Collection of published 5S, 5.8S and 4.5S ribosomal RNA sequences

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The 1984 collection (1) of mature 5 S and 5.8 S rRNA sequences is updated. The sequences reported here are based on actual sequence determinations and not on oligonucleotide catalogues. Some of the earlier published oligonucleotide catalogues are given in reference 2.

We would like to thank those colleagues who have sent us their pre- or reprints on small ribosomal RNA sequences in 1984, and who have pointed out mistakes in our previous collection.

ACCESSIBILITY OF THE DATA

The 5 S, 5.8 S, and 4.5 S rRNA databases are part of the Berlin RNA Databank which is online accessible worldwide via the I.P.Sharp Timesharing Network. The Berlin RNA Databank uses the formats of the EMBL Nucleotide Sequence Data Library and is always updated as soon as a new RNA sequence is available. Downloading the data only requires a modem and costs US\$ 60 per hour connect-time with 300 baud (US\$ 120/h 1200 baud). Requests should be sent to Volker A. Erdmann (mailbox code VAEFU in the I.P.Sharp electronic mail system). Copies on magnetic tape of the 5 S RNA sequence alignment with superimposed secondary structure model are available on request from Rupert De Wachter in Antwerpen.

ABBREVIATIONS AND CONVENTIONS USED IN THE ALIGNMENTS AND REFERENCES

Each sequence is preceded by a number, repeated on the reference page. If identical 5 S rRNA sequences are found in two or more species, the sequence is aligned only once, preceded by the name of the species first examined. Additional species with the same sequence are listed only on the reference page.

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. The reference is to the paper reporting the correction, and is followed by the reference to the original paper, put in parentheses.
- 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 RNA variant due to gene polymorphism. If the variants have been isolated and separately sequenced, each variant sequence is aligned. The species name is followed by the character or number, in parentheses, used by the authors to identify the variant, e.g. Gallus gallus (I) and Gallus gallus (II). If heterogeneity was detected during sequencing of a mixture, a single sequence is aligned and heterogeneous positions are indicated as recommended by the IUB-IUPAC joint commission on biochemical nomenclature :

<u>symbol</u>	<u>nucleotides present</u>
R	A and G
Y	U and C
S	G and C
W	A and U
K	G and U
M	A and C

A nucleotide not identified due to an incomplete sequence analysis, is indicated by the symbol X.

5 S rRNA SEQUENCES

Alignment

The alignment of the 5 S RNA sequences is divided in 5 groups : eubacteria, plastids, mitochondria, archaebacteria, and eukaryotes. The procedure followed to align the sequences, described in detail elsewhere (3), 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. The number of positions needed to align the 238 sequences of the present compilation is 147. This does not include a 108 nucleotide insertion

between positions 123 and 128 in the *Halococcus morrhuae* 5 S rRNA. Terminal residues found in submolar amounts because of length heterogeneity in a 5 S RNA preparation are written in lower case characters.

The boxes labeled A-A', B-B', C-C', D-D' and E-E' correspond to double-stranded areas according to the secondary structure model defined below. 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.

The taxonomic position indicated for each species on the reference page is according to Kaestner (4) for the metazoa and protozoa, Ainsworth et al. (5) for the Ascomycota, Mastigomycota and Zygomycota, Oberwinkler (6) and Moore (7) for the Basidiomycota, Fritsch (8) for the algae and phytoflagellates, Engler (9) for the higher plants, Balch et al. (10) and Schnabel et al. (11) for the archaeobacteria. For eubacteria, the systematics based on 16 S rRNA oligonucleotide catalogues (12-15) is used. Taxonomic positions corresponding with an established taxonomic level, are followed by the appropriate abbreviation : Ph. (phylum), Sph. (subphylum), Cl. (classis) or O. (ordo).

