonella bacilliformis 2 NCTC 12138
 Bartonella bacilliformis 3 ATCC 35685

Beijerinckia indica
 Blastobacter denitrificans LMG 8443 (T)
 Bradyrhizobium japonicum LMG 6138 (T)
 Brucella abortus
 Caulobacter bacteroides
 Caulobacter crescentus 1
 Caulobacter crescentus 2
 Caulobacter crescentus 3
 Caulobacter subvibrioides
 Caulobacter sp. 1
 Caulobacter sp. 2
 Caulobacter sp. 3
 Caulobacter sp. 4
 Caulobacter sp. 5
 Caulobacter sp. 6
 Caulobacter sp. 7
 Caulobacter sp. 8
 Caulobacter sp. 9
 Caulobacter sp. 10
 Cowdria ruminantium 1
 Cowdria ruminantium 2
 Ehrlichia canis 1
 Ehrlichia canis 2
 Ehrlichia chafetszsis
 Ehrlichia equi
 Ehrlichia ewingii 1
 Ehrlichia ewingii 2
 Ehrlichia phagocytophila 1
 Ehrlichia phagocytophila 2
 Ehrlichia risticii
 Ehrlichia sennetsu 1
 Ehrlichia sennetsu 2
 Erythrobacter longus 1
 Erythrobacter longus 2
 Erythrobacter longus 3
 Erythrobacter sp.
 Flavobacterium capsulatum
 Flavobacterium devorans
 Hirschia baltica
 Hyphomicrobium vulgare
 Hyphomonas jannaschiana
 Hyphomonas sp.
 Magnetite-containing magnetic vibrio
 Magnetospirillum gryphiswaldense DSM 6361
 Magnetospirillum magnetotacticum ATCC 31632
 Methylbacterium extorquens 1
 Methylbacterium extorquens 2
 Methylbacterium organophilum
 Methylbacterium sp. 1
 Methylbacterium sp. 2
 Methylbacterium sp. 3
 Methylocystis parvus
 Methylosinus sporium
 Methylosinus trichosporium
 Methylosinus sp. 1
 Methylosinus sp. 2
 Methylosporovibrio methanicus
 Porphyrobacter neustonensis 1
 Porphyrobacter neustonensis 2
 Pseudomonas diminuta
 Rhinocylus conicus endosymbiont
 Rhodobacter capsulatus 1
 Rhodobacter capsulatus 2
 Rhodobacter sphaeroides 1
 Rhodobacter sphaeroides 2
 Rhodobacter sphaeroides 3
 Rhodomicrobium vannielii
 Rhodopseudomonas acidophila
 Rhodopseudomonas globiformis
 Rhodopseudomonas marina
 Rhodopseudomonas palustris
 Rhodospirillum centenum
 Rhodospirillum fulvum
 Rhodospirillum molischianum
 Rhodospirillum rubrum
 Rhodospirillum salexigenes
 Rhodospirillum salinarum

Table 1. continued

| | |
|--|---|
| Rhodospirillum sodomense | PROTEOBACTERIA GAMMA* ^b |
| Rickettsia prowazekii Brieni | Acinetobacter calcoaceticus |
| Rickettsia rickettsii | Alteromonas vaga ATCC 27119 |
| Rickettsia typhi Wilmington | Arhodomonas oleiferhydrans |
| Rochalimaea americana | Bacteroides nodosus |
| Rochalimaea quintana 1 | Bathymodiolus thermophilus gill symbiont |
| Rochalimaea quintana 2 | Calyptogena magnifica symbiont |
| Rochalimaea saintelizabethsina | Cardiobacterium hominis ATCC 16826 (T) |
| Rochalimaea vinsonii 1 | Chromatium tepidum |
| Rochalimaea vinsonii 2 | Chromatium vinosum ATCC 17899 |
| Roseobacter denitrificans 1 | Codakia orbicularis gill symbiont |
| Roseobacter denitrificans 2 | Coxiella burnetii |
| Simonsiella muelleri | Ectothiorhodospira halochloris |
| Sitophilus oryzae endosymbiont | Ectothiorhodospira halophila |
| Wolbachia pipiensis | Ectothiorhodospira shaposhnikovi |
| Zoogloea ramigera | Flavobacterium halmophilum |
| PROTEOBACTERIA BETA | |
| Alcaligenes eutrophus | Flavobacterium lutescens |
| Alcaligenes faecalis ATCC 8750 (T) | Halomonas elongata ATCC 33173 |
| Alcaligenes xylosoxidans ATCC 15173 (T) | Kingella indologenes ATCC 25869 (T) |
| Bordetella bronchiseptica | Legionella bozemani NCTC 11368 (T) |
| Chromobacterium fluvatile ATCC 33051 (T) | Legionella erythra NCTC 11977 (T) |
| Chromobacterium violaceum ATCC 12472 (T) | Legionella hackeliae NCTC 11979 (T) |
| Eikenella corrodens 1 ATCC 23834 (T) | Legionella longbeachae NCTC 11477 (T) |
| Eikenella corrodens 2 FDC 373 | Legionella maceachernii NCTC 11982 |
| Eikenella corrodens 3 FDC 558 | Legionella micdadei NCTC 11371 (T) |
| Eikenella corrodens 4 FDC 1073 | Legionella pneumophila 1 NCTC 11192 (T) |
| Eikenella sp. | Legionella pneumophila 2 NCTC 11286 |
| Gallionella ferruginea | Legionella pneumophila 3 NCTC 11233 (T) |
| Kingella denitrificans 1 ATCC 33394 (T) | Legionella pneumophila 4 NCTC 11405 |
| Kingella denitrificans 2 | Legionella pneumophila 5 |
| Kingella kingae ATCC 23330 (T) | Legionella spiralis NCTC 11990 (T) |
| Kingella orale | Legionella sp. |
| Leptothrix discophora | Lucinoma aequizonata gill symbiont |
| Methylobacillus flagellatum | Marinobacter hydrocarbonoclasticus |
| Methylobacillus glycogenes | Methylococcus capsulatus |
| Methyloimonas methanolica | Methylococcus luteus |
| Methyloimonas methyllovora | Methyloimonas albus |
| Methylophilus methylotrophicus | Methyloimonas methanica |
| Neisseria animalis | Methyloimonas rubra |
| Neisseria canis | Methyloimonas sp. |
| Neisseria denitrificans 1 ATCC 14686 (T) | Nitrosococcus oceanus 1 |
| Neisseria denitrificans 2 | Nitrosococcus oceanus 2 |
| Neisseria elongata 1 | Oceanospirillum linum ATCC 11336 (T) |
| Neisseria elongata 2 | Pseudomonas aeruginosa 1 ATCC 11996 |
| Neisseria flavescens | Pseudomonas aeruginosa 2 ATCC 25330 |
| Neisseria gonorrhoeae 1 NCTC 83785 | Pseudomonas mendocina |
| Neisseria gonorrhoeae 2 | Riftia pachyptila trophosome symbiont |
| Neisseria macaca | Solemya reidi symbiont |
| Neisseria polysaccharea | Solemya velum symbiont |
| Nitrosococcus mobilis | Thiobacillus hydrothermalis |
| Nitrosolobus multiformis 1 | Xanthomonas maltophilia |
| Nitrosolobus multiformis 2 | Xylella fastidiosa |
| Nitrosomonas europaea | |
| Nitrosomonas europaea | |
| Nitrosomonas eutropha | |
| Nitrovibrio tenuis 1 | PROTEOBACTERIA GAMMA |
| Nitrovibrio tenuis 2 | Actinobacillus actinomycetemcomitans 1 ATCC 29524 |
| Nitrovibrio tenuis 3 | Actinobacillus actinomycetemcomitans 2 ATCC 29523 |
| Nitrospira briensis | Actinobacillus actinomycetemcomitans 3 ATCC 33384 (T) |
| Pseudomonas cepacia ATCC 25416 (T) | Actinobacillus actinomycetemcomitans 4 FDC Y4 |
| Pseudomonas testosteroni ATCC 11996 | Actinobacillus actinomycetemcomitans 5 ATCC 29522 |
| Rhodococcus gelatinosus | Actinobacillus capsulatus 1 NCTC 11408 (T) |
| Rhodococcus purpureus | Actinobacillus capsulatus 2 CCUG 19799 |
| Sphaerotilus natans | Actinobacillus capsulatus 3 CCUG 12396 (T) |
| Spirillum volutans ATCC 19554 (T) | Actinobacillus equuli NCTC 8529 (T) |
| Thiobacillus thioparus ATCC 8158 | Actinobacillus hominis |
| Vitreoscilla stercoraria 1 | Actinobacillus lignieresii 1 ATCC 19393 (T) |
| Vitreoscilla stercoraria 2 | Actinobacillus lignieresii 2 NCTC 4189 (T) |
| Zoogloea ramigera 1 | Actinobacillus pleuropneumoniae ATCC 27088 (T) |
| Zoogloea ramigera 2 | Actinobacillus salpingitidis |
| Zoogloea ramigera 3 | Actinobacillus seminis ATCC 15768 (T) |
| | Actinobacillus suis ATCC 15557 |
| | Actinobacillus ureae |
| | Acyrhosyphon pisum symbiont P |
| | Acyrhosyphon pisum symbiont S |

- Aeromonas caviae* 1 NCIMB 13016 (T)
Aeromonas caviae 2 ATCC 15467
Aeromonas eucrenophila NCIMB 74 (T)
Aeromonas hydrophila 1
Aeromonas hydrophila 2 ATCC 7966 (T)
Aeromonas jandaei ATCC 49568 (T)
Aeromonas media ATCC 33907 (T)
Aeromonas salmonicida 1 NCIMB 1102 (T)
Aeromonas salmonicida 2 NCIMB 1102
Aeromonas salmonicida 3 NCIMB 1110
Aeromonas schubertii DSM 4882 (T)
Aeromonas sobria NCIMB 12065 (T)
Aeromonas trota ATCC 49657 (T)
Aeromonas veronii NCIMB 13015 (T)
Aeromonas sp. ATCC 35941
Alteromonas haloplanktis ATCC 14393
Arsenophonus nasoniae ATCC 49151 (T)
Barophile 1
Barophile 2
Bisgaard Taxon 2
Bisgaard Taxon 3
Bisgaard Taxon 5
Bisgaard Taxon 6
Bisgaard Taxon 7
Bisgaard Taxon 8
Bisgaard Taxon 9
Bisgaard Taxon 13
Bisgaard Taxon 14 1
Bisgaard Taxon 14 2
Buchnera aphidicola 1
Buchnera aphidicola 2
Buchnera aphidicola 3
Buchnera aphidicola 4
Buchnera aphidicola 5
Buchnera aphidicola 6
Buchnera aphidicola 7
Buchnera aphidicola 8
Buchnera aphidicola 9
Buchnera aphidicola 10
Citrobacter freundii
Cryptosaras couesi symbiont
Erwinia carotovora
Erwinia herbicola
Escherichia coli
Euscelidius variegatus parasite
Haemophilus aegyptius NCTC 8502 (T)
Haemophilus aphrophilus ATCC 33389 (T)
Haemophilus ducreyi 1 CIP 542 (T)
Haemophilus ducreyi 2 CIP 542 (T)
Haemophilus ducreyi 3
Haemophilus ducreyi 4 ATCC 27722
Haemophilus haemoglobinophilus NCTC 1659 (T)
Haemophilus haemolyticus NCTC 10659 (T)
Haemophilus influenzae ATCC 33391 (T)
Haemophilus paracuniculus ATCC 29986 (T)
Haemophilus paragallinarum NCTC 11296 (T)
Haemophilus parahaemolyticus NCTC 8479 (T)
Haemophilus parainfluenzae 1 ATCC 7901
Haemophilus parainfluenzae 2 ATCC 33392 (T)
Haemophilus paraphrophyliticus NCTC 10670 (T)
Haemophilus paraphrophilus 1 ATCC 29241 (T)
Haemophilus paraphrophilus 2 ATCC 29242
Haemophilus parasuis 1 NCTC 4557 (T)
Haemophilus parasuis 2
Haemophilus segnis ATCC 33393 (T)
Haemophilus somnus
Haemophilus sp.
Haemophilus taxon
Hafnia alvei
Melanocetus johnsoni symbiont
Pasteurella aerogenes ATCC 27883 (T)
Pasteurella anatis ATCC 43329 (T)
Pasteurella avium NCTC 11297 (T)
Pasteurella betti
Pasteurella canis ATCC 43326 (T)
- Pasteurella dagmatis* ATCC 43325 (T)
Pasteurella gallinarum NCTC 11188 (T)
Pasteurella haemolytica 1 NCTC 10624
Pasteurella haemolytica 2 NCTC 9380 (T)
Pasteurella langaa ATCC 43328 (T)
Pasteurella multocida NCTC 10322 (T)
Pasteurella pneumotropica NCTC 8141 (T)
Pasteurella stomatis ATCC 43327 (T)
Pasteurella testudinis
Pasteurella volantium 1 NCTC 4101
Pasteurella volantium 2 NCTC 3438 (T)
Pasteurella sp. 1 CCUG 19794
Pasteurella sp. 2 CCUG 18782
Photobacterium phosphoreum
Piscirickettsia salmonis
Plesiomonas shigelloides 1
Plesiomonas shigelloides 2 NCIMB 9242 (T)
Proteus vulgaris 1
Proteus vulgaris 2
Ruminobacter amylophilus DSM 1361 (T)
Serratia entomophila ATCC 43705
Serratia ficaria ATCC 33105
Serratia fonticola ATCC 29844
Serratia grimesii ATCC 14460
Serratia liquefaciens ATCC 27592
Serratia marcescens 1 ATCC 13880
Serratia marcescens 2
Serratia odorifera ATCC 33077
Serratia plymuthica ATCC 183
Serratia proteamaculans ATCC 19323
Serratia rubidaea ATCC 27593
Sitophilus zeamais endosymbiont 1
Sitophilus zeamais endosymbiont 2
Thiomicrospira sp.
Vibrio alginolyticus ATCC 17749 (T)
Vibrio anguillarum NCMB 6, ATCC 12964 (T)
Vibrio campbellii ATCC 25920 (T)
Vibrio diazotrophicus ATCC 33466 (T)
Vibrio harveyi 1
Vibrio harveyi 2 ATCC 14126 (T)
Vibrio hollisae ATCC 33564 (T)
Vibrio natriegens ATCC 14048 (T)
Vibrio parahaemolyticus 1
Vibrio parahaemolyticus 2 ATCC 17802 (T)
Vibrio proteolyticus ATCC 15338 (T)
Vibrio vulnificus ATCC 27562 (T)
Wolbachia persica ATCC VR 331
Xenorhabdus nematophilus
Yersinia enterocolitica

