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Compilation of small ribosomal subunit RNA sequences

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INTRODUCTION

The database on small ribosomal subunit RNA (further abbreviated as SSU rRNA) structure has more than doubled in size in one year's time and currently contains 927 aligned sequences. Table 1 only lists the 475 sequences (references 1–475) that were added to the database since publication of the last compilation (476). The latter should be consulted for data and references concerning the sequences entered previously. The total set of 927 entries now consists of 197 eukaryotic cytoplasmic, 21 archaeal, 625 bacterial, 21 plastidial, and 63 mitochondrial SSU rRNAs. This set includes partial sequences, but only if they satisfy the criterion defined in detail in the previous compilation (476) and in footnote (f) of Table 1, in short if the combined lengths of the sequenced segments corresponds to at least 70% of the *Escherichia coli* 16S rRNA sequence.

Sequence alignment is based largely on the adopted secondary structure model, which in turn is corroborated by the observation of compensating substitutions in the alignment. Therefore, the secondary structure model can be gradually refined as more sequences become available. Some improvements to the secondary structure model for eukaryotic SSU rRNAs are described below.

SECONDARY STRUCTURE MODEL

Prokaryotic and eukaryotic models

Fig. 1 shows the prokaryotic secondary structure model, applicable to SSU rRNAs from archaea, bacteria, plastids and mitochondria. The model of Fig. 2 applies to eukaryotic cytoplasmic SSU rRNAs. Areas of conserved primary and secondary structure are drawn in bold lines. Areas of variable primary and secondary structure, drawn in thin lines, are labelled V1 to V9. Variability in secondary structure often consists in extension or reduction in size of helices in some species with respect to others. Long insertions present in a limited number of species result in the presence of extra helices, drawn in broken lines.

The prokaryotic model is identical to the one shown in the previous compilation (476), but the eukaryotic model has been adapted, the changes being enumerated below. The two models are distinguished, even though they have many helices in common, because helix P21, which usually forms variable area V4 of prokaryotic SSU rRNAs, apparently is not homologous to any of the helices E21-1 to E21-10 forming area V4 in eukaryotic SSU rRNAs.

Helix numbering system

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 30). A single number is attributed to 48 '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 that of the microsporidian *Vairimorpha necatrix*, which lacks helices 10, 11, and 44. Additional helices specific to the prokaryotic model (Fig. 1) 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. 2) are similarly numbered Ea-b. 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 the previous compilation (476). 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 sequences are very monotonous due to a high A+U content.

Changes made to the eukaryotic secondary structure model (Fig. 2)

Alignment of additional sequences has brought to light new compensating substitutions, leading to changes in the base pairing scheme adopted for helices 8 and 18. In addition, helices E21-1 to E21-4 of the previous model (476) have been rejected in favour of a different structure, and the numbering of the helices in area V4 was changed in consequence. Table 2 gives the helix occupancy for area V4 of eukaryotic SSU rRNAs according to the new structure and numbering system. Fig. 3 shows the secondary structure presently adopted for *Saccharomyces cerevisiae* SSU rRNA, which is typical for the majority of eukaryotic structures. Fig. 4 shows the new secondary structure for *Drosophila melanogaster* SSU rRNA, which is one of the species containing extra helices E21-3 and E21-4. The structure in the area of helix E21-10 (Fig. 2) remains uncertain. The insert present in this area in a number of species (see Table 2) may

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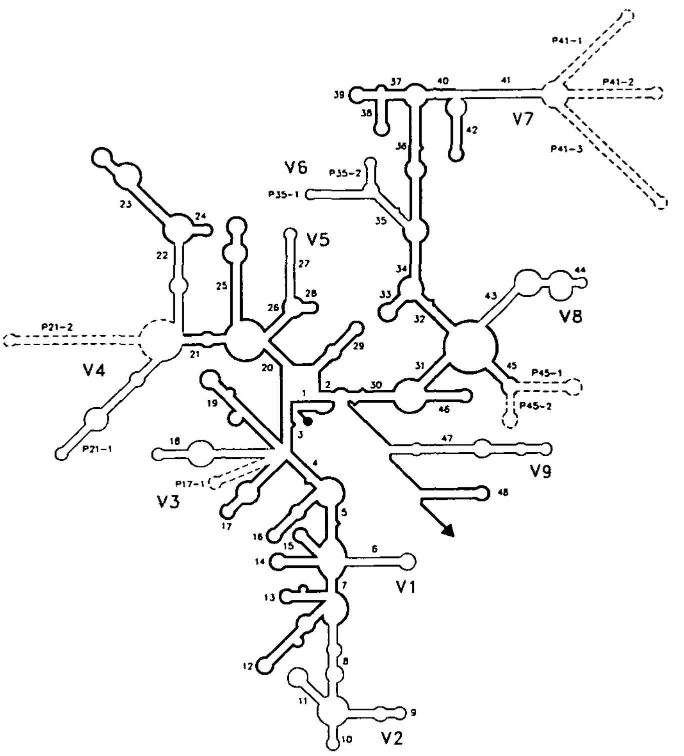

Fig. 1. Secondary structure model for prokaryotic SSU rRNAs. The 5′-terminus is symbolized by a dot, the 3′-terminus by an arrowhead. Helices are numbered in the order of occurrence from 5′- to 3′-terminus. Helices bearing a single number are common to the prokaryotic and eukaryotic (Fig. 2) models. Helices bearing a composite number preceded by P are prokaryote-specific. Areas of relatively conserved structure are drawn in bold lines. Nine variable areas labeled V1 to V9 are drawn in thin lines. Helices drawn in broken lines are present exceptionally.

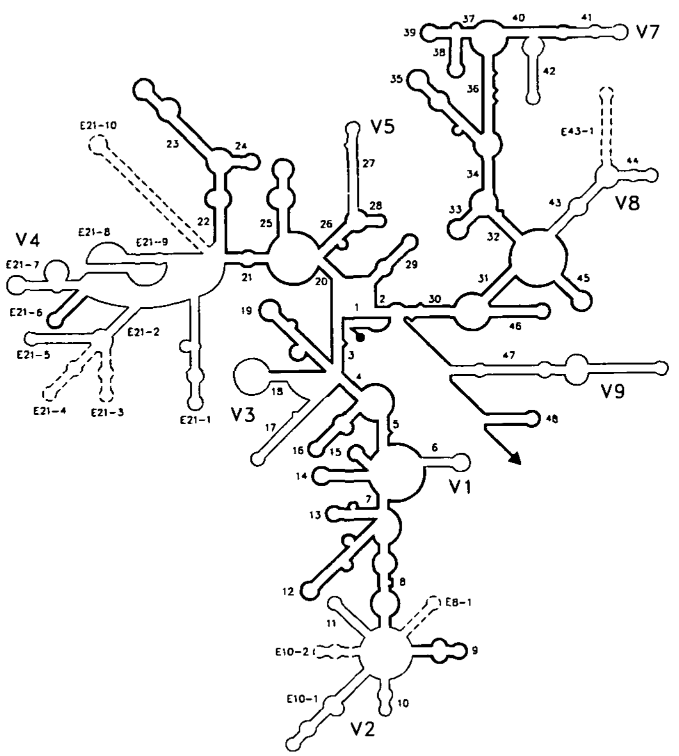

Fig. 2. Secondary structure model for eukaryotic SSU rRNAs. Symbols are as in Fig. 1. Helices bearing a composite number preceded by E are eukaryote-specific. The area corresponding to V6 in Fig. 1 is more conserved among eukaryotic SSU rRNAs. See Table 2 for a complete survey of helix occupancy in known structures.

actually form more than one extra helix, but it is not possible as yet to derive a reliable model on the basis of the available sequences.

COMPLETENESS, ACCURACY, AND AVAILABILITY OF THE DATA

SSU rRNA sequences deposited into the GenBank and EMBL nucleotide sequence libraries are obtained weekly from the EMBL file server by electronic mail. An appropriate set of programs is used for alignment of a new sequence, indication of secondary structure elements by comparison with a closely related sequence, checking the consistency of the postulated secondary structure, and checking for errors by comparison with the original record.

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 these files, each sequence covers 4284 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 structure elements. The alignment is divided into 43 pages each comprising 100 positions containing a nucleotide or a gap. These positions alternate with extra 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 these files.

In addition, there are files containing a taxonomic list of species and general documentation on the database.

The database will be made available through 'anonymous ftp' on host uiam3.uia.ac.be (143.169.8.1). A previous, less complete version of the database was written on the CD-ROM disk distributed in December 1991 by the EMBL nucleotide sequence library at Heidelberg. Updates of the database will be similarly put at the disposal of the EMBL nucleotide sequence library for distribution on future releases of the CD-ROM, and in order to be made available on the EMBL file server as well. 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 inquire about the availability of the database on magnetic media by writing to the authors or by sending an electronic mail message to DEWACHTER@CCV.UIA.AC.BE or to RRNA@CCV.UIA.AC.BE.