Secondary structure model

The fundamental premise of the comparative approach to secondary structure investigation is that functionally equivalent molecules will exhibit a functionally equivalent secondary structure. A universal function implies an overall universal secondary structure. On the other hand, parts of the molecule could serve a function adapted to the special molecular biology of distinct groups of organisms.

The differences in the regulation of 5 S rRNA transcription (intragenic promoter elements in eukaryotes) and ribosome assembly between prokaryotes and eukaryotes might have some influence on primary and secondary structure. For a summary of the possible structure and function of the 5 S rRNA, the reader referred to references 3 and 16-20.

Five double-stranded areas postulated in the uniform 5 S rRNA secondary structure model proposed by De Wachter et al. (3) are indicated in the sequence alignment and labeled A to E. It should be stressed that this model is based purely on comparative examination of sequences, which shows the existence of universal complementarities in certain areas of the alignment, and of compensating substitutions in each of the postulated double stranded areas.

The length of helix D in eubacterial-, plastid- and mitochondrial 5 S RNA

is still a matter of controversy. According to some authors it contains only two base pairs, according to others it can be extended by additional base pairs, the number of which varies with the species considered. A two base-pair helix might not be recognized by experimental methods employed in secondary structure investigation.

In order to state the topological rules obeyed by the secondary structure model, which is represented in Fig. 1, 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 odd base pair occurring in such a segment should be intercalated between two standard base pairs.

The odd 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 5 S RNAs. It is extremely rare to find more than one odd base pair in any one double-stranded area.

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.

SEQUENCES OF THE 5.8S-SUBDOMAIN OF LARGE SUBUNIT RIBOSOMAL RNA

This year, the 5.8S rRNA sequences, which gained just one new species, are aligned with the equivalent structure at the 5'end of large subunit rRNA (L-rRNA). The 5.8S rRNA exists as a separate entity only in eukaryotes, in

Fig. 1. General shape of the secondary structure model in eubacteria and in eukaryotes. A to E, double-stranded areas; M, multibranched loop; I₁, I₂, interior loops; H₁, H₂, hairpin loops. Wavy lines between bases in area D of eubacterial 5 S RNA indicate a helix extension open to discussion (see text). Residues conserved at the 90% level are indicated by the symbols defined in the text, less conserved positions by filled circles. Terminal bases that are not present in all 5 S 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 5 S RNAs are numbered to facilitate comparison with the alignment.

diptera (5808, 5809), it is further processed into two fragments. In *Paramecium* mitochondria a fragment of about the same size and in *Chlamydomonas* plastids (5832) a 7S and a 3S rRNA are split off at the 5' end of L-rRNA. For secondary structure models and possible function we refer to (5801 [1], 5813, 5814, 5820, 156, 157, 158). Unfortunately, the authors of the most recent publication on 5.8S rRNA secondary structure (158) overlooked the "5.8S" fragment in *Paramecium* mitochondria and erroneously aligned the 5' end of the 20S fragment. In *Saccharomyces* (154) and *Aspergillus* (155) mitochondria no significant homology, in *Paramecium* (4515) and *Zea* (4514) mitochondria only partial homology could be detected, so that these sequences have been omitted.

The alignment has been obtained by running the program ALIGNSTAT (159) and adjusted manually to account for potential secondary structure interactions. The program ALIGNSTAT was purchased as part of the program package SAGE for the IBM PC/XT 370 from Technoma GmbH, Heidelberg, West Germany. It was run on the IBM 3081 computer of I.P. Sharp Associates in Toronto, Canada. To facilitate the recognition of species, the name of a higher taxon, believed to represent a monophyletic group, is given in parentheses. 2'-O-methyl-riboses are indicated by underscoring and pseudouridine by P.

