Volume 12, Supplement Nucleic Acids Research

Collection of published 5S and 5.8S ribosomal RNA sequences

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The 1983 collection (1) of mature 5S RNA sequences is updated. The sequences reported are based on actual sequence determinations and not on the basis of oligonucleotide catalogues. Some of the earlier published oligonucleotide catalogues are given in reference 2.

For a summary of the possible structure and function of the ribosomal 5S and 5.8S RNAs the reader is refered to references 3-8.

For this year the collection of 5S RNA sequences will be presented according to the recently proposed secondary structure model of De Wachter, Chen and Vandenberghe (8), even though we realize that these structures, being deduced by a comparative approach, have not been experimentally proven to be correct. Not all investigators agree that the double-stranded area D-D' (see below) is present in eubacterial as well as in eukaryotic 5S RNAs.

We would like to thank those colleagues who have sent us their pre- or reprints on small ribosomal RNA sequences in 1983, and who have pointed out several mistakes in our previous collection.

ALIGNMENT OF 5S rRNA SEQUENCES

The alignment of 5S RNA sequences is divided in 5 groups : eubacteria, chloroplasts, plant mitochondria, archaebacteria, and eukaryotes. The procedure followed to align the sequences, described in detail elsewhere (8), is based on the presence of conserved bases, indicated on the secondary structure models in Fig. 1. The set of conserved bases differs slightly from one group to another, but there is a sufficient number of universally conserved positions to allow an alignment of each of the 5 groups with respect to the others. Although the number of 5S RNA sequences has increased from 93 in the previous collection (1) to 175 in the present one, the number of positions needed to align all these sequences has decreased from 150 to 148. This is because some superfluous positions could be eliminated as a consequence of sequence corrections (9,10) whereas only one new position had to be created to accomodate new sequences. Other corrections which are in progress may allow further simplification in the future. The 148 positions needed do not include a 108 nucleotide insertion between positions 124 and 129 in *Halococcus morrhuae* 5S RNA.

SECONDARY STRUCTURE MODEL

All presently known 5S RNA sequences can be fitted in a uniform secondary structure model (8) featuring 5 double-stranded areas indicated on the alignments as A-A', B-B', C-C', D-D' and E-E', in the order of occurrence from 5'- to 3'-end. In order to state the topological rules that this model obeys it is useful to consider the following definitions :

- Double-stranded area: an area consisting of a single helix segment or of several helix segments connected by bulges or, more exceptionally, by small interior loops.
- Helix segment: a stretch of double helix uninterrupted by bulges or interior loops.
- Standard base pair: one of the base pairs G·C, A·U and G·U.
- Non-standard or odd base pair: one of the 7 other conceivable base pairs.

The topological rules can then be summarized as follows. A hairpin loop cannot contain less than 3 bases. A helix segment should consist of at least two standard base pairs. Any non-standard base pair occurring in such a segment should be intercalated between two standard base pairs.

The non-standard base pairs postulated in the secondary structure model occur most frequently in area E-E', as well as in area D-D' of plant and eubacterial 5S RNAs. It is extremely rare to find more than one non-standard pair in any one double stranded area.

The secondary structure is represented in Fig. 1. There are slight variations in the dimensions of helices and loops, as well as in the set of conserved bases, among the 5 major groups of sequences. Even within one group such as the eukaryotes, there are variations. Fig. 1 shows the most commonly encountered structure within each of the two groups, eubacteria and eukaryotes, for which the largest set of sequences is known. It should be realized that the set of residues conserved at the 90% level, which are indicated on both models, may change slightly as the number of known sequences will increase in the future.

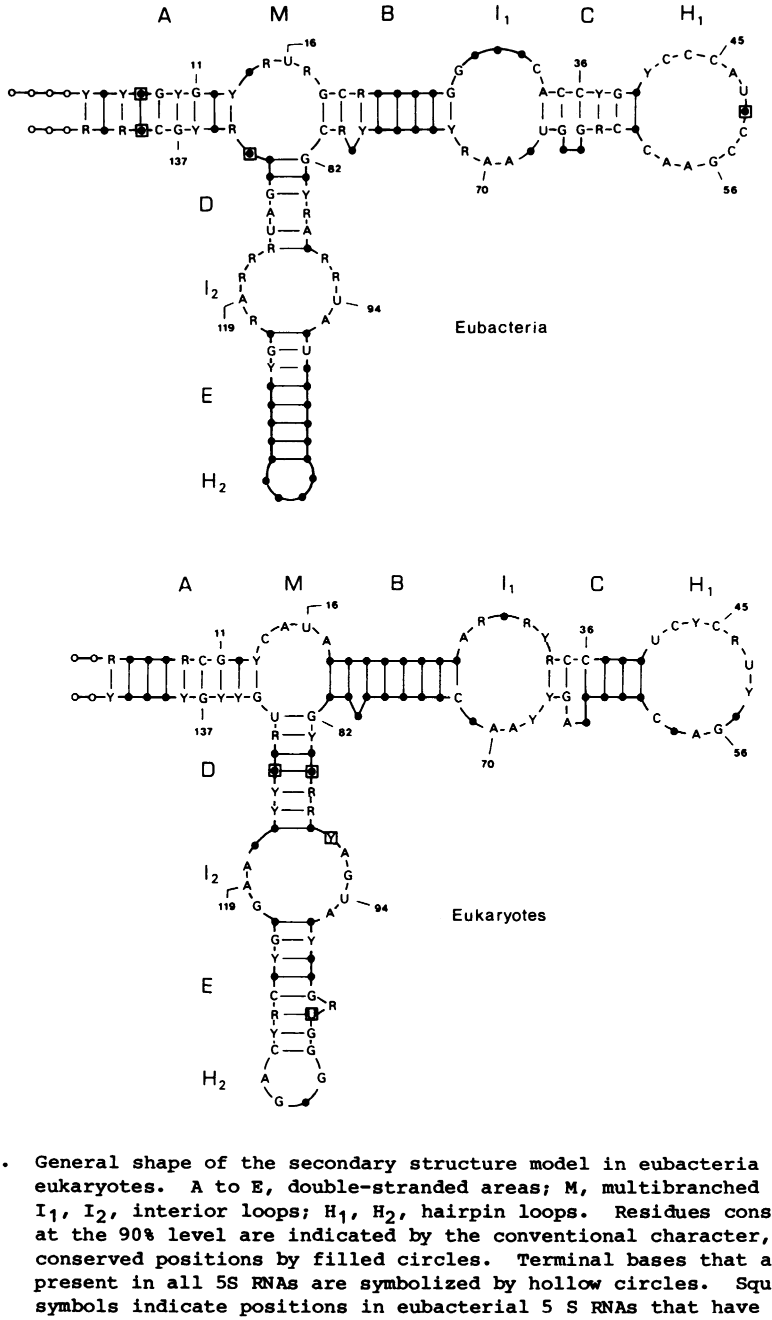

Fig. 1. General shape of the secondary structure model in eubacteria and in eukaryotes. A to E, double-stranded areas; M, multibranched loop; I_1, I_2, interior loops; H_1, H_2, hairpin loops. Residues conserved at the 90% level are indicated by the conventional character, less conserved positions by filled circles. Terminal bases that are not present in all 5S RNAs are symbolized by hollow circles. Squared symbols indicate positions in eubacterial 5 S RNAs that have no eukaryotic counterpart and vice versa. Some of the conserved residues common to eubacterial and eukaryotic 5S RNAs are numbered to facilitate comparison with the alignment.

ABBREVIATIONS AND CONVENTIONS USED IN THE 5S rRNA ALIGNMENTS AND REFERENCES

The double-stranded areas A-A', B-B', C-C', D-D' and E-E' are boxed. Bulges or small interior loops connecting helix segments within a double-stranded area are indicated by nested boxes. Bases belonging to odd base pairs within a helix segment are put in parentheses. Terminal residues found in submolar amounts because of length heterogeneity in the 5S RNA preparations are written in lower case characters.

For some species, more than one sequence has been published. The following cases may be distinguished:

- A published sequence has been reexamined later and corrected: in this case only the corrected sequence appears in the alignment, but the reference of the original paper is mentioned, followed by the reference of the correction.
- Different sequences have been published and it is not known which is the correct one, or different strains have been examined: all reported sequences are aligned and numbered sequentially.
- A single species contains more than one 5S RNA variant due to gene polymorphism: if the variants have been isolated and separately sequenced, each variant sequence is aligned. If heterogeneity was detected during sequencing of a mixture, a single sequence is aligned and heterogeneous positions are mentioned in a footnote on the reference page. The position numbers refer to the alignment and not to the distance from the 5'-terminus.

The taxonomic position indicated for each species on the reference page is according to Kaestner (11) for the metazoa and protozoa, Ainsworth et al. (12) for the fungi, Engler (13) for the plants, Fritsch (14) for the algae and phytoflagellates, Zillig et al. (15) for the archaebacteria, and according to the 8th edition of Bergey's Manual (16) for the eubacteria. In some cases the rank of a taxon has been altered according to newer systematic insights as discerned by the authors.

ALIGNMENT OF 5.8S rRNA SEQUENCES

The alignment of 5.8S rRNA sequences does not take into account any potential secondary structure interaction. To facilitate the recognition of species, the name of a higher taxon, beleived to represent a monophyletic group, is given in parentheses. Sequences solely determined at the DNA level are marked by an asterisk in front of the species name. 2'-0-methylriboses are indicated by underscoring and pseudouridine by P. The position of the internal transcribed spacer in diptera is marked by ◊. As explained previously (141), the vertebrate sequences published before 1978 probably all contain the same sequencing error, which was revealed when the Xenopus laevis (132,133), rat (123) and mouse (128) sequences were reexamined at the DNA level. In analogy the GC at position 50 of the original sequences of Xenopus borealis, chick, turtle and trout has been omitted. We would like to point out that the latter sequence alterations have not been confirmed by sequencing data.

The program ALIGNSTAT (152) available as part of the program package SAGE for the IBM PC/XT was purchased from Technoma, Heidelberg, West Germany. It was run on the IBM 3081 computer of I.P. Sharp Associates in Toronto, Canada.

ACCESSIBILITY OF THE DATA

The 5S and 5.8S rRNA databases are now also online accessible worldwide via the I.P. Sharp Timesharing Network. Requests should be sent either to Volker A. Erdmann or to mailbox code VAEFU in the I.P. Sharp electronic mail system. In the near future the databases will also be integrated into the EMBL nucleotide sequence data library.

Eubacterial 5S RNA Sequences

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                                   ....|....10...|....20...|....30...|....40...|....50...|....60...|....70...|....80
CLOSTRIDIUM PASTEURIANUM           ----UCCAGUGUCUAUGAC--UUAGAGGUAACAC-UCCUUC--CCAUUCCGAACAGGC-----AGGUUAAGCUCUAAUGU
BACILLUS STEAROTHERMOPHILUS        ----CCUAGUGACAAUAGC--GGAGAGGAAACAC-CCGUUC--CCAUCCCGAACACGG-----AAGUUAAGCUCUCCAGC
BACILLUS SUBTILIS                  ----UUUGGUGGCGAUAGC--GAAGAGGUCACAC-CCGUUC--CCAUACCGAACACGG-----AAGUUAAGCUCUUCAGC
BACILLUS LICHENIFORMIS             ----UUUGGUGGCGAUAGC--GAAGAGGUCACAC-CCGUUC--CCAUGCCGAACACGG-----AAGUUAAGCUCUUCAGC
BACILLUS MEGATERIUM                ----UCURGUGGCGAUAGC--GAAGAGGUCACAC-CCGUUC--CCAUACCGAACACGG-----AAGUUAAGCUCUUUAGC
BACILLUS PASTEURII                 ----UNUGGUGGCGAUAGC--GAAGAGGUCACAC-CCGUUC--CCAUACCGAACACGG-----AAGUUAAGCUCUUCAGC
BACILLUS FIRMUS                    ----UCYGGUGGCGAUAGC--GAGAAGGUCACAC-CCGUUC--CCAUACCGAACACGG-----AAGUUAAGCUUCUCAGC
BACILLUS BREVIS                    ----UCUGGUGAUGAUGGC--GGAGGGGACACAC-CCGUUC--CCAUACCGAACACGG-----CCGUUAAGCCCUCCAGC
BACILLUS ACIDOCALDARIUS            ----UCUGGUGACUAUAGC--GGAGGGGCAACAC-CCGUAC--CCAUCCCGAACACGG-----ACGUGAAGACCUCCAGC
LACTOBACILLUS VIRIDESCENS(MAJ)     ----UGUUGUGAUGAUGGC--AUUGAGGUCACAC-CUGUUC--CCAUACCGAACACAG-----AAGUUAAGCUCAAUAGC
LACTOBACILLUS VIRIDESCENS(MIN)     ----UGUUGUGAUGAUGGC--AUUGAGGCCACAC-CUGUUC--CCAUACCGAACACAG-----AAGUUAAGCUCAAUAGC
LACTOBACILLUS BREVIS               ----UGUGGUGGCGAUAGC--CUGAAGGAUACAC-CUGUUC--CCAUGCCGAACACAG-----AAGUUAAGCUUCAGCAC
STREPTOCOCCUS CREMORIS             ---UUUUGGUCAUCAUUGC--GAUGGAGAUACAC-CUGUUC--CCAUGUCGAACACAG-----AAGUUAAGUCCAUCUAC
STREPTOCOCCUS FAECALIS             ----UGUGGUGGCGAUAGC--GAGAAGGAUACAC-CUGUAA--CCAUGCCGAACACAG-----AAGUUAAGCUUCUUAGC
MICROCOCCUS LYSODEIKTICUS          --GUUACGGCGGCUAUAGC--GUGGGGGAAACGC-CCGGCC--GUAUAUCGAACCCGG-----AAGCUAAGCCCCAUAGC
SPIROPLASMA SP.                    ----UCUGGUGCUUAUGGC--AUAGUGGACACAC-CCGUUC--CCAUCCCGAACACGG-----AAGUUAAGCACUAUUAC
MYCOPLASMA CAPRICOLUM              -----UUGGUGGU-AUAGC--AUAGAGGUCACAC-CUGUUC--CCAUGCCGAACACAG-----AAGUUAAGCUCUAUUAC
MYCOPLASMA MYCOIDES                -----UUGGUGGU-AUAGC--AUAGAGGUCACAC-CUGUUC--CCAUGCCGAACACAG-----AAGUUAAGCUCUAUUAC

                                          A               B          C                     C'           B'

                                   ....|....90...|....100..|....110..|....120..|....130..|....140..|....150
CLOSTRIDIUM PASTEURIANUM           -GCU--(G)AU--GGU-ACUGCAG-GGGAAGCCCUGUGGAAGAGU(A)----GGU-CGACGCUGGGU------
BACILLUS STEAROTHERMOPHILUS        -GCC--(G)AU--GGU-AGU(U)GGG-GCCAGCGCCCC(U)GCAAGAGU(A)----GGU-CGUUGCUAGGC------
BACILLUS SUBTILIS                  -GCC--(G)AU--GGU-AGU(C)GGG-GGUUU-CCCCC(U)GUGAGAGU(A)----GGA-CGCCGCCAAGC------
BACILLUS LICHENIFORMIS             -GCC--(G)AU--GGU-AGU(U)GGG-GGCUU-CCCCC(U)GUGAGAGU(A)----GGA-CGCCGCCAAGC------
BACILLUS MEGATERIUM                -GCC--(R)AU--GGU-AGU(U)GGG-ACUUU-GUCCC(U)GNGAGAGU(A)----GGA-CGUUGCYAGGC------
BACILLUS PASTEURII                 -GCC--(G)AU--GGU-AGU(U)GGG-GUGUUAGCCCC(U)GCAAGAGU(A)----GGA-CGUUGCCARGC------
BACILLUS FIRMUS                    -GCC--(G)AU--GGU-AGU(U)RGG-GGCUG-UCCCC(U)GUGAGAGU(A)----GGA-CGCUGCCRGGC------
BACILLUS BREVIS                    -GCC--(A)AU--GGU-ACU(U)GCU-CCGCAGGGAGC(C)GGGAGAGU(A)----GGA-CGUCGCCAGGC------
BACILLUS ACIDOCALDARIUS            -GCC--GAG--AAU-ACUGGGA-GGGCAGCCUCCUGGGAAAGU(A)----GGU-CGUUGCCAGGC------
LACTOBACILLUS VIRIDESCENS(MAJ)     -GCC--GAA--AGU-AGU(U)GGA-GGAUCUCUUCC(U)GCGAGGAU(A)----GGA-CGUCGCAAUGC------
LACTOBACILLUS VIRIDESCENS(MIN)     -ACC--(G)AA--AGU-AGU(U)GGA-GGAUCUCUUCC(U)GCGAGGAU(A)----GGA-CGUCGCGAUGC------
LACTOBACILLUS BREVIS               -GCC--(G)AU--AGU-AGU(U)GGG-GGAUCGCCCCC(U)GCGAGGAU(A)----GGA-CGUUGCCACGC------
STREPTOCOCCUS CREMORIS             GGCG--GA---AGU-ACUUGGG-GG-UUGCCCCCUGGGAGA-U(A)----UGCGAGUGGCCAAGU------
STREPTOCOCCUS FAECALIS             -GCC--(G)AU--UGU-AGUGAGG-GGGUUGCCCCUUGUGAGAGU(A)----GGA-CGUCGCCACGC------
MICROCOCCUS LYSODEIKTICUS          -GCC--(G)AU--GGUUACUGUAA-CCGGGAGGUUGUGGGAGAGU(A)----GGU-CGCCGCCGUGA------
SPIROPLASMA SP.                    -GCC--(G)AC--GAU-AG------CCGCAAGG-----UGAAAAU(A)----GGG-CAGUGCCAGGU------
MYCOPLASMA CAPRICOLUM              -GGU--(G)AA--GAU-AUU-----ACUGAUGU----GAGAAAAU(A)----GCA-AGCUGCCAGUU------
MYCOPLASMA MYCOIDES                -GGU--(G)AA--AAU-AUU-----ACUUAUGU----GAGAAGAU(A)----GCA-AGCUGCCAGUU------