Saccharomyces cerevisiae

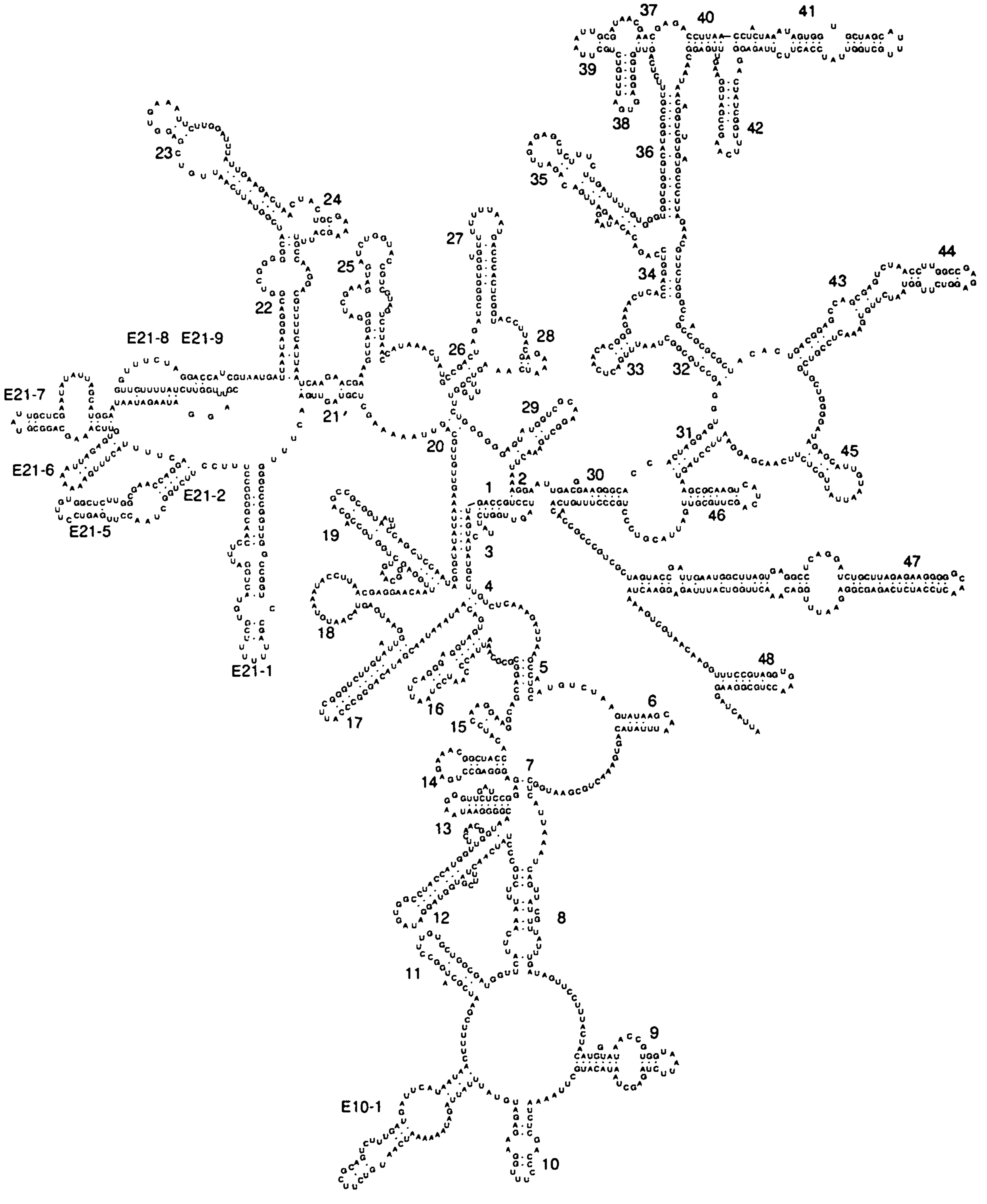

Fig. 3. Secondary structure model for *Saccharomyces cerevisiae* SSU rRNA. With respect to the previously published model (476), a different base pairing scheme has been adopted for helices 8, 18, and the area formed by helices E21-1 to E21-5.

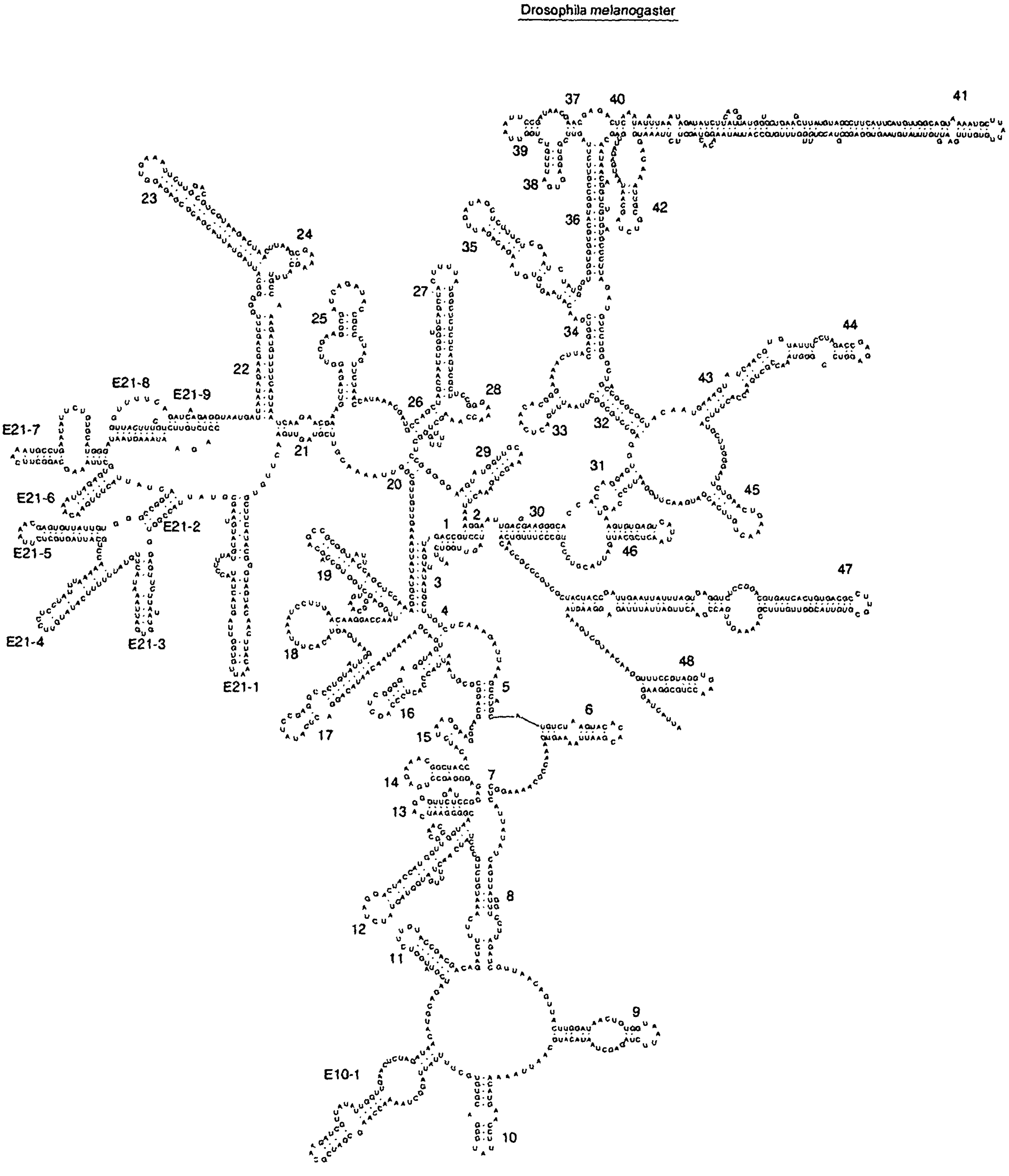

Fig. 4. Secondary structure model for *Drosophila melanogaster* SSU rRNA. With respect to the previously published model (476), a different base pairing scheme has been adopted for helices 8 and 18, while helices E21-1 to E21-5 replace a set of 4 different helices in the older model.

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Table 1. List of SSU rRNA sequences added to the database since publication of the previous compilation (477).