PROTEOBACTERIA DELTA

- Angiococcus disciformis*
Archangium gephyra
Bdellovibrio bacteriovorus
Bdellovibrio stolpii
Chondromyces apiculatus
Chondromyces crocatus
Cystobacter fuscus
Desulfobacter curvatus DSM 3379
Desulfobacter hydrogenophilus DSM 3380
Desulfobacter latus DSM 3381
Desulfobacter postgatei DSM 2034
Desulfobacter sp. 1 DSM 2035
Desulfobacter sp. 2 DSM 2057
Desulfobacterium autotrophicum DSM 3382
Desulfobacterium niaci DSM 2650
Desulfobacterium vacuolatum DSM 3385
Desulfobulbus propionicus ATCC 33891
Desulfobulbus sp. DSM 2058
Desulfococcus multivorans ATCC 33890
Desulfomonas pigra ATCC 29098
Desulfomonile tiedjei ATCC 49306
Desulfosarcina variabilis 1
Desulfosarcina variabilis 2 DSM 2060
Desulfovibrio africanus

Table 1. continued

| | |
|--|---|
| Desulfovibrio baarsii DSM 2075 | GREEN SULFUR |
| Desulfovibrio baculatus DSM 1743 | <i>Chlorobium limicola</i> |
| Desulfovibrio desulfuricans 1 ATCC 27774 | <i>Chlorobium tepidum</i> ATCC 49652 |
| Desulfovibrio desulfuricans 2 | <i>Chlorobium vibrioforme</i> |
| Desulfovibrio desulfuricans 3 | <i>Clathrochloris sulfurica</i> |
| Desulfovibrio gigas ATCC 19364 | |
| Desulfovibrio longus | |
| Desulfovibrio salexigens ATCC 14822 | FLAVOBACTERIA AND RELATIVES |
| Desulfovibrio sapovorans ATCC 33892 | <i>Antarcticum vesiculatum</i> |
| Desulfovibrio vulgaris DSM 644 | <i>Bacteroides distasonis</i> |
| Desulfovibrio sp. | <i>Bacteroides fragilis</i> 1 ATCC 25285 |
| Desulfuromonas acetoxidans DSM 684 | <i>Bacteroides fragilis</i> 2 |
| Magnetotactic bacterium | <i>Bacteroides thetaiotaomicron</i> |
| Melittangium lichenicola | <i>Bacteroides vulgatus</i> |
| Myxococcus coralloides | <i>Capnocytophaga gingivalis</i> |
| Myxococcus xanthus | <i>Capnocytophaga ochracea</i> |
| Nannocystis exedens | <i>Capnocytophaga sputigena</i> ATCC 33612 |
| Polyangium cellulosum | <i>Cytophaga aquatilis</i> |
| Stigmatella aurantiaca | <i>Cytophaga diffluens</i> |
| | <i>Cytophaga fermentans</i> |
| | <i>Cytophaga levensis</i> |
| | <i>Cytophaga heparina</i> IFO 12017, ATCC 13125 |
| PROTEOBACTERIA EPSILON | <i>Cytophaga hutchinsonii</i> |
| <i>Bacteroides gracilis</i> | <i>Cytophaga johnsonae</i> 1 |
| <i>Bacteroides ureolyticus</i> | <i>Cytophaga johnsonae</i> 2 |
| <i>Campylobacter coli</i> 1 | <i>Cytophaga latercula</i> |
| <i>Campylobacter coli</i> 2 | <i>Cytophaga lytica</i> ATCC 23178 |
| <i>Campylobacter concisus</i> 1 | <i>Cytophaga marinoflava</i> |
| <i>Campylobacter concisus</i> 2 | <i>Cytophaga salmonicolor</i> |
| <i>Campylobacter curvus</i> 1 | <i>Flavobacterium aquatile</i> ATCC 11947 |
| <i>Campylobacter curvus</i> 2 | <i>Flavobacterium balustum</i> |
| <i>Campylobacter fetus</i> | <i>Flavobacterium breve</i> |
| <i>Campylobacter fetus</i> subsp. <i>fetus</i> ATCC 27374 | <i>Flavobacterium ferrugineum</i> ATCC 13524 |
| <i>Campylobacter fetus</i> subsp. <i>venerealis</i> ATCC 19438 | <i>Flavobacterium gleum</i> |
| <i>Campylobacter hyoilealis</i> 1 | <i>Flavobacterium gondwanense</i> |
| <i>Campylobacter hyoilealis</i> 2 ATCC 25317 | <i>Flavobacterium indologenes</i> |
| <i>Campylobacter jejuni</i> 1 | <i>Flavobacterium indoltheticum</i> |
| <i>Campylobacter jejuni</i> 2 | <i>Flavobacterium meningosepticum</i> |
| <i>Campylobacter lari</i> | <i>Flavobacterium odoratum</i> |
| <i>Campylobacter mucosalis</i> | <i>Flavobacterium salegens</i> |
| <i>Campylobacter rectus</i> 1 | <i>Flavobacterium spiritivorum</i> |
| <i>Campylobacter rectus</i> 2 | <i>Flavobacterium thalpophilum</i> |
| <i>Campylobacter showae</i> 1 | <i>Flavobacterium uliginosum</i> ATCC 14397 |
| <i>Campylobacter showae</i> 2 | <i>Flectobacillus glomeratus</i> |
| <i>Campylobacter sputorum</i> 1 LMG 7795 | <i>Flectobacillus major</i> ATCC 29496 |
| <i>Campylobacter sputorum</i> 2 | <i>Flectobacillus marinus</i> ATCC 43824 |
| <i>Flexispira rappini</i> | <i>Flexibacter aggregans</i> 1 |
| <i>Helicobacter acinonyx</i> 1 | <i>Flexibacter aggregans</i> 2 |
| <i>Helicobacter acinonyx</i> 2 | <i>Flexibacter aurantiacus</i> ATCC 23107 |
| <i>Helicobacter cinaedi</i> | <i>Flexibacter canadensis</i> ATCC 29591 |
| <i>Helicobacter felis</i> 1 ATCC 49179 | <i>Flexibacter columnaris</i> |
| <i>Helicobacter felis</i> 2 | <i>Flexibacter elegans</i> 1 |
| <i>Helicobacter felis</i> 3 | <i>Flexibacter elegans</i> 2 |
| <i>Helicobacter fennelliae</i> | <i>Flexibacter elegans</i> 3 |
| <i>Helicobacter muridarum</i> | <i>Flexibacter elegans</i> 4 |
| <i>Helicobacter mustelae</i> 1 ATCC 43772 | <i>Flexibacter flexilis</i> ATCC 23079 |
| <i>Helicobacter mustelae</i> 2 | <i>Flexibacter litoralis</i> |
| <i>Helicobacter pylori</i> | <i>Flexibacter maritimus</i> 1 |
| <i>Helicobacter</i> sp. 1 | <i>Flexibacter maritimus</i> 2 |
| <i>Helicobacter</i> sp. 2 | <i>Flexibacter polymorphus</i> |
| <i>Helicobacter</i> sp. 3 | <i>Flexibacter roseolus</i> |
| <i>Helicobacter</i> sp. 4 | <i>Flexibacter ruber</i> |
| <i>Helicobacter</i> sp. 5 | <i>Flexibacter sancti</i> ATCC 23092 |
| <i>Helicobacter</i> sp. 6 | <i>Flexibacter tractuosus</i> |
| <i>Helicobacter</i> sp. 7 | <i>Haliscomonobacter hydrossis</i> |
| <i>Helicobacter</i> sp. 8 | <i>Microscilla aggregans</i> subsp. <i>catalytica</i> |
| <i>Helicobacter</i> sp. 9 | <i>Microscilla arenaria</i> |
| <i>Helicobacter</i> sp. 10 | <i>Microscilla furvescens</i> |
| <i>Helicobacter</i> sp. 11 | <i>Microscilla marina</i> |
| <i>Helicobacter</i> sp. 12 | <i>Microscilla sericea</i> |
| <i>Wolinella succinogenes</i> 1 ATCC 29453 | <i>Ranunculus silthiformis</i> ATCC 29530 |
| <i>Wolinella succinogenes</i> 2 | <i>Saprosphaera grandis</i> |
| <i>Wolinella succinogenes</i> 3 | <i>Sphingobacter mizutae</i> |
| | <i>Spirosoma linguale</i> ATCC 23276 |
| PROTEOBACTERIA, UNCERTAIN AFFILIATION | <i>Sporocytophaga cauliniformis</i> |
| <i>Thiobacillus thiooxidans</i> DSM 612 | |

Weeksella virosa
Weeksella zoohelcum

CHLAMYDIAE

Chlamydia pneumoniae
Chlamydia psittaci
Chlamydia trachomatis

FIBROBACTER

Fibrobacter intestinales 1
Fibrobacter intestinales 2
Fibrobacter intestinales 3
Fibrobacter intestinales 4
Fibrobacter intestinales 5
Fibrobacter succinogenes 1
Fibrobacter succinogenes 2
Fibrobacter succinogenes 3
Fibrobacter succinogenes 4
Fibrobacter succinogenes 5
Fibrobacter succinogenes 6
Fibrobacter succinogenes 7
Fibrobacter succinogenes 8
Fibrobacter succinogenes 9
Fibrobacter succinogenes 10

SPIROCHETES

Borrelia anserina 1
Borrelia anserina 2
Borrelia burgdorferi
Borrelia burgdorferi 1
Borrelia burgdorferi 2
Borrelia burgdorferi 3
Borrelia burgdorferi 4
Borrelia burgdorferi 5
Borrelia burgdorferi 6
Borrelia burgdorferi 7 ATCC 35210 (T)
Borrelia burgdorferi 8
Borrelia burgdorferi 9
Borrelia burgdorferi 10
Borrelia burgdorferi 11
Borrelia burgdorferi 12
Borrelia coriaceae ATCC 43381
Borrelia hermsii 1 ATCC 35209
Borrelia hermsii 2
Borrelia hermsii 3
Borrelia hermsii 4
Borrelia hermsii 5
Borrelia sp.
Leptonema illini
Leptospira illini
Leptospira interrogans 1 ATCC 23606
Leptospira interrogans 2
Leptospira sp.
Serpula hydysenteriae 1 ATCC 27164 (T)
Serpula hydysenteriae 2
Serpula hydysenteriae 3
Serpula innocens 1 ATCC 29796 (T)
Serpula innocens 2
Spirochaeta aurantia ATCC 25082 (T)
Spirochaeta bajacaliforniensis ATCC 35968 (T)
Spirochaeta halophila ATCC 29478 (T)
Spirochaeta isovalerica
Spirochaeta litoralis ATCC 27000 (T)
Spirochaeta stenostrepta ATCC 25083 (T)
Spirochaeta thermophila DSM 6192
Spirochaeta zuelzeri ATCC 19044 (T)
Spirochaeta sp. 1
Spirochaeta sp. 2
Treponema bryantii ATCC 33254 (T)
Treponema denticola ATCC 33520
Treponema pallidum 1
Treponema pallidum 2
Treponema pectinovorum ATCC 33768 (T)
Treponema phagedenis
Treponema saccharophilum ATCC 43261 (T)
Treponema succinifaciens ATCC 33096 (T)