The numbering of the helices is adapted from that of Maly and Brimacombe (160) introduced for L-rRNA of *E. coli*. Helix 1 is only present in eubacteria and plastids. Helices 2, 3, 4, and 10 of eukaryotic 5.8S/28S rRNA are defined by comparison to eubacterial 23S rRNA. In some instances, helices could not be drawn because of missing complementarity (helices 5, 7, and 8). No significant structural homology between eukaryotic and eubacterial helix 7 was found; in eukaryotes the hairpin loop of helix 7 is considerably conserved and modified. Please note that for 5.8S rRNAs the sequence numbers and reference numbers are identical. In the specification table the position numbers are those of the original sequence and therefore not identical to those in the alignment.

SEQUENCES OF THE 4.5S-SUBDOMAIN OF LARGE SUBUNIT RIBOSOMAL RNA

Included for the first time are sequences of 4.5S rRNA, found as a distinct entity in the plastids of land plants (bryophyta, pteridophyta, spermatophyta) (4506) but not in those of green algae (chlorophyta) (5832) or in any other plastid type (4507). These are aligned with their equivalent structure at the 3' end of L-rRNA of other plastids, eubacteria, and plant mito-

chondria. The eukaryotic correspondent shows significant sequence homology but fails to show structural homology. In other mitochondria, none (154, 155) or only partial (4515) homology has been found. For secondary structure models and possible function we refer to (4509, 152, 153).

The alignment was performed as described for 5.8S rRNAs. Please note that for 4.5S rRNAs the sequences numbers and reference numbers are identical. In the specification table the position numbers are those of the original sequence and therefore not identical to those in the alignment.

	10	20	30	40	50	60	70	80
1 CLOSTRIDIUM PASTERIANUM	UCCAGUGGCUAUGAC	UUAGAGGUAACA	C-UCCUUC	CCAUUCGGACA	GGG	AGGUAAGC	CCUUAAGU	UGU
2 BACILLUS STEAROTERMOPHILUS	UCCAGUGGCUAUAAC	SSAGAGGUAACA	C-CCGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
3 BACILLUS SUBTILIS(NAU)	UUUGUGGGCGUAABC	GAAGAGGUAACA	C-CCGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
4 BACILLUS LICHENIFORMIS(NAU)	UUUGUGGGCGUAABC	GAAGAGGUAACA	C-CCGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
5 BACILLUS NEGATIVUM	UUUGUGGGCGUAABC	GAAGAGGUAACA	C-CCGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
6 BACILLUS PASTERIUM	UUUGUGGGCGUAABC	GAAGAGGUAACA	C-CCGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
7 BACILLUS FINNIS	UYUGUGGGCGUAABC	GAAGAGGUAACA	C-CCGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
8 BACILLUS PASTERIANUS	UUUGUGGGCGUAABC	GAAGAGGUAACA	C-CCGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
9 BACILLUS ACTINOMARITIS	UCUGUGGACUAUAGC	SSAGAGGUAACA	C-CCGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
10 BACILLUS ACTINOMARITIS	UCUGUGGACUAUAGC	SSAGAGGUAACA	C-CCGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
11 LACTONICILLUS VIRIDESCENS(NAU)	UUUGUGGACUAUAGC	AUUGAGGUAACA	C-CUGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
12 LACTONICILLUS VIRIDESCENS(MIN)	UUUGUGGACUAUAGC	AUUGAGGUAACA	C-CUGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
13 STREPTOCOCCUS FAECALIS	UUUGUGGGCGUAUAC	CUAGAGGUAACA	C-CUGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
14 STREPTOCOCCUS FAECALIS	UUUGUGGGCGUAUAC	CUAGAGGUAACA	C-CUGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
15 STREPTOCOCCUS FAECALIS	UUUGUGGGCGUAUAC	CUAGAGGUAACA	C-CUGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC
16 STREPTOCOCCUS FAECALIS	UUUGUGGGCGUAUAC	CUAGAGGUAACA	C-CUGUUC	CCAUUCGGACA	CBB	AAGUUAAGC	CCUUAAGU	CGC