Nr. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)
	EUKARYOTES							
1	Turdus migratorius	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Aves (Cl.)	(1621)	87.9	M59402	RT
2	Alligator mississippiensis	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Reptilia (Cl.)	(1560)	83.6	M59383	RT
3	Heterodon platyrhinos	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Reptilia (Cl.)	(1594)	86.1	M59392	RT
4	Pseudemys scripta	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Reptilia (Cl.)	(1506)	80.2	M59398	RT
5	Sceloporus undulatus	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Reptilia (Cl.)	(1410)	72.2	M59400	RT
6	Ambystoma mexicanum	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1592)	86.1	M59384	RT
7	Amphiuma tridactylum	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1430)	75.9	M59385	RT
8	Bufo valliceps	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1605)	83.3	M59386	RT
9	Discoglossus pictus	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1345)	70.1	M59387	RT
10	Eleutherodactylus cuneatus	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1456)	75.7	M59388	RT
11	Gastrophryne carolinensis	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1489)	79.4	M59390	RT
12	Grandisonia alternans	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1414)	75.0	M59391	RT
13	Hyla cinerea	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1576)	81.6	M59393	RT
14	Ichthyophis bannanicus	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1399)	73.9	M59395	RT
15	Nesomantis thomasseti	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1504)	77.0	M59396	RT
16	Plethodon yonhalossee	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1417)	75.4	M59397	RT
17	Scaphiopus holbrooki	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1410)	75.0	M59399	RT
18	Siren intermedia	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1492)	80.0	M59401	RT
19	Typhlonectes natans	Liver/Ova	Chordata (Ph.), Vertebrata (SPh.)	Amphibia (Cl.)	(1465)	76.5	M59403	RT
20	Latimeria chalumnae	Frozen skeletal muscle	Chordata (Ph.), Vertebrata (SPh.)	Actinistia (Cl.)	(1749)	94.9	no acc	PCR
21	Herdmania momus	Sperm	Chordata (Ph.), Urochordata (SPh.)	Ascidiacea (Cl.)	1803	100.0	X53538	
22	Aedes albopictus	Larvae, cell line ATC-15, Chromosome 3	Arthropoda (Ph.), Uniramia (SPh.)	Insecta (Cl.)	1950	100.0	X57172	
23	Amblyomma americanum		Arthropoda (Ph.), Cheliceriformes (SPh.)	Chelicerata (Cl.)	(1431)	76.5	M60487	PCR
24	Callinectes sapidus		Arthropoda (Ph.), Crustacea (SPh.)	Malacostraca (CL.)	(1522)	83.0	M34360	RT
25	Palaemonetes kadiakensis		Arthropoda (Ph.), Crustacea (SPh.)	Malacostraca (Cl.)	1372	74.8	M34359	RT
26	Penaeus aztecus		Arthropoda (Ph.), Crustacea (SPh.)	Malacostraca (Cl.)	1468	73.7	M34362	RT
27	Procambarus leonensis		Arthropoda (Ph.), Crustacea (SPh.)	Malacostraca (Cl.)	(1699)	89.5	M34363	RT
28	Stenopus hispidus		Arthropoda (Ph.), Crustacea (SPh.)	Malacostraca (Cl.)	1461	76.7	M34361	RT
29	Opisthorchis viverrini	Stage Adult	Platyhelminthes (Ph.)	Trematoda (Cl.)	1992	100.0	X55357	
30	*Schistosoma mansoni*	Strain NMRI	Platyhelminthes (Ph.)	Trematoda (Cl.)	1992	100.0	X53047	
31	Crassostrea virginica	Adult, hemocyte and sperm	Mollusca (Ph.)	Bivalvia (Cl.)	1816	100.0	X60315	PCR
32	Alnus glutinosa	Strain Gaertner, leaves	Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1697)	92.0	X54984	PCR
33	Buckleya distichophylla		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1717)	93.7	X16598	RT
34	Buxus sempervirens		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1646)	90.4	X16599	RT
35	Cornus florida		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1676)	91.1	X17370	RT
36	Cornus racemosa		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1710)	93.6	X16602	RT
37	Dendrophthora domingensis		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1727)	94.2	X16601	RT
38	Euonymus alatus		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1699)	93.1	X16600	RT
39	Hedera helix		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1679)	91.8	X16604	RT
40	Hydrocotyle sibthorpioides		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1647)	89.9	X16605	RT
41	Nyssa sylvatica		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1664)	91.0	X16603	RT
42	Phoradendron serotinum		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1734)	94.5	X16607	RT
43	Schoepfia arenaria		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	(1697)	92.7	X16606	RT
44	Aspergillus fumigatus 1	Strain ATCC 36607, clone sequence	Ascomycotina (Ph.)		1799	100.0	M60300	PCR
45	Aspergillus fumigatus 2	Strain ATCC 36607, rRNA sequence	Ascomycotina (Ph.)		(1630)	88.9	M60301	RT
46	Aspergillus fumigatus 3		Ascomycotina (Ph.)		1798	100.0	M55626	
47	Aureobasidium pullulans	Isolate Y117	Ascomycotina (Ph.)		1800	100.0	M55639	PCR
48	Blastomyces dermatitidis		Ascomycotina (Ph.)		1799	100.0	M55624	
49	Candida albicans 2	Strain MUCL 29800, ATCC 18804	Ascomycotina (Ph.)		1787	100.0	M60302	PCR
50	Candida glabrata 2	Strain MUCL 29833, CBS 138, ATCC 2001	Ascomycotina (Ph.)		(1661)	90.3	M60311	RT
51	Candida parapsilosis	Strain MUCL 29868, CBS 604, ATCC 22019	Ascomycotina (Ph.)		(1633)	89.5	M60307	RT
52	Candida tropicalis 2	Strain CBS 94, ATCC 750	Ascomycotina (Ph.)		(1638)	89.8	M60308	RT
53	Candida viswanathii	Strain MUCL 29893, CBS 4024, ATCC 22891	Ascomycotina (Ph.)		(1607)	87.9	M60309	RT
54	Clavispora lusitaniae 2	Strain ATCC 42720	Ascomycotina (Ph.)		(1603)	89.2	M60306	RT
55	Coccidioides immitis		Ascomycotina (Ph.)		1798	100.0	M55627	
56	Colletotrichum gloeosporioides		Ascomycotina (Ph.)		1795	100.0	M55640	PCR
57	Debaryomyces hansenii	Strain MUCL 29826, CBS 1795	Ascomycotina (Ph.)		1802	100.0	X58053	
58	Dekkera bruxellensis	Strain MUCL 27700, CBS 72, ATCC 10560	Ascomycotina (Ph.)		1799	100.0	X58052	
59	Issatchenkia orientalis 2	Strain MUCL 29849, CBS 573, ATCC 6258	Ascomycotina (Ph.)		(1595)	88.7	M60305	RT
60	Kluyveromyces lactis 2	Strain MUCL 29873, ATCC 4135, CBS 607	Ascomycotina (Ph.)		(1365)	73.2	M60303	RT
61	Penicillium notatum		Ascomycotina (Ph.)		1797	100.0	M55628	
62	Pichia angusta	Strain ATCC 34438, CBS 4732	Ascomycotina (Ph.)		(1632)	89.0	M60310	RT
63	Pichia anomala	Strain MUCL 28639, CBS 5759	Ascomycotina (Ph.)		1795	99.9	X58054	
64	Pichia guilliermondii	Strain MUCL 29837, CBS 566, ATCC 6260	Ascomycotina (Ph.)		(1632)	88.5	M60304	RT
65	Pichia membranaefaciens	Strain MUCL 30004, CBS 107, ATCC 26288	Ascomycotina (Ph.)		1765	99.9	X58055	
66	Schizosaccharomyces pombe 2	Strain MUCL 30245, CBS 356	Ascomycotina (Ph.)		1839	100.0	X58056	
67	Yarrowia lipolytica	Strain MUCL 29853, ATCC 18942, CBS 6124	Ascomycotina (Ph.)		(1521)	88.8	M60312	RT
68	Zygosaccharomyces rouxii	Strain MUCL 30254, CBS 732, ATCC 2623	Ascomycotina (Ph.)		1801	100.0	X58057	
69	Athelia bombacina	Strain ATCC 20629	Basidiomycotina (Ph.)		1809	100.0	M55638	PCR
70	Bullera alba	Strain MUCL 30301, CBS 501, ATCC 18568	Basidiomycotina (Ph.)		1807	100.0	X60179	
71	Filobasidiella neoformans 1	Strain MUCL 30453, CBS 6886, ATCC 28958	Basidiomycotina (Ph.)		1797	100.0	X60183	
72	*Filobasidiella neoformans 2*		Basidiomycotina (Ph.)		(1735)	95.2	M55625	
73	Rhodosporidium toruloides	Strain MUCL 30249, CBS 14, ATCC 15385	Basidiomycotina (Ph.)		1804	100.0	X60180	
74	Sporobolomyces roseus	Strain MUCL 30251, CBS 486, ATCC 24257	Basidiomycotina (Ph.)		1805	99.9	X60181	
75	Trichosporon cutaneum	Strain MUCL 30308, CBS 2466, ATCC 28592	Basidiomycotina (Ph.)		1799	100.0	X60182	