                                      D                E            E'          D'         A'
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Eubacterial 5 S RNA Sequences

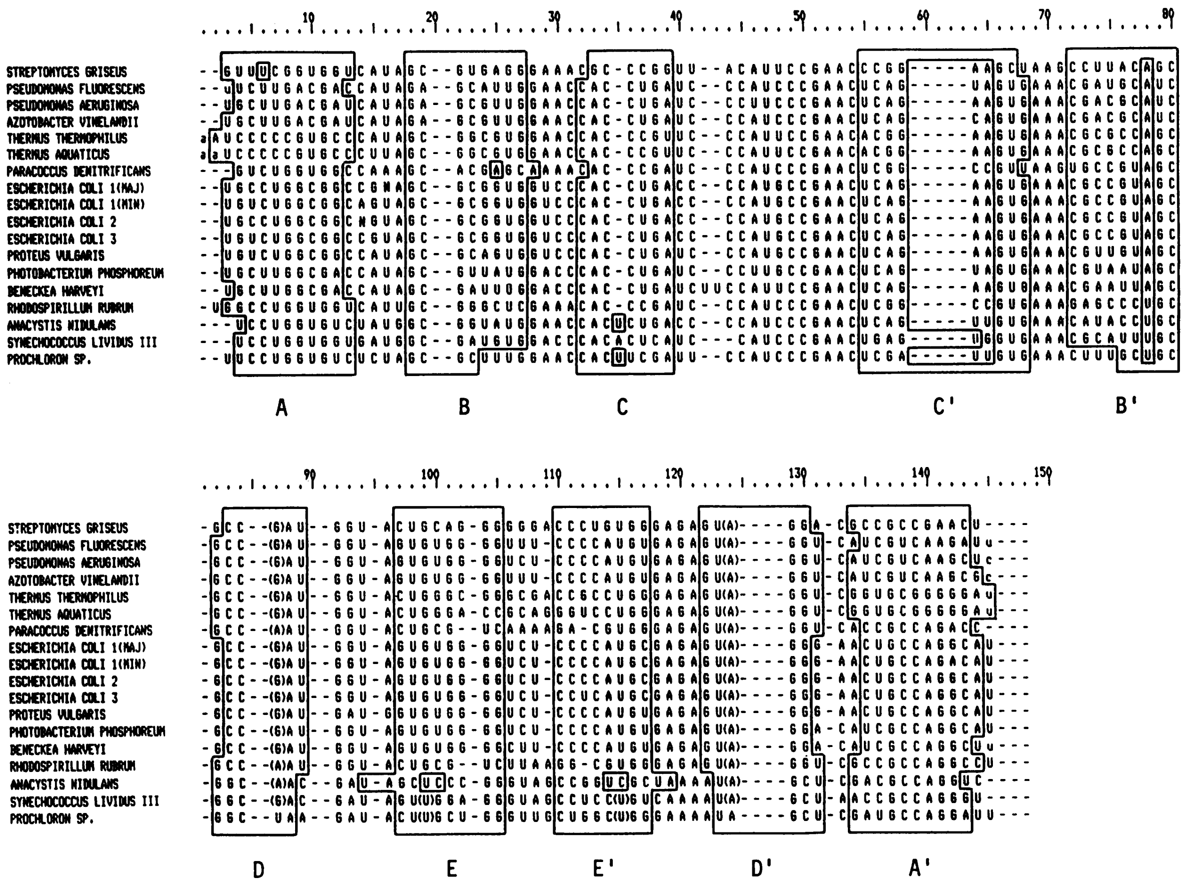
Species	Specification	Taxonomic position		Reference
Clostridium pasteurianum	ATCC 6013	Grampositive, endosporous	Clostridiaceae	17
Bacillus stearothermophilus	Strain 1430FV		Bacillaceae	18
Bacillus subtilis	Strain BD170,major fract.			18
Bacillus licheniformis	Strain S244,major fract.			19
Bacillus megaterium[a]	Strain KM			20
Bacillus pasteurii[b]	ATCC 11859			20
Bacillus firmus[c]	ATCC 14575			20
Bacillus brevis	ATCC 8185			20
Bacillus acidocaldarius	—			10
Lactobacillus viridescens (maj)	ATCC 12706	Grampositive, non endosporous	Lactobacillaceae	21
Lactobacillus viridescens (min)	ATCC 12706			22
Lactobacillus brevis	Strain X-2			20
Streptococcus cremoris	ATCC 11603		Streptococcaceae	23
Streptococcus faecalis	—			20
Micrococcus lysodeikticus	ATCC 4698		Micrococcaceae	24
Spiroplasma sp.	Strain BC3	Mycoplasmatales		25
Mycoplasma capricolum	ATCC 27343			26
Mycoplasma mycoides	*subsp. capri*, strain PG3			25

(a) Sequence heterogeneities : G/A_8, G/A_{87}, U/G_{117}, C/U_{139}.

(b) Sequence heterogeneities : G/U_6, G/A_{141}.

(c) Sequence heterogeneities : C/U_7, G/A_{100}, G/A_{140}.

Eubacterial 5 S RNA Sequences



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                             ....|....10...|....20...|....30...|....40...|....50...|....60...|....70...|....80
STREPTOMYCES GRISEUS         --GUUUCGGUGGUCAUAGC--GUGAGGGAAACGC-CCGGUU--ACAUUCCGAACCCGG-----AAGCUAAGCCUUACAGC
PSEUDOMONAS FLUORESCENS      --uUCUUGACGACCAUAGA--GCAUUGGAACCAC-CUGAUC--CCAUCCCGAACUCAG-----UAGUGAAACGAUGCAUC
PSEUDOMONAS AERUGINOSA       --UGCUUGACGAUCAUAGA--GCGUUGGAACCAC-CUGAUC--CCUUCCCGAACUCAG-----AAGUGAAACGACGCAUC
AZOTOBACTER VINELANDII       --UGCUUGACGAUCAUAGA--GCGUUGGAACCAC-CUGAUC--CCAUCCCGAACUCAG-----CAGUGAAACGACGCAUC
THERMUS THERMOPHILUS         aAUCCCCCGUGCCCAUAGC--GGCGUGGAACCAC-CCGUUC--CCAUUCCGAACACGG-----AAGUGAAACGCGCCAGC
THERMUS AQUATICUS            aaUCCCCCGUGCCCUUAGC--GGCGUGGAACCAC-CCGUUC--CCAUUCCGAACACGG-----AAGUGAAACGCGCCAGC
PARACOCCUS DENITRIFICANS     ---GUCUGGUGGCCAAAGC--ACGAGCAAAACAC-CCGAUC--CCAUCCCGAACUCGG-----CCGUUAAGUGCCGUAGC
ESCHERICHIA COLI 1(MAJ)      --UGCCUGGCGGCCGNAGC--GCGGUGGUCCCAC-CUGACC--CCAUGCCGAACUCAG-----AAGUGAAACGCCGUAGC
ESCHERICHIA COLI 1(MIN)      --UGUCUGGCGGCAGUAGC--GCGGUGGUCCCAC-CUGACC--CCAUGCCGAACUCAG-----AAGUGAAACGCCGUAGC
ESCHERICHIA COLI 2           --UGCCUGGCGGCNGUAGC--GCGGUGGUCCCAC-CUGACC--CCAUGCCGAACUCAG-----AAGUGAAACGCCGUAGC
ESCHERICHIA COLI 3           --UGUCUGGCGGCCGUAGC--GCGGUGGUCCCAC-CUGACC--CCAUGCCGAACUCAG-----AAGUGAAACGCCGUAGC
PROTEUS VULGARIS             --UGUCUGGCGGCCAUAGC--GCAGUGGUCCCAC-CUGAUC--CCAUGCCGAACUCAG-----AAGUGAAACGUUGUAGC
PHOTOBACTERIUM PHOSPHOREUM   --UGCUUGGCGACCAUAGC--GUUAUGGACCCAC-CUGAUC--CCUUGCCGAACUCAG-----UAGUGAAACGUAAUAGC
BENECKEA HARVEYI             --UGCUUGGCGACCAUAGC--GAUUUGGACCCAC-CUGAUCUUCCAUUCCGAACUCAG-----AAGUGAAACGAAUUAGC
RHODOSPIRILLUM RUBRUM        -UGGCCUGGUGGUCAUUGC--GGGCUCGAAACAC-CCGAUC--CCAUCCCGAACUCGG-----CCGUGAAAGAGCCCUGC
ANACYSTIS NIDULANS           ---UCCUGGUGUCUAUGGC--GGUAUGGAACCACUCUGACC--CCAUCCCGAACUCAG-----UUGUGAAACAUACCUGC
SYNECHOCOCCUS LIVIDUS III    ---UCCUGGUGGUGAUGGC--GAUGUGGACCCACACUCAUC---CAUCCCGAACUGAG-----UGGUGAAACGCAUUUGC
PROCHLORON SP.               --UUCCUGGUGUCUCUAGC--GCUUUGGAACCACUUCGAUU--CCAUCCCGAACUCGA-----UUGUGAAACUUUGCUGC

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                             ....|....90...|....100..|....110..|....120..|....130..|....140..|....150
STREPTOMYCES GRISEUS         -GCC--(G)AU--GGU-ACUGCAG-GGGGGACCCUGUGGGAGAGU(A)----GGA-CGCCGCCGAACU----
PSEUDOMONAS FLUORESCENS      -GCC--(G)AU--GGU-AGUGUGG-GGUUU-CCCCAUGUGAGAGU(A)----GGU-CAUCGUCAAGAUu---
PSEUDOMONAS AERUGINOSA       -GCC--(G)AU--GGU-AGUGUGG-GGUCU-CCCCAUGUGAGAGU(A)----GGU-CAUCGUCAAGCUc---
AZOTOBACTER VINELANDII       -GCC--(G)AU--GGU-AGUGUGG-GGUUU-CCCCAUGUGAGAGU(A)----GGU-CAUCGUCAAGCGc---
THERMUS THERMOPHILUS         -GCC--(G)AU--GGU-ACUGGGC-GGGCGACCGCCUGGGAGAGU(A)----GGU-CGGUGCGGGGGAu---
THERMUS AQUATICUS            -GCC--(G)AU--GGU-ACUGGGA-CCGCAGGGUCCUGGGAGAGU(A)----GGU-CGGUGCGGGGGAu---
PARACOCCUS DENITRIFICANS     -GCC--(A)AU--GGU-ACUGCG--UCAAAAGA-CGUGGGAGAGU(A)----GGU-CACCGCCAGACC----
ESCHERICHIA COLI 1(MAJ)      -GCC--(G)AU--GGU-AGUGUGG-GGUCU-CCCCAUGCGAGAGU(A)----GGG-AACUGCCAGGCAU---
ESCHERICHIA COLI 1(MIN)      -GCC--(G)AU--GGU-AGUGUGG-GGUCU-CCCCAUGCGAGAGU(A)----GGG-AACUGCCAGACAU---
ESCHERICHIA COLI 2           -GCC--(G)AU--GGU-AGUGUGG-GGUCU-CCCCAUGCGAGAGU(A)----GGG-AACUGCCAGGCAU---
ESCHERICHIA COLI 3           -GCC--(G)AU--GGU-AGUGUGG-GGUCU-CCUCAUGCGAGAGU(A)----GGG-AACUGCCAGGCAU---
PROTEUS VULGARIS             -GCC--(G)AU--GAU-GGUGUGG-GGUCU-CCCCAUGUGAGAGU(A)----GGG-AACUGCCAGGCAU---
PHOTOBACTERIUM PHOSPHOREUM   -GCC--(G)AU--GGU-AGUGUGG-GGUCU-CCCCAUGUGAGAGU(A)----GGA-CAUCGCCAGGCAU---
BENECKEA HARVEYI             -GCC--(G)AU--GGU-AGUGUGG-GGCUU-CCCCAUGUGAGAGU(A)----GGA-CAUCGCCAGGCUu---
RHODOSPIRILLUM RUBRUM        -GCC--(A)AU--GGU-ACUGCG--UCUUAAGG-CGUGGGAGAGU(A)----GGU-CGCCGCCAGGCCU---
ANACYSTIS NIDULANS           -GGC--(A)AC--GAU-AGCUCCC-GGGUAGCCGGUCGCUAAAAU(A)----GCU-CGACGCCAGGUC----
SYNECHOCOCCUS LIVIDUS III    -GGC--(G)AC--GAU-AGU(U)GGA-GGGUAGCCUCC(U)GUCAAAAU(A)----GCU-AACCGCCAGGGU----
PROCHLORON SP.               -GGC--UAA--GAU-ACU(U)GCU-GGGUUGCUGGC(U)GGGAAAAUA----GCU-CGAUGCCAGGAUU---

                               D               E           E'          D'          A'
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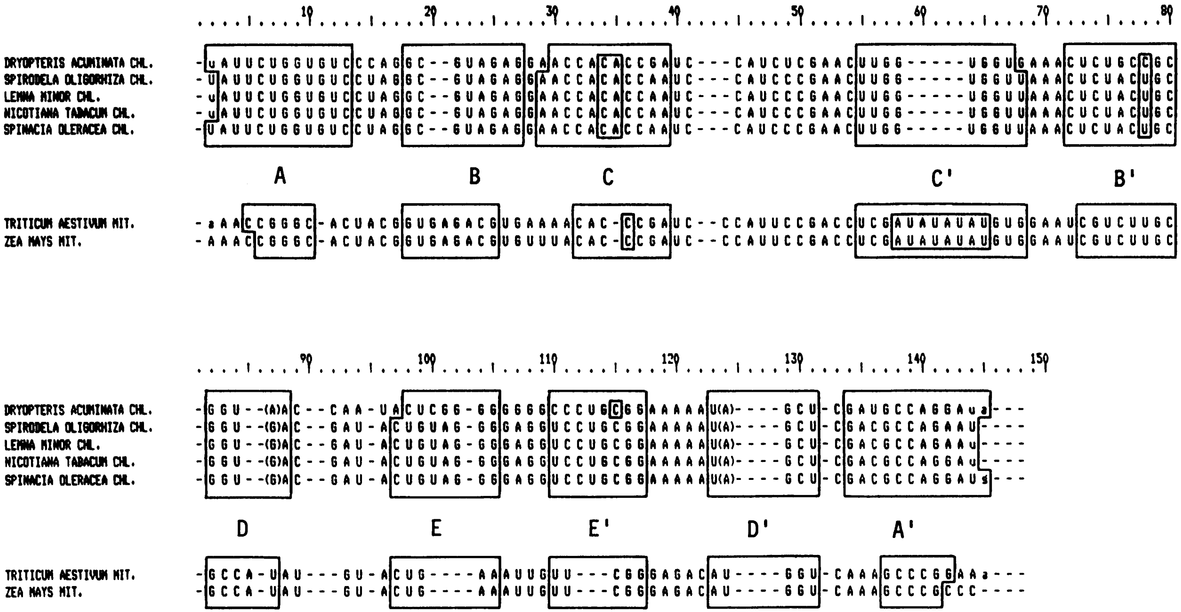
Eubacterial 5 S RNA Sequences

Species	Specification	Taxonomic position		Reference
Streptomyces griseus	Strain 45-H	Actinomycetales	Streptomycetaceae	27
Pseudomonas fluorescens	ATCC 13525	Gram negative, aerobic	Pseudomonaceae	28, 9
Pseudomonas aeruginosa	CCEB 481			9
Azotobacter vinelandii	NCIB 8789		Azotobacteraceae	9
Thermus thermophilus	Strain HB 8		Uncertain affiliation	29,30
Thermus aquaticus	ATCC 25104			31,10
Paracoccus denitrificans	ATCC 13543		Uncertain affiliation	32
Escherichia coli 1 (maj)[a]	MRE 600	Gram negative, fac.anaerobic	Enterobacteriaceae	33
Escherichia coli 1 (min)	MRE 600			34
Escherichia coli 2[b]	CA 265			33
Escherichia coli 3	A 19			35
Proteus vulgaris	—			34
Photobacterium phosphoreum	Strain 8265		Vibrionaceae	36
Beneckea harveyi	Strain 392		Uncertain affiliation	37
Rhodospirillum rubrum	Strain S1	Rhodospirillales	Rhodospirillaceae	38
Anacystis nidulans	Strain 1405/1 Kratz/Allen	Cyanobacteria		39
Synechococcus lividus (III)	—			40
Prochloron sp.	Lissoclinum patella host			32

(a) Sequence heterogeneity : G/U_{16}.