Treponema sp. 1 ATCC 43811
Treponema sp. 2
Treponema sp. 3
Treponema sp. 4

FUSOBACTERIUM AND RELATIVES

Bacteroides termitidis
Fusobacterium alocis ATCC 35896 (T)
Fusobacterium gonidiaformans ATCC 25563 (T)
Fusobacterium gonidoformans
Fusobacterium mortiferum 1
Fusobacterium mortiferum 2 ATCC 25557 (T)
Fusobacterium necrogenes ATCC 25556 (T)
Fusobacterium necrophorum ATCC 25286 (T)
Fusobacterium nucleatum
Fusobacterium nucleatum ssp. *animalis* NCTC 12276 (T)
Fusobacterium nucleatum ssp. *fusiformis* NCTC 11326 (T)
Fusobacterium nucleatum ssp. *nucleatum* ATCC 25586 (T)
Fusobacterium nucleatum ssp. *polymorphum* ATCC 10953
Fusobacterium perfoetens
Fusobacterium periodonticum ATCC 33693 (T)
Fusobacterium russii 1
Fusobacterium russii 2 ATCC 25533 (T)
Fusobacterium simiae 1
Fusobacterium simiae 2 ATCC 33568 (T)
Fusobacterium ulcerans NCTC 12111 (T)
Fusobacterium varium 1
Fusobacterium varium 2 NCTC 10560 (T)
Leptotrichia buccalis
Propionigenium modestum

CYANOBACTERIA

Anabaena sp.
Anacystis nidulans
Cyanobacterium sp.
Cyanophora paradoxa cyanelle
Mastigocladus laminosus
Prochlorococcus marinus
Prochloron sp.
Prochlorothrix hollandica

GRAM POSITIVES AND RELATIVES, LOW G+C

Acetomaculum ruminis
Acetonebema longum DSM 6540 (T)
Acholeplasma entomophilum ATCC 43706
Acholeplasma laidlawii
Acholeplasma modicum ATCC 29102
Acidaminococcus fermentans ATCC 25085
Aerococcus urinae NCTC 12142 (T)
Aerococcus viridans
Alloiococcus otitis
Anaeroplasma abactoclasticum ATCC 27879
Anaeroplasma bactoclasticum ATCC 27112
Anaeroplasma varium ATCC 43167
Asteroleplasma anaerobium ATCC 27880
Bacillus acidocaldarius 1 ATCC 43034
Bacillus acidocaldarius 2 DSM 446 (T)
Bacillus acidoterrestris 1 DSM 3922
Bacillus acidoterrestris 2 DSM 3923
Bacillus alcalophilus DSM 485
Bacillus alvei 1 ATCC 6344
Bacillus alvei 2 NCDO 1153
Bacillus amyloliquefaciens ATCC 23350
Bacillus amylolyticus NCIMB 8144
Bacillus aneurinolyticus NCIMB 10056
Bacillus anthracis
Bacillus atropaeus NCIMB 12899
Bacillus azotofixans ATCC 35681
Bacillus azotoformans ATCC 29788
Bacillus badius NCDO 1760
Bacillus benzevorans NCIMB 12555
Bacillus brevis 1 NCIMB 9372
Bacillus brevis 2
Bacillus cereus 1 NCTC 11143
Bacillus cereus 2 NCDO 1771 (T)
Bacillus circulans NCDO 1775

Table 1. continued

| | |
|--|---|
| Bacillus coagulans NCDO 1761 | Clostridium estertheticum NCIMB 12511 |
| Bacillus cycloheptanicus DSM 4006 (T) | Clostridium fallax |
| Bacillus fastidiosus DSM 91 | Clostridium histolyticum |
| Bacillus firmus NCIMB 9366 | Clostridium innocuum ATCC 14501 |
| Bacillus globisporus 1 NCIMB 11434 | Clostridium kluveri |
| Bacillus globisporus 2 ATCC 23301, DSM 4 (T) | Clostridium leptum |
| Bacillus gordonae ATCC 29948 | Clostridium limosum |
| Bacillus insolitus DSM 5 | Clostridium lituseburense |
| Bacillus kaustophilus NCIMB 8547 | Clostridium ljungdahlii |
| Bacillus larvae ATCC 9545 | Clostridium malenominatum |
| Bacillus laterosporus 1 ATCC 6344, DSM 25 | Clostridium mangenotii |
| Bacillus laterosporus 2 NCDO 1763 | Clostridium mayombeii DSM 6539 (T) |
| Bacillus laetus NCIMB 12780 | Clostridium novyi |
| Bacillus lentimorbus ATCC 14707 | Clostridium oceanicum |
| Bacillus lentus NCDO 1127 | Clostridium oroticum |
| Bacillus licheniformis NCDO 1772 | Clostridium paraperfringens |
| Bacillus macerans 1 ATCC 8244, DSM 24 | Clostridium pasteurianum |
| Bacillus macerans 2 NCDO 1764 | Clostridium perfringens 1 |
| Bacillus macquariensis 1 DSM/ATCC 23464 (T) | Clostridium perfringens 2 |
| Bacillus macquariensis 2 NCTC 10419 | Clostridium piliforme |
| Bacillus maroccanus NCIMB 10500 | Clostridium purinolyticum |
| Bacillus medusa NCIMB 10437 | Clostridium quercicolum |
| Bacillus megaterium DSM 32 | Clostridium ramosum ATCC 25582 |
| Bacillus mycoides DSM 2048 (T) | Clostridium scatologenes |
| Bacillus pabuli NCIMB 12781 | Clostridium sordellii |
| Bacillus pantothenticus NCDO 1765 | Clostridium sporogenes |
| Bacillus pasteurii NCIMB 8841 | Clostridium sporosphaeroides |
| Bacillus polymyxa 1 DSM 36 | Clostridium sticklandii 1 |
| Bacillus polymyxa 2 NCDO 1774 | Clostridium sticklandii 2 |
| Bacillus popilliae ATCC 14706 | Clostridium subterminale |
| Bacillus psychrophilus 1 ATCC 23304 | Clostridium symbiosum |
| Bacillus psychrophilus 2 ATCC 23304, DSM 3 (T) | Clostridium tetanomorphum NCIMB 11547 |
| Bacillus psychrophilus 3 ATCC 23306, DSM 2273 | Clostridium thermaceticum |
| Bacillus psychrosaccharolyticus ATCC 23296 | Clostridium thermoaceticum |
| Bacillus pulifaciens NCDO 1141 | Clostridium thermoautotrophicum 1 |
| Bacillus pumilus NCDO 1766 | Clostridium thermoautotrophicum 2 |
| Bacillus simplex DSM 1321 | Clostridium thermohydrosulfuricum |
| Bacillus smithii DSM 4216 | Clostridium thermosaccharolyticum |
| Bacillus sphaericus NCDO 1767 | Clostridium thermosulfurogenes |
| Bacillus stearothermophilus 1 | Clostridium tyrobutyricum 1 |
| Bacillus stearothermophilus 2 NCDO 1768 | Clostridium tyrobutyricum 2 |
| Bacillus subtilis 1 | Desulfovotaculum nigricans NCIMB 8395 (T) |
| Bacillus subtilis 2 NCDO 1769 | Desulfovotaculum orientis NCIMB 8382 |
| Bacillus thermoglucosadicus ATCC 43742 | Desulfovotaculum ruminis NCIMB 8452 |
| Bacillus thuringiensis NCIMB 9134 (T) | Enterococcus avium NCDO 2369 (T) |
| Brochotrichix campestris ATCC 43754 (T) | Enterococcus casseliflavus NCDO 2376 |
| Brochotrichix thermosphacta 1 NCDO 1676 (T) | Enterococcus columbae NCIMB 13013 |
| Brochotrichix thermosphacta 2 | Enterococcus dispar |
| Carnobacterium divergens NCDO 2763 (T) | Enterococcus durans NCDO 596 (T) |
| Carnobacterium gallinarum | Enterococcus faecalis |
| Carnobacterium mobile | Enterococcus faecium NCDO 942 (T) |
| Carnobacterium piscicola NCDO 2762 (T) | Enterococcus gallinarum NCDO 2313 (T) |
| Clostridium acetobutylicum NCIMB 8052 | Enterococcus hirae NCDO 1258 (T) |
| Clostridium aciduriuci | Enterococcus malodoratus NCDO 846 (T) |
| Clostridium aminophilum | Enterococcus mundtii NCDO 2375 (T) |
| Clostridium aminovalericum | Enterococcus pseudoavium NCDO 2138 (T) |
| Clostridium aurantibutyricum NCIMB 10659 | Enterococcus raffinosus NCTC 12192 (T) |
| Clostridium barati 1 ATCC 27638 | Enterococcus sulfureus NCDO 2379 |
| Clostridium barati 2 ATCC 43756 | Epulopiscium sp. 1 |
| Clostridium barkeri | Epulopiscium sp. 2 |
| Clostridium beijerinckii 1 DSM 791 | Erysipelothrix rhusiopathiae ATCC 19414 |
| Clostridium beijerinckii 2 NCIMB 9362 | Eubacterium alactolyticum DSM 3980 |
| Clostridium botulinum 1 | Eubacterium biforme |
| Clostridium botulinum 2 | Eubacterium limosum |
| Clostridium botulinum 3 | Eubacterium tenue |
| Clostridium botulinum 4 NCTC 10281 | Gemella haemolysans |
| Clostridium botulinum 5 ATCC 25765 | Heliobacterium chlorum |
| Clostridium butyricum 1 ATCC 43755 | Kurthia zopfii |
| Clostridium butyricum 2 DSM 2478 | Lactobacillus acetolentans |
| Clostridium butyricum 3 NCIMB 8082 | Lactobacillus acidophilus 1 NCDO 1748 (T) |
| Clostridium cadaveris | Lactobacillus acidophilus 2 |
| Clostridium carnis | Lactobacillus agilis |
| Clostridium clostridiiformes | Lactobacillus alimentarius |
| Clostridium coccoides | Lactobacillus amylophilus |
| Clostridium cochlearium | Lactobacillus amylovorus |