Table 1. continued

Nr. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)
76	Ustilago maydis (i)	Strain MUCL 30488	Basidiomycotina (Ph.)		1798	100.0	X62396	
77	Chlorella sorokiniana	Strain 211-8k (T)	Chlorobionts (assemblage)	Chlorophyta (Ph.)	1796	100.0	X62441	
78	Mallomonas papillosa	Strain CCMP A3807	Chromobionts (assemblage)	Chrysophyta (Ph.)	1790	100.0	M55285	PCR
79	Tribonema aequale	Strain UTEX 50	Chromobionts (assemblage)	Xanthophyta (Ph.)	1829	100.0	M55286	PCR
80	Neocallimastix joyonii	Strain NJ1	Mastigomycetes (assemblage)	Chytridiomycota (Ph.)	(1513)	82.6	M62705	
81	Neocallimastix frontalis	Strain MCH3	Mastigomycetes (assemblage)	Chytridiomycota (Ph.)	(1509)	82.3	M62704	
82	Piromonas communis	Strain FL	Mastigomycetes (assemblage)	Chytridiomycota (Ph.)	(1502)	81.8	M62706	
83	Colpidium campylum		Ciliates (assemblage)	Ciliophora (Ph.)	(1708)	96.2	X56532	PCR
84	Glaucoma chattoni		Ciliates (assemblage)	Ciliophora (Ph.)	(1695)	96.0	X56533	PCR
85	Onychodromus quadricornutus		Ciliates (assemblage)	Ciliophora (Ph.)	1771	100.0	X53485	PCR
86	Opisthonecta henneguyi	Strain ATTC 30600	Ciliates (assemblage)	Ciliophora (Ph.)	(1686)	96.2	X56531	PCR
87	Oxytricha granulifera		Ciliates (assemblage)	Ciliophora (Ph.)	1778	100.0	X53486	PCR
88	Crypthecodinium cohnii		Dinoflagellates (assemblage)	Peridinea (Ph.)	1796	100.0	M64245	PCR
89	Plasmodium fragile		Sporozoa (assemblage)	Sporozoa (Ph.)	(2071)	98.9	M61722	
90	Plasmodium gallinaceum		Sporozoa (assemblage)	Sporozoa (Ph.)	(2102)	98.4	M61723	
91	Plasmodium malariae	Strain Uganda-I-CDC	Sporozoa (assemblage)	Sporozoa (Ph.)	2147	100.0	M54897	
92	Sarcocystis muris		Sporozoa (assemblage)	Sporozoa (Ph.)	1809	100.0	M64244	PCR
93	Theileria annulata		Sporozoa (assemblage)	Sporozoa (Ph.)	1744	100.0	M64243	PCR
94	Cryptomonas phi 1	Nuclei	Cryptomonads (assemblage)	Cryptophyta (Ph.)	1773	100.0	X57162	PCR
95	Cryptomonas phi 2	Nucleomorph	Cryptomonads (assemblage)	Cryptophyta (Ph.)	2039	100.0	X57008	PCR
96	Pyrenomonas salina 1	Nuclei	Cryptomonads (assemblage)	Cryptophyta (Ph.)	1762	100.0	X54276	
97	Pyrenomonas salina 2	Nucleomorph	Cryptomonads (assemblage)	Cryptophyta (Ph.)	1884	99.9	X55032	
98	Babesia bigemina 1	Erythrocytes	Microsporidia (assemblage)	Microsporidia (Ph.)	1693	100.0	X59604	
99	Babesia bigemina 2	Erythrocytes	Microsporidia (assemblage)	Microsporidia (Ph.)	1693	100.0	X59605	
100	Babesia bigemina 3	Erythrocytes	Microsporidia (assemblage)	Microsporidia (Ph.)	1693	100.0	X59607	
	ARCHAEBACTERIA							
101	Halobacterium marismortui 1	Clone pHC8, operon rrnA	Halobacteria		1472	100.0	X61688	
102	Halobacterium marismortui 2	Clone HH10, operon rrnB	Halobacteria		1472	100.0	X61689	
	EUBACTERIA							
103	Afipia clevelandensis	CCI Strain B91-007353	Proteobacteria	Alpha group	(1420)	95.5	M69186	RT
104	Afipia felis	Strain B91-007352, ATCC 53690	Proteobacteria	Alpha group	(1420)	95.5	M65248	RT
105	Alpha-proteobacterium 1		Proteobacteria	Alpha group	(1269)	87.8	M63810	PCR
106	Alpha-proteobacterium 2		Proteobacteria	Alpha group	(1293)	87.5	M63812	PCR
107	Anaplasma marginale		Proteobacteria	Alpha group	1493	99.9	M60313	PCR
108	Ancylobacter aquaticus	Strain ATCC 25396	Proteobacteria	Alpha group	(1420)	95.6	M62790	
109	Aquaspirillum magnetotacticum	Strain MS1, ATCC 31632	Proteobacteria	Alpha group	(1402)	94.6	M58171	PCR
110	Bartonella bacilliformis 1	Strain ATCC 35685	Proteobacteria	Alpha group	(1419)	95.4	M65249	RT
111	Bartonella bacilliformis 2	Strain NCTC 12138	Proteobacteria	Alpha group	(1393)	94.0	X60042	
112	Rhodobacter capsulatus 2		Proteobacteria	Alpha group	(1380)	93.1	M60671	
113	Rhodobacter sphaeroides 1	Strain 2.4.1, operon rrnA	Proteobacteria	Alpha group	1466	100.0	X53853	
114	Rhodobacter sphaeroides 2	Strain 2.4.1, operon rrnB	Proteobacteria	Alpha group	1466	100.0	X53854	
115	Rhodobacter sphaeroides 3	Strain 2.4.1, operon rrnC	Proteobacteria	Alpha group	1466	100.0	X53855	
116	Kingella indologenes	Strain ATCC 25869 (T)	Proteobacteria	Beta group	(1464)	95.8	M35015	RT
117	Neisseria denitrificans	Strain ATCC 14686 (T)	Proteobacteria	Beta group	(1467)	95.2	M35020	RT
118	Actinobacillus actinomycetemcomitans 1		Proteobacteria	Gamma group	(1478)	96.0	M75037	
119	Actinobacillus actinomycetemcomitans 2		Proteobacteria	Gamma group	(1468)	95.3	M75038	
120	Actinobacillus actinomycetemcomitans 3		Proteobacteria	Gamma group	(1477)	95.7	M75039	
121	Actinobacillus actinomycetemcomitans 4		Proteobacteria	Gamma group	(1476)	95.8	M75035	
122	Actinobacillus actinomycetemcomitans 5		Proteobacteria	Gamma group	(1472)	95.7	M75036	
123	Actinobacillus capsulatus 1		Proteobacteria	Gamma group	(1457)	94.7	M75062	
124	Actinobacillus capsulatus 2		Proteobacteria	Gamma group	(1475)	95.8	M75067	
125	Actinobacillus capsulatus 3		Proteobacteria	Gamma group	(1462)	95.0	M75069	
126	Actinobacillus equuli		Proteobacteria	Gamma group	(1464)	95.1	M75072	
127	Actinobacillus lignieresii 1	Strain ATCC 19393 (T)	Proteobacteria	Gamma group	(1456)	93.8	M35017	RT
128	Actinobacillus lignieresii 2		Proteobacteria	Gamma group	(1481)	96.1	M75068	
129	Actinobacillus pleuropneumoniae		Proteobacteria	Gamma group	(1464)	95.0	M75074	
130	Actinobacillus seminis		Proteobacteria	Gamma group	(1465)	95.0	M75047	
131	Actinobacillus suis		Proteobacteria	Gamma group	(1459)	94.8	M75071	
132	Actinobacillus ureae		Proteobacteria	Gamma group	(1459)	94.8	M75075	
133	Bacteroides nodosus	Strain 198A	Proteobacteria	Gamma group	1529	99.8	M35016	RT
134	Cardiobacterium hominis	Strain ATCC 16826 (T)	Proteobacteria	Gamma group	(1466)	95.7	M35014	RT
135	Gamma-proteobacterium		Proteobacteria	Gamma group	(1347)	87.5	M63811	PCR
136	Haemophilus aegyptius		Proteobacteria	Gamma group	(1457)	94.7	M75044	
137	Haemophilus aphrophilus		Proteobacteria	Gamma group	(1463)	95.1	M75041	
138	Haemophilus ducreyi 1	Strain CIP 542 (T)	Proteobacteria	Gamma group	(1495)	97.1	M63900	PCR
139	Haemophilus ducreyi 2		Proteobacteria	Gamma group	(1471)	95.5	M75078	
140	Haemophilus ducreyi 3		Proteobacteria	Gamma group	(1457)	94.6	M75079	
141	Haemophilus ducreyi 4		Proteobacteria	Gamma group	(1467)	95.3	M75084	
142	Haemophilus haemoglobinophilus		Proteobacteria	Gamma group	(1469)	95.5	M75064	
143	Haemophilus haemolyticus		Proteobacteria	Gamma group	(1450)	94.3	M75045	
144	Haemophilus influenzae	Strain ATCC 33391 (T)	Proteobacteria	Gamma group	(1480)	96.0	M35019	RT
145	Haemophilus paracuniculus		Proteobacteria	Gamma group	(1467)	95.4	M75061	
146	Haemophilus parahaemolyticus		Proteobacteria	Gamma group	(1455)	94.3	M75073	
147	Haemophilus parainfluenzae 1		Proteobacteria	Gamma group	(1465)	95.2	M75040	

Table 1. continued

Nr. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)
148	Haemophilus parainfluenzae 2		Proteobacteria	Gamma group	(1459)	94.6	M75081	
149	Haemophilus paraphrophaemolyticus		Proteobacteria	Gamma group	(1449)	94.3	M75076	
150	Haemophilus paraphrophilus 1		Proteobacteria	Gamma group	(1457)	94.7	M75042	
151	Haemophilus paraphrophilus 2		Proteobacteria	Gamma group	(1452)	94.1	M75082	
152	Haemophilus parasuis 1		Proteobacteria	Gamma group	(1463)	95.1	M75065	
153	Haemophilus parasuis 2		Proteobacteria	Gamma group	(1467)	95.3	M75066	
154	Haemophilus segnis		Proteobacteria	Gamma group	(1458)	94.8	M75043	
155	Haemophilus sp.		Proteobacteria	Gamma group	(1479)	95.7	M75077	
156	Haemophilus taxon C		Proteobacteria	Gamma group	(1475)	95.7	M75056	
157	Legionella bozemanii	Strain NCTC 11368	Proteobacteria	Gamma group	(1393)	89.7	M36031	RT
158	Legionella erythra	Strain NCTC 11977	Proteobacteria	Gamma group	(1389)	89.5	M36027	RT
159	Legionella hackeliae	Strain NCTC 11979	Proteobacteria	Gamma group	(1416)	91.4	M36028	RT
160	Legionella longbeachae	Strain NCTC 11477	Proteobacteria	Gamma group	(1426)	92.3	M36029	RT
161	Legionella pneumophila 1	Strain NCTC 11192	Proteobacteria	Gamma group	(1425)	92.0	M36023	RT
162	Legionella pneumophila 2	Strain NCTC 11286	Proteobacteria	Gamma group	(1420)	91.7	M36024	RT
163	Legionella pneumophila 3	Strain NCTC 11233	Proteobacteria	Gamma group	(1406)	90.6	M36025	RT
164	Legionella pneumophila 4	Strain NCTC 11405	Proteobacteria	Gamma group	(1411)	90.9	M36026	RT
165	Legionella spiritensis	Strain NCTC 11990	Proteobacteria	Gamma group	(1424)	92.2	M36030	RT
166	Oceanospirillum linum	Strain ATCC 11336 (T)	Proteobacteria	Gamma group	(1511)	97.1	M22365	
167	Pasteurella aerogenes		Proteobacteria	Gamma group	(1461)	94.8	M75048	
168	Pasteurella anatis		Proteobacteria	Gamma group	(1469)	95.6	M75054	
169	Pasteurella canis		Proteobacteria	Gamma group	(1466)	94.7	M75049	
170	Pasteurella dagmatis		Proteobacteria	Gamma group	(1475)	95.7	M75051	
171	Pasteurella gallinarum		Proteobacteria	Gamma group	(1469)	94.9	M75059	
172	Pasteurella haemolytica 1		Proteobacteria	Gamma group	(1469)	95.5	M75063	
173	Pasteurella haemolytica 2		Proteobacteria	Gamma group	(1462)	95.0	M75080	
174	Pasteurella langaa		Proteobacteria	Gamma group	(1463)	95.1	M75053	
175	Pasteurella multocida	Strain NCTC 10322 (T)	Proteobacteria	Gamma group	(1500)	96.4	M35018	RT
176	Pasteurella pneumotropica		Proteobacteria	Gamma group	(1464)	95.5	M75083	
177	Pasteurella sp. 1		Proteobacteria	Gamma group	(1482)	96.2	M75052	
178	Pasteurella sp. 2		Proteobacteria	Gamma group	(1470)	95.4	M75055	
179	Pasteurella stomatis		Proteobacteria	Gamma group	(1454)	94.4	M75050	
180	Pasteurella volantium 1		Proteobacteria	Gamma group	(1460)	94.4	M75060	
181	Pasteurella volantium 2		Proteobacteria	Gamma group	(1473)	95.5	M75070	
182	Serratia entomophila	Strain ATCC 43705	Proteobacteria	Gamma group	(1495)	97.3	no Acc	RT
183	Serratia ficaria	Strain G4024, ATCC 33105	Proteobacteria	Gamma group	(1483)	96.5	no Acc	RT
184	Serratia fonticola	Strain G3965, ATCC 29844	Proteobacteria	Gamma group	(1486)	96.6	no Acc	RT
185	Serratia grimesii	Strain G503, ATCC 14460	Proteobacteria	Gamma group	(1499)	97.4	no Acc	RT
186	Serratia liquefaciens	Strain G866, ATCC 27592	Proteobacteria	Gamma group	(1490)	97.0	no Acc	RT
187	Serratia marcescens	Strain G504, ATCC 13880	Proteobacteria	Gamma group	(1491)	97.3	no Acc	RT
188	Serratia odorifera	Strain G1073, ATCC 33077	Proteobacteria	Gamma group	(1491)	97.0	no Acc	RT
189	Serratia plymuthica	Strain G510, ATCC 183	Proteobacteria	Gamma group	(1490)	96.7	no Acc	RT
190	Serratia proteamaculans	Strain G3630, ATCC 19323	Proteobacteria	Gamma group	(1491)	97.0	no Acc	RT
191	Serratia rubidaea	Strain G864, ATCC 27593	Proteobacteria	Gamma group	(1494)	97.2	no Acc	RT
192	Vibrio harveyi		Proteobacteria	Gamma group	(1268)	82.7	M58172	
193	Campylobacter coli		Proteobacteria	Uncertain affiliation	(1379)	91.2	no acc	
194	Campylobacter fetus subsp. fetus	Strain ATCC 27374	Proteobacteria	Uncertain affiliation	(1447)	95.6	M65012	
195	Campylobacter fetus subsp. venerealis	Strain ATCC 19438	Proteobacteria	Uncertain affiliation	(1423)	94.2	M65011	
196	Campylobacter hyointestinalis 1	Strain NADC 2006	Proteobacteria	Uncertain affiliation	(1446)	95.6	M65009	
197	Campylobacter hyointestinalis 2	Strain ATCC 35217	Proteobacteria	Uncertain affiliation	(1448)	95.3	M65010	
198	Campylobacter jejuni		Proteobacteria	Uncertain affiliation	(1437)	94.9	no acc	
199	Fibrobacter intestinales 1	Strain JG1	Proteobacteria	Uncertain affiliation	(1347)	88.5	M62690	
200	Fibrobacter intestinales 2	Strain LH1	Proteobacteria	Uncertain affiliation	(1344)	88.3	M62691	
201	Fibrobacter intestinales 3	Strain NR9	Proteobacteria	Uncertain affiliation	(1349)	88.4	M62695	
202	Fibrobacter intestinales 4	Strain C1a	Proteobacteria	Uncertain affiliation	(1332)	87.3	M62686	
203	Fibrobacter intestinales 5	Strain DR7	Proteobacteria	Uncertain affiliation	(1337)	87.9	M62687	
204	Fibrobacter succinogenes 1	Strain REH9-1	Proteobacteria	Uncertain affiliation	(1142)	75.1	M62682	
205	Fibrobacter succinogenes 2	Strain A3C	Proteobacteria	Uncertain affiliation	(1329)	87.5	M62683	
206	Fibrobacter succinogenes 3	Strain B1	Proteobacteria	Uncertain affiliation	(1328)	87.7	M62684	
207	Fibrobacter succinogenes 4	Strain BL2	Proteobacteria	Uncertain affiliation	(1344)	88.7	M62685	
208	Fibrobacter succinogenes 5	Strain GC5	Proteobacteria	Uncertain affiliation	(1333)	88.1	M62688	
209	Fibrobacter succinogenes 6	Strain HM2	Proteobacteria	Uncertain affiliation	(1335)	88.0	M62689	
210	Fibrobacter succinogenes 7	Strain MB4	Proteobacteria	Uncertain affiliation	(1319)	87.2	M62692	
211	Fibrobacter succinogenes 8	Strain MC1	Proteobacteria	Uncertain affiliation	(1332)	88.1	M62693	
212	Fibrobacter succinogenes 9	Strain MM4	Proteobacteria	Uncertain affiliation	(1328)	87.8	M62694	
213	Fibrobacter succinogenes 10	Strain S85	Proteobacteria	Uncertain affiliation	(1428)	94.1	M62696	
214	Helicobacter felis 1	Strain CS1 (T)	Proteobacteria	Uncertain affiliation	(1413)	94.6	M57398	
215	Helicobacter felis 2	Strain DS3	Proteobacteria	Uncertain affiliation	(1434)	95.8	M37643	RT
216	Bacillus acidoterrestris	Strain DSM 3922	Firmicuta	Low G+C	(1415)	91.2	X60602	
217	Bacillus alcalophilus	Strain DSM 485	Firmicuta	Low G+C	(1419)	91.6	X60603	
218	Bacillus alvei 1	Strain ATCC 6344	Firmicuta	Low G+C	(1379)	89.4	X57304	
219	Bacillus alvei 2	Strain NCDO 1153	Firmicuta	Low G+C	(1332)	85.5	X60604	
220	Bacillus amyloliquefaciens	Strain ATCC 23350	Firmicuta	Low G+C	(1409)	91.2	X60605	
221	Bacillus amylolyticus	Strain NCIMB 8144	Firmicuta	Low G+C	(1389)	89.4	X60606	
222	Bacillus aneurinolyticus	Strain NCIMB 10056	Firmicuta	Low G+C	(1407)	91.5	X60645	
223	Bacillus atrophaeus	Strain NCIMB 12899	Firmicuta	Low G+C	(1334)	86.3	X60607	