(b) Sequence heterogeneity : C/A_{14}.

Chloroplast and Mitochondrial 5 S RNA Sequences



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                              ....|....10....|....20....|....30....|....40....|....50....|....60....|....70....|....80
DRYOPTERIS ACUMINATA CHL.     -uAUUCUGGUGUCCCAGGC--GUAGAGGAACCACACCGAUC---CAUCUCGAACUUGG------UGGUGAAACUCUGCCGC
SPIRODELA OLIGORHIZA CHL.     -UAUUCUGGUGUCCUAGGC--GUAGAGGAACCACACCAAUC---CAUCCCGAACUUGG------UGGUUAAACUCUACUGC
LEMNA MINOR CHL.              -uAUUCUGGUGUCCUAGGC--GUAGAGGAACCACACCAAUC---CAUCCCGAACUUGG------UGGUUAAACUCUACUGC
NICOTIANA TABACUM CHL.        -uAUUCUGGUGUCCUAGGC--GUAGAGGAACCACACCAAUC---CAUCCCGAACUUGG------UGGUUAAACUCUACUGC
SPINACIA OLERACEA CHL.        -UAUUCUGGUGUCCUAGGC--GUAGAGGAACCACACCAAUC---CAUCCCGAACUUGG------UGGUUAAACUCUACUGC

                                     A               B          C                        C'              B'

TRITICUM AESTIVUM MIT.        -aAACCGGGC-ACUACGGUGAGACGUGAAAACAC-CCGAUC--CCAUUCCGACCUCGAUAUAUAUGUGGAAUCGUCUUGC
ZEA MAYS MIT.                 -AAACCGGGC-ACUACGGUGAGACGUGUUUACAC-CCGAUC--CCAUUCCGACCUCGAUAUAUAUGUGGAAUCGUCUUGC


                              ....|....90....|....100...|....110...|....120...|....130...|....140...|....150
DRYOPTERIS ACUMINATA CHL.     -GGU--(A)AC--CAA-UACUCGG-GGGGGGCCCUGCGGAAAAAU(A)----GCU-CGAUGCCAGGAua---
SPIRODELA OLIGORHIZA CHL.     -GGU--(G)AC--GAU-ACUGUAG-GGGAGGUCCUGCGGAAAAAU(A)----GCU-CGACGCCAGAAU----
LEMNA MINOR CHL.              -GGU--(G)AC--GAU-ACUGUAG-GGGAGGUCCUGCGGAAAAAU(A)----GCU-CGACGCCAGAAu----
NICOTIANA TABACUM CHL.        -GGU--(G)AC--GAU-ACUGUAG-GGGAGGUCCUGCGGAAAAAU(A)----GCU-CGACGCCAGGAu----
SPINACIA OLERACEA CHL.        -GGU--(G)AC--GAU-ACUGUAG-GGGAGGUCCUGCGGAAAAAU(A)----GCU-CGACGCCAGGAUs---

                                  D               E            E'          D'          A'

TRITICUM AESTIVUM MIT.        -GCCA-UAU---GU-ACUG----AAAUUGUU---CGGGAGACAU----GGU-CAAAGCCCGGAAa---
ZEA MAYS MIT.                 -GCCA-UAU---GU-ACUG----AAAUUGUU---CGGGAGACAU----GGU-CAAAGCCCGCCC----
```

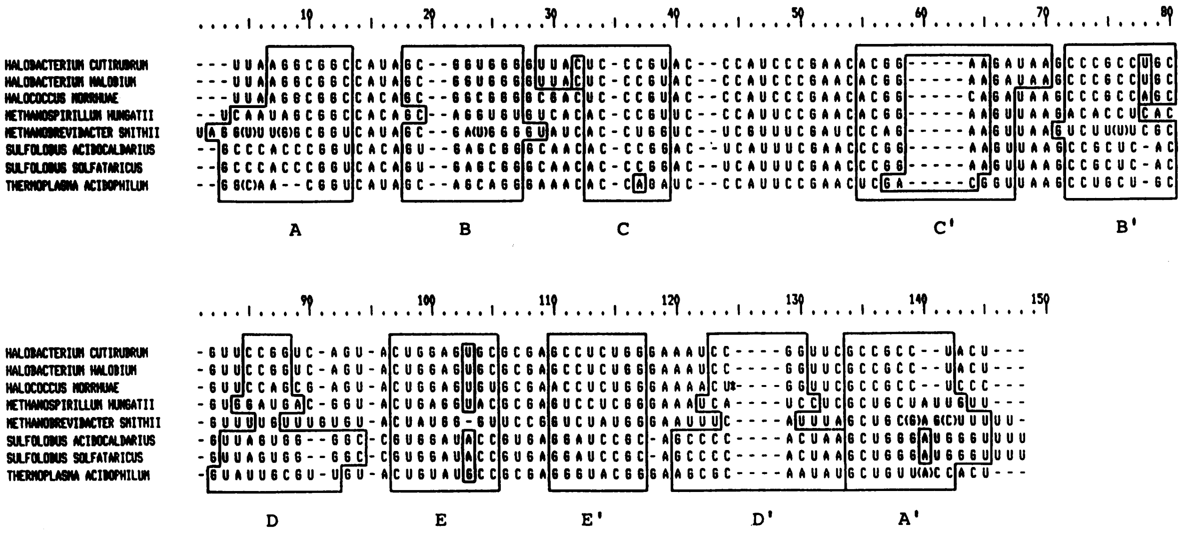
Chloroplast 5 S RNA Sequences

Species	Specifications	Taxonomic position	Reference
Dryopteris acuminata chl.	—	Pteridophyta	41
Spirodela oligorhiza chl.	clone pSpoC18M	Spermatophyta	42
Lemna minor chl.	—		43
Nicotiana tabacum chl.	var. bright-yellow		44,45
Spinacia oleracea chl.	var. 424		46

Mitochondrial 5 S RNA Sequences

Triticum aestivum mit.	var. thatcher	Spermatophyta	47
Zea mays mit.	clone Zmmt N542		48

Archaebacterial 5S RNA Sequences



```
                                      10        20        30        40        50        60        70        80
HALOBACTERIUM CUTIRUBRUM      ---UUAAGGCGGCCAUAGC--GGUGGGGUUACUC-CCGUAC--CCAUCCCGAACACGG-----AAGAUAAGCCCGCCUGC
HALOBACTERIUM HALOBIUM        ---UUAAGGCGGCCAUAGC--GGUGGGGUUACUC-CCGUAC--CCAUCCCGAACACGG-----AAGAUAAGCCCGCCUGC
HALOCOCCUS MORRHUAE           ---UUAAGGCGGCCACAGC--GGCGGGGCGACUC-CCGUAC--CCAUCCCGAACACGG-----CAGAUAAGCCCGCCAGC
METHANOSPIRILLUM HUNGATII     --UCAAUAGCGGCCACAGC--AGGUGUGUCACAC-CCGUUC--CCAUUCCGAACACGG-----AAGUUAAGACACCUCAC
METHANOBREVIBACTER SMITHII    UAGG(U)UU(G)GCGGUCAUAGC--GA(U)GGGGUAUCAC-CUGGUC--UCGUUUCGAUCCCAG-----AAGUUAAGUCUU(U)UCGC
SULFOLOBUS ACIDOCALDARIUS     --GCCCACCCGGUCACAGU--GAGCGGGCAACAC-CCGGAC--UCAUUUCGAACCCGG-----AAGUUAAGCCGCUC-AC
SULFOLOBUS SOLFATARICUS       --GCCCACCCGGUCACAGU--GAGCGGGCAACAC-CCGGAC--UCAUUUCGAACCCGG-----AAGUUAAGCCGCUC-AC
THERMOPLASMA ACIDOPHILUM      --GG(C)AA--CGGUCAUAGC--AGCAGGGAAACAC-CAGAUC--CCAUUCCGAACUCGA-----CGGUUAAGCCUGCU-GC

                                      90        100       110       120       130       140       150
HALOBACTERIUM CUTIRUBRUM      -GUUCCGGUC-AGU-ACUGGAGUGCGCGAGCCUCUGGGAAAUCC----GGUUCGCCGCC--UACU---
HALOBACTERIUM HALOBIUM        -GUUCCGGUC-AGU-ACUGGAGUGCGCGAGCCUCUGGGAAAUCC----GGUUCGCCGCC--UACU---
HALOCOCCUS MORRHUAE           -GUUCCAGCG-AGU-ACUGGAGUGUGCGAACCUCUGGGAAAACU*----GGUUCGCCGCC--UCCC---
METHANOSPIRILLUM HUNGATII     -GUGGAUGAC-GGU-ACUGAGGUACGCGAGUCCUCGGGAAAUCA----UCCUCGCUGCUAUUGUU---
METHANOBREVIBACTER SMITHII    -GUUUUGUUUGUGU-ACUAUGG-GUUCCGGUCUAUGGGAAUUUC----AUUUAGCUGC(G)AG(C)UUUUU-
SULFOLOBUS ACIDOCALDARIUS     -GUUAGUGG--GGC-CGUGGAUACCGUGAGGAUCCGC-AGCCCC----ACUAAGCUGGGAUGGGUUUU
SULFOLOBUS SOLFATARICUS       -GUUAGUGG--GGC-CGUGGAUACCGUGAGGAUCCGC-AGCCCC----ACUAAGCUGGGAUGGGUUUU
THERMOPLASMA ACIDOPHILUM      -GUAUUGCGU-UGU-ACUGUAUGCCGCGAGGGUACGGGAAGCGC----AAUAUGCUGUU(A)CCACU---
```

Archaebacterial 5 S RNA Sequences

Species	Specification	Taxonomic position	Reference
Halobacterium cutirubrum	NRC 34001	Halobacteriales	49,50
Halobacterium halobium	Strain R1		51
Halococcus morrhuae[a]	ATCC 17082		52
Methanospirillum hungatii	—	Methanobacteriales	50
Metanobrevibacter smithii	Strain PS		50
Sulfolobus acidocaldarius[b]	—	Sulfolobales	53
Sulfolobus solfataricus[b]	MT 4		10
Thermoplasma acidophilum	Strain 122-1B2 or 122-1B3	Thermoplasmatales	54

(a) The chain length of the complete 5 S RNA is 231 nucleotides. The following sequence has to be inserted between positions 124 and 129 : GCCUCGCAAGAGGGGCCAAGUGUGAGCCCAGGAGCGCAAUCGGUAGUACACGCGGAGUCCGUCCCGGUGGAACCCGAGACCGCUCCGUUACAACGGCUCAUAACUAGU.

(b) The C residue at position 37 has an unidenified modification.

Eukaryotic 5 S RNA Sequences

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                            ....|....10....|....20....|....30....|....40....|....50....|....60....|....70....|....80
HOMO SAPIENS                ---GUCU-ACGGCCAUACC--ACCCUGAACGCGC-CCGAUC--UCGU-CUGAUCUCGG------AAGCUAAGCAGGGUCGG
RATTUS RATTUS               ---GUCU-ACGGCCAUACC--ACCCUGAACGCGC-CCGAUC--UCGU-CUGAUCUCGG------AAGCUAAGCAGGGUCGG
GALLUS GALLUS (I)           ---GCCU-ACGGCCAUCCC--ACCCUGGUAACGC-CCGAUC--UCGU-CUGAUCUCGG------AAGCUAAGCAGGGUCGG
GALLUS GALLUS (II)          ---GCCU-ACGGCCAUACC--ACCCUGGAAACGC-CCGAUC--UCGU-CUGAUCUCGG------AAGCUAAGCAGGGUCGG
XENOPUS LAEVIS              ---GCCU-ACGGCCACACC--ACCCUGAAAGUGC-CUGAUC--UCGU-CUGAUCUCAG------AAGCGAUACAGGGUCGG
XENOPUS BOREALIS 1          ---GCCU-ACGGCCACACC--CCCCUGAAAGUGC-CCGAUC--UCGU-CUGAUCUCGG------AAGCGAUGCAGGGCCGG
XENOPUS BOREALIS 2          ---GCCU-ACGGCCACACC--CCC(C)UGAAAGUGC-CCGAUC--UCGU-CUGAUCUCGG------AAGCGAUGCA(A)GGUCGG
XENOPUS BOREALIS 3          ---CCCU-GCGGCUACACC--CCCCUGAAAGAGC-CUGAUC--UUGU-CUGAUCUCAG------AAGCCAUGCGGGGCCGA
NOTOPHTALMUS VIRIDESCENS    ---GCUU-ACGGCCAUACC--ACCCUGAAAGCAC-CUGAUC--UCGU-CUGAUCUCAG------AAGUUAAGCAGGGUCGG
SALMO GAIRDNERI              ---GCUU-ACGGCCAUACC--A(G)CCUGAAUACGC-CCGAUC--UCGU-CCGAUCUCGG------AAGCUAAGCAGG(G)UCGG
MISGURNUS FOSSILIS(S)       ---GCUU-ACGGCCAUACC--ACCCUGAGCACGC-CCGAUC--UCGU-CCGAUCUCGG------AAGCUAAGCAGGGUCGG
MISGURNUS FOSSILIS(O)       ---GCUU-ACGGCCACACC--A(A)CCUGAGCAAGC-CCGAUC--UCGU-CUGAUCUCGG------AAGCCAAGCAGG(G)UUGG
HALOCYNTHIA RORETZI         ---AUCU-ACGGCCAUACC--ACAUUGAGAGCAC-CCGAUC--UCGU-UCGAUCUCGG------AAGUUAAGCAAUGUAGG
ACYRTHOSIPHON MAGNOLIAE     ---G(G)CA-ACG(A)CCAUACC--ACGUUGAAUACAC-CAGUUC--UCGU-CCGAUCACUG------AAGUUAAGCAACGUCGG
DROSOPHILA MELANOGASTER     ---GCCA-ACGACCAUACC--ACGCUGAAUACAU-CGGUUC--UCGU-CCGAUCACCG------AAAUUAAGCAGCGUCGG
PHILOSAMIA CYNTHIA-RICINI   ---GCCA-ACG(U)CCAUACC--ACGUUGAAAACAC-CGGUUC--UCGU-CCGAUCACCG------AAGUUAAGCAACGUCGG
BOMBYX MORI                 ---GCCA-ACGUCCAUACC--AUGUUGAAUACAC-CGGUUC--UCGU-CCGAUCACCG------AAGUCAAGCAACAUCGG
ARTEMIA SALINA              ---ACCA-ACGGCCAUACC--ACGUUGAAAGUAC-CCAGUC--UCGU-CAGAUCCUGG------AAGUCACACAACGUCGG

                                 A            B           C                      C'          B'
```
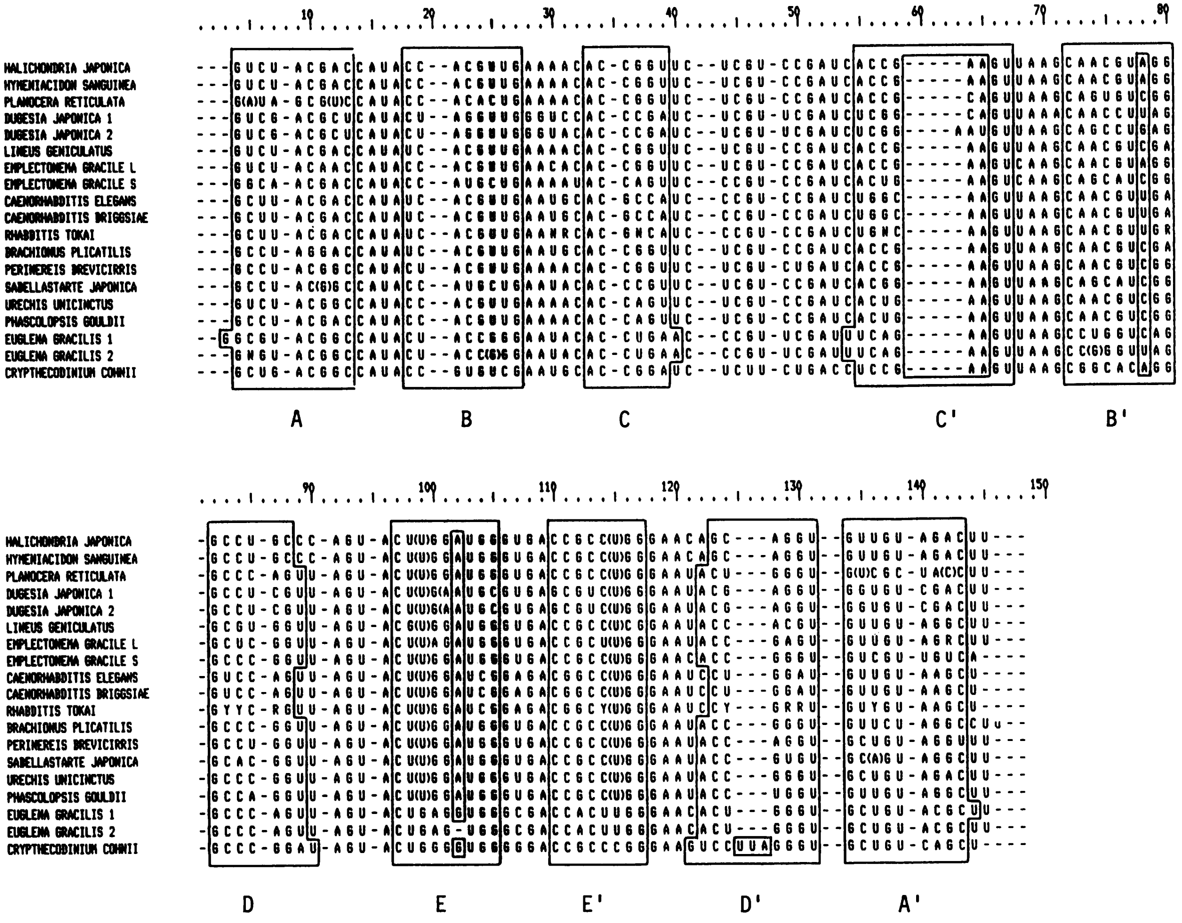

```
                            ....|....90....|....100....|....110....|....120....|....130....|....140....|....150
HOMO SAPIENS                -GCCU-GGUU-AGU-ACU(U)GGAUGGGAGACCGCC(U)GGGAAUACC---GGGU--GCUGU-AGGCUu---
RATTUS RATTUS               -GCCU-GGUU-AGU-ACU(U)GGAUGGGAGACCGCC(U)GGGAAUACC---GGGU--GCUGU-AGGCUUU--
GALLUS GALLUS (I)           -GCCU-GGUU-AGU-ACU(U)GGAUGGGAGACCUCC(U)GGGAAUACC---GGGU--GCUGU-AGGCUu---
GALLUS GALLUS (II)          -GCUC-GGUU-AGU-ACU(U)GGAUGGGAGACUGCC(U)GGGAAUACC---GAGU--GUCGU-AGGCGu---
XENOPUS LAEVIS(O)           -GCCU-GGUU-AGU-ACC(U)GGAUGGGAGACCGCC(U)GGGAAUACC---AGGU--GUCGU-AGGCUU---
XENOPUS BOREALIS(O) 1       -GCCU-GGUU-AGU-ACC(U)GGAUGGGAGACCGCC(U)GGGAAUACC---AGGU--GUCGU-AGGCUU---
XENOPUS BOREALIS(O) 2       -GCCU-GGUU-AGU-ACC(U)GGAUGGGAGACCGCC(U)GGGAAUACC---AGGU--GUCGU-AGGCUU---
XENOPUS BOREALIS(O) 3       -CCCU-(G)GUU-AGU-ACC(U)GGAUGGGAGACCACC(U)GGGAAUAC(A)---AGGU--GUUGU-AGUCUU---
NOTOPHTALMUS VIRIDESCENS    -GCCU-GGUU-AGU-ACCUGGAUGGGAGACCGCCUUGGAAUACC---AGGU--GCUGU-AGGCUU---
SALMO GAIRDNERI             -GCCU-GGUU-AGU-ACU(U)GGAUGGGAGACCGCC(U)GGGAAUACC---AGGU--GCUGU-AAGCUu---
MISGURNUS FOSSILIS(S)       -GCCU-GGUU-AGU-ACU(U)GGAUGGGAGACUGCC(U)GGGAAUACC---AGGU--GUUGU-AAGCUu---
MISGURNUS FOSSILIS(O)       -GCCU-GGUU-AGU-ACU(U)GGAUGGGAGACUGCC(U)GGGAAUACC---AGGU--GUUGU-AAGCUu---
HALOCYNTHIA RORETZI         -GAUC-AGUU-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACU---GGUU--GCUGU-AGAAA----
ACYRTHOSIPHON MAGNOLIAE     -GCGU-AGUU-AGU-ACU(U)GGAUGGGUGACCGCU(U)GGGAACACU---ACGU--G(C)CGU-UG(G)CAU---
DROSOPHILA MELANOGASTER     -GCGC-GGUU-AGU-ACU(U)AGAUGRGGGACCGCU(U)GGGAACACC---GCGU--GUUGU-UGGCCU---
PHILOSAMIA CYNTHIA-RICINI   -GCGC-GGUC-AGU-ACU(U)GGAUGGGUGACCACC(U)GGGAACACC---GCGU--G(C)CGU-UGGCU----
BOMBYX MORI                 -GCGU-GGUC-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAACACC---ACGU--GAUGU-UGGCUU---
ARTEMIA SALINA              -GCCC-GGUC-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAACACC---GGGU--GCUGU-UGGCAU---

                              D               E          E'           D'          A'
```