- Lactobacillus animalis 1 NCDO 2425 (T)
 Lactobacillus animalis 2
 Lactobacillus aviarus
 Lactobacillus bifementans
 Lactobacillus brevis 1 NCDO 1749 (T)
 Lactobacillus brevis 2
 Lactobacillus buchneri 1 NCDO 110 (T)
 Lactobacillus buchneri 2
 Lactobacillus carnis
 Lactobacillus casei 1
 Lactobacillus casei 2 NCDO 161 (T)
 Lactobacillus casei 3
 Lactobacillus catenaforme ATCC 25536 (T)
 Lactobacillus confusus 1 NCDO 5186
 Lactobacillus confusus 2 DSM 20196
 Lactobacillus coryniformis
 Lactobacillus delbrueckii 1
 Lactobacillus delbrueckii 2 NCDO 213
 Lactobacillus divergens
 Lactobacillus farciminis
 Lactobacillus fermentum 1 NCDO 1750 (T)
 Lactobacillus fermentum 2
 Lactobacillus fructivorans
 Lactobacillus fructosus NCDO 2345 (T)
 Lactobacillus gasseri 1 NCDO 2233 (T)
 Lactobacillus gasseri 2
 Lactobacillus halotolerans DSM 20190
 Lactobacillus helveticus NCDO 2712 (T)
 Lactobacillus hilgardii
 Lactobacillus kandleri 1 NCDO 2753
 Lactobacillus kandleri 2 DSM 20593
 Lactobacillus lactis
 Lactobacillus mali
 Lactobacillus maltaromaticus 1
 Lactobacillus maltaromaticus 2 JCM 1154
 Lactobacillus minor 1 NCDO 1973
 Lactobacillus minor 2 DSM 20014
 Lactobacillus murinus
 Lactobacillus oris NCDO 2160 (T)
 Lactobacillus plantarum 1
 Lactobacillus plantarum 2 NCDO 1752
 Lactobacillus ruminis
 Lactobacillus sake
 Lactobacillus salivarius
 Lactobacillus sanfrancisco 1 JCM 5668
 Lactobacillus sanfrancisco 2
 Lactobacillus sharpeae
 Lactobacillus thermophilus
 Lactobacillus vaginalis NCTC 12197
 Lactobacillus vermiciforme
 Lactobacillus viridescens 1 NCDO 1655
 Lactobacillus viridescens 2 ATCC 12706
 Lactobacillus vitulinus ATCC 27783
 Lactobacillus sp.
 Lactococcus garviae NCDO 2156
 Lactococcus lactis 1 ssp. lactis NCDO 2118
 Lactococcus lactis 2
 Lactococcus piscium
 Lactococcus plantarum NCDO 1871
 Lactococcus raffinolactis NCDO 2112
 Leuconostoc amelobiosum
 Leuconostoc carnosum
 Leuconostoc citreum NCDO 1837
 Leuconostoc cremoris DSM 20346
 Leuconostoc fallax DSM 20189
 Leuconostoc gelidum
 Leuconostoc lactis 1 DSM 20202
 Leuconostoc lactis 2 NCDO 533
 Leuconostoc mesenteroides 1 DSM 20343
 Leuconostoc mesenteroides 2 NCDO 523
 Leuconostoc oenos 1 DSM 20252
 Leuconostoc oenos 2 NCDO 1674
 Leuconostoc parmesenteroides 1 DSM 20288
 Leuconostoc parmesenteroides 2 NCDO 803
 Leuconostoc pseudomesenteroides NCDO 768
 Listeria grayi CIP 6818 (T)
 Listeria innocua NCTC 11288 (T)
- Listeria ivanovii NCTC 11846 (T)
 Listeria monocytogenes 1
 Listeria monocytogenes 2 NCTC 10357 (T)
 Listeria murrayi NCTC 10812 (T)
 Listeria seeligeri NCTC 11856 (T)
 Listeria welshimeri NCTC 11857 (T)
 Marinococcus halophilus NCIMB 2178 (T)
 Megasphaera elsdenii
 Mycoplasma agalactiae NCTC 10123
 Mycoplasma arginini ATCC 23838
 Mycoplasma arthritidis ATCC 19611
 Mycoplasma bovis genitalium ATCC 19852
 Mycoplasma californicum ATCC 33461
 Mycoplasma capricolum
 Mycoplasma coragypsorum
 Mycoplasma ellychniae ATCC 43707
 Mycoplasma fermentans ATCC 19989
 Mycoplasma flocculare ATCC 27716
 Mycoplasma gallisepticum 1
 Mycoplasma gallisepticum 2
 Mycoplasma gallisepticum 3
 Mycoplasma hominis 1 ATCC 23114
 Mycoplasma hominis 2
 Mycoplasma hyopneumoniae ATCC 27719
 Mycoplasma hyorhinis ATCC 17981
 Mycoplasma iowae 1 ATCC 33552
 Mycoplasma iowae 2
 Mycoplasma-like organism 1
 Mycoplasma-like organism 2
 Mycoplasma-like organism 3
 Mycoplasma lipophilum ATCC 27104
 Mycoplasma mobile ATCC 43663
 Mycoplasma muris ATCC 33757
 Mycoplasma mycoides
 Mycoplasma neurolyticum ATCC 19988
 Mycoplasma orale ATCC 23714
 Mycoplasma pirum ATCC 25960
 Mycoplasma pneumoniae ATCC 15531
 Mycoplasma pulmonis ATCC 19612
 Mycoplasma putrefaciens ATCC 15718
 Mycoplasma salivarium ATCC 23064
 Mycoplasma sualvi ATCC 33004
 Mycoplasma sp. 1
 Mycoplasma sp. 2
 Mycoplasma sp. 3 ATCC 49193
 Mycoplasma sp. 4 ATCC 49191
 Oenothera hookeri MLO
 Pectinatus cerevisiiphilus ATCC 29359
 Pectinatus frisigenensis ATCC 33332
 Pediococcus acidilactici
 Pediococcus pentosaceus
 Peptococcus niger DSM 20475 (T)
 Peptostreptococcus anaerobius
 Planococcus citreus NCIMB 1493 (T)
 Planococcus kocurii NCIMB 629
 Quinella ovalis
 Selenomonas lacticifex DSM 20757
 Selenomonas ruminantium 1 subsp. lacticilytica DSM 2872
 Selenomonas ruminantium 2
 Selenomonas ruminantium 3
 Selenomonas sputigena ATCC 35185
 Spiroplasma ATCC 43302
 Spiroplasma apis ATCC 33834
 Spiroplasma citri 1 ATCC 27556
 Spiroplasma citri 2
 Spiroplasma mirum ATCC 29335
 Spiroplasma sp. 1 ATCC 43153
 Spiroplasma sp. 2 ATCC 33827
 Spiroplasma sp. 3 ATCC 33835
 Spiroplasma sp. 4 ATCC 33825
 Spiroplasma sp. 5 ATCC 43210
 Spiroplasma sp. 6 ATCC 43525
 Sporolactobacillus inulinus
 Sporomusa paucivorans
 Sporomusa termitida
 Sporosarcina halophila NCIMB 2269
 Sporosarcina ureae NCIB 9251

Table 1. continued

| | |
|---|--|
| Staphylococcus aureus NCDO 949 | Atopobium rimae |
| Staphylococcus muscae CCM 4175 (T) | Bifidobacterium adolescentis |
| Staphylococcus schleiferi DSM 4807 (T) | Bifidobacterium asteroides |
| Staphylococcus sciuri | Bifidobacterium bifidum |
| Streptococcus acidominimus NCDO 2025 (T) | Bifidobacterium breve |
| Streptococcus agalactiae NCDO 1348 (T) | Bifidobacterium catenulatum |
| Streptococcus alactolyticus NCDO 1091 (T) | Bifidobacterium coryneforme |
| Streptococcus anginosus NCTC 10713 (T) | Bifidobacterium cuniculi |
| Streptococcus bovis 1 NCDO 597 (T) | Bifidobacterium dentium |
| Streptococcus bovis 2 | Bifidobacterium globosum |
| Streptococcus canis DSM 20715 (T) | Bifidobacterium indicum |
| Streptococcus cecorum NCDO 2674 (T) | Bifidobacterium infantis |
| Streptococcus constellatus NCTC 11325 (T) | Bifidobacterium longum |
| Streptococcus cremoris | Bifidobacterium magnum |
| Streptococcus crieae NCDO 2772 (T) | Bifidobacterium minimum |
| Streptococcus cricetus NCDO 2720 (T) | Bifidobacterium pseudolongum |
| Streptococcus downei NCTC 11391 (T) | Bifidobacterium suis |
| Streptococcus dysgalactiae NCDO 2023 (T) | Clavibacter xyli |
| Streptococcus equi NCDO 2493 (T) | Corynebacterium renale ATCC 19412 |
| Streptococcus equinus NCDO 1037 (T) | Corynebacterium variabile NCIB 9455, NCDO 2097 (T) |
| Streptococcus hansenii | Corynebacterium xerosis |
| Streptococcus hyoilectinalis DSM 20770 (T) | Dermatophilus congolensis |
| Streptococcus intermedius NCTC 11324 (T) | Eubacterium suis DSM 20639, ATCC 33144 (T) |
| Streptococcus lactis | Faenia rectivirgula ATCC 33515 (T) |
| Streptococcus macacae NCTC 11558 (T) | Frankia sp. 1 |
| Streptococcus mutans NCTC 10449 (T) | Frankia sp. 2 |
| Streptococcus oralis NCTC 11427 (T) | Frankia sp. 3 |
| Streptococcus parasanguis NCTC 7863 (T) | Frankia sp. 4 |
| Streptococcus parauberis NCDO 651 | Frankia sp. 5 |
| Streptococcus pleomorphus ATCC 29734 | Fusobacterium prausnitzi |
| Streptococcus pneumoniae NCTC 7465 (T) | Gardnerella vaginalis |
| Streptococcus porcinus NCDO 600 (T) | Gordona terrae DSM 43249 |
| Streptococcus pyogenes NCDO 2381 (T) | Kibdelosporangium aridum ATCC 39323 |
| Streptococcus ratus NCDO 2723 (T) | Kitasatosporia griseola NRRL B-16229 |
| Streptococcus saccharolyticus NCDO 2594 | Kitasatosporia phosalacinea NRRL B-16230 |
| Streptococcus salivarius 1 NCDO 1779 (T) | Kitasatosporia setae NRRL B-16185 |
| Streptococcus salivarius 2 | Lactobacillus minutus |
| Streptococcus sanguis NCTC 7863 | Micrococcus luteus |
| Streptococcus sobrinus DSM 20742 (T) | Mobiluncus curtisi ATCC 35421 |
| Streptococcus suis NCTC 10237 (T) | Mobiluncus mulieris ATCC 35423 |
| Streptococcus thermophilus NCDO 573 (T) | Mycobacterium aichense ATCC 27280 |
| Streptococcus uberis NCDO 643 | Mycobacterium asiaticum 1 ATCC 25276 |
| Streptococcus vestibularis NCTC 12166 (T) | Mycobacterium asiaticum 2 ATCC 25276 |
| Syntrophomonas wolfei | Mycobacterium aurum 1 ATCC 23366 |
| Syntrophospora bryantii | Mycobacterium aurum 2 ATCC 23366 |
| Ureaplasma urealyticum NCTC 10177 | Mycobacterium avium 1 |
| Vagococcus fluvialis NCDO 2497 | Mycobacterium avium 2 |
| Vagococcus salmoninarum | Mycobacterium avium 3 DSM 43216 |
| Western aster yellow MLO isolated from celery | Mycobacterium avium 4 |
| Zymophilus paucivorans DSM 20756 | Mycobacterium avium 5 |
| GRAM POSITIVES AND RELATIVES, HIGH G+C | |
| Actinomyces bovis 1 DSM 43014 | Mycobacterium avium 6 |
| Actinomyces bovis 2 DSM 43014 | Mycobacterium avium 7 |
| Actinomyces israelii 1 DSM 43020 | Mycobacterium avium 8 |
| Actinomyces israelii 2 DSM 43020 | Mycobacterium avium 9 |
| Actinomyces naeslundii 1 DSM 43013 | Mycobacterium avium 10 |
| Actinomyces naeslundii 2 DSM 43013 | Mycobacterium bovis 1 |
| Actinomyces odontolyticus 1 DSM 43331 | Mycobacterium bovis 2 |
| Actinomyces odontolyticus 2 DSM 43331 | Mycobacterium chelonae ATCC 14472 |
| Actinomyces pyogenes ATCC 19411 | Mycobacterium chelonei ATCC 19977 |
| Actinomyces viscosus 1 DSM 43027 | Mycobacterium chitae 1 ATCC 19627 |
| Actinomyces viscosus 2 DSM 43027 | Mycobacterium chitae 2 |
| Actinoplyspora halophila ATCC 279 | Mycobacterium chitae 3 ATCC 19627 |
| Aeromicrobium erythreum NRRL B-3381 (T) | Mycobacterium chubuense ATCC 27278 |
| Amycolata autotrophica DSM 43210 | Mycobacterium confluentis |
| Amycolata nitrificans DSM new | Mycobacterium cookii ATCC 49103, DSM 43922 (T) |
| Amycolata petroleophila DSM new | Mycobacterium diernhoferi ATCC 19340 |
| Amycolatopsis azurae NRRL 11412 | Mycobacterium fallax ATCC 35219 |
| Amycolatopsis fastidiosa ATCC 31181 | Mycobacterium farcinogenes DSM 43294 |
| Amycolatopsis methanolica NCIB 11946 (T) | Mycobacterium flavescens 1 ATCC 14474 |
| Arthrobacter globiformis | Mycobacterium flavescens 2 ATCC 14474 |
| Arthrobacter simplex ATCC 6946 | Mycobacterium fortuitum ATCC 6841 (T) |
| Arthrobacter sp. | Mycobacterium gadium 1 |
| Atopobium parvulum | Mycobacterium gadium 2 ATCC 27726 |
| | Mycobacterium gastri ATCC 15754 |