Table 1. continued

Nr. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)
224	Bacillus azotofixans	Strain ATCC 35681	Firmicuta	Low G+C	(1378)	88.8	X60608	
225	Bacillus azotoformans	Strain ATCC 29788	Firmicuta	Low G+C	(1343)	87.0	X60609	
226	Bacillus badius	Strain NCDO 1760	Firmicuta	Low G+C	(1386)	89.3	X60610	
227	Bacillus benzeovorans	Strain NCIMB 12555	Firmicuta	Low G+C	(1420)	91.7	X60611	
228	Bacillus brevis	Strain NCIMB 9372	Firmicuta	Low G+C	(1383)	90.1	X60612	
229	Bacillus circulans	Strain NCDO 1775	Firmicuta	Low G+C	(1374)	89.0	X60613	
230	Bacillus coagulans	Strain NCDO 1761	Firmicuta	Low G+C	(1394)	90.1	X60614	
231	Bacillus fastidiosus	Strain DSM 91	Firmicuta	Low G+C	(1415)	91.5	X60615	
232	Bacillus firmus	Strain NCIMB 9366	Firmicuta	Low G+C	(1421)	91.7	X60616	
233	Bacillus globisporus	Strain NCIMB 11434	Firmicuta	Low G+C	(1362)	87.9	X60644	
234	Bacillus gordonae	Strain ATCC 29948	Firmicuta	Low G+C	(1373)	89.3	X60617	
235	Bacillus insolitus	Strain DSM 5	Firmicuta	Low G+C	(1384)	89.3	X60642	
236	Bacillus kaustophilus	Strain NCIMB 8547	Firmicuta	Low G+C	(1420)	91.6	X60618	
237	Bacillus larvae	Strain ATCC 9545	Firmicuta	Low G+C	(1414)	90.9	X60619	
238	Bacillus laterosporus 1	Strain ATCC 6344, DSM 25	Firmicuta	Low G+C	(1432)	93.2	X57307	
239	Bacillus laterosporus 2	Strain NCDO 1763	Firmicuta	Low G+C	(1383)	90.2	X60620	
240	Bacillus lautus	Strain NCIMB 12780	Firmicuta	Low G+C	(1411)	91.2	X60621	
241	Bacillus lentimorbus	Strain ATCC 14707	Firmicuta	Low G+C	(1383)	89.4	X60622	
242	Bacillus lentus	Strain NCDO 1127	Firmicuta	Low G+C	(1340)	86.6	X60601	
243	Bacillus licheniformis	Strain NCDO 1772	Firmicuta	Low G+C	(1387)	89.6	X60623	
244	Bacillus macerans 1	Strain ATCC 8244, DSM 24	Firmicuta	Low G+C	(1476)	95.2	X57306	
245	Bacillus macerans 2	Strain NCDO 1764	Firmicuta	Low G+C	(1359)	87.4	X60624	
246	Bacillus macquariensis 1	Strain DSM/ATCC23464	Firmicuta	Low G+C	(1476)	94.9	X57305	
247	Bacillus macquariensis 2	Strain NCTC 10419	Firmicuta	Low G+C	(1419)	91.1	X60625	
248	Bacillus maroccanus	Strain NCIMB 10500	Firmicuta	Low G+C	(1397)	90.3	X60626	
249	Bacillus medusa	Strain NCIMB 10437	Firmicuta	Low G+C	(1368)	88.2	X60628	
250	Bacillus megaterium	Strain DSM 32	Firmicuta	Low G+C	(1369)	88.3	X60629	
251	Bacillus pabuli	Strain NCIMB 12781	Firmicuta	Low G+C	(1400)	90.1	X60630	
252	Bacillus pantothenticus	Strain NCDO 1765	Firmicuta	Low G+C	(1357)	87.0	X60627	
253	Bacillus pasteurii	Strain NCIMB 8841	Firmicuta	Low G+C	(1379)	89.0	X60631	
254	Bacillus polymyxa 1	Strain DSM 36	Firmicuta	Low G+C	(1176)	75.9	X57308	
255	Bacillus polymyxa 2	Strain NCDO 1774	Firmicuta	Low G+C	(1380)	88.8	X60632	
256	Bacillus popilliae	Strain ATCC 14706	Firmicuta	Low G+C	(1411)	91.3	X60633	
257	Bacillus psychrophilus	Strain ATCC 23304	Firmicuta	Low G+C	(1362)	88.1	X60634	
258	Bacillus psychrosaccharolyticus	Strain ATCC 23296	Firmicuta	Low G+C	(1388)	89.9	X60635	
259	Bacillus pulvifaciens	Strain NCDO 1141	Firmicuta	Low G+C	(1381)	88.8	X60636	
260	Bacillus pumilus	Strain NCDO 1766	Firmicuta	Low G+C	(1384)	89.6	X60637	
261	Bacillus simplex	Strain DSM 1321	Firmicuta	Low G+C	(1362)	88.0	X60638	
262	Bacillus smithii	Strain DSM 4216	Firmicuta	Low G+C	(1389)	89.8	X60643	
263	Bacillus sphaericus	Strain NCDO 1767	Firmicuta	Low G+C	(1378)	89.0	X60639	
264	Bacillus stearothermophilus 1	Strain T10	Firmicuta	Low G+C	(1507)	97.0	X57309	
265	Bacillus stearothermophilus 2	Strain NCDO 1768	Firmicuta	Low G+C	(1364)	87.8	X60640	
266	Bacillus subtilis 2	Strain NCDO 1769	Firmicuta	Low G+C	(1418)	91.8	X60646	
267	Bacillus thermoglucosadicus	Strain ATCC 43742	Firmicuta	Low G+C	(1351)	86.9	X60641	
268	Clavibacter xyli		Firmicuta	Low G+C	1524	100.0	M60935	
269	Clostridium mayombeii		Firmicuta	Low G+C	(1308)	88.0	M62421	
270	Clostridium perfringens	rrnB operon	Firmicuta	Low G+C	1517	100.0	M69264	
271	Enterococcus avium	Strain NCDO 2369 (T)	Firmicuta	Low G+C	(1441)	92.5	no Acc	RT
272	Enterococcus casseliflavus	Strain NCDO 2376	Firmicuta	Low G+C	(1383)	88.9	no Acc	RT
273	Enterococcus durans	Strain NCDO 596 (T)	Firmicuta	Low G+C	(1437)	92.4	no Acc	RT
274	Enterococcus faecium	Strain NCDO 942 (T)	Firmicuta	Low G+C	(1437)	92.2	no Acc	RT
275	Enterococcus gallinarum	Strain NCDO 2313 (T)	Firmicuta	Low G+C	(1423)	91.4	no Acc	RT
276	Enterococcus hirea	Strain NCDO 1258 (T)	Firmicuta	Low G+C	(1445)	92.8	no Acc	RT
277	Enterococcus malodoratus	Strain NCDO 846 (T)	Firmicuta	Low G+C	(1426)	91.7	no Acc	RT
278	Enterococcus mundtii	Strain NCDO 2375 (T)	Firmicuta	Low G+C	(1451)	93.1	no Acc	RT
279	Enterococcus pseudoavium	Strain NCDO 2138 (T)	Firmicuta	Low G+C	(1449)	93.1	no Acc	RT
280	Enterococcus raffinosus	Strain NCTC 12192 (T)	Firmicuta	Low G+C	(1452)	93.4	no Acc	RT
281	Enterococcus sulfureus	Strain NCDO 2379 (MUTK31)	Firmicuta	Low G+C	(1484)	95.2	X55133	RT
282	Eubacterium biforme		Firmicuta	Low G+C	(1475)	95.7	M59230	
283	Lactobacillus acidophilus	Strain NCDO 1748 (T)	Firmicuta	Low G+C	(1341)	86.6	X61138	RT
284	Lactobacillus animalis	Strain NCDO 2425 (T)	Firmicuta	Low G+C	(1369)	88.1	X61133	RT
285	Lactobacillus brevis	Strain NCDO 1749 (T)	Firmicuta	Low G+C	(1431)	91.2	X61134	RT
286	Lactobacillus buchneri	Strain NCDO 110 (T)	Firmicuta	Low G+C	(1338)	86.4	X61139	RT
287	Lactobacillus casei 2	Strain NCDO 161 (T)	Firmicuta	Low G+C	(1398)	90.1	X61135	RT
288	Lactobacillus fermentum	Strain NCDO 1750 (T)	Firmicuta	Low G+C	(1332)	85.3	X61142	RT
289	Lactobacillus fructosus	Strain NCDO 2345 (T)	Firmicuta	Low G+C	(1304)	84.2	X61140	RT
290	Lactobacillus gasseri	Strain NCDO 2233 (T)	Firmicuta	Low G+C	(1282)	82.7	X61137	RT
291	Lactobacillus helveticus	Strain NCDO 2712 (T)	Firmicuta	Low G+C	(1268)	81.8	X61141	RT
292	Lactobacillus oris	Strain NCDO 2160 (T)	Firmicuta	Low G+C	(1304)	84.0	X61131	RT
293	Lactobacillus sanfrancisco	Strain JCM 5668	Firmicuta	Low G+C	(1446)	91.8	X61132	RT
294	Lactobacillus vaginalis	Strain NCTC 12197	Firmicuta	Low G+C	(1411)	91.1	X61136	RT
295	Mycoplasma iowae 2	Strain PPAV	Firmicuta	Low G+C	1511	100.0	X55271	
296	Quinella ovalis		Firmicuta	Low G+C	(1443)	96.3	M62701	
297	Streptococcus acidominimus	Strain NCDO 2025 (T)	Firmicuta	Low G+C	(1299)	83.7	X58301	RT
298	Streptococcus alactolytiens	Strain NCDO 1091 (T)	Firmicuta	Low G+C	(1295)	83.5	X58319	RT
299	Streptococcus anginosus	Strain NCTC 10713 (T)	Firmicuta	Low G+C	(1311)	84.5	X58309	RT