Eukaryotic 5 S RNA Sequences

Species	Specification	Taxonomic position		Reference
		Phylum	Classis	
Homo sapiens	KB cells	Chordata	Mammalia	55
Rattus rattus	liver			56
Gallus gallus I	liver and brain cells		Aves	57,58
Gallus gallus II	liver and brain cells			58
Xenopus laevis	oocytes		Amphibia	59
Xenopus borealis 1	clone pXb01, oocytes			60
Xenopus borealis 2	clone pXb01, oocytes			60
Xenopus borealis 3	clone pXb01, oocytes			60
Notophtalmus viridescens	clone p5510			61
Salmo gairdneri	liver		Osteichtyes	62
Misgurnus fossilis (s)	liver			63
Misgurnus fossilis (o)	oocytes			63
Halocynthia roretzi	branchial pouches		Tunicata	64
Acyrthosiphon magnoliae	whole organism	Arthropoda	Hexapoda	65
Drosophila melanogaster[a]	clone N1			66,67
Philosamia cynthia-ricini	posterior silkglands			68
Bombyx mori	silkglands			69
Artemia salina	cysts		Crustacea	70

(a) Sequence heterogeneity : G/A_{105}.

Eukaryotic 5 S RNA Sequences



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HALICHONDRIA JAPONICA         ---GUCU-ACGACCAUACC--ACGUUGAAAACAC-CGGUUC--UCGU-CCGAUCACCG-----AAGUUAAGCAACGUAGG
HYMENIACIDON SANGUINEA        ---GUCU-ACGACCAUACC--ACGUUGAAAACAC-CGGUUC--UCGU-CCGAUCACCG-----AAGUUAAGCAACGUAGG
PLANOCERA RETICULATA          ---G(A)UA-GCG(U)CCAUACC--ACACUGAAAACAC-CGGUUC--UCGU-CCGAUCACCG-----CAGUUAAGCAGUGUCGG
DUGESIA JAPONICA 1            ---GUCG-ACGCUCAUACU--AGGUUGGGUCCAC-CCGAUC--UCGU-UCGAUCUCGG-----CAGUUAAACAACCUUAG
DUGESIA JAPONICA 2            ---GUCG-ACGCUCAUACU--AGGUUGGGUACAC-CCGAUC--UCGU-UCGAUCUCGG----AAUGUUAAGCAGCCUGAG
LINEUS GENICULATUS            ---GUCU-ACGACCAUAUC--ACGUUGAAAACAC-CGGUUC--UCGU-CCGAUCACCG-----AAGUUAAGCAACGUCGA
EMPLECTONEMA GRACILE L        ---GUCU-ACAACCAUACC--ACGUUGAACACAC-CGGUUC--UCGU-CCGAUCACCG-----AAGUCAAGCAACGUAGG
EMPLECTONEMA GRACILE S        ---GGCA-ACGACCAUACC--AUGCUGAAAAUAC-CAGUUC--CCGU-CCGAUCACUG-----AAGUCAAGCAGCAUCGG
CAENORHABDITIS ELEGANS        ---GCUU-ACGACCAUAUC--ACGUUGAAUGCAC-GCCAUC--CCGU-CCGAUCUGGC-----AAGUUAAGCAACGUUGA
CAENORHABDITIS BRIGGSIAE      ---GCUU-ACGACCAUAUC--ACGUUGAAUGCAC-GCCAUC--CCGU-CCGAUCUGGC-----AAGUUAAGCAACGUUGA
RHABDITIS TOKAI               ---GCUU-ACGACCAUAUC--ACGUUGAANRCAC-GNCAUC--CCGU-CCGAUCUGNC-----AAGUUAAGCAACGUUGR
BRACHIONUS PLICATILIS         ---GCCU-AGGACCAUAUC--ACGUUGAAUGCAC-CGGUUC--UCGU-CCGAUCACCG-----AAGUUAAGCAACGUCGA
PERINEREIS BREVICIRRIS        ---GCCU-ACGGCCAUACU--ACGUUGAAAACAC-CGGUUC--UCGU-CUGAUCACCG-----AAGUUAAGCAACGUCGG
SABELLASTARTE JAPONICA        ---GCCU-AC(G)GCCAUACC--AUGCUGAAUACAC-CCGUUC--UCGU-CCGAUCACGG-----AAGUUAAGCAGCAUCGG
URECHIS UNICINCTUS            ---GUCU-ACGGCCAUACC--ACGUUGAAAACAC-CAGUUC--UCGU-CCGAUCACUG-----AAGUUAAGCAACGUCGG
PHASCOLOPSIS GOULDII          ---GCCU-ACGACCAUACC--ACGUUGAAAACAC-CAGUUC--UCGU-CCGAUCACUG-----AAGUUAAGCAACGUCGG
EUGLENA GRACILIS 1            --GGCGU-ACGGCCAUACU--ACCGGGAAUACAC-CUGAAC--CCGU-UCGAUUUCAG-----AAGUUAAGCCUGGUCAG
EUGLENA GRACILIS 2            ---GNGU-ACGGCCAUACU--ACC(G)GGAAUACAC-CUGAAC--CCGU-UCGAUUUCAG-----AAGUUAAGCC(G)GGUUAG
CRYPTHECODINIUM COHNII        ---GCUG-ACGGCCAUACC--GUGUCGAAUGCAC-CGGAUC--UCUU-CUGACCUCCG-----AAGUUAAGCGGCACAGG
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HALICHONDRIA JAPONICA         -GCCU-GCCC-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAACAGC---AGGU--GUUGU-AGACUU---
HYMENIACIDON SANGUINEA        -GCCU-GCCC-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAACAGC---AGGU--GUUGU-AGACUU---
PLANOCERA RETICULATA          -GCCC-AGUU-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACU---GGGU--G(U)CGC-UA(C)CUU---
DUGESIA JAPONICA 1            -GCCU-CGUU-AGU-ACU(U)G(AAUGCGUGAGCGUC(U)GGGAAUACG---AGGU--GGUGU-CGACUU---
DUGESIA JAPONICA 2            -GCCU-CGUU-AGU-ACU(U)G(AAUGCGUGAGCGUC(U)GGGAAUACG---AGGU--GGUGU-CGACUU---
LINEUS GENICULATUS            -GCGU-GGUU-AGU-ACG(U)GGAUGGGUGACCGCC(U)CGGAAUACC---ACGU--GUUGU-AGGCUU---
EMPLECTONEMA GRACILE L        -GCUC-GGUU-AGU-ACU(U)AGAUGGGUGACCGCU(U)GGGAAUACC---GAGU--GUUGU-AGRCUU---
EMPLECTONEMA GRACILE S        -GCCC-GGUU-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAACACC---GGGU--GUCGU-UGUCA----
CAENORHABDITIS ELEGANS        -GUCC-AGUU-AGU-ACU(U)GGAUCGGAGACGGCC(U)GGGAAUCCU---GGAU--GUUGU-AAGCU----
CAENORHABDITIS BRIGGSIAE      -GUCC-AGUU-AGU-ACU(U)GGAUCGGAGACGGCC(U)GGGAAUCCU---GGAU--GUUGU-AAGCU----
RHABDITIS TOKAI               -GYYC-RGUU-AGU-ACU(U)GGAUCGGAGACGGCY(U)GGGAAUCCY---GRRU--GUYGU-AAGCU----
BRACHIONUS PLICATILIS         -GCCC-GGUU-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACC---GGGU--GUUCU-AGGCCUu--
PERINEREIS BREVICIRRIS        -GCCU-GGUU-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACC---AGGU--GCUGU-AGGUUU---
SABELLASTARTE JAPONICA        -GCAC-GGUU-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACC---GUGU--GC(A)GU-AGGCUU---
URECHIS UNICINCTUS            -GCCC-GGUU-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACC---GGGU--GCUGU-AGACUU---
PHASCOLOPSIS GOULDII          -GCCA-GGUU-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACC---UGGU--GUUGU-AGGCUU---
EUGLENA GRACILIS 1            -GCCC-AGUU-AGU-ACUGAGGUGGGCGACCACUUGGGAACACU---GGGU--GCUGU-ACGCUU---
EUGLENA GRACILIS 2            -GCCC-AGUU-AGU-ACUGAG-UGGGCGACCACUUGGGAACACU---GGGU--GCUGU-ACGCUU---
CRYPTHECODINIUM COHNII        -GCCC-GGAU-AGU-ACUGGGGUGGGGGACCGCCCGGGAAGUCCUUAGGGU--GCUGU-CAGCU----
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Eukaryotic 5 S RNA Sequences

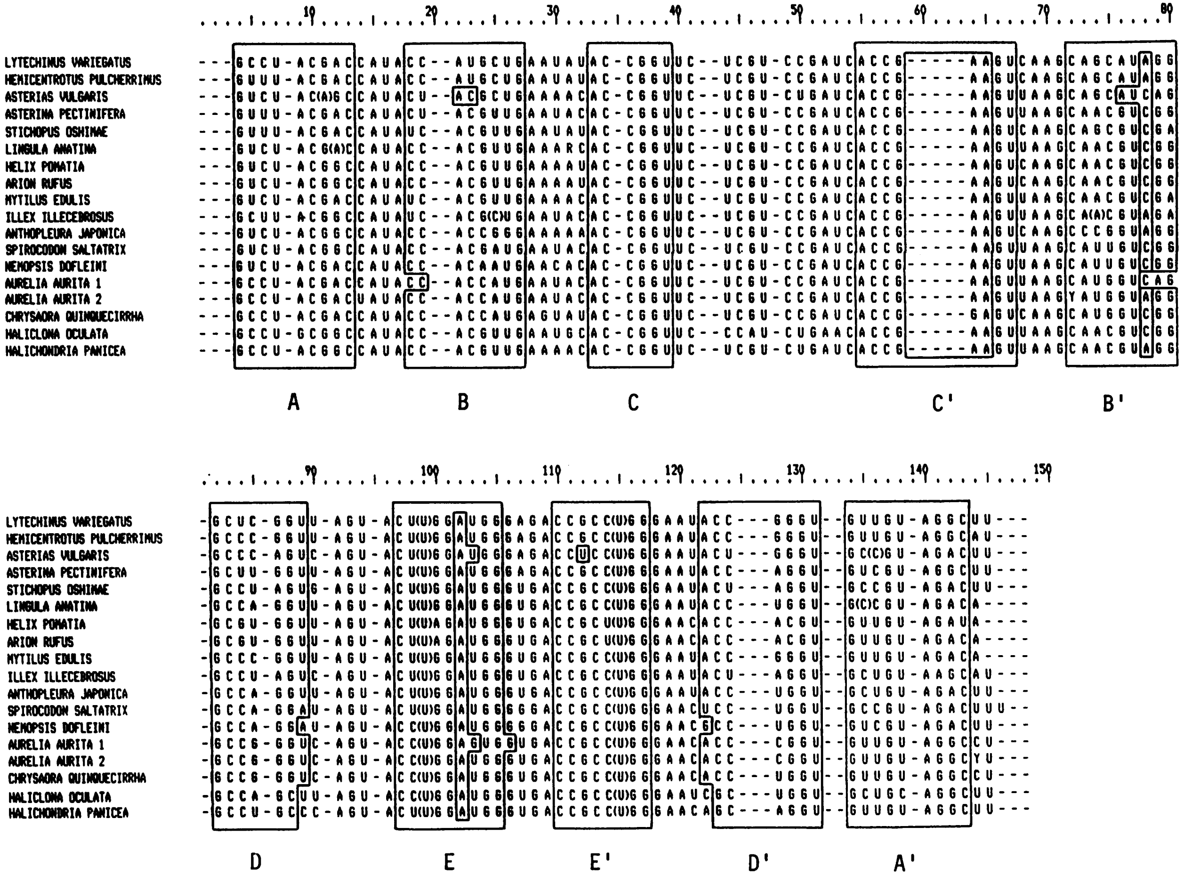
Species	Specification	Taxonomic position		Reference
		Phylum	Classis	
Halichondria japonica	whole organism	Porifera		64
Hymeniacidon sanguinea	whole organism			78
Planocera reticulata	whole organism	Plathelminthes	Polycladida	79
Dugesia japonica 1	whole organism, from Furugu		Seriata	79
Dugesia japonica 2	whole organism, from Sanage			79
Lineus geniculatus	whole organism	Nemertini	Heteronermetini	80
Emplectonema gracile L[a]	whole organism		Hoplonermetini	80
Emplectonema gracile S	whole organism			80
Caenorhabditis elegans	var. bristol, strain N2	Nemathelminthes	Nematoda	81
Caenorhabditis briggsiae	—			81
Rhabditis tokai[b]	whole organism			82
Brachionus plicatilis	whole organism		Rotatoria	82
Perinereis brevicirris	whole organism	Annelida	Polychaeta	83
Sabellastarte japonica	whole organism			83
Urechis unicinctus	ovaries	Echiurida		83
Phascolopsis gouldii	coelomic fluid	Sipunculida		73
Euglena gracilis 1	strain Z	Euglenophyta		84
Euglena gracilis 2[c]	strain Z, CM500			85
Crypthecodinium cohnii	—	Dinophyta		86

(a) Sequence heterogeneity : A/G_{142}.