- Mycobacterium gilvum ATCC 43909
 Mycobacterium gordonaie 1 ATCC 14470
 Mycobacterium gordonaie 2 ATCC 14470
 Mycobacterium intracellulare 1 ATCC 15985
 Mycobacterium intracellulare 2
 Mycobacterium intracellulare 3
 Mycobacterium intracellulare 4
 Mycobacterium intracellulare 5
 Mycobacterium intracellulare 6
 Mycobacterium kansasii 1 DSM 43224
 Mycobacterium kansasii 2 ATCC 12478
 Mycobacterium komossense ATCC 33013
 Mycobacterium leprae 1
 Mycobacterium leprae 2
 Mycobacterium leprae 3
 Mycobacterium madagascariense
 Mycobacterium malmoense 1 ATCC 29571
 Mycobacterium malmoense 2
 Mycobacterium marinum
 Mycobacterium neoaurum ATCC 25795
 Mycobacterium nonchromogenicum 1 ATCC 19530
 Mycobacterium nonchromogenicum 2 ATCC 19530
 Mycobacterium obuense ATCC 27023
 Mycobacterium paratuberculosis 1
 Mycobacterium paratuberculosis 2
 Mycobacterium paratuberculosis 3
 Mycobacterium paratuberculosis 4
 Mycobacterium paratuberculosis 5
 Mycobacterium paratuberculosis 6
 Mycobacterium paratuberculosis 7
 Mycobacterium paratuberculosis 8
 Mycobacterium paratuberculosis 9 ATCC 19698
 Mycobacterium phlei ATCC 11758
 Mycobacterium scrofulaceum ATCC 19981
 Mycobacterium senegalense ATCC 35796
 Mycobacterium simiae ATCC 25275
 Mycobacterium smegmatis ATCC 14468
 Mycobacterium sphagni ATCC 33026
 Mycobacterium szulgai 1 ATCC 25799
 Mycobacterium szulgai 2
 Mycobacterium terrae 1 ATCC 15755
 Mycobacterium terrae 2 ATCC 15755
 Mycobacterium thermoresistibile 1 ATCC 19527
 Mycobacterium thermoresistibile 2 ATCC 19527
 Mycobacterium triviale ATCC 23292
 Mycobacterium tuberculosis 1
 Mycobacterium tuberculosis 2
 Mycobacterium tuberculosis 3 NCTC 7416
 Mycobacterium ulcerans
 Mycobacterium vaccae ATCC 15483
 Mycobacterium xenopi 1 ATCC 19250
 Mycobacterium xenopi 2 ATCC 19250
 Mycobacterium sp. 1
 Mycobacterium sp. 2
 Mycobacterium sp. 3
 Nocardia asteroides 1 DSM 43005
 Nocardia asteroides 2 ATCC 3306
 Nocardia otitidis-caviae
 Nocardioides albus DSM 43109
 Nocardioides fastidiosa NCIB 12713 (T)
 Nocardioides jensenii DSM 29641
 Nocardioides luteus NCIB 11455
 Nocardioides simplex 1 NCIB 8929
 Nocardioides simplex 2 NCIB 8929 (T)
 Propionibacterium acidi-propionicum DSM 20272
 Propionibacterium acnes 1 DSM 1897
 Propionibacterium acnes 2
 Propionibacterium freudenreichii DSM 20271
 Propionibacterium jensenii DSM 20535
 Propionibacterium propionicum DSM 43307
 Propionibacterium thoenii DSM 20276
 Pseudonocardia thermophila 1 ATCC 19285 (T)
 Pseudonocardia thermophila 2 ATCC 19285 (T)
 Renibacterium salmoninarum ATCC 33209 (T)
 Rhodococcus equi Equine lung
 Rhodococcus erythropolis DSM 43188
 Rhodococcus fascians DSM 20131
- Rothia dentocariosa
 Saccharomonospora viridis ATCC 15386
 Saccharopolyspora erythraea NRRL 2338
 Saccharopolyspora hirsuta 1 ATCC 27875 (T)
 Saccharopolyspora hirsuta 2
 Saccharopolyspora hordei
 Saccharothrix australiensis ATCC 31947
 Streptomyces albus DSM 40313, ISP 5313 (T)
 Streptomyces ambofaciens ATCC 23877
 Streptomyces brasiliensis DSM 43159 (T)
 Streptomyces coelicolor 1
 Streptomyces coelicolor 2
 Streptomyces diastaticus DSM 40496, ISP 5496 (T)
 Streptomyces griseus subsp. griseus ATCC 10137
 Streptomyces lavendulae DSM 2014, ISP 5069 (T)
 Streptomyces lividans
 Streptomyces purpureus DSM 43460 (T)
 Streptoverticillium abikoense DSM 40831 (T)
 Streptoverticillium baldacii
 Streptoverticillium cinnamoneum spp. azacolutum
 Streptoverticillium cinnamoneum spp. cinnamoneum
 Streptoverticillium ladakanum DSM 40587 (T)
 Streptoverticillium luteoreticuli
 Streptoverticillium olivoreticuli ssp. cellulophilum
 Streptoverticillium salmonis
 Terrabacter tumescens NCIB 8914
 Tropheryma whippelii
 Tsukamurella aurantiacus NCTC 10741
 Tsukamurella paurometabolum 1 DSM 20162, NCTC 10741
 Tsukamurella paurometabolum 2 NCTC 10741
- GREEN NON SULFUR**
 Chloroflexus aurantiacus
 Herpetosiphon aurantiacus ATCC 23779
 Sphaerobacter thermophilus DSM 20745 (T)
 Thermomicrobium roseum ATCC 27502
- RADIORESISTANT MICROCOCCI AND RELATIVES**
 Deinococcus radiodurans UWO 298
 Thermus aquaticus 1
 Thermus aquaticus 2
 Thermus aquaticus 3 ATCC 27978
 Thermus filiformis 1 ATCC 43280
 Thermus filiformis 2
 Thermus flavus 1 ATCC 33923
 Thermus flavus 2
 Thermus ruber 1 ATCC 35948
 Thermus ruber 2
 Thermus thermophilus 1
 Thermus thermophilus 2 ATCC 27634
 Thermus thermophilus 3 ATCC 27634
 Thermus thermophilus 4
 Thermus sp. 1
 Thermus sp. 2
 Thermus sp. 3
 Thermus sp. 4
 Thermus sp. 5
 Thermus sp. 6
 Thermus sp. 7
 Thermus sp. 8
 Thermus sp. 9
 Thermus sp. 10
- THERMOTOGALES**
 Fervidobacterium nodosum ATCC 35602
 Fervidobacterium islandicum DSM 5733 (T)
 Thermosiphon africanus
 Thermotoga maritima DSM 3109
- PLANCTOMYCES AND RELATIVES**
 Gemmata obscuriglobus 1 UQM 2246
 Gemmata obscuriglobus 2 UQM 2246
 Isosphaera pallida
 Pirellula marina DSM 3645
 Planctomyces limnophilus ATCC 43296
 Planctomyces maris ATCC 29209 (T)
 Planctomyces staleyi

Table 1. continued

| | |
|-----------------------------------|----------------------------------|
| UNCERTAIN AFFILIATION | |
| Aquifex pyrophilus | Antilocapra americana |
| Flexistipes sinusarabici DSM 4947 | Atelerix albiventris |
| Haloanaerobium praevalens | Balaenoptera physalus |
| Leptospirillum sp. DSM 2391 | Bathyergus janetta |
| Sporohalobacter lortetii | Bathyergus suillus |
| Synergistis jonesii | Blarina brevicauda |
| PLASTIDS | |
| PLANTAE | |
| BRYOPHYTA | |
| MARCHANTIOPSIDA | |
| Marchantia polymorpha | Cryptomys hottentotus 1 |
| MAGNOLIOPHYTA | |
| LILIOPSIDA | |
| Oryza sativa | Cryptomys hottentotus 2 |
| Zea mays | Cryptomys hottentotus damarensis |
| MAGNOLIOPSIDA | |
| Conopholis americana | Damaliscus dorcus |
| Epifagus virginiana | Gazella thomsoni |
| Glycine max | Georychus capensis |
| Nicotiana plumbaginifolia | Gorilla gorilla |
| Nicotiana tabacum 1 | Heliothobius argenteocinereus |
| Nicotiana tabacum 2 | Heterocephalus glaber |
| Pisum sativum 1 | Homo sapiens 1 |
| Pisum sativum 2 | Homo sapiens 2 |
| PROTISTA | |
| ASSEMBLAGE CHLOROBIONTS | |
| CHLOROPHYTA | |
| Chlamydomonas eugametos | Hydropotes inermis |
| Chlamydomonas moewusii | Kobus ellipsiprymnus |
| Chlamydomonas reinhardtii | Madoqua kirki |
| Chlorella ellipoidea | Muntiacus reevesi |
| Chlorella kessleri | Mus musculus |
| Chlorella mirabilis | Odocoileus virginianus |
| Chlorella protothecoides | Oryx gazella |
| Chlorella sorokiniana | Pan paniscus |
| Chlorella vulgaris | Pan troglodytes |
| ASSEMBLAGE CHROMOBIONTS | |
| CHRYSOPHYTA | |
| Ochromonas danica | Petromus typicus |
| Olisthodiscus luteus | Phoca vitulina |
| HAPTOPHYTA | |
| Ochrosphaera spec. | Pongo pigmaeus |
| PHAEOPHYTA | |
| Pylaiella littoralis 1 | Rattus norvegicus 1 |
| ASSEMBLAGE CRYPTOMONADS | |
| CRYPTOPHYTA | |
| Cryptomonas phi | Rattus norvegicus 2 |
| Pyrenomonas salina | Thryonomys swinderianus |
| ASSEMBLAGE EUGLENOZOA | |
| EUGLENOPHYTA | |
| Astasia longa | Tragelaphus imberbis |
| Euglena gracilis | Tragulus napu |
| ASSEMBLAGE RHODOPHYNTHES | |
| RHODOPHYTA | |
| Antithamnion sp. | AVES |
| Cyanidium caldarium | Coturnix japonica |
| MITOCHONDRIA | |
| ANIMALIA | |
| CHORDATA | |
| VERTEBRATA | |
| MAMMALIA | |
| Aepycoerus melampus | Gallus gallus |
| Amblysomus hottentotus | AMPHIBIA |
| | Rana catesbeiana |
| | Xenopus laevis |
| INSECTA | |
| OSTEICHTYES | |
| Crossostoma lacustre | ECHINODERMATA |
| Cyprinus carpio | ECHINOIDEA |
| | Paracentrotus lividus |
| | Strongylocentrotus purpuratus |
| ARTHROPODA | |
| INSECTA | |
| Apis mellifera ligustica | NEMATODA |
| Drosophila virilis | SECERNENTEA |
| Drosophila yakuba | Ascaris suum |
| PLANTAE | |
| BRYOPHYTA | |
| MARCHANTIOPSIDA | |
| Marchantia polymorpha | MAGNOLIOPHYTA |
| LILIOPSIDA | |
| Secale cereale | LILIOPSIDA |
| Triticum aestivum | |

Zea

diploperennis
mays 1
mays 2

MAGNOLIOPSIDA

Glycine max
Lupinus luteus
Oenothera sp.

FUNGI**ASCOMYCOTINA****HEMIASCOMYCETES**

Saccharomyces cerevisiae 1
cerevisiae 2
cerevisiae 3
cerevisiae 4
cerevisiae 5

EUASCOMYCETES

Aspergillus nidulans
Podospora anserina

UNCERTAIN AFFILIATION

Schizosaccharomyces pombe

PROTISTA**ASSEMBLAGE CHLOROBIONTS****CHLOROPHYTA**

Chlamydomonas reinhardtii
Prototheca wickerhamii

ASSEMBLAGE CILIATES**CILIOPHORA**

Paramecium aurelia
primaurelia
tetraurelia
Tetrahymena pyriformis 1
Tetrahymena pyriformis 2

ASSEMBLAGE EUGLENOZOA**KINETOPLASTIDS**

Crithidia fasciculata
Leishmania tarentolae
Leptomonas sp.
Trypanosoma brucei

ASSEMBLAGE SPOROZOA**APICOMPLEXA**

Plasmodium falciparum 1
falciparum 2

(a) Some species names are listed several times followed by a sequential number. This means that the SSU rRNA sequence has been determined several times, usually by different authors. The sequences are not necessarily the same since they may have been determined for different varieties or strains of a species, or for different genes of the same organism. The systematics followed for the three domains are mentioned in the text. Plastidial and mitochondrial structures are listed according to the systematics followed for the host organism. In the case of Archaea and Bacteria, the species name is followed by the culture collection name and number if specified by the author. This number is followed by (T) if it is a type species. Abbreviations of culture collection names can be found in the catalogs of the American Type Culture Collection (ATCC), Deutsche Sammlung von Mikroorganismen (DSM), and Laboratorium voor Microbiologie Universiteit Gent (LMG). The assignment of the archaeal and bacterial species to taxa is based on the tree shown in outline in Fig. 1. These taxa correspond to the divisions and subdivisions distinguished by Woese and coworkers (10–12), except for the bacterial genera *Fibrobacter* and *Fusobacterium*, which form separate clusters and therefore are listed as separate taxa. The taxon of Gram positive bacteria of low GC contents and relatives comprises a number of genera with gram negative cell walls: *Megasphaera*, *Pectinatus*, *Selenomonas*, *Sporomusa*, and *Zymophilus*. For the Archaea, the classification is slightly different from that followed by Olsen and Woese (12), as explained in the text.