Table 1. continued

Nr. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)
300	Streptococcus bovis	Strain NCDO 597 (T)	Firmicuta	Low G+C	(1294)	83.4	X58317	RT
301	Streptococcus cecorum	Strain NCDO 2674	Firmicuta	Low G+C	(1457)	93.6	no Acc	RT
302	Streptococcus constellatus	Strain NCTC 11325 (T)	Firmicuta	Low G+C	(1262)	81.5	X58310	RT
303	Streptococcus cricetus	Strain NCDO 2720 (T)	Firmicuta	Low G+C	(1293)	83.3	X58305	RT
304	Streptococcus downei	Strain NCTC 11391 (T)	Firmicuta	Low G+C	(1215)	78.3	X58306	RT
305	Streptococcus equi	Strain NCDO 2493 (T)	Firmicuta	Low G+C	(1276)	82.2	X58314	RT
306	Streptococcus equinus	Strain NCDO 1037 (T)	Firmicuta	Low G+C	(1300)	83.8	X58318	RT
307	Streptococcus hyointestinalis	Strain DSM 20770 (T)	Firmicuta	Low G+C	(1215)	78.3	X58313	RT
308	Streptococcus iniae	Strain NCDO 2772 (T)	Firmicuta	Low G+C	(1285)	82.8	X58316	RT
309	Streptococcus intermedius	Strain NCTC 11324 (T)	Firmicuta	Low G+C	(1242)	80.0	X58311	RT
310	Streptococcus macacae	Strain NCTC 11558 (T)	Firmicuta	Low G+C	(1286)	83.0	X58302	RT
311	Streptococcus mutans	Strain NCTC 10449 (T)	Firmicuta	Low G+C	(1307)	84.3	X58303	RT
312	Streptococcus oralis	Strain NCTC 11427 (T)	Firmicuta	Low G+C	(1291)	83.3	X58308	RT
313	Streptococcus pneumoniae	Strain NCTC 7465 (T)	Firmicuta	Low G+C	(1290)	83.1	X58312	RT
314	Streptococcus porcinus	Strain NCDO 600 (T)	Firmicuta	Low G+C	(1256)	81.1	X58315	RT
315	Streptococcus rattus	Strain NCDO 2723 (T)	Firmicuta	Low G+C	(1308)	84.3	X58304	RT
316	Streptococcus salivarius	Strain NCDO 1779 (T)	Firmicuta	Low G+C	(1301)	83.9	X58320	RT
317	Streptococcus sobrinus	Strain DSM 20742 (T)	Firmicuta	Low G+C	(1306)	84.2	X58307	RT
318	Streptococcus vestibularis	Strain NCTC 12166 (T)	Firmicuta	Low G+C	(1284)	83.0	X58321	RT
319	Propionigenium modestum		new line of descent	related to low G+C Firmicuta	1518	99.9	X54275	
320	Selenomonas ruminantium 2	Strain GA192	Firmicuta	Species with Gram-negative walls	(1481)	94.7	M62702	
321	Selenomonas ruminantium 3	Strain HD4	Firmicuta	Species with Gram-negative walls	(1387)	88.5	M62703	
322	Actinomyces viscosus 2	Strain DSM 43027	Firmicuta	High G+C	(1313)	86.6	M33908	
323	Amycolata nitrificans	Strain DSM new (IFAM 379)	Firmicuta	High G+C	(1241)	81.8	X55609	
324	Amycolata petroleophila	Strain DSM new (IFAM 78)	Firmicuta	High G+C	(1390)	91.2	X55608	
325	Brevibacterium bifidum		Firmicuta	High G+C	(1501)	97.1	M38018	
326	Frankia sp.		Firmicuta	High G+C	1512	100.0	M55343	
327	Micrococcus luteus		Firmicuta	High G+C	(1493)	97.0	M38242	
328	Mycobacterium avium 3	Strain DSM 43216	Firmicuta	High G+C	(1460)	95.2	X52918	PCR
329	Mycobacterium avium 4		Firmicuta	High G+C	(1320)	86.6	M61667	
330	Mycobacterium avium 5		Firmicuta	High G+C	(1346)	87.9	M61668	
331	Mycobacterium avium 6		Firmicuta	High G+C	(1337)	87.3	M61669	
332	Mycobacterium avium 7		Firmicuta	High G+C	(1346)	87.9	M61670	
333	Mycobacterium avium 8		Firmicuta	High G+C	(1356)	88.5	M61671	
334	Mycobacterium avium 9		Firmicuta	High G+C	(1351)	88.2	M61672	
335	Mycobacterium avium 10		Firmicuta	High G+C	(1363)	89.0	M61673	
336	Mycobacterium bovis 2	Strain vallee	Firmicuta	High G+C	(1416)	92.4	X55589	
337	Mycobacterium chelonae	Strain ATCC 14472	Firmicuta	High G+C	(1447)	95.4	X52921	PCR
338	Mycobacterium chitae 2		Firmicuta	High G+C	(1298)	85.6	M61662	
339	Mycobacterium farcinogenes	Strain DSM 43294	Firmicuta	High G+C	(1416)	93.3	X55592	
340	Mycobacterium flavescens 2	Strain ATCC 14474	Firmicuta	High G+C	(1446)	95.1	X52932	PCR
341	Mycobacterium fortuitum	Strain ATCC 6841 (T)	Firmicuta	High G+C	(1443)	95.1	X52933	PCR
342	Mycobacterium gadium		Firmicuta	High G+C	(1327)	87.6	M61663	
343	Mycobacterium gastri	Strain ATCC 15754	Firmicuta	High G+C	(1455)	95.0	X52919	
344	Mycobacterium gordonae 2	Strain ATCC 14470	Firmicuta	High G+C	(1453)	95.0	X52923	PCR
345	Mycobacterium intracellulare 1	Strain ATCC 15985	Firmicuta	High G+C	(1446)	94.5	X52927	PCR
346	Mycobacterium intracellulare 2		Firmicuta	High G+C	(1354)	88.5	M61682	
347	Mycobacterium intracellulare 3		Firmicuta	High G+C	(1353)	88.3	M61683	
348	Mycobacterium intracellulare 4		Firmicuta	High G+C	(1361)	88.8	M61684	
349	Mycobacterium intracellulare 5		Firmicuta	High G+C	(1355)	88.5	M61685	
350	Mycobacterium intracellulare 6		Firmicuta	High G+C	(1339)	87.4	M61686	
351	Mycobacterium kansasii 2	Strain ATCC 12478	Firmicuta	High G+C	(1357)	88.7	M29575	
352	Mycobacterium komossense	Strain ATCC 33013	Firmicuta	High G+C	(1458)	95.9	X55591	
353	Mycobacterium leprae 2		Firmicuta	High G+C	(1478)	95.5	X55587	
354	Mycobacterium leprae 3		Firmicuta	High G+C	(1443)	93.3	X55022	PCR
355	Mycobacterium malmoense 1	Strain ATCC 29571	Firmicuta	High G+C	(1457)	95.1	X52930	PCR
356	Mycobacterium malmoense 2		Firmicuta	High G+C	(1344)	87.7	M61666	
357	Mycobacterium marinum		Firmicuta	High G+C	(1488)	97.1	X52920	PCR
358	Mycobacterium nonchromogenicum 2	Strain ATCC 19530	Firmicuta	High G+C	(1461)	95.2	X52928	PCR
359	Mycobacterium paratuberculosis 2		Firmicuta	High G+C	(1337)	87.6	M61674	
360	Mycobacterium paratuberculosis 3		Firmicuta	High G+C	(1344)	87.7	M61675	
361	Mycobacterium paratuberculosis 4		Firmicuta	High G+C	(1330)	87.2	M61676	
362	Mycobacterium paratuberculosis 5		Firmicuta	High G+C	(1349)	88.3	M61677	
363	Mycobacterium paratuberculosis 7		Firmicuta	High G+C	(1341)	87.5	M61679	
364	Mycobacterium paratuberculosis 8		Firmicuta	High G+C	(1337)	87.4	M61680	
365	Mycobacterium paratuberculosis 9	Strain ATCC 19698	Firmicuta	High G+C	(1458)	95.1	X52934	PCR
366	Mycobacterium scrofulaceum	Strain ATCC 19981	Firmicuta	High G+C	(1451)	95.0	X52924	PCR
367	Mycobacterium simiae	Strain ATCC 25275	Firmicuta	High G+C	(1442)	95.0	X52931	PCR
368	Mycobacterium smegmatis	Strain ATCC 14468	Firmicuta	High G+C	(1449)	95.2	X52922	PCR
369	Mycobacterium sphagni	Strain ATCC 33026	Firmicuta	High G+C	(1450)	95.5	X55590	
370	Mycobacterium szulgai 1	Strain ATCC 25799	Firmicuta	High G+C	(1454)	95.0	X52926	PCR
371	Mycobacterium szulgai 2		Firmicuta	High G+C	(1347)	87.9	M61665	
372	Mycobacterium terrae 2	Strain ATCC 15755	Firmicuta	High G+C	(1461)	95.2	X52925	PCR
373	Mycobacterium tuberculosis 1	Strain H37	Firmicuta	High G+C	(1464)	95.5	X52917	PCR
374	Mycobacterium tuberculosis 2	Strain H37/Rv	Firmicuta	High G+C	(1416)	92.4	X55588	
375	Mycobacterium xenopi 1		Firmicuta	High G+C	(1370)	95.2	M61664	