(b) Sequence heterogeneity : A/U_{30}, A/G_{31}, G/C_{37}, C/G_{57}, G/A_{80}, C/U_{83}, U/C_{84}, G/A_{86}, U/C_{114}, U/C_{124}, A/G_{129}, G/A_{130}, C/U_{136}.

(c) Sequence heterogeneity : C/A_5; U_{47} stands for pseudouridine

Eukaryotic 5 S RNA Sequences



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                              ....|....10...|....20...|....30...|....40...|....50...|....60...|....70...|....80
LYTECHINUS VARIEGATUS         ---GCCU-ACGACCAUACC--AUGCUGAAUAUAC-CGGUUC--UCGU-CCGAUCACCG------AAGUCAAGCAGCAUAGG
HEMICENTROTUS PULCHERRIMUS    ---GUUU-ACGACCAUACC--AUGCUGAAUAUAC-CGGUUC--UCGU-CCGAUCACCG------AAGUCAAGCAGCAUAGG
ASTERIAS VULGARIS             ---GUCU-AC(A)GCCAUACU--ACGCUGAAAACAC-CGGUUC--UCGU-CUGAUCACCG------AAGUUAAGCAGCAUCAG
ASTERINA PECTINIFERA          ---GUUU-ACGACCAUACU--ACGUUGAAUACAC-CGGUUC--UCGU-CCGAUCACCG------AAGUUAAGCAACGUCGG
STICHOPUS OSHIMAE             ---GUUU-ACGACCAUAUC--ACGUUGAAUAUAC-CGGUUC--UCGU-CCGAUCACCG------AAGUCAAGCAGCGUCGA
LINGULA ANATINA               ---GUCU-ACG(A)CCAUACC--ACGUUGAAARCAC-CGGUUC--UCGU-CCGAUCACCG------AAGUUAAGCAACGUCGG
HELIX POMATIA                 ---GUCU-ACGGCCAUACC--ACGUUGAAAAUAC-CGGUUC--UCGU-CCGAUCACCG------AAGUCAAGCAACGUCGG
ARION RUFUS                   ---GUCU-ACGGCCAUACC--ACGUUGAAAAUAC-CGGUUC--UCGU-CCGAUCACCG------AAGUCAAGCAACGUCGG
MYTILUS EDULIS                ---GUCU-ACGACCAUAUC--ACGUUGAAAACAC-CGGUUC--UCGU-CCGAUCACCG------AAGUUAAGCAACGUCGA
ILLEX ILLECEBROSUS            ---GCUU-ACGGCCAUAUC--ACG(C)UGAAUACAC-CGGUUC--UCGU-CCGAUCACCG------AAGUUAAGCA(A)CGUAGA
ANTHOPLEURA JAPONICA          ---GUCU-ACGGCCAUACC--ACCGGGAAAAAAC-CGGUUC--UCGU-CCGAUCACCG------AAGUCAAGCCCGGUAGG
SPIROCODON SALTATRIX          ---GUCU-ACGGCCAUACC--ACGAUGAAUACAC-CGGUUC--UCGU-CCGAUCACCG------AAGUUAAGCAUUGUCGG
NEMOPSIS DOFLEINI             ---GUCU-ACGACCAUACC--ACAAUGAACACAC-CGGUUC--UCGU-CCGAUCACCG------AAGUUAAGCAUUGUCGG
AURELIA AURITA 1              ---GCCU-ACGACCAUACC--ACCAUGAAUACAC-CGGUUC--UCGU-CCGAUCACCG------AAGUUAAGCAUGGUCAG
AURELIA AURITA 2              ---GCCU-ACGACUAUACC--ACCAUGAAUACAC-CGGUUC--UCGU-CCGAUCACCG------AAGUUAAGYAUGGUAGG
CHRYSAORA QUINQUECIRRHA       ---GCCU-ACGACCAUACC--ACCAUGAGUAUAC-CGGUUC--UCGU-CCGAUCACCG------GAGUCAAGCAUGGUCGG
HALICLONA OCULATA             ---GCCU-GCGGCCAUACC--ACGUUGAAUGCAC-CGGUUC--CCAU-CUGAACACCG------AAGUUAAGCAACGUCGG
HALICHONDRIA PANICEA          ---GCCU-ACGGCCAUACC--ACGUUGAAAACAC-CGGUUC--UCGU-CUGAUCACCG------AAGUUAAGCAACGUAGG

                                   A          B            C                         C'          B'

                              ....|....90...|....100..|....110..|....120..|....130..|....140..|....150
LYTECHINUS VARIEGATUS         -GCUC-GGUU-AGU-ACU(U)GGAUGGGAGACCGCC(U)GGGAAUACC---GGGU--GUUGU-AGGCUU---
HEMICENTROTUS PULCHERRIMUS    -GCCC-GGUU-AGU-ACU(U)GGAUGGGAGACCGCC(U)GGGAAUACC---GGGU--GUUGU-AGGCAU---
ASTERIAS VULGARIS             -GCCC-AGUC-AGU-ACU(U)GGAUGGGAGACCUCC(U)GGGAAUACU---GGGU--GC(C)GU-AGACUU---
ASTERINA PECTINIFERA          -GCUU-GGUU-AGU-ACU(U)GGAUGGGAGACCGCC(U)GGGAAUACC---AGGU--GUCGU-AGGCUU---
STICHOPUS OSHIMAE             -GCCU-AGUG-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACU---AGGU--GCCGU-AGACUU---
LINGULA ANATINA               -GCCA-GGUU-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACC---UGGU--G(C)CGU-AGACA----
HELIX POMATIA                 -GCGU-GGUU-AGU-ACU(U)AGAUGGGUGACCGCU(U)GGGAACACC---ACGU--GUUGU-AGAUA----
ARION RUFUS                   -GCGU-GGUU-AGU-ACU(U)AGAUGGGUGACCGCU(U)GGGAACACC---ACGU--GUUGU-AGACA----
MYTILUS EDULIS                -GCCC-GGUU-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACC---GGGU--GUUGU-AGACA----
ILLEX ILLECEBROSUS            -GCCU-AGUC-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACU---AGGU--GCUGU-AAGCAU---
ANTHOPLEURA JAPONICA          -GCCA-GGUU-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAAUACC---UGGU--GCUGU-AGACUU---
SPIROCODON SALTATRIX          -GCCA-GGAU-AGU-ACU(U)GGAUGGGGGACCGCC(U)GGGAACUCC---UGGU--GCCGU-AGACUUU--
NEMOPSIS DOFLEINI             -GCCA-GGAU-AGU-ACC(U)GGAUGGGGGACCGCC(U)GGGAACGCC---UGGU--GUCGU-AGACUU---
AURELIA AURITA 1              -GCCG-GGUC-AGU-ACC(U)GGAGUGGUGACCGCC(U)GGGAACACC---CGGU--GUUGU-AGGCCU---
AURELIA AURITA 2              -GCCG-GGUC-AGU-ACC(U)GGAUGGGUGACCGCC(U)GGGAACACC---CGGU--GUUGU-AGGCYU---
CHRYSAORA QUINQUECIRRHA       -GCCG-GGUC-AGU-ACC(U)GGAUGGGUGACCGCC(U)GGGAACACC---UGGU--GUUGU-AGGCCU---
HALICLONA OCULATA             -GCCA-GCUU-AGU-ACC(U)GGAUGGGUGACCGCC(U)GGGAAUCGC---UGGU--GCUGC-AGGCUU---
HALICHONDRIA PANICEA          -GCCU-GCCC-AGU-ACU(U)GGAUGGGUGACCGCC(U)GGGAACAGC---AGGU--GUUGU-AGGCUU---

                                 D              E           E'           D'        A'
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Eukaryotic 5 S RNA Sequences

Species	Specification	Taxonomic position		Reference
		Phylum	Classis	
Lytechinus variegatus	clone pLu103	Echinodermata	Echinoidea	71
Hemicentrotus pulcherrimus	ovaries			72
Asterias vulgaris	ovaries		Asteroidea	73
Asterina pectinifera	ovaries			72
Stichopus oshimae	waterlungs		Holothuroidea	72
Lingula anatina[a]	whole organism	Lophophorata		74
Helix pomatia	whole organism	Mollusca	Gastropoda	75
Arion rufus	whole organism			75
Mytilus edulis	whole organism		Bivalvia	75
Illex illecebrosus	digestive gland		Cephalopoda	73
Anthopleura japonica	whole organism	Cnidaria	Anthozoa	76
Spirocodon saltatrix	whole organism		Hydrozoa	77
Nemopsis dofleini	whole organism			77
Aurelia aurita 1	whole organism		Scyphozoa	77
Aurelia aurita 2[b]	ovaries			73
Chrysaora quinquecirrha	whole organism			77
Haliclona oculata	whole organism	Porifera		78
Halichondria panicea	whole organism			78

(a) Sequence heterogeneity : G/A_{31}.

(b) Sequence heterogeneity : U/C_{72}, U/C_{144}.

Eukaryotic 5S RNA Sequences

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                                ....|....10...|....20...|....30...|....40...|....50...|....60...|....70...|....80

CRITHIDIA FASCICULATA           ---GAGU-ACG(A)CCAUACU--UG(A)GUGAAAACAC-CAUAUC--CCGU-CCGAUUUGUG------AAGUUAAGCAC(C)CACAG
TETRAHYMENA THERMOPHILA 1       ---GYUR-UCGGCCAUACU--AAGGUGAAAACAC-CGGAUC--CCAU-UCGAACUCCG------AAGUUAAGCGCCUUAAG
TETRAHYMENA THERMOPHILA 2       ---GUUR-UCGGCCAUACU--AAGGUGAAAACAC-CGGAUC--CCAU-UCGAACUCCG------AAGUUAAGCGCCUUAAG
BLEPHARISMA JAPONICUM           ---GUUG-UCGGCCAUACU--AUGCCUAACGCAC-CAGAUC--CCAU-CCGAACUCUG------AAGUUAAGCGGCAUAAG
PARAMECIUM TETRAURELIA          ---GUUG-(G)UGGCCAUACU--AAGCCUAAAGCAC-CRGAUC--CCAU-UCGAACUCCG------AAGUUAAGCGGCUUAAG
BRESSLAUA VORAX                 ---GUUA-UCGGCCAUACU--AAGCCAAAAGCAC-CGGAUC--CCAU-UCGAACUCCG------AAGUUAAGCGGCUUAAG
EUPLOTES WOODRUFFI              ---GCUA-UCGGCCAUACU--AAGCCAAAUGCAC-CGGAUC--CCAU-CCGAACUCCG------AAGUUAAGCGGUUUAAG
ACANTHAMOEBA CASTELLANII        ---GGAU-ACGGCCAUACU--GCGCAGAAAGCAC-CGCUUC--CCAU-CCGAACAGCG------AAGUUAAGCUGCGCCAG
PHYSARUM POLYCEPHALUM           ---GGAU-GCGGCCAUACU--AAGGAGAAAGCAC-CUCAUC--CCGU-CCGAUCUGAG------AAGUUAAGCUCCUUCAG
DICTYOSTELIUM DISCOIDEUM        ---GUAU-ACGGCCAUACU--AGGUUGGAAACAC-AUCAUC--CCGU-UCGAUCUGAU------AAGUAAAUCGACCUCAG
PHYCOMYCES BLAKESLEEANUS        --AAUCU-ACGGCCAUACA--GA(U)AGUAACACAC-CGGAUC--CCGU-CUGAUCUCCG------CAGUUAAGUCU(C)UCCUG
BLASTOCLADIELLA SIMPLEX         ---AGCU-ACGGCCAUACA--CACCAGAAAGCUC-CGCAUC--CCGU-CCGAUCUGCG------AAGAUAAUCUGGUGCUG
PHLYCTOCHYTRIUM IRREGULARE      ---AGCU-ACGGCCAUACA--UAGAUGAAAAUAC-CGGAUC--CCGU-CCGAUCUCCG------AAGUCAAGCAUCUAAUG
THRAUSTOCHYTRIUM VISURGENSE     ---AUGA-GCCCUCAUAUC--AUGUGGAGUGCAC-CGGAUC--UCAU-CCGAACUCCG------UAGUUAAGCCACAUAGA
SCHIZOCHYTRIUM AGGREGATUM       ---ACAG-CCGUUCAUACC--ACACGGAGAAUAC-CGGAUC--UCGU-UCGAACUCCG------CAGUCAAGCCGUGUCGG
SAPROLEGNIA FERAX               ---GGAA-UCGGCCAUAUU--AGCCUGACUAGAC-UGCAUC--CCGU-CCGCUCUGCA------AAGUUAACCAGGCUCAA
PYTHIUM HYDNOSPORUM             ---GUAG-ACGGCCAUCUU--AGGCUGAGAACAC-CGUAUC--CCGU-UCGCUCUGCG------AAGUUAAGCAGCCUCAA

                                     A             B             C                               C'          B'

                                ....|....90...|....100..|....110..|....120..|....130..|....140..|....150

CRITHIDIA FASCICULATA           -GCUU-AGUU-AGU-ACUGAGGUCAGUGAUGACUCGGGAACCCU---GAGU--G(C)CGU-ACUCCC---
TETRAHYMENA THERMOPHILA 1       -GCUG-GGUU-AGU-ACUAAGGUGGGGGACCGCUUGGGAAGUCC---CAGU--GUCGA-YARCCU---
TETRAHYMENA THERMOPHILA 2       -GCUG-GGUU-AGU-ACUAAGGUGGGGGACCGCUUGGGAAGUCC---CAGU--GUCGA-UAGCCU---
BLEPHARISMA JAPONICUM           -GCGA-GGUU-AGU-ACUUGGGUGGGGGACCGCCAGGGAAGCCC---UCGU--GCUGA-CAGCUA---
PARAMECIUM TETRAURELIA          -GCGA-GGUU-AGU-ACUAAGGUGGGGGACCGCUUGGGAAGUCC---UCGU--GUUG(A)-CAACCC---
BRESSLAUA VORAX                 -GCAU-GGUU-AGU-ACUAAGGUGGGGGACCGCUUGGGAAGCCC---AUGU--GCUGA-UAGCUU---
EUPLOTES WOODRUFFI              -GCCU-GUUA-AGU-ACUGAGGUGGGGGACCACUCGGGAACUUC---AGGU--GCUGA-UAGCUU---
ACANTHAMOEBA CASTELLANII        -GCGG-UGUU-AGU-ACUGGGGUGGGCGACCACCCGGGAAUCCA---CCGU--GCCGU-AUCCU----
PHYSARUM POLYCEPHALUM           -GCGU-GGUU-AGU-ACUGGGGUGGGGGACCACCUGGGAAUCCC---ACGU--GCUGC-AUUCUU---
DICTYOSTELIUM DISCOIDEUM        -GCCU-UCCA-AGU-ACUCUGGUUGGAGACAACAGGGGAACAUA---GGGU--GCUGU-AUACU----
PHYCOMYCES BLAKESLEEANUS        -GUAG-CGUC-AGU-ACUAUGGUGGGGGACCACAUGGGAAUACG---CUAU--GUCGU-AGGUU----
BLASTOCLADIELLA SIMPLEX         -GCGC-GGUC-AGU-ACUGUCGUGGGAGACCAGAUGGGAAUACC---GCGU--GCUGU-AGUU-----
PHLYCTOCHYTRIUM IRREGULARE      -GCGA-CGUC-AGU-ACUGUGAUGGGGGACCGCACGGGAAUACG---UCGU--GCUGU-AGUU-----
THRAUSTOCHYTRIUM VISURGENSE     -GCGC-GUCU-AGU-ACUGCCGUAGGGGACUAGGUGGGAAGCAC---GCGU--GGGGC-UCAUU----
SCHIZOCHYTRIUM AGGREGATUM       -GCGU-GCUC-AGU-ACUACCAUAGGGGACUGGGUGGGAAGCGU---GCGU--GACGG-CUGUU----
SAPROLEGNIA FERAX               -GCGU-GGGU-AGU-ACUCAGGUGGGUGACCACUGGGGAAGUCC---ACGU--GCUGA-UUCU-----
PYTHIUM HYDNOSPORUM             -GCUC-GGGU-AGU-ACUCGGGUGGGUGACCACCGGGGAAGUCC---GAGU--GCUGU-CUAC-----