(b) Most of the species listed under the heading 'Proteobacteria gamma*' are attributed to the Proteobacteria γ group by Woese (11), although they cluster with the Proteobacteria β in the tree of Fig. 1. Exceptions are *Xanthomonas maltophilia* and *Xylella fastidiosa* which belong to the Proteobacteria β group according to the same author (11).

Table 2. Helix occupancy in eukaryotic SSU rRNAs.

| Taxon & Species ^a | Helices ^b | | | | | | | | | | | | | | E45 | | | |
|--|----------------------|----------|----------|-----|---|---|---|---|---|---|---|---|---|---|-----|----|----|---|
| | E8 1 | E10 1 | E10 2 | E23 | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 1 |
| Insecta | — | * | — | * | * | * | * | * | * | * | * | * | * | * | — | — | — | — |
| Platyhelminthes | — | * | — | * | * | * | * | * | * | * | * | * | * | * | — | — | — | — |
| <i>Schizosaccharomyces pombe</i> | — | * | — | * | * | — | — | * | * | * | * | * | * | * | — | — | — | * |
| (Ascomycotina) | — | * | — | * | * | — | — | * | * | * | * | * | * | * | — | — | — | * |
| <i>Euploites aediculus</i> (Ciliophora) | * | * | — | * | * | — | — | * | * | * | * | * | * | * | — | — | — | * |
| <i>Euglena gracilis</i> (Euglenophyta) | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | — | * | * |
| <i>Bodo caudatus</i> (Kinetoplastidea) | * | * | — | * | * | — | — | * | * | * | * | * | * | * | * | — | — | * |
| <i>Tritrichomonas foetus</i> (Kinetoplastidea) | — | * | — | * | * | — | — | * | * | * | * | * | * | * | — | — | — | * |
| <i>Trypanosoma cruzi</i> (Kinetoplastidea) | * | * | — | * | * | — | — | * | * | * | * | * | * | * | * | * | * | * |
| Other Kinetoplastidea | * | * | — | * | * | — | — | * | * | * | * | * | * | * | * | — | * | * |
| <i>Blastocladia emersonii</i> | — | * | — | * | * | — | — | * | * | * | * | * | * | * | — | — | — | * |
| (Chytridiomycota) | — | * | — | * | * | — | — | * | * | * | * | * | * | * | — | — | — | * |
| <i>Encephalitozoon cuniculi</i> | — | — | — | — | — | — | — | — | — | — | — | * | * | — | — | — | — | — |
| (Microsporidia) | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — |
| <i>Vairimorpha necatrix</i> (Microsporidia) | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — | — |
| <i>Giardia</i> (Polymastigotes) | — | — | — | — | — | — | — | — | — | * | * | * | * | * | — | — | — | — |
| <i>Acanthamoeba castellanii</i> (Amoebozoa) | — | * | — | * | * | — | * | * | * | * | * | * | * | * | — | — | — | * |
| <i>Naegleria gruberi</i> (Amoebozoa) | — | * | * | * | * | — | * | * | * | * | * | * | * | * | — | — | — | * |
| Other Amoebozoa | — | * | — | * | * | — | — | * | * | * | * | * | * | * | — | — | — | * |
| <i>Physarum polycephalum</i> (Eumycetozoa) | * | * | — | * | * | — | * | * | * | * | * | * | * | * | — | — | — | — |
| <i>Babesia</i> (Apicomplexa) | — | * | — | — | * | — | — | * | * | * | * | * | * | * | — | — | — | — |
| <i>Plasmodium</i> (Apicomplexa) | — | * | — | * | * | — | — | * | * | * | * | * | * | * | — | — | — | * |
| Other Eukarya | — | * | — | * | * | — | — | * | * | * | * | * | * | * | — | — | — | — |

(a) In the case of the genera *Giardia*, *Babesia*, and *Plasmodium*, the helix occupancy applies to all species of the genus.

(b) The presence of a helix is indicated by an asterisk. Only eukaryote-specific helices are listed since universal helices are present in all known eukaryotic SSU rRNAs except those of *Vairimorpha necatrix*, which lacks helices 10, 11, 43, and 46 and of *Encephalitozoon cuniculi*, which lacks helices 11, 18, 43, and 46. The structure of the SSU rRNA of the insect *Acyrtosiphon pisum* in area V4 (helices E23-n), which is exceptionally large in this species, is not yet known.

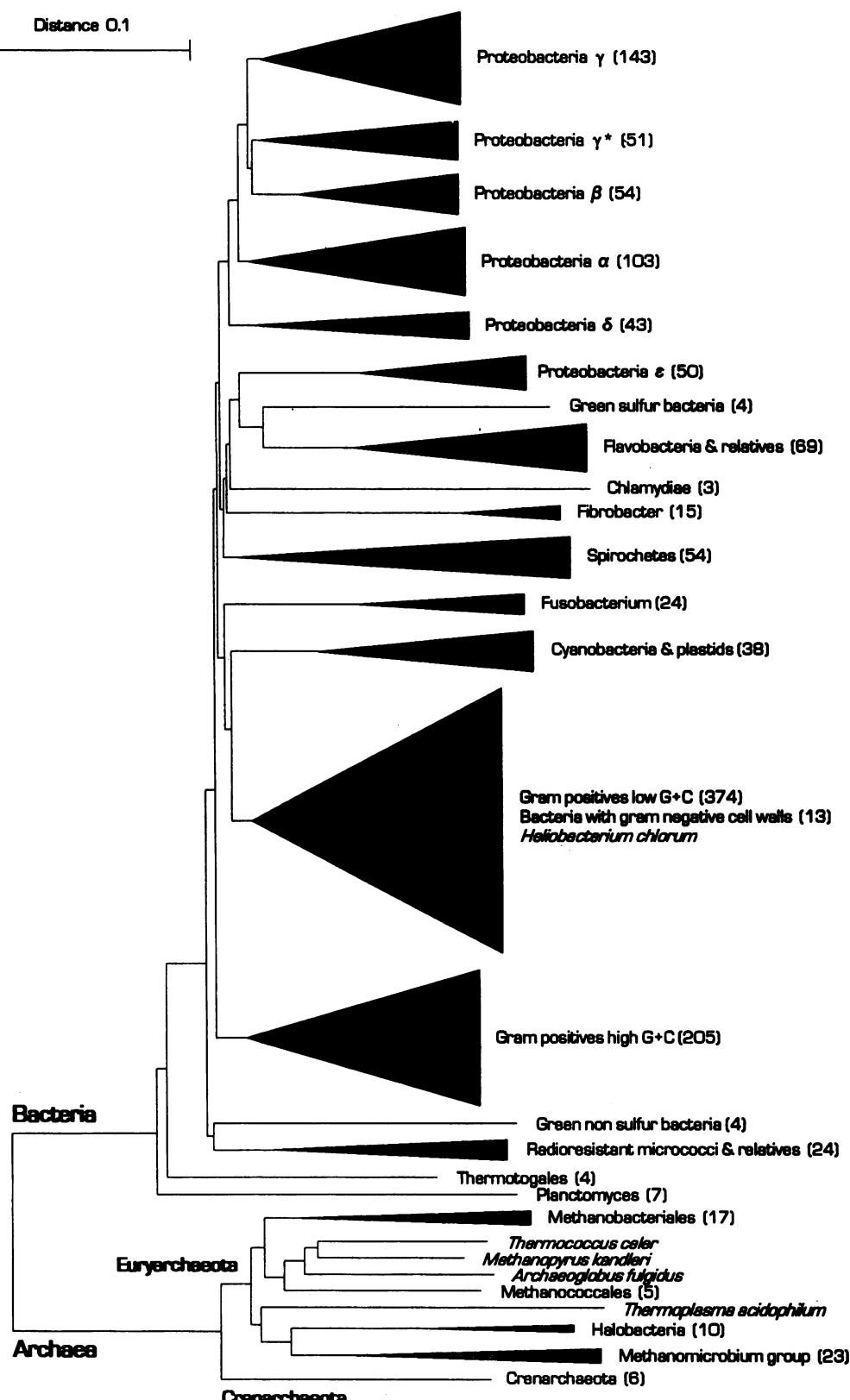


Figure 1. Evolutionary tree reconstructed from archaeal, bacterial and plastidial SSU rRNA sequences. The tree was constructed as described in the text from a total of 1348 SSU rRNA sequences. Clusters distinguishable in the tree are simplified to isosceles triangles with a height approximately equal to the average distance separating the terminal nodes from the deepest branching point within the cluster, and a base proportional to the number of sequences composing it, mentioned in brackets after the taxon name. If a taxon is represented by a single sequence, the species name is mentioned in italics. Each cluster corresponds to a taxon listed in Table 1. The cluster labeled Proteobacteria γ^* is in fact more closely related to the Proteobacteria β than to the Proteobacteria γ in the present tree. However, its position between the latter two clusters is not stable and it consists mainly of species classified as Proteobacteria γ by Woese (11) (see also footnote b to Table 1). The scale on top measures evolutionary distance expressed in substitutions per nucleotide.

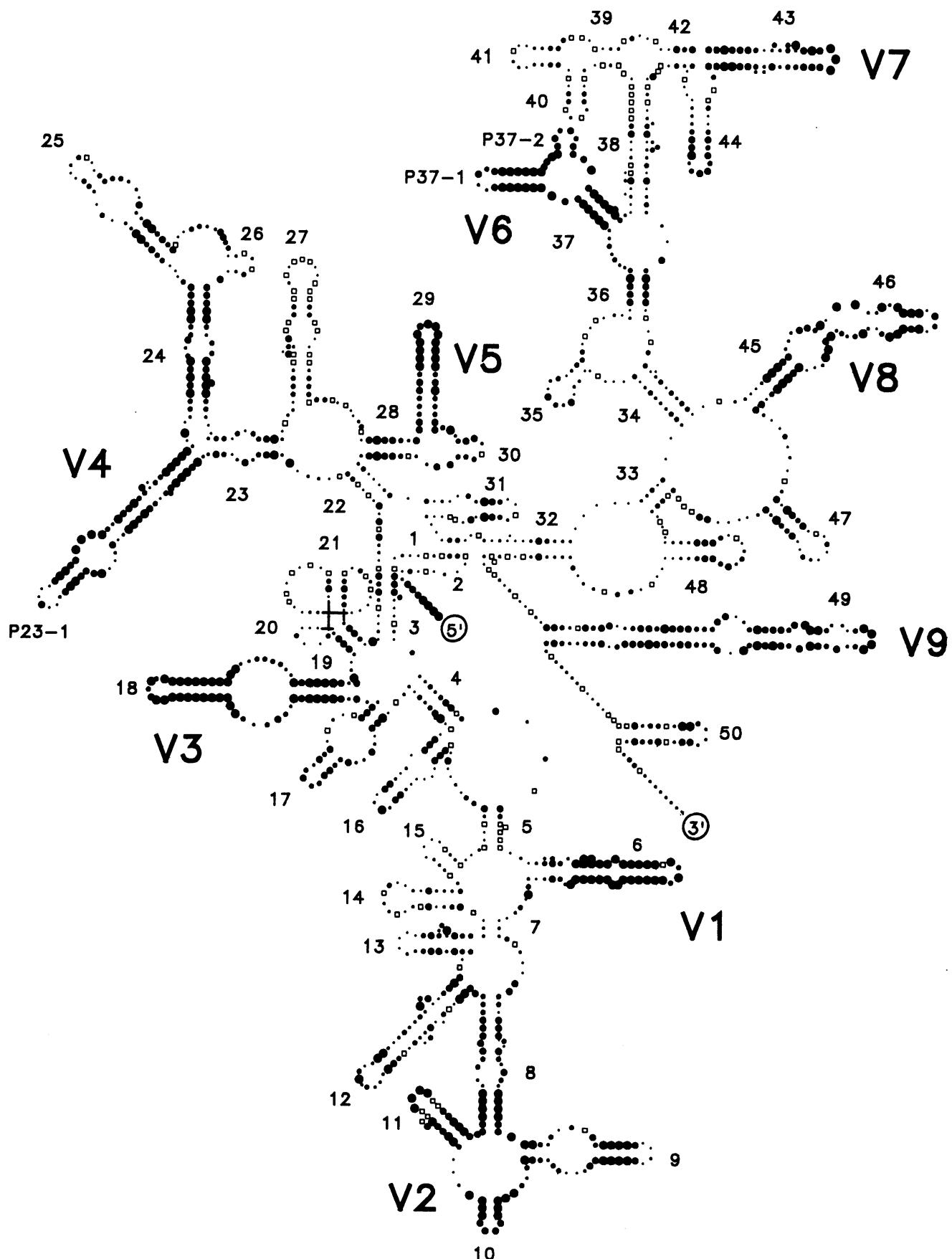


Figure 2. Secondary structure model for prokaryotic SSU rRNAs. Sites are divided into five equally numerous categories of increasing variability, indicated by full circles of increasing diameter. Sites that are invariant among presently known sequences are indicated as hollow squares. Areas containing the most variable sites are labeled V1 to V9. The helices P37-1 and P37-2 are absent in archaeal SSU rRNAs.