Table 1. continued

Nr. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)
376	Mycobacterium xenopi 2	Strain ATCC 19250	Firmicuta	High G+C	(1469)	89.1	X52929	PCR
377	Nocardia asteroides 2	Strain ATCC 3306	Firmicuta	High G+C	(1443)	95.1	X57949	PCR
378	Propionibacterium acnes		Firmicuta	High G+C	(1513)	98.0	M61903	
379	Renibacterium salmoninarum	Strain ATCC 33209 (T)	Firmicuta	High G+C	(1460)	94.9	X51601	RT
380	Streptomyces albus	Strain DSM 40313 (T) ISP 5313	Firmicuta	High G+C	(1240)	81.5	X53163	
381	Streptomyces brasiliensis	Strain DSM 43159 (T)	Firmicuta	High G+C	(1238)	81.6	X53162	
382	Streptomyces coelicolor 2	Strain A3(2) M145	Firmicuta	High G+C	1528	100.0	X60514	
383	Streptomyces diastaticus	Strain DSM 40496 (T) ISP 5496	Firmicuta	High G+C	(1189)	78.5	X53161	
384	Streptomyces griseus subsp. griseus	Strain KCTC 9080, operon rrnE	Firmicuta	High G+C	1525	100.0	X55435	
385	Streptomyces lavendulae	Strain DSM 2014 (T) ISP 5069	Firmicuta	High G+C	(1183)	78.1	X53173	
386	Streptomyces purpureus	Strain DSM 43460 (T)	Firmicuta	High G+C	(1185)	78.2	X53170	
387	Streptoverticillium abikoense	Strain DSM 40831 (T)	Firmicuta	High G+C	(1161)	75.7	X53168	
388	Streptoverticillium baldacii	Strain DPDU 0819 (T)	Firmicuta	High G+C	(1144)	74.6	X53164	
389	Streptoverticillium cinnamoneum 1	Strain spp. azacolutum DPDU 0074 (T)	Firmicuta	High G+C	(1174)	78.1	X53165	
390	Streptoverticillium cinnamoneum 2	Strain spp. cinnamoneum DPDU 0093 (T)	Firmicuta	High G+C	(1214)	80.1	X53171	
391	Streptoverticillium ladakanum	Strain var. ladakanum DSM 40587 (T)	Firmicuta	High G+C	(1182)	78.0	X53167	
392	Streptoverticillium luteoreticuli	Strain DPDU 0081 ISP 5509.	Firmicuta	High G+C	(1175)	77.6	X53172	
393	Streptoverticillium olivoreticuli	Strain ssp. cellulophilum DPDU 0278 (T)	Firmicuta	High G+C	(1209)	79.8	X53166	
394	Streptoverticillium salmonis	Strain DPDU 0098 (T)	Firmicuta	High G+C	(1131)	73.8	X53169	
395	Tsukamurella aurantiacus	Strain NCTC 10741	Firmicuta	High G+C	(1303)	86.1	no Acc	
396	Acetonema longum 1		Firmicuta	Uncertain affiliation	(1211)	78.3	M61919	
397	Acetonema longum 2		Firmicuta	Uncertain affiliation	(1348)	86.8	M61920	
398	Borrelia anserina 1		Spirochetes & rel.		(1449)	94.7	M64312	
399	Borrelia anserina 2	Strain ES	Spirochetes & rel.		(1459)	94.7	M72397	RT
400	Borrelia burgdorferi 1		Spirochetes & rel.		(1464)	96.0	M60967	
401	Borrelia burgdorferi 2		Spirochetes & rel.		(1457)	95.0	M60969	
402	Borrelia burgdorferi 3		Spirochetes & rel.		(1466)	95.9	M64309	
403	Borrelia burgdorferi 4		Spirochetes & rel.		(1467)	95.7	M64310	
404	Borrelia burgdorferi 5		Spirochetes & rel.		(1451)	95.1	X57404	
405	Borrelia burgdorferi 6		Spirochetes & rel.		(1464)	95.5	M64311	
406	Borrelia coriaceae		Spirochetes & rel.		(1449)	94.9	M60970	
407	Borrelia hermsii		Spirochetes & rel.		(1485)	97.2	M60968	
408	Borrelia hermsii	Strain M1001	Spirochetes & rel.		(1283)	83.4	M72398	RT
409	Borrelia sp.	Strain 19941	Spirochetes & rel.		(1376)	89.6	M72396	RT
410	Leptospira interrogans 2	Strain Kennewicki	Spirochetes & rel.		(1294)	85.7	M71241	RT
411	Serpula hyodysenteriae 1	Strain ATCC 27164 (T)	Spirochetes & rel.		(1375)	90.9	M57743	RT
412	Serpula hyodysenteriae 2	Strain B204	Spirochetes & rel.		(1441)	95.2	M57741	RT
413	Serpula hyodysenteriae 3	Strain A-1	Spirochetes & rel.		(1431)	94.7	M57742	RT
414	Serpula innocens 1	Strain B256, ATCC 29796 (T)	Spirochetes & rel.		(1443)	95.3	M57744	RT
415	Serpula innocens 2	Strain 4/71	Spirochetes & rel.		(1436)	94.7	M57745	RT
416	Spirochaeta aurantia	Strain J1	Spirochetes & rel.		(1518)	96.4	M57740	RT
417	Spirochaeta bajacaliforniensis	Strain BA2, ATCC 35968 (T)	Spirochetes & rel.		(1480)	94.5	M71239	RT
418	Spirochaeta thermophila		Spirochetes & rel.		(1327)	86.1	X62809	
419	Thermophilic spirochete	Strain H1	Spirochetes & rel.		(1504)	95.7	M71240	RT
420	Treponema bryantii	Strain RUS-1 (T)	Spirochetes & rel.		(1523)	96.0	M57737	RT
421	Treponema denticola	Strain ATCC 33520	Spirochetes & rel.		(1481)	94.0	M71236	RT
422	Treponema pectinovorum	Strain DR-36-DR-2, ATCC 33768 (T)	Spirochetes & rel.		(1471)	93.5	M71237	RT
423	Treponema phagedenis	Strain K5	Spirochetes & rel.		(1531)	95.8	M57739	RT
424	Treponema saccharophilum	Strain ATCC 43261 (T)	Spirochetes & rel.		(1482)	94.6	M71238	RT
425	Treponema succinifaciens	Strain 6091, ATCC 33096 (T)	Spirochetes & rel.		(1484)	94.1	M57738	RT
426	Thermus aquaticus	Strain X-1, ATCC 27978	Radioresistant micrococci & rel.	Thermophiles group	(1158)	75.7	X58340	RT
427	Thermus thermophilus 2	Strain HB8, ATCC 27634	Radioresistant micrococci & rel.	Thermophiles group	1521	100.0	M26923	
428	Bacteroides fragilis 2		Bacteroides, Flavobact., Cytophaga	Flavobacterium group	1536	99.9	M61006	
429	Cytophaga lytica	Strain ATCC 23178	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1483)	96.4	M62796	
430	Flavobacterium aquatile	Strain ATCC 11947	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1494)	97.5	M62797	RT
431	Flavobacterium ferrugineum	Strain ATCC 13524	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1496)	96.6	M62798	RT
432	Flavobacterium uliginosum	Strain ATCC 14397	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1505)	97.6	M62799	RT
433	Flectobacillus major	Strain ATCC 29496	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1458)	96.6	M62787	RT
434	Flectobacillus marinus	Strain ATCC 43824	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1465)	95.7	M62788	RT
435	Flexibacter aurantiacus	Strain ATCC 23107	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1446)	95.4	M62792	RT
436	Flexibacter canadensis	Strain ATCC 29591	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1447)	95.0	M62793	RT
437	Flexibacter flexilis	Strain ATCC 23079	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1441)	95.2	M62794	RT
438	Flexibacter sancti	Strain ATCC 23092	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1462)	95.5	M62795	RT
439	Runella slithyformis	Strain ATCC 29530	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1444)	95.7	M62786	RT
440	Spirosoma linguale	Strain ATCC 23276	Bacteroides, Flavobact., Cytophaga	Flavobacterium group	(1423)	93.6	M62789	RT
441	Chlamydia trachomatis		Chlamydiae		1555	100.0	M59178	
442	Chlorobium vibrioforme		Green sulfur bacteria		1503	99.7	M62791	
443	Anabaena sp.	Strain PCC 7120	Cyanobacteria		1489	100.0	X59559	
444	Prochlorococcus marinus	Strain SSW5	Cyanobactaria		1147	100.0	X63140	
445	Prochloron sp.		Cyanobacteria		1377	100.0	X63141	
446	Unknown Cyanobacterium 1		Cyanobacteria		(1292)	87.5	M63813	
447	Unknown Cyanobacterium 2		Cyanobacteria		(1296)	87.9	M63814	
448	Fervidobacterium islandicum	Isolate H21, DSM 5733	Thermophilic eubacteria		(1434)	95.1	M59176	RT
449	Fervidobacterium nodosum	Strain Rt17-B, ATCC 35602	Thermophilic eubacteria		(1423)	94.3	M59177	RT
450	Flexistipes sinusarabici	Isolate MAS 10, DSM 4947	Uncertain affiliation		(1473)	94.8	M59231	RT
451	Gemmata obscuriglobus	Strain UQM 2246	Uncertain affiliation		1490	99.9	X54522	