                                   D               E          E'         D'         A'
```

Eukaryotic 5 S RNA Sequences

Species	Specification	Taxonomic position		Reference
		Phylum	Classis	
Crithidia fasciculata	—	Flagellata		87
Tetrahymena thermophila 1[a]	strain B	Ciliata	Holotricha	88
Tetrahymena thermophila 2[b]	mating type IV			89
Blepharisma japonicum	strain R13			89
Paramecium tetraurelia	mating type VIII			89
Bresslaua vorax	—			90
Euplotes woodruffi	—		Hypotricha	90
Acanthamoeba castellanii	ATCC 30010	Rhizopoda		91
Physarum polycephalum	—	Myxomycota	Myxomycetes	92
Dictyostelium discoideum	strain NC4		Acrasiomycetes	93
Phycomyces blakesleeanus	NRRL 155	Zygomycota		94
Blastocladiella simplex	ATCC 24579	Mastigomycota	Chytridiomycetes	95
Phlyctochytrium irregulare	ATCC 32066			95
Thraustochytrium visurgense	ATCC 28208		Oomycetes	96
Schizochytrium aggregatum	ATCC 28209			96
Saprolegnia ferax	ATCC 26116			95
Pythium hydnosporum	ATCC 26929			95

(a) Sequence heterogeneities : C/U_5, A/G_7, U/C_{140}, G/A_{142}.

(b) Sequence heterogeneity : A/G_7.

Eukaryotic 5 S RNA Sequences

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                            ....|....10...|....20...|....30...|....40...|....50...|....60...|....70...|....80
AURICULARIA AURICULA-JUDAE  ---A(U)CC-ACGGCCAUAGG--ACUCUGAAAGCAC-UGCAUC--CCGU-CCGAUCUGCA-----AAGUUAACCAGAGUACC
TREMELLA MESENTERICA        ---A(U)CC-ACGGCCAUAGG--ACUC(U)GAAAAUAC-CGCAUC--CCGU-CCGAUCUGCG-----AAGUCAAGC(C)GAGUACC
AGARICUS EDULIS             ---A(U)CC-ACGGCCAUAGG--ACUGUGAAAGCAC-CGCAUC--CCGU-CUGAUCUGCG-----CAGUUAAACACAGUGCC
RUSSULA CYANOXANTHA         ---A(U)CC-ACGGCCAUAGG--ACUCUGAAAGCAC-CGCAUC--CCGU-UCGAUCUGCG-----CAGUUAACCAGAGUGCC
PLEUROTUS OSTREATUS         ---A(U)CC-ACGGCCAUAGG--ACUCUGAAAGCAC-CGCAUC--CCGU-CUGAUCUGCG-----CAGUUAACCAGAGUGCC
COPRINUS RADIATUS           ---A(U)CC-(A)CGGCCAUAGG--ACUCUGAAAGCAC-CGCAUC--CCGU-CCGAUCUGCG-----CAGUUAACCAGAGUGCC
COPRINUS CINEREUS           ---A(U)CC-(A)CGGCCAUAGG--ACUCUGAAAGCAC-CGCAUC--CCGU-CCGAUCUGCG-----CAGUUAACCAGAGUGCC
BJERKANDERA ADUSTA          ---A(U)CC-ACGGCCAUAGG--ACUCUGAAAGCAC-CGCAUC--CCGU-CCGAUCUGCG-----AAGUUAACCAGAGUGCC
SCHIZOPHYLLUM COMMUNE       ---A(U)CC-ACGGCCAUAGG--ACUCUGAAAGCAC-CGCAUC--CCGU-CCGAUCUGCG-----CAGUUAACCAGAGUGCC
DACRYMYCES DELIQUESCENS     ---A(U)CC-ACGGCCAUAGG--ACACUGAAAGCAC-CGCAUC--CCGU-CCGAUCUGCG-----AAGUUAACCAGUGUGCC
EXOBASIDIUM VACCINII        ---A(U)CU-GCGGCCAUAGA--ACCGUGAAAAUAC-CGCAUC--CCGU-CCGAUCUGCG-----AAGUCAAGCACGGUAUC
FILOBASIDIUM CAPSULIGENUM   ---A(U)CC-ACGGCCAUAGG--ACUCUGAAAACAC-CGCAUC--CCGU-CCGAUCUGCG-----CAGUUAACCAGAGUGCC
FILOBASIDIUM FLORIFORME     ---A(U)CC-ACGGCCAUAGG--ACCCUGAAAGCAC-CGCAUC--CCGU-CCGAUCUGCG-----CAGUUAACCAGGGUGCC
RHIZOCTONIA HIEMALIS        ---AUCU-GGGGCCAUACC--ACAGUUAAAUCAC-CGCAUC--CCGU-CUGAUCUGCG-----AAGUUAAGCACUGUAGG
RHIZOCTONIA CROCORUM        ---AUCU-GGGGCCAUACC--ACAGCCGAAUCAC-CGCAUC--CCGU-UCGAUCUGCG-----CAGUUAAAUGCUGUAGG
TRICHOSPORON ORYZAE         ---A(U)CU-GCGGCCAUAGA--ACCUUGAAAGCAC-CGCAUC--CCGU-CCGAUCUGCG-----AAGUUAAGCAAGGUAUC
TILLETIARIA ANOMALA         ---A(U)CC-GCGGCCAUAGG--AUCAGGAAAGCAC-CGCAUC--CCGU-CCGAUCUGCG-----AAGUUAAGCCUGAUACC

                               A             B             C                      C'              B'

                            ....|....90...|....100..|....110..|....120..|....130..|....140..|....150
AURICULARIA AURICULA-JUDAE  -GCCC-AGUU-AGU-ACC(A)CGGUGGGGGACCACG(C)GGGAAUCCU---GGGU--GCUGU-GG(U)U-----
TREMELLA MESENTERICA        -GCUC-AGUU-AGU-ACCACGGUGGGGGACCACGUGGGAAUCCU---GGGU--GCUGU-GG(U)U-----
AGARICUS EDULIS             -GCCU-AGUU-AGU-ACCAUGGUGGGGGACCACAUGGGAAUCCU---GGGU--GCUGU-GG(U)U-----
RUSSULA CYANOXANTHA         -GCCC-AGUU-AGU-ACC(A)CGGUGGGGGACCACG(C)GGGAAUCCU---GGGU--GCUGU-GG(U)UUu----
PLEUROTUS OSTREATUS         -GCUC-AGUU-AGU-ACC(A)CGGUGGGGGACCACG(C)GGGAAUCCU---GGGU--GCUGU-GG(U)U-----
COPRINUS RADIATUS           -GCCU-AGUU-AGU-ACC(A)CGGUGGGGGACCACG(C)GGGAAUCCU---GGGU--GCUGU-GG(U)U-----
COPRINUS CINEREUS           -GCUC-AGUU-AGU-ACC(A)CGGUGGGGGACCACG(C)GGGAAUCCU---GGGU--GCUGU-GG(U)U-----
BJERKANDERA ADUSTA          -GCCU-AGUU-AGU-ACC(A)CGGUGGGGGACCACG(C)GGGAAUCCU---AGGU--GCUGU-GG(U)U-----
SCHIZOPHYLLUM COMMUNE       -GCUC-AGUU-AGU-ACC(A)CGGUGGGGGACCACG(C)GGGAAUCCU---GGGU--GCUGU-GG(U)U-----
DACRYMYCES DELIQUESCENS     -GCCC-GGUU-AGU-ACC(A)CGGUGGGGGACCACG(C)GGGAAUCCU---GGGU--GCUGU-GG(U)U-----
EXOBASIDIUM VACCINII        -GCCU-AGUC-AGU-ACUGCGGUGGGGGACCACGCGGGAAUCCU---GGGU--GCUGC-AG(U)U-----
FILOBASIDIUM CAPSULIGENUM   -GCCU-AGUU-AGU-ACC(A)CGGUGGGGGACCACG(C)GGGAAUCCU---AGGU--GCUGU-GG(U)U-----
FILOBASIDIUM FLORIFORME     -GCCU-AGUU-AGU-ACC(A)CGGUGGGGGACCACG(C)GGGAAUCCU---AGGU--GCUGU-GG(U)U-----
RHIZOCTONIA HIEMALIS        -GCCG-AGUC-AGU-AGUGCGGUGGGGGACCACGCGCGAAUACU--CUGGU--GCCCC-AGGU-----
RHIZOCTONIA CROCORUM        -GCCG-AGUC-AGU-AGUGCGGUGGGGGACCACGCGCGAAUACU--CUGGU--GCCCC-AGGU-----
TRICHOSPORON ORYZAE         -GCCU-AGUC-AGU-ACUGCGGUGGGGGACCACGCGGGAAUCCU---AGGU--GCUGC-AG(U)U-----
TILLETIARIA ANOMALA         -GCCG-AGUU-AGU-ACUAAGGUAGGGGACUACUUGGGAAUCCU---CGGU--GCUGC-GG(U)U-----

                               D              E           E'          D'         A'
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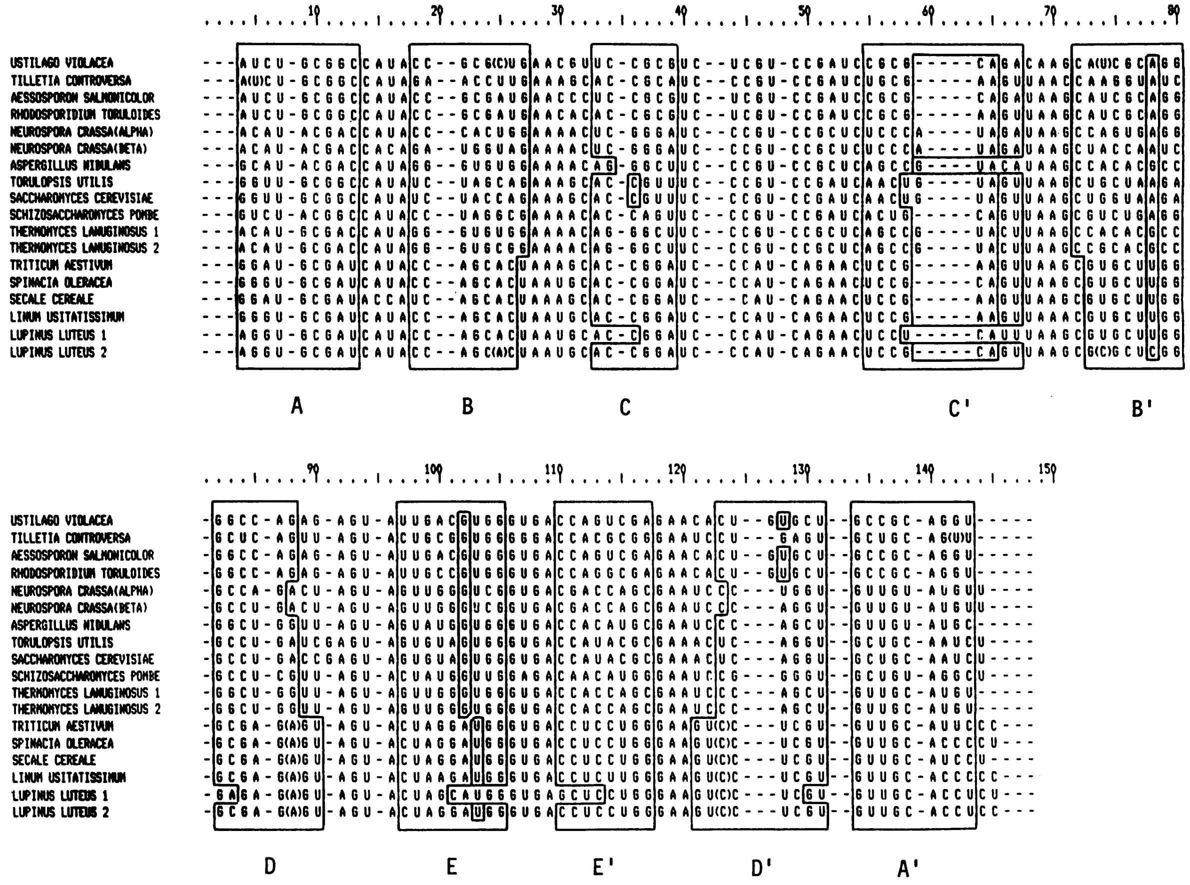
Eukaryotic 5 S RNA Sequences

Species	Specification	Taxonomic position		Reference
		Phylum	Classis	
Auricularia auricula-judae	fruitbody	Basidiomycota	Phragmobasidiomycetes	97
Tremella mesenterica	yeast phase			98
Agaricus edulis	fruitbody		Holobasidiomycetes	97
Russula cyanoxantha	fruitbody			97
Pleurotus ostreatus	fruitbody			97
Coprinus radiatus	—			99
Coprinus cinereus	mycelia			100
Bjerkandera adusta	mycelia			98
Schizophyllum commune	mycelia			98
Dacrymyces deliquescens	ATCC 13292			99
Exobasidium vaccinii	ATCC 24312			99
Filobasidum capsuligenum	yeast phase			98
Filobasidum floriforme	yeast phase			98
Rhizoctonia hiemalis	ATCC 14016	basidiomycetous deuteromycete		99
Rhizoctonia crocorum	ATCC 11070			99
Trichosporon oryzae	ATCC 28323	basidiomycetous yeast		99
Tilletiaria anomala	ATCC 24038	Basidiomycota	Teliomycetes	99

Eukaryotic 5 S RNA Sequences



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                                  ....|....10....|....20....|....30....|....40....|....50....|....60....|....70....|....80

USTILAGO VIOLACEA                 - - - A U C U - G C G G C C A U A C C - - G C G(C)U G A A C G U U C - C G C G U C - - U C G U - C C G A U C C G C G - - - - - C A G A C A A G C A(U)C G C A G G
TILLETIA CONTROVERSA              - - - A(U)C U - G C G G C C A U A G A - - A C C U U G A A A G C A C - C G C A U C - - C C G U - C C G A U C U G C G - - - - - A A G U U A A C C A A G G U A U C
AESSOSPORON SALMONICOLOR          - - - A U C U - G C G G C C A U A C C - - G C G A U G A A C C C U C - C G C G U C - - U C G U - C C G A U C C G C G - - - - - C A G A U A A G C A U C G C A G G
RHODOSPORIDIUM TORULOIDES         - - - A U C U - G C G G C C A U A C C - - G C G A U G A A C A C A C - C G C G U C - - U C G U - C C G A U C C G C G - - - - - A A G U U A A G C A U C G C A G G
NEUROSPORA CRASSA(ALPHA)          - - - A C A U - A C G A C C A U A C C - - C A C U G G A A A A C U C - G G G A U C - - C C G U - C C G C U C U C C C A - - - - U A G A U A A G C C A G U G A G G
NEUROSPORA CRASSA(BETA)           - - - A C A U - A C G A C C A C A G A - - U G G U A G A A A A C U C - G G G A U C - - C C G U - C C G C U C U C C C A - - - - U A G A U A A G C U A C C A A U C
ASPERGILLUS NIDULANS              - - - G C A U - A C G A C C A U A G G - - G U G U G G A A A A C A G - G G C U U C - - C C G U - C C G C U C A G C C G - - - - U A C A U A A G C C A C A C G C C
TORULOPSIS UTILIS                 - - - G G U U - G C G G C C A U A U C - - U A G C A G A A A G C A C - C G U U U C - - C C G U - C C G A U C A A C U G - - - - U A G U U A A G C U G C U A A G A
SACCHAROMYCES CEREVISIAE          - - - G G U U - G C G G C C A U A U C - - U A C C A G A A A G C A C - C G U U U C - - C C G U - C C G A U C A A C U G - - - - U A G U U A A G C U G G U A A G A
SCHIZOSACCHAROMYCES POMBE         - - - G U C U - A C G G C C A U A C C - - U A G G C G A A A A C A C - C A G U U C - - C C G U - C C G A U C A C U G - - - - - C A G U U A A G C G U C U G A G G
THERMOMYCES LANUGINOSUS 1         - - - A C A U - G C G A C C A U A G G - - G U G U G G A A A A C A G - G G C U U C - - C C G U - C C G C U C A G C C G - - - - U A C U U A A G C C A C A C G C C
THERMOMYCES LANUGINOSUS 2         - - - A C A U - G C G A C C A U A G G - - G U G C G G A A A A C A G - G G C U U C - - C C G U - C C G C U C A G C C G - - - - U A C U U A A G C C G C A C G C C
TRITICUM AESTIVUM                 - - - G G A U - G C G A U C A U A C C - - A G C A C U A A A G C A C - C G G A U C - - C C A U - C A G A A C U C C G - - - - - A A G U U A A G C G U G C U U G G
SPINACIA OLERACEA                 - - - G G G U - G C G A U C A U A C C - - A G C A C U A A U G C A C - C G G A U C - - C C A U - C A G A A C U C C G - - - - - C A G U U A A G C G U G C U U G G
SECALE CEREALE                    - - - G G A U - G C G A U A C C A U C - - A G C A C U A A A G C A C - C G G A U C - - - C A U - C A G A A C U C C G - - - - - A A G U U A A G C G U G C U U G G
LINUM USITATISSIMUM               - - - G G G U - G C G A U C A U A C C - - A G C A C U A A U G C A C - C G G A U C - - C C A U - C A G A A C U C C G - - - - - A A G U U A A A C G U G C U U G G
LUPINUS LUTEUS 1                  - - - A G G U - G C G A U C A U A C C - - A G C A C U A A U G C A C - C G G A U C - - C C A U - C A G A A C U C C U - - - - - C A U U U A A G C G U G C U U G G
LUPINUS LUTEUS 2                  - - - A G G U - G C G A U C A U A C C - - A G C(A)C U A A U G C A C - C G G A U C - - C C A U - C A G A A C U C C G - - - - - C A G U U A A G C G(C)G C U C G G

                                           A               B               C                                    C'               B'


                                  ....|....90....|....100...|....110...|....120...|....130...|....140...|....150

USTILAGO VIOLACEA                 - G G C C - A G A G - A G U - A U U G A C G U G G G U G A C C A G U C G A G A A C A C U - - G U G C U - - G C C G C - A G G U - - - - -
TILLETIA CONTROVERSA              - G C U C - A G U U - A G U - A C U G C G G U G G G G G A C C A C G C G G G A A U C C U - - - G A G U - - G C U G C - A G(U)U - - - - -
AESSOSPORON SALMONICOLOR          - G G C C - A G A G - A G U - A U U G A C G U G G G U G A C C A G U C G A G A A C A C U - - G U G C U - - G C C G C - A G G U - - - - -
RHODOSPORIDIUM TORULOIDES         - G G C C - A G A G - A G U - A U U G C C G U G G G U G A C C A G G C G A G A A C A C U - - G U G C U - - G C C G C - A G G U - - - - -
NEUROSPORA CRASSA(ALPHA)          - G C C A - G A C U - A G U - A G U U G G G U C G G U G A C G A C C A G C G A A U C C C - - - U G G U - - G U U G U - A U G U U - - - -
NEUROSPORA CRASSA(BETA)           - G C C U - G A C U - A G U - A G U U G G G U C G G U G A C G A C C A G C G A A U C C C - - - A G G U - - G U U G U - A U G U U - - - -
ASPERGILLUS NIDULANS              - G G C U - G G U U - A G U - A G U A U G G U G G G U G A C C A C A U G C G A A U C C C - - - A G C U - - G U U G U - A U G C - - - - -
TORULOPSIS UTILIS                 - G C C U - G A U C G A G U - A G U G U A G U G G G U G A C C A U A C G C G A A A C U C - - - A G G U - - G C U G C - A A U C U - - - -
SACCHAROMYCES CEREVISIAE          - G C C U - G A C C G A G U - A G U G U A G U G G G U G A C C A U A C G C G A A A C U C - - - A G G U - - G C U G C - A A U C U - - - -
SCHIZOSACCHAROMYCES POMBE         - G C C U - C G U U - A G U - A C U A U G G U U G G A G A C A A C A U G G G A A U C C G - - - G G G U - - G C U G U - A G G C U - - - -
THERMOMYCES LANUGINOSUS 1         - G G C U - G G U U - A G U - A G U U G G G U G G G U G A C C A C C A G C G A A U C C C - - - A G C U - - G U U G C - A U G U - - - - -
THERMOMYCES LANUGINOSUS 2         - G G C U - G G U U - A G U - A G U U G G G U G G G U G A C C A C C A G C G A A U C C C - - - A G C U - - G U U G C - A U G U - - - - -
TRITICUM AESTIVUM                 - G C G A - G(A)G U - A G U - A C U A G G A U G G G U G A C C U C C U G G G A A G U(C)C - - - U C G U - - G U U G C - A U U C C C - - -
SPINACIA OLERACEA                 - G C G A - G(A)G U - A G U - A C U A G G A U G G G U G A C C U C C U G G G A A G U(C)C - - - U C G U - - G U U G C - A C C C C U - - -
SECALE CEREALE                    - G C G A - G(A)G U - A G U - A C U A G G A U G G G U G A C C U C C U G G G A A G U(C)C - - - U C G U - - G U U G C - A U C C U - - - -
LINUM USITATISSIMUM               - G C G A - G(A)G U - A G U - A C U A A G A U G G G U G A C C U C U U G G G A A G U(C)C - - - U C G U - - G U U G C - A C C C C C - - -
LUPINUS LUTEUS 1                  - G A G A - G(A)G U - A G U - A C U A G C A U G G G U G A G C U C C U G G G A A G U(C)C - - - U C G U - - G U U G C - A C C U C U - - -
LUPINUS LUTEUS 2                  - G C G A - G(A)G U - A G U - A C U A G G A U G G G U G A C C U C C U G G G A A G U(C)C - - - U C G U - - G U U G C - A C C U C C - - -

                                       D                E                E'             D'              A'
```