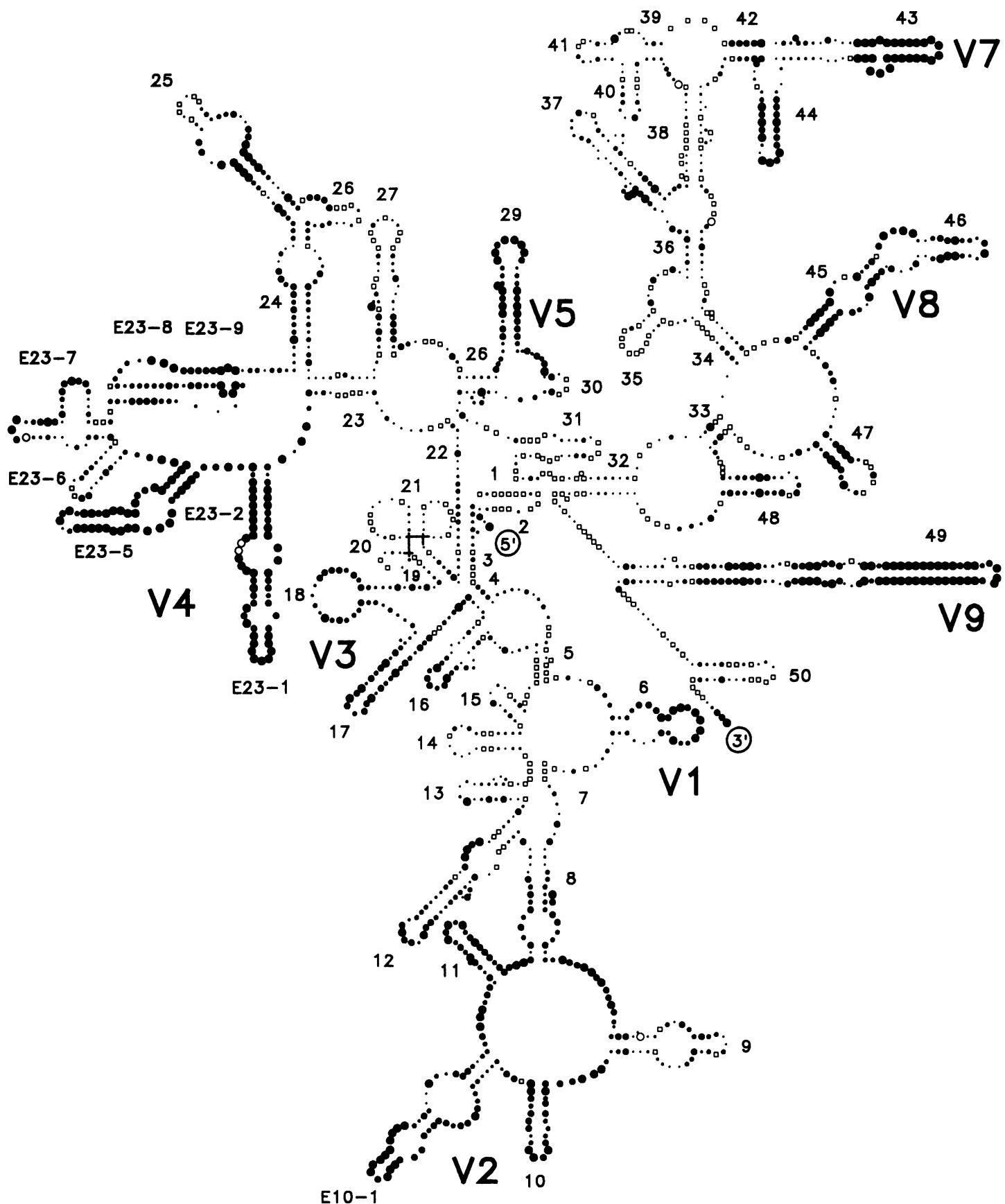


Figure 3. Secondary structure model for eukaryotic SSU rRNAs. Conventions are as in Fig. 2. The shape of the model is based on *Saccharomyces cerevisiae* SSU rRNA, and hollow circles represent nucleotides deleted in most other eukaryotic SSU rRNAs. The area corresponding to V6 in prokaryotic SSU rRNAs is more conserved among eukaryotic SSU rRNAs.

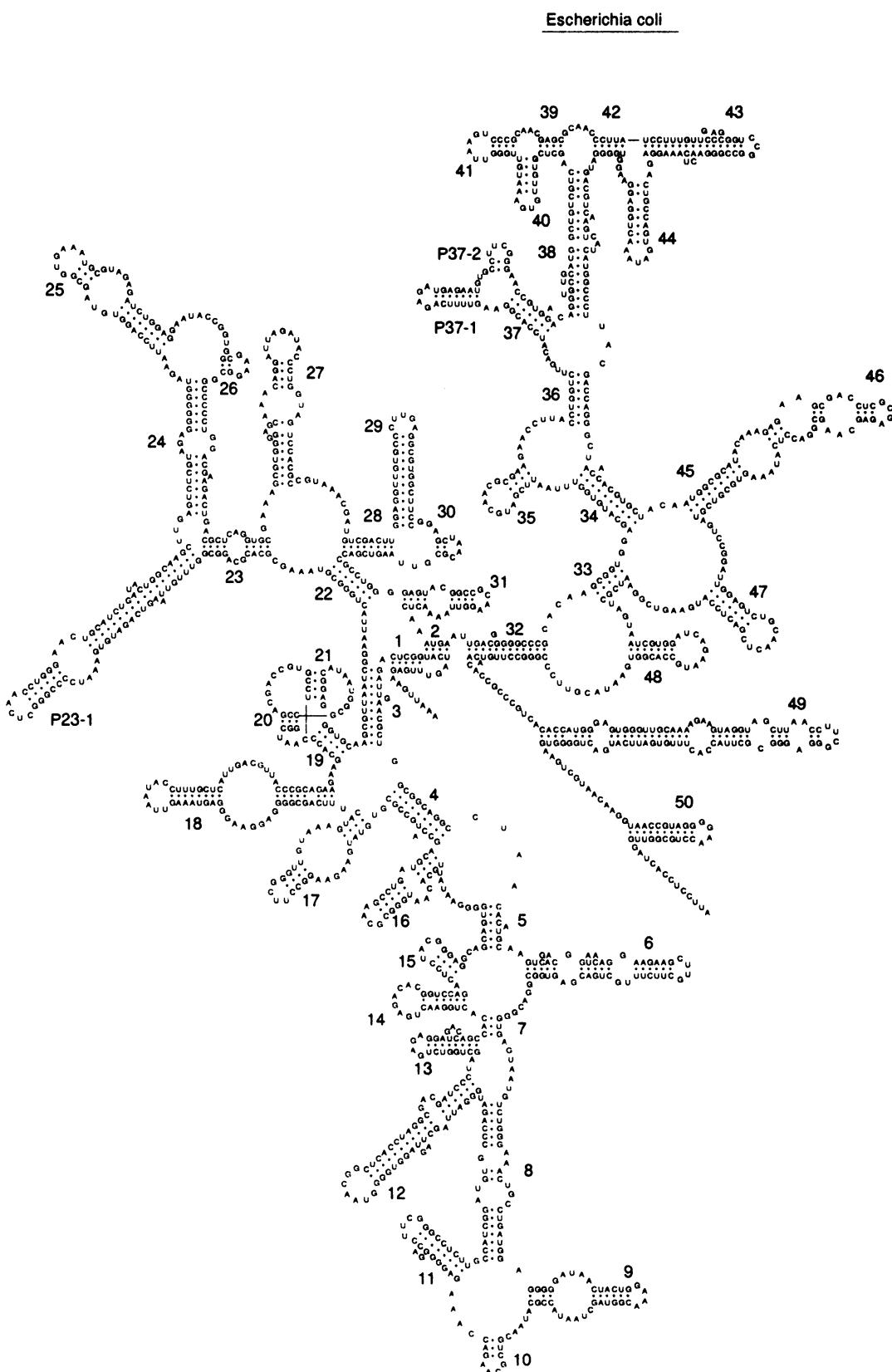


Figure 4. Secondary structure model for SSU rRNA of the bacterium *Escherichia coli*.

Halobacterium halobium

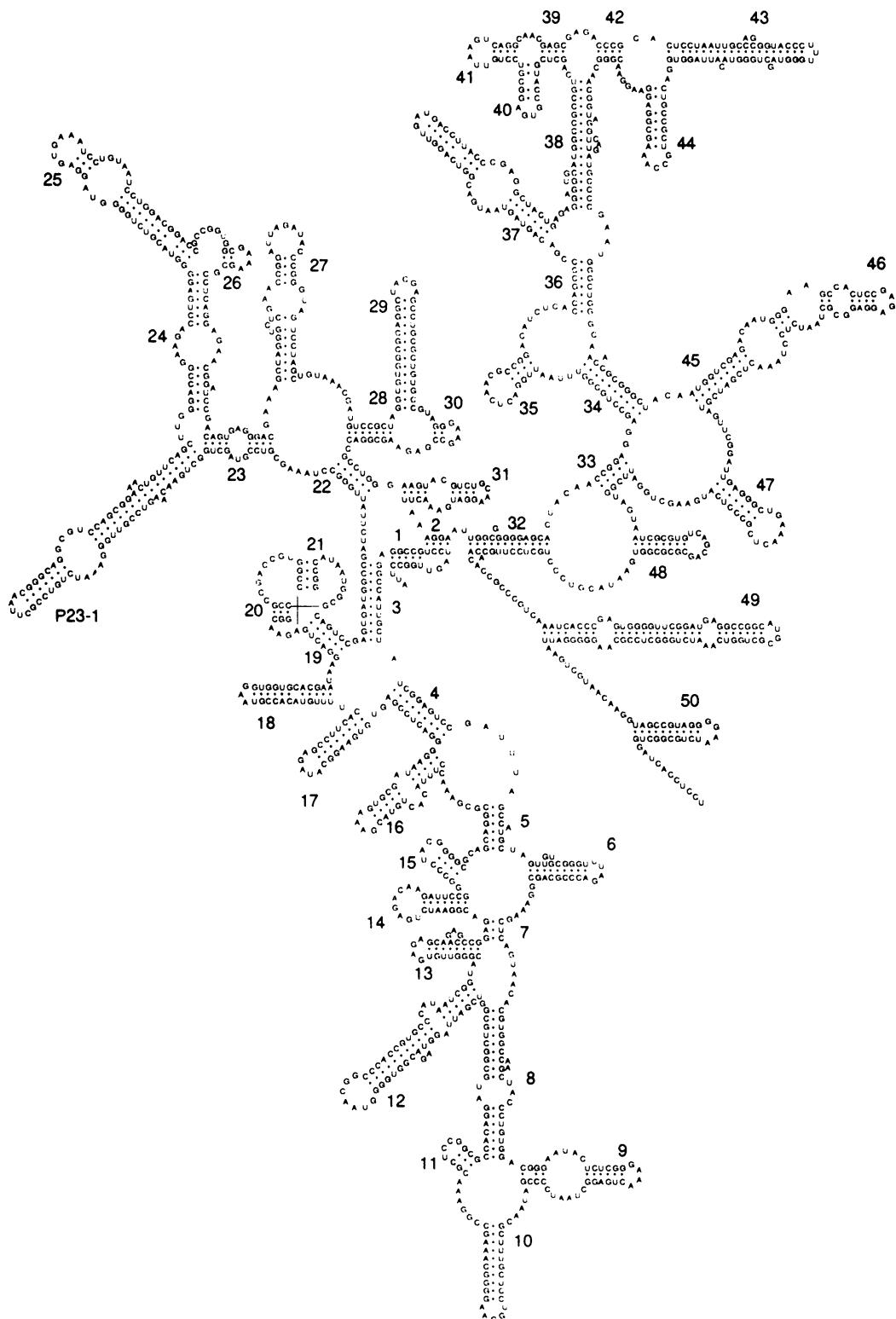


Figure 5. Secondary structure model for SSU rRNA of the archaeabacterium *Halobacterium halobium*.