Table 1. continued

Nr. (a)	Species (b)	Specification (c)	Taxonomic Position (d)		Length (e)	E.coli % (f)	Access. (g)	Method (h)
	PLASTIDS							
452	Pisum sativum		Magnoliophyta (Div.)	Magnoliopsida (Cl.)	1487	100.0	M37430	
453	Olisthodiscus luteus		Chromobionts (assemblage)	Chrysophyta (Ph.)	1520	100.0	M82860	
454	Cryptomonas Phi	Strain F	Cryptomonads (assemblage)	Cryptophyta (Ph.)	1493	100.0	X56806	
455	Pyrenomonas salina		Cryptomonads (assemblage)	Cryptophyta (Ph.)	1490	100.0	X55015	
456	Antithamnion sp.		Rhodophytes (assemblage)	Rhodophyta (Ph.)	1486	100.0	X54299	
	MITOCHONDRIA							
457	Antilocapra americana		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	958	100.0	M55540	
458	Balaenoptera physalus	Adult female, liver, isolate no 27	Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	976	100.0	X61145	
459	Bathyergus janetta		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	(784)	86.3	M63565	
460	Bathyergus suillus		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	(783)	86.3	M63564	
461	Capra hircus		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	956	100.0	M55541	
462	Cryptomys damarensis		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	(788)	86.3	M63569	
463	Cryptomys hottentotus 1		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	(782)	86.3	M63567	
464	Cryptomys hottentotus 2		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	(783)	84.6	M63568	
465	Georychus capensis		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	(782)	86.3	M63566	
466	Heliophobius argenteocinereus		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	(791)	86.3	M63562	
467	Heterocephalus glaber		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	(786)	86.3	M63563	
468	Petromus typicus		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	(752)	83.9	M63571	
469	Thryonomys swinderianus		Chordata (Ph.), Vertebrata (SPh.)	Mammalia (Cl.)	(790)	86.3	M63570	
470	Cyprinus carpio		Chordata (Ph.), Vertebrata (SPh.)	Osteichthyes (Cl.)	951	100.0	X61010	
471	Caenorhabditis elegans	Strain N2 Bristol.	Nematoda (Ph.)	Secernentea (Cl.)	697	100.0	X54252	
472	Ascaris suum	Tissue body wall muscle and egg	Nematoda (Ph.)	Secernentea (Cl.)	701	100.0	X54253	
473	Lupinus luteus	Strain cv. Topaz, seedlings	Magnoliophyta (Div.)	Magnoliopsida (Cl.)	2023	100.0	Z11512	
474	Saccharomyces cerevisiae 5	Strain V25T-R5	Ascomycotina (Ph.)		1651	100.0	X14966	
475	Plasmodium falciparum		Sporozoa (assemblage)	Sporozoa (Ph.)	1427	100.0	X57167	

Footnotes to Table 1

a)This number corresponds with the literature reference.

b)Species are classified alphabetically within each taxonomic group as defined in columns 4 and 5. When different sequences are determined for various strains or genes of the same organism, the sequences are listed separately and the species name is followed by a number.

c)This column contains the following data, if specified by the authors:

-Strain name for laboratory animals, (cultivated) variety for plants, culture collection and strain number in the case of microorganisms

-Tissue from which the DNA used for cloning or amplification was extracted in the case of differentiated organisms.

-Ribosomal RNA operon to which belongs the cloned SSU rRNA gene in the case of bacteria.

The absence of a specification is often due to the fact that a sequence is unpublished and that the specification is not mentioned in the submission to a nucleotide sequence library.

d)The taxonomic position is described according to the following references:

477 for the Metazoa (No. 1 to 31), 478 for the higher plants (No. 32 to 43), 57, 70, and 479 for the higher fungi (No. 44 to 76). The taxonomic position of the remaining eukaryotes is decribed according to Corliss (480). The archaebacteria are classified according to Woese (481). The classification of the eubacteria is according to Stackebrandt et al. (482) for the Proteobacteria, according to Wayne et al. (483) for the Firmicuta, and according to Woese (481) for the remaining taxa. We have no information yet on the taxonomic position of species 450 and 451. Taxon designations corresponding to an established taxonomic level are followed by the abbreviation Ph. (Phylum), SPh. (Subphylum), Div. (Division) and Cl. (Class).

e)The SSU rRNA termini are located experimentally (e.g. by S1 nuclease mapping) by some authors, but more often deduced by comparison with structures from related species. In case of length heterogeneity the length of the longest variant is listed. A number enclosed in brackets means that the sequence is incomplete and gives the number of sequenced nucleotides. This includes partially identified nucleotides denoted as B, D, H, K, M, R, S, V, W or Y, but not unidentified nucleotides denoted as N.

f)For incomplete sequences, this is the combined length of the corresponding *E. coli* SSU rRNA segments as a fraction of the total *E. coli* SSU rRNA length. This may amount to 100% even for an incomplete sequence because a missing segment may be situated in an insertion relative to the *E. coli* sequence. In order for an SSU rRNA sequence to be listed, the sequenced segments should correspond to segments in the E. coli sequence amounting to a combined length of at least 70% of the complete *E. coli* SSU rRNA (477).

g)Accession number in the EMBL and Genbank nucleotide sequence libraries. The accession number for a sequence is the same in both libraries but there can be a delay before a sequence submitted to one library arrives in the other one.

h)RT: the SSU rRNA was sequenced by the dideoxynucleotide method using reverse transcriptase. PCR: amplification of the DNA involved use of polymerase chain reaction. In the remaining cases, specific information about the methods used was not available (e.g. unpublished results) or DNA was amplified by cloning only. Sequencing of amplified DNA was then performed in most cases by the dideoxynucleotide method.

i)The SSU rRNA sequence of *Ustilago maydis* contains a 411-base pair intron between bases 1158 and 1159.

Table 2. Helix occupancy in eukaryotic SSU rRNAs.

Taxon	Taxonomic level	Helices (a)													
		E8	E10		E21										E43
		1	1	2	1	2	3	4	5	6	7	8	9	10	1
Insecta	Class	-	*	-	*	*	*	*	*	*	*	*	*	-	-
Platyhelminthes	Phylum	-	*	-	*	*	*	*	*	*	*	*	*	-	-
Schizosaccharomyces pombe	Species	-	*	-	*	*	-	-	*	*	*	*	*	-	*
Yarrowia lipolytica	Species	-	*	-	*	*	-	-	-	*	*	*	*	-	*
Blastocladiella emersonii	Species	-	*	-	*	*	-	-	*	*	*	*	*	-	*
Euplotes aediculatus	Species	*	*	-	*	*	-	-	*	*	*	*	*	-	*
Plasmodium	Genus	-	*	-	*	*	-	-	*	*	*	*	*	-	*
Physarum polycephalum	Species	*	*	*	*	*	-	*	*	*	*	*	*	-	*
Kinetoplastidea	Phylum	*	*	-	*	*	-	-	*	*	*	*	*	*	*
Euglena gracilis	Species	*	*	*	*	*	-	*	*	*	*	*	*	*	*
Babesia bigemina	Species	-	*	-	*	*	-	-	-	*	*	*	*	-	-
Vairimorpha necatrix	Species	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Giardia	Genus	-	-	-	-	-	-	-	-	*	*	*	*	-	-
Naegleria gruberi	Species	-	*	*	*	*	-	*	*	*	*	*	*	-	*
Acanthamoeba castellanii	Species	-	*	-	*	*	-	*	*	*	*	*	*	-	*
All other eukaryotes		-	*	-	*	*	-	-	*	*	*	*	*	-	-

a) The presence of a helix is indicated by an asterisk. Only eukaryote-specific helices are listed since universal helices are present in all eukaryotic SSU rRNAs, except for Vairimorpha necatrix SSU rRNA, which misses helices 10, 11 and 44.