Eukaryotic 5 S RNA Sequences

Species	Specification	Taxonomic position		Reference
		Phylum	Classis	
Ustilago violacea	yeast phase	Basidiomycota	Teliomycetes	98
Tilletia controversa				99
Aessosporon salmonicolor	yeast phase	teliomycetous yeast		98
Rhodosporidium toruloides	yeast phase			98
Neurospora crassa (alpha)	clone pKD52	Ascomycota	Pyrenomycetes	101,102
Neurospora crassa (beta)	clone pKD51			102
Aspergillus nidulans	strain pabaA1,biA1		Plectomycetes	101
Torulopsis utilis	clone pTU824		Hemiascomycetes	103,104
Saccharomyces cerevisiae	clone pDB25			105
Schizosaccharomyces pombe	IFO 0345			106
Thermomyces lanuginosus 1	ATCC 16455	ascomycetous deuteromycete		107
Thermomyces lanuginosus 2	ATCC 16455			107
Triticum aestivum	clone pTA	Spermatophyta	Magnoliopsida	108,109
Spinacia oleracea	var. 424			110
Secale cereale[a]	cv. lavoszpatonai			111
Linum usitatissimum	clone p8G6,clone p8G13			112
Lupinus luteus 1	clone pAR1			113
Lupinus luteus 2	clone pAR4			113

(a) The sequence in positions 14 to 18, 44 and 139 to 144 is questioned by McKay et al.[109]

Eukaryotic 5S RNA Sequences

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                                                 10        20        30        40        50        60        70        80
                                        ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
MARCHANTIA POLYMORPHA                   ---GGAU-GCGGUCAUACC--AGGGCUACUACAC-CAGAUC--CCAU-CAGAACUCUG-----CAGUUAAGCGCCCUUGG
LOPHOCOLEA HETEROPHYLLA                 ---GGAU-GCGGUCAUACC--ARGGCUACUACAC-CAGAUC--CCAU-CAGAACUCUG-----CAGUUAAGCGCCUUUGG
PLAGIOMNIUM TRICHOMANES                 ---GGAU-GCGGUCAUACC--AAGGCUACUACAC-CAGAUC--CCAU-CAGAACUCUG-----AAGUUAAGCGCCUUUGG
ANTHOCEROS PUNCTATUS                    ----GGU-GCGGUCAUACC--AGGGCUACUACAC-CGGAUC--CCAU-CAGAACUCCG-----UAGUUAAGCGCCCUUGG
CHLAMYDOMONAS REINHARDTII(I)            --AUGG(A)-UCGUUCAAACC--UUCAAGGCCCCUC-CCCAUC--CCAU-CAGCACUGGG-----AAGAUAAGCCUGAAUGG
CHLAMYDOMONAS REINHARDTII(II)           --AUGG(A)-UUGCUUAUACC--UUUAUGAAAACUC-CCCAUC--CCAU-UAGCACUGGG-----AAGAUAAGUAUGAAUGG
CHLAMYDOMONAS SP.                       --AUGG--UCGUUCAUACU--AGCACUACUGCAC-CCUAAC--CCGU-CAGAUCUAGG-----AAGUUAAGCGUGCUCAG
CHLORELLA SP.                           --AUGCU-ACGUUCAUACC--ACCACGAAAGCAC-CCGAUC--CCAU-CAGAACUCGG-----AAGUUAAACGUGGUUGG
SCENEDESMUS QUADRICAUDUS                --AUGCU-ACGUUCAUACC--ACCACGAAAGCAC-CCGAUC--CCAU-CAGAACUCGG-----AAGUUAAACGUGGUUGG
SCENEDESMUS OBLIQUUS                    --AUGCU-ACGUUCAUACC--ACCACGAAAGCAC-CCGAUC--CCAU-CAGAACUCGG-----AAGUUAAACGUGGUUGG
ULVA PERTUSA                            --GUGAU-ACGGUCAUACC--ACCAGGAAAACAG-GCGAUC--CCAU-CAGAACUCGC-----AACUUAAGCCUGGUUGG
CHILOMONAS PARAMECIUM                   -UUCUGU-ACGGUCAUACC--UGGUUGGAAACGC-CGGAUC--CCGU-CCGAUCUCCG-----AAGCUAAGCAACCAUGG
EISENIA BICYCLIS                        ---AGGA-ACGGCCAUACC--ACGUCGAUCGCAC-CACAUC--CCGU-CCGCUCUGUG-----AAGUUAAGCGGCGUCGG
SARGASSUM FULVELLUM                     ---AGGA-ACGGCCAUACC--ACGUCGAUCGCAC-CACAUC--CCGU-CCGCUCUGUG-----AAGUUAAGCGGCGUCGG
PORPHYRA YEZOENSIS                      ---ACGU-ACGGCCAUAUCC-GAGAC(A)CGCGUAC-CGGAAC--CCAUUCCGAAUUCCG-----AAGUCAAG(C)GUCCGCGA
PORPHYRA TENERA                         ---ACGU-ACGGCCAUAUCC-GAGAC(A)CGCGUAC-CGGAAC--CCAUUCCGAAUUCCG-----AAGUCAAG(C)GUCCGCGA
GRACILARIA COMPRESSA                    ---ACAU-UCGGCCAUAUCA-AGUUGACAAACGC-CGUAUC--CCAUCCCGAACUACG-----AAGCUAAGUCACUUUGA

                                            A             B              C                              C'            B'

                                                 90        100       110       120       130       140       150
                                        ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
MARCHANTIA POLYMORPHA                   -GCCG-G(A)AU-AGU-ACUGGGAUGGGUGACCUCCCGGGAAGU(C)C---CGGU--GCUGC-AUCCA----
LOPHOCOLEA HETEROPHYLLA                 -GCCG-G(A)AU-AGU-ACUGGGAUGGGUGACCUCCCGGGAAGU(C)C---CGGU--GCUGC-AUCCA----
PLAGIOMNIUM TRICHOMANES                 -GCCG-G(A)AU-AGU-ACUGGGAUGGGUGACCUCCCGGGAAGU(C)C---CGGU--GCUGC-AUCCA----
ANTHOCEROS PUNCTATUS                    -GCCG-GAUC-AGU-ACUGGGAUGGGUGACCUCCCGGGAAGUCC---CGGU--GCUGC-ACCCU----
CHLAMYDOMONAS REINHARDTII(I)            -GCUG-AACU-AGU-AGUACGGUGGGGGACCACGUGCGAAUCCU---CAGU--GACGA-(C)CUGGUU--
CHLAMYDOMONAS REINHARDTII(II)           -GCUG-AAUC-AGU-AGUACGGUGGGGGACCACGUGCGAACCCU---CAGU--G(A)CGA-(C)CUGUU---
CHLAMYDOMONAS SP.                       -GCGA-GGCC-AGU-AGUACGGUGGGUGACCACGUGCGAAGCCC---UCGU--GACGA--UCGU----
CHLORELLA SP.                           -GCUC-GACU-AGU-ACUGGGUUGAGGGAUUACCUGGGAACCCC---GAGU--GACGU-AGUGU----
SCENEDESMUS QUADRICAUDUS                -GCUC-GACU-AGU-ACUGGGUUGAGGGAUCACCUGGGAACCCC---GAGU--GACGU-AGUGU----
SCENEDESMUS OBLIQUUS                    -GCUU-GAUU-AGU-ACUGGGUUGAGGGAUCACCUGGGAACCCC---GAGU--GACGU-AGUGU----
ULVA PERTUSA                            -GCAG-GAUU-AGU-ACUGGGCUGAGUGAUCUCCUGGGAAUCCC---CUGU--GCUGU-AUCGC----
CHILOMONAS PARAMECIUM                   -GCGU-GUCU-AGU-ACUCAGGUGGGGGACCACUGGGGAAGCGC---ACGU--ACUGU-ACAGC----
EISENIA BICYCLIS                        -GCCA-GGCU-AGU-ACUACGGUGGGGGACCACGUGGGGGACCC---UGGU--GCUGU-UCCU-----
SARGASSUM FULVELLUM                     -GCCG-GGCU-AGU-ACUACGGUGGGGGACCACGUGGGAAGCCC---CGGU--GCUGU-UCCU-----
PORPHYRA YEZOENSIS                      -GUUG-GGUU-AGU-AAUCUGGUGAAAGAUCACAGGCGAACCCC---CAAU--GCUGU-ACGUC----
PORPHYRA TENERA                         -GUUG-GGUU-AGU-AGUCUGGUGAGGGAUCACAGGCGAACCCC---CAAU--GCUGU-ACGUC----
GRACILARIA COMPRESSA                    -GCUG-GGCU-AGU-AC(U)GAGAUGAGGGAUCGGUC(U)GGAAUCCC---CAGU--GCUGA-AUGUU----

                                          D                E           E'           D'          A'
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Eukaryotic 5 S RNA Sequences

Species	Specification	Taxonomic position		Reference
		Phylum	Classis	
Marchantia polymorpha	whole thallus	Bryophyta	Hepaticopsida	114
Lophocolea heterophylla[a]	whole thallus			114
Plagiomnium trichokanes	whole thallus		Bryopsida	114
Anthoceros punctatus	whole thallus		Anthoceropsida	114
Chlamydomonas reinhardtii (I)	cell wall mutant CW15	Chlorophyta	Monadophyceae	115
Chlamydomonas reinhardtii (II)	cell wall mutant CW15			115
Chlamydomonas sp.	—			90
Chlorella sp.	ATCC 11469		Coccophyceae	116
Scenedesmus quadricaudus	ATCC 11460			116
Scenedesmus obliquus[b]	—			117
Ulva pertusa	whole thallus		Septophyceae	118
Chilomonas paramecium	whole organism	Cryptophyta		119
Eisenia bicyclis	whole thallus	Phaeophyta		118
Sargassum fulvellum	whole thallus			118
Porphyra yezoensis	—	Rhodophyta	Bangiophyceae	120
Porphyra tenera	—			121
Gracilaria compressa	—		Florideophyceae	121

(a) Sequence heterogeneity : A/G_{23}.

(b) The residue in position 142 was not identified, but in the alignment it is assumed to be U as in *Scenedesmus quadricaudus*