	99	100	110	120	130	140
1 CLOSTRIDIUM PASTERIANUM	-	6CU--(G)AU	-	66UAUGCAG	-	-
2 MACILLUS STENOCHROMIDULUS	-	6CC--(G)AU	-	66UAUGCAG	-	-
3 MACILLUS STOMATIDULUS	-	6CC--(G)AU	-	66UAUGCAG	-	-
4 MACILLUS LICKENTIFORMIS(NAJ)	-	6CC--(G)AU	-	66UAUGCAG	-	-
5 MACILLUS NEVATIUM	-	6CC--(G)AU	-	66UAUGCAG	-	-
6 MACILLUS PASTERI	-	6CC--(G)AU	-	66UAUGCAG	-	-
7 MACILLUS FINNIS	-	6CC--(G)AU	-	66UAUGCAG	-	-
8 MACILLUS MEVIS	-	6CC--(G)AU	-	66UAUGCAG	-	-
9 MACILLUS ACTINOMARTIS	-	6CC--(G)AU	-	66UAUGCAG	-	-
10 LACTONICILLUS VIRIDIS(NAJ)	-	6CC--(G)AU	-	66UAUGCAG	-	-
11 LACTONICILLUS VITREUS(NAJ)	-	6CC--(G)AU	-	66UAUGCAG	-	-
12 LACTONICILLUS VITREUS(NAJ)	-	6CC--(G)AU	-	66UAUGCAG	-	-
13 STREPTOCOCCUS MEVIS	-	6CC--(G)AU	-	66UAUGCAG	-	-
14 STREPTOCOCCUS CREBRIS	-	6CC--(G)AU	-	66UAUGCAG	-	-
15 STREPTOCOCCUS MEVIS	-	6CC--(G)AU	-	66UAUGCAG	-	-
16 STREPTOCOCCUS EPIDERMIS	-	6CC--(G)AU	-	66UAUGCAG	-	-

Eubacterial 5S RNA sequences

Nr	Species	Specification	Taxonomic position		Reference
1	CLOSTRIDIUM PASTEURIANUM	ATCC 6013	gram-positives	clostridia	21
2	BACILLUS STEAROTHEROPHILUS	Strain 1430 FV			22
3	BACILLUS SUBTILIS(MAJ)	Strain BB 170			22
4	BACILLUS LICHENIFORMIS(MAJ)	Strain S244			23
5	BACILLUS NEGATIVUM	Strain KN			24
6	BACILLUS PASTEURII	ATCC 11859			24
7	BACILLUS FINNIS	ATCC 14575			24
8	BACILLUS BREVIS	ATCC 8185			24
9	BACILLUS ACIDOCALDARIUS				25
10	LACTOBACILLUS VIRIDESCENS(MAJ)	ATCC 12706			26
11	LACTOBACILLUS VIRIDESCENS(MIN)	ATCC 12706			27
12	LACTOBACILLUS BREVIS	Strain X-2			24
13	STREPTOCOCCUS FAECALIS				24
14	STREPTOCOCCUS CREMORIS	ATCC 11603			28
15	STAPHYLOCOCCUS AUREUS				29
16	STAPHYLOCOCCUS EPIDERMIDIS	ATCC 14990			29

[illegible][illegible]

17. STROPHOMYXIN SP.
18. MYCOPHLYXIN CAPRILICOL
19. MYCOPHLYXIN CAPRILICOL
20. MYCOPHLYXIN CAPRILICOL
21. MYCOPHLYXIN CAPRILICOL
22. MYCOPHLYXIN CAPRILICOL
23. MYCOPHLYXIN CAPRILICOL
24. MYCOPHLYXIN CAPRILICOL
25. MYCOPHLYXIN CAPRILICOL
26. MYCOPHLYXIN CAPRILICOL
27. MYCOPHLYXIN CAPRILICOL
28. MYCOPHLYXIN CAPRILICOL
29. MYCOPHLYXIN CAPRILICOL