Palmaria palmata

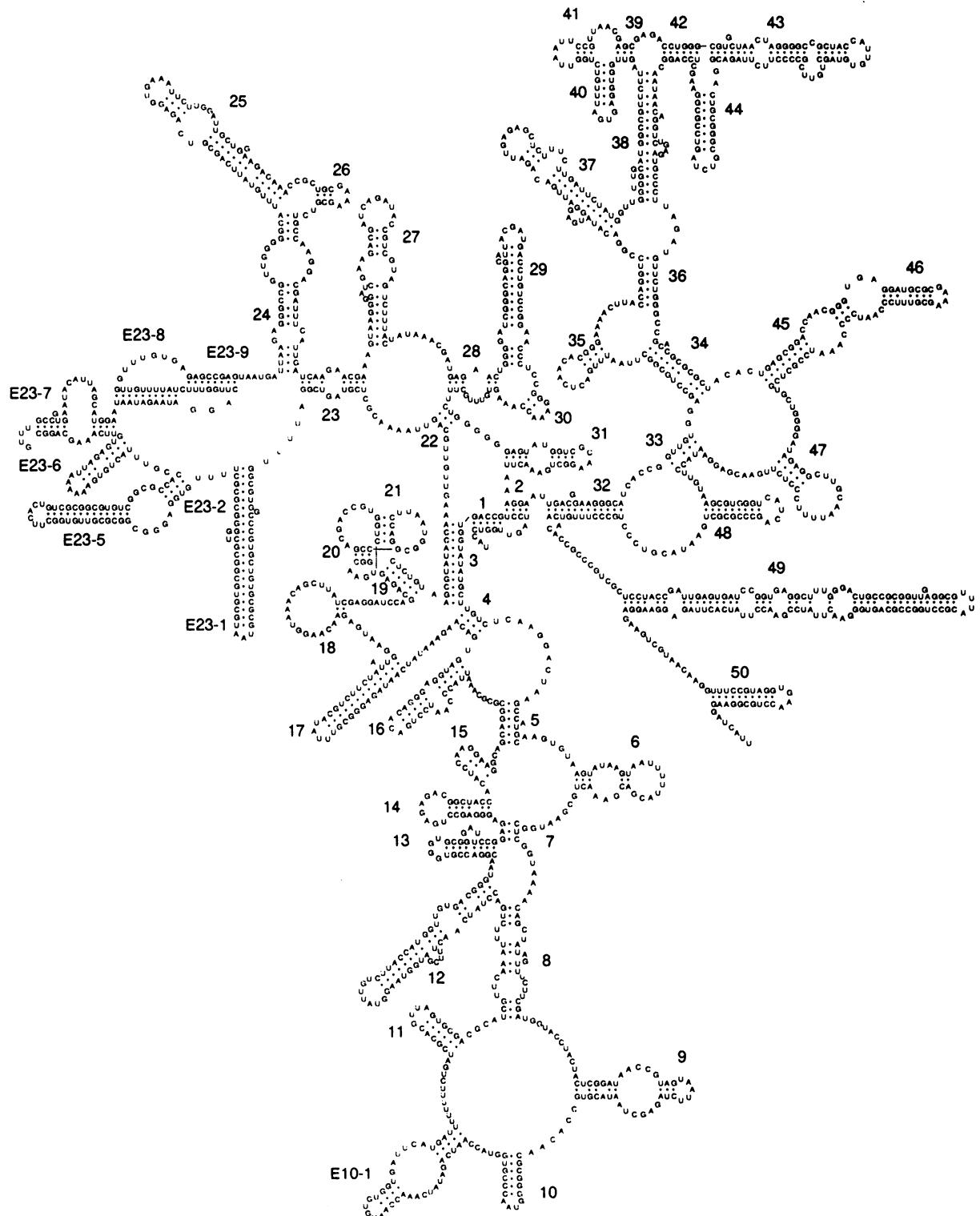


Figure 6. Secondary structure model for SSU rRNA of the red alga *Palmaria palmata*.

Giardia duodenalis

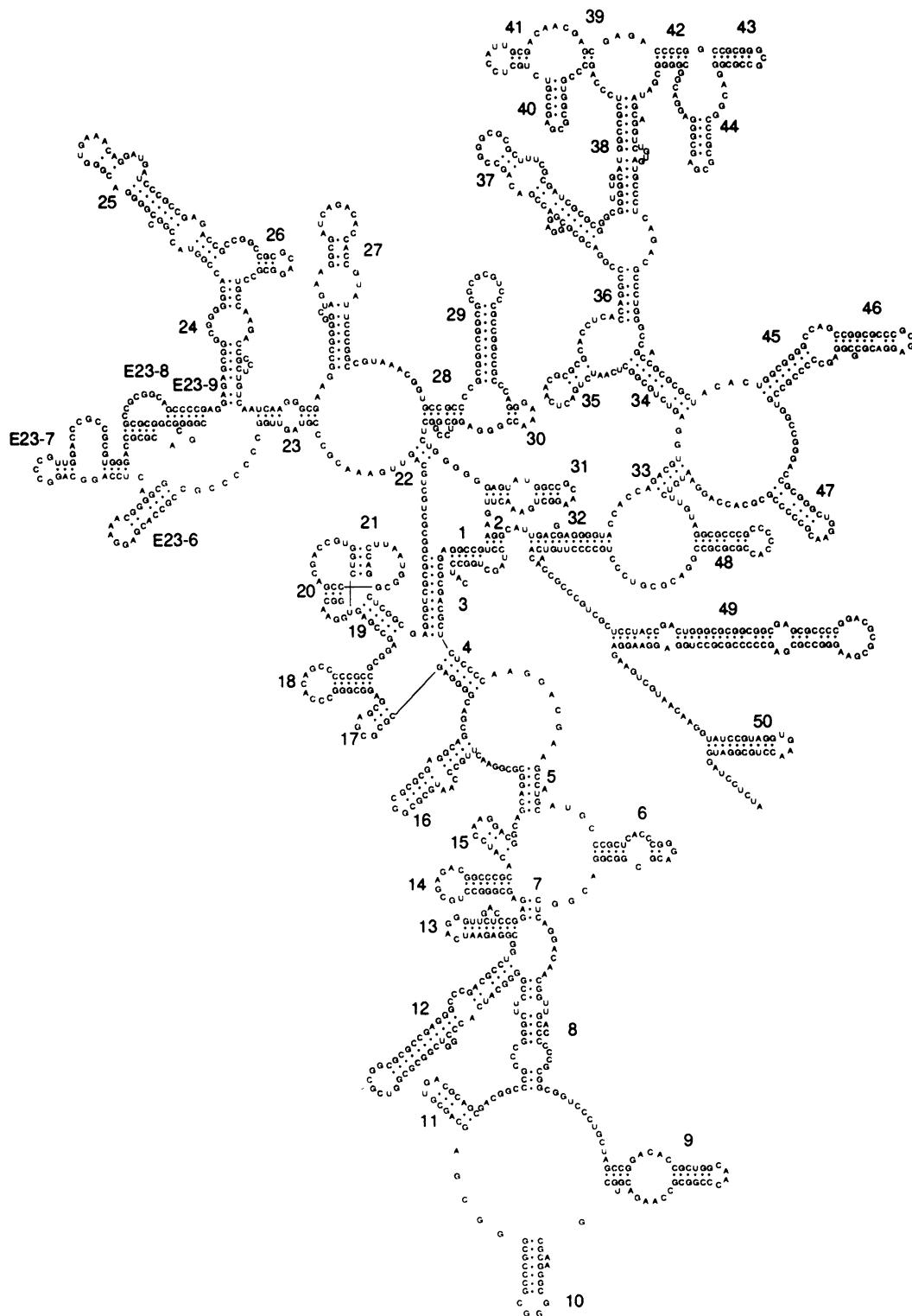


Figure 7. Secondary structure model for SSU rRNA of the polymastigote *Giardia duodenalis*.

Homo sapiens mitochondrion

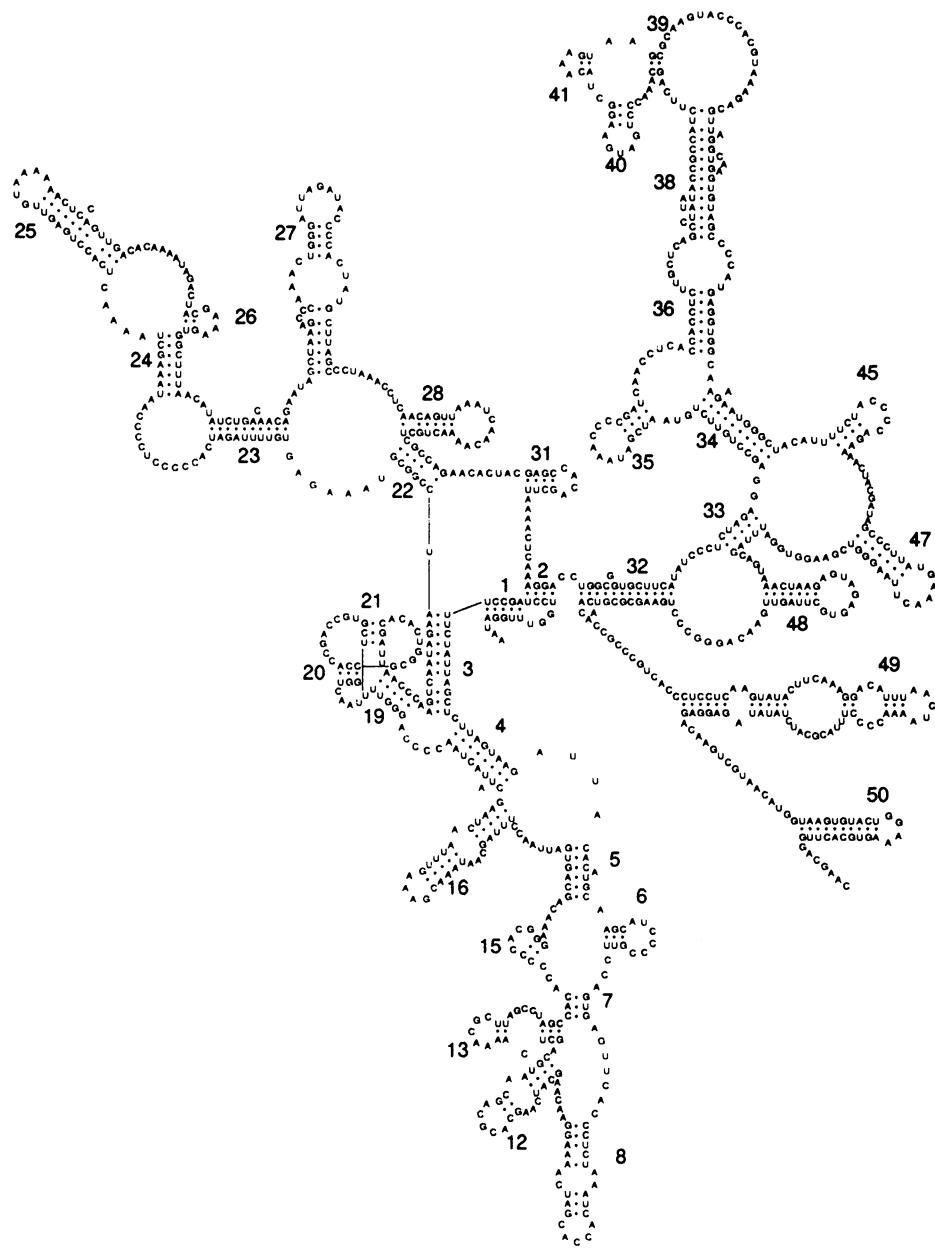


Figure 8. Secondary structure model for SSU rRNA of *Homo sapiens* mitochondrion.