ALIGNMENT OF 5.8S RRNA SEQUENCES

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            10        20        30        40        50        60        70        80        90       100
             .         .         .         .         .         .         .         .         .         .
  1  ------CGACUCUUAGCGGUGGAUCACUCGGC-UCGUGCGUCGAUGAAGAACGCAGCUAGCPGCGAGAAUUAAUGPGAAUUGCAGGACACAU-UGAUCAU  RATTUS RATTUS (MAMMALIA)
  2  ------CGACUCUUAGCGGUGGAUCACUCGGC-UCGUGCGUCGAUGAAGAACGCAGCUAGCPGCGAGAAUUAAUGPGAAUUGCAGGACACAU-UGAUCAU  MUS MUSCULUS, HOMO SAPIENS (MAMMALIA)
  3  ------CAACUCUUAGCGGUGGAUCACUCGGC-UCGUGCGUCGAUGAAGAACGCAGCUAGCUGCGAGAAUUAAUGPGAAUUGCAGGACACAU-UGAUCAU  TERRAPENE CAROLINA (REPTILIA)
  4  ------CAACUCUUAGCGGUGGAUCACUCGGC-UCGUGGGUCGAUGAAGAACGCAGCUAGCPGCGAGAAUUAAUGPGAAUUGCAGGACACAU-UGAUCAU  GALLUS GALLUS (AVES)
  5  -----UCGACUCUUAGCGGUGGAUCACUCGGC-UCGUGCGUCGAUGAAGAACGCAGCUAGCPGCGAGAAUUAGUGPGAAUUGCAGGACACAU-UGAUCAU  XENOPUS LAEVIS (AMPHIBIA)
  6  -----UCGACUCUUAGCGGUGGAUCACUCGGC-UCGUGCGUCGAUGAAGAACGCAGCUAGCPGCGAGAAUUAGUGPGAAUUGCAGGACACAU-UGAUCAU  XENOPUS BOREALIS (AMPHIBIA)
  7  ------CAACUCUUAGCGGUGGAUCACUCGGC-UCGUGCGUCGAUGAAGAACGCAGCUAGCPGCGAGAACUAAUGPGAAUUGCAGGACACAU-UGAUCAU  SALMO GAIRDNERI (OSTEICHTHYES)
  8  A-------ACUCUAAGCGGUGGAUCACUCGGC-UCAUGGGUCGAUGAAGAACGCAGCAAACUGUGCGUCAUCGUGUGAACUGCAGGACACA--UGAACAU  DROSOPHILA MELANOGASTER (INSECTA)
  9  A-------ACCCUAAGCGGGGGAUCACUUGGU-UUGUGGGUCGAUGAAGAACGCAGCAAACUGCGUGUUGACAUGUGAACUGCAGGACACA--UGAACAU  *SCIARA COPROPHILA (INSECTA)
 10  AAAUGAUUACCCUGGACGGUGGAUCACUUGGC-UCGCGGGUCGAUGAAGAACGCAGUUAACPGCGCGUCAUAGUGUGAACUGCAGGACACAUUUGAACAU  BOMBYX MORI (INSECTA)
 11  AAACCAUUACCCUGGACGGUGGAUCACUUGGC-UCGCGGGUCGAUGAAGAACGCAGUUAACUGCGCGUCAUAGUGUGAACUGCAGGACACAUUUGAACAU  PHILOSAMIA CYNTHIA RICINI (INSECTA)
 12  CGU------CCCCGAACGGCGGAUCACUUGGC-UCGUGGAUCGAUGAAGACCGCAGCUAUCUGCGCGUCGUCGUGUAAUCCGCAGGUUAUAC--GAACAU  ACYRTHOSIPHON MAGNOLIAE (INSECTA)
 13  AGA--AUGACCCUGGAGGAUGGAUCACUUGGC-UCACAUUACGAAGACGAACGCAGCUAGACGCGUGAUUCCAUGCGAACUGCAGGACACAUG-GAACGU  ARTEMIA SALINA (CRUSTACEA)
 14  ------UAACUUUGUGCGGUGGAUCACUCGGC-UCGUGCGUCGAUGAAGAGCGCAGCCAGCUGCGUGAAUUAAUGUGAAPUGCAGAACACAU-UGAACAU  ARION RUFUS (GASTROPODA)
 15  ------CAACUUCCAACGGUGGACCCCUCGGC-UCGUGCAUCGAUGAAGAACGCAGCAAACUGCGAUACGPAGUGUGAAPUGCAGAAUUCAGUGAAUCAU  HYMENIACIDON SANGUINEA (PORIFERA)
 16  A------AACUUUCAACAAUGGAPCUCUUGGU-UCCGGCAUCGAUGAAGAACGCAGCGAAAPGCGAUAAGUAAUGUGAAPUGCAGAAUUCCGUGAAUCAU  THERMOMYCES LANUGINOSUS (PLECTOMYCETES)
 17  A------AACUUUCAACAACGGAUCUCUUGGU-UCUGGCAUCGAUGAAGAACGCAGCGAAAUGCGAUAGGUAAUGUGAAUUGCAGAAUUCAGUGAAUCAU  *NEUROSPORA CRASSA (PYRENOMYCETES)
 18  A------AACUUUCAGCAACGGAUCUCUUGGC-UCUCGCAUCGAUGAAGAACGCAGCGAAAUGCGAUACGUAAUGUGAAUUGCAGAAUUCCGUGAAUCAU  *SCHIZOSACCHAROMYCES POMBE (ENDOMYCETES)
 19  A------AACUUUCAACAACGGAUCUCUUGGU-UCUCGCAUCGAUGAAGAACGCAGCGAAAUGCGAUACGUAAUGUGAAPUGCAGAAUUCCGUGAAUCAU  SACCHAROMYCES CEREVISIAE (ENDOMYCETES)
 20  A-------ACUCUCAACAACGGAUAUCUUGGC-UCUCGGAUCGAUGAAGGACGCAGCGAAAUGCGAUACGUAGUGUGAACUGCAGAAAUACGUGAACUAU  CHLAMYDOMONAS REINHARDII (VOLVOCALES)
 21  CAC--ACGACUCUCGGCAACGGAPAUCUCGGC-UCUCGCAUCGAUGAAGAACGUAGCGAAAUGCGAUACCUGGUGUGAAUPGCAGAAUCCCGCGAACCAU  TRITICUM AESTIVUM (ANGIOSPERMAE)
 22  CUA--AAGACUCUCGGCAACGGAUAUCUCGGC-UCUUGCAUCGAUGAAGAACGUAGCGAAAUGCGAUACUUGGUG-GAAUUGCAGAAUCCCGUGAACCAU  *LUPINUS LUTEUS (ANGIOSPERMAE)
 23  AGA--AUGACUCUCGGCAACGGAPAUCUAGGC-UCUUGCAUCGAUGAAGAACGUAGCGAAAUGCGAUACUUGGUGUGAAUPGCAGAAUCCCGUGAACCAU  VICIA FABA (ANGIOSPERMAE)
 24  -------AACPCCUAACAACGGAPAUCUUGGU-UCUCGCGAGGAUGAAGAACGCAGCGAAAUGCGAUACGUAGUGUGAAUCGCAGGGAUCAGUGAAUCAP  ACANTHAMOEBA CASTELLANII (AMOEBINA)
 25  -----UUAAGCAUAAACGGUGAAUACCUCGAC-UCCCAAAUUGAUGAAGACCGUAGCAAACUGCGAUAAUUCACUUGAAUUGCAGCCUACUGGGA-UAGU  DICTYOSTELIUM DISCOIDEUM (DICTYOSTELIIA)
 26  -------ACCGUUGGGCGAUGGAUUGCUUGGU-GCCUGCUUCGACGAAGAGCGCAGUGAAACGCGAUAACUUUUGUGACUCGCACUCU-CUGUGA-UCAA  *PHYSARUM POLYCEPHALUM (MYXOGASTRIA)
 27  -----ACAACUUUCAGCAGUUGAUUCCUUGGU-UCAGACCUCGAUGAAGGGCACUGCGAAA-GUGA-AUGGCAUGUGAAU-GCAGGCAUCCGGGAAUUGA  CRYPTHECODINIUM COHNII (PYRRHOPHYTA)
 28  AG---AAAACUUUCAACGGUGGAUAUCUUGGU-UCCCGUGACGAUGAAGAACGCAGCGAAAUGCGAUACGUAAUGCGAAUUGCAG--AACCGCGAGUCAA  TETRAHYMENA PYRIFORMIS (CILIOPHORA)
 29  A-------ACGUGUCGCGAUGGAUGACUUGGCUUCCUAUCUCGUUGAAGAACGCAGUAAAGUGCGAUAAGUGGUAPCAAUUGCAGAAU-CAUUCAAUUAC  CRITHIDIA FASCICULATA (KINETOPLASTIDA)
                            *   ** *            *  ** *  *   *  *   * *            *    **

             .         .         .         .         .         .         .         .         .         .
  1  CGACACUUCGAACGCA-CUUGCGGCCCC--G--G---GUUCCUCCCGGGGCUACGCCUGUCUGAGCGUCG-C--U-----                      RATTUS RATTUS (MAMMALIA)
  2  CGACACUUCGAACGCA-CUUGCGGCCCC--G--G---GUUCCUCCCGGGGCUACGCCUGUCUGAGCGUCG-CU-U-----                      MUS MUSCULUS, HOMO SAPIENS (MAMMALIA)
  3  CGACACUUCGAACGCA-CUUGCGGCCCC--G--G---GUUCCUCCCGGGGCUACGCCUGUCUGAGCGUCG-CU-U-----                      TERRAPENE CAROLINA (REPTILIA)
  4  CGACACUUCGAACGCA-CUUGCGGCCCC--G--G---GUUCCUCCCGGGGCUACGCCUGCCUGAGCGUCG-CU-U-----                      GALLUS GALLUS (AVES)
  5  CGACACUUCGAACGCACCUUGCGGCCCC--G--G---GUUCCUCCCGGGGCCACGCCUGUCUGAGGGUCG-CUCC-----                      XENOPUS LAEVIS (AMPHIBIA)
  6  CGACACUUCGAACGCACCUUGCGGCCCC--G--G---GUUCCUCCCGGGGCUACGCCUGUCUGAGGGUCG-CUC------                      XENOPUS BOREALIS (AMPHIBIA)
  7  UGACACUUCGAACGCACUUUGCGGCCCCAGG--G---GUUCCUCCUGGGGCUACGCCUGUCUGAGUGUCG-CU-U-----                      SALMO GAIRDNERI (OSTEICHTHYES)
  8  CGACAUUUUGAACGCAUAUCGCAG--UCCAU--G-CUG◊◊◊◊UGCUUGGACUACAUAUGGUUGAGGGUUG---UA-----                      DROSOPHILA MELANOGASTER (INSECTA)
  9  UGACAUUUUGAACGCAUAUUGCGG--UCCAU--A-CUG◊◊◊◊UGUAUGGACCACACAUGGUUGAGGGUCG---UU-----                      *SCIARA COPROPHILA (INSECTA)
 10  CGACAUUUCGAACGCACAUUGCGG--UCCGU--G-GAGACACAUCCAGGACCACUCCUGUCUGAGGGCCGGCU-------                      BOMBYX MORI (INSECTA)
 11  CGACAUUUCGAACGCACAUUGCGG--UCCGU--G-GAGACACAUCCAGGACCACUCCUGUCUGAGGGCCGAUUAA-----                      PHILOSAMIA CYNTHIA RICINI (INSECTA)
 12  CGACCAGUCGAACGCACAUUGCGGCCUCGGU--GACCCGCGGGCCCCGGGCCACGCCUGUCUGAGGGUCG---UA-----                      ACYRTHOSIPHON MAGNOLIAE (INSECTA)
 13  CUAUAUUUPGAACGCAAAUUGCAG--UCCA---GCCUUUGAGGU--UGGACUACGUCUGGCUGAGAGACGGAU-------                      ARTEMIA SALINA (CRUSTACEA)
 14  CGACAUCUUGAACGCAUAUGGCGGCCUCGG-------GUCCAUCCCGGGGCCACGCCCGUCUGAGGGUCGGC--------                      ARION RUFUS (GASTROPODA)
 15  CGAGUCUUUGAACGCAAAUGGC-GCUUCUG-------GUCUCACCAGGAGC-ACGUCUGUCUGAGAGUUUGC--------                      HYMENIACIDON SANGUINEA (PORIFERA)
 16  CGAAUCUUUGAACGCACAUUGCGCCCUCUGG--------UAUUCCGGGGGGCAUGCCUGUCCGAGCGUC--A-UU-----                      THERMOMYCES LANUGINOSUS (PLECTOMYCETES)
 17  CGAAUCUUUGAACGCACAUUGCGCUCGCCAG--------UAUUCUGGCGAGCAUGCCUGUUCGAGCGUC--AUUU-----                      *NEUROSPORA CRASSA (PYRENOMYCETES)
 18  CGAAUCUUUGAACGCACAUUGCGCCUUUGGG--------UUCUACCAAAGGCAUGCCUGUUUGAGUGUC--A-UU-----                      *SCHIZOSACCHAROMYCES POMBE (ENDOMYCETES)
 19  CGAAUCUUUGAACGCACAUUGCGCCCCUUGG--------UAUUCCAGGGGGCAUGCCUGUUUGAGCGUC--AUUU-----                      SACCHAROMYCES CEREVISIAE (ENDOMYCETES)
 20  CGAAUCCCUGAACGUAUACUGCG--CCCGAG--GCCC-C--GGU--AGAGC-AUGUCUGCCUUAGUGCUGGGUU------                      CHLAMYDOMONAS REINHARDII (VOLVOCALES)
 21  CGAGUCUUUGAACGCAAGUUGCG--CCCGA---GCCA-CU-CGCCGAGGGC-ACGCCUGCCUGGGCG-UCACGC------                      TRITICUM AESTIVUM (ANGIOSPERMAE)
 22  CGAGUCUUUGAACGCAAGUUGCG--CCCGAA--GCCA-UUAGGCCGAGGGC-ACGCCUGCCUGGGUG-UUGCAC------                      *LUPINUS LUTEUS (ANGIOSPERMAE)
 23  CGAGUCUUUGAACGCAAGUUGCG--CCCGAU--GCCA-UUAGGUUGAGGGC-ACGUCUGCCUGGGUG-UCACAU------                      VICIA FABA (ANGIOSPERMAE)
 24  CGAAUCUPUGAACGCA-AGUUGCGCUCUCGU--GGUUUAACCCCCCGGGAGCACGUUCGCUUGAGUGCCGC--UU-----                      ACANTHAMOEBA CASTELLANII (AMOEBINA)
 25  UGAAAUGUUGAACGCACAUGAUGACAUCGGU--CCUUUCGGAUUAGGUGUUAUACUUGGG-UG-AGAGUGG--UC-----                      DICTYOSTELIUM DISCOIDEUM (DICTYOSTELIIA)
 26  CGUCUCCUUGAAC----AUUAGUGCGGCCUU--GCCUUCGGGCAC--UGGCCCCCUUGGGAUGCCUUGUCC--UU-----                      *PHYSARUM POLYCEPHALUM (MYXOGASTRIA)
 27  GAGCUUCUUGAAUGCAUACUGCUCCAGCUGA--CUUGUCAG-UUGGAUAAUCUCCCUCAGG-GACUA-------------                      CRYPTHECODINIUM COHNII (PYRRHOPHYTA)
 28  CAGAUCUUUGAAAGCA-AGUGGUG-----GA--GGUGUAAAAACC----UUCAUGUUUGUAUUAGU-GUGG--CA-----                      TETRAHYMENA PYRIFORMIS (CILIOPHORA)
 29  CGAAUCUUUGAACGCAAACGGCGCAUGGGAGAAGCUCUUUUGAGUCAUCCCCGUGCAUGCCAUAUUCUCCAGUGUCGAAC                      CRITHIDIA FASCICULATA (KINETOPLASTIDA)
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Eukaryotic 5.8S RNS Sequences

SPECIES (Higher Taxon)	SPECIFICATIONS	REMARKS	REFERENCES
RATTUS RATTUS (MAMMALIA)	NOVIKOFF HEPATOMA ASCITES; DNA	C1 HET; U14 P57 PART MOD	122 123 124
MUS MUSCULUS, HOMO SAPIENS (MAMMALIA)	MPC-11; HELA; DNA	C1 HET; U14 P57 PART MOD	125 126 127 128
TERRAPENE CAROLINA (REPTILIA)	HEAR CELLS CCL50	U14 PART MOD	129
GALLUS GALLUS (AVES)	EMBRYO	C1 HET; U14 P57 PART MOD	126
XENOPUS LAEVIS (AMPHIBIA)	SOMATIC; DNA	U1 40% C2 20% HET; U14 P57 PART MOD	130 131 132 133
XENOPUS BOREALIS (AMPHIBIA)	SOMATIC	U1 40% C2 20% HET; U14 P57 PART MOD	131
SALMO GAIRDNERI (OSTEICHTHYES)	RTG-2	C1 HET; U14 P57 PART MOD	134
DROSOPHILA MELANOGASTER (INSECTA)	OREGON R, WHOLE TISSUE		135
*SCIARA COPROPHILA (INSECTA)	DNA		136
BOMBYX MORI (INSECTA)	POSTERIOR SILKGLAND		137
PHILOSAMIA CYNTHIA RICINI (INSECTA)	POSTERIOR SILKGLAND		138
ACYRTHOSIPHON MAGNOLIAE (INSECTA)	WHOLE TISSUE		139
ARTEMIA SALINA (CRUSTACEA)	CYSTS	A1 25% G2 25% GUA1 5% Het; ?U→P	140
ARION RUFUS (GASTROPODA)	WHOLE TISSUE		141
HYMENIACIDON SANGUINEA (PORIFERA)	AUDRESSELLES (F), WHOLE TISSUE	C1 ≤50% HET	141
THERMOMYCES LANUGINOSUS (PLECTOMYCETES)			142
*NEUROSPORA CRASSA (PYRENOMYCETES)	DNA		143
*SCHIZOSACCHAROMYCES POMBE (ENDOMYCETES)	DNA	AUUAUUUAA1 HET (8 SPECIES)	144
SACCHAROMYCES CEREVISIAE (ENDOMYCETES)	A364A (ATCC 22244)		145
CHLAMYDOMONAS REINHARDII (VOLVOCALES)	CELL WALL DEFICIENT MUT CW15		115
TRITICUM AESTIVUM (ANGIOSPERMAE)	EMBRYO	C1 79% HET; C119 A125 UNCERTAIN	109
*LUPINUS LUTEUS (ANGIOSPERMAE)	DNA		146
VICIA FABA (ANGIOSPERMAE)	LEAVES		147 148
ACANTHAMOEBA CASTELLANII (AMOEBINA)	ATCC 30010	U162 HET	91
DICTYOSTELIUM DISCOIDEUM (DICTYOSTELIIA)	AX3		149
*PHYSARUM POLYCEPHALUM (MYXOGASTRIA)	DNA		150
CRYPTHECODINIUM COHNII (PYRRHOPHYTA)			86
TETRAHYMENA PYRIFORMIS (CILIOPHORA)	W		139
CRITHIDIA FASCICULATA (KINETOPLASTIDA)		A171 34% C172 63% HET; U7 80% MOD	151

ABBREVIATIONS: HET = HETEROGENEITY, PART MOD = PARTIALLY MODIFIED

ACKNOWLEDGEMENTS

We would like to thank C. Kansy and A. Schreiber for the help with the input of the 5.8S rRNA sequences. The financial support of the "Deutsche Forschungsgemeinschaft" (Sfb 9/B5) and the "Fonds der chemischen Industrie" through grants to Volker A. Erdmann are deeply appreciated.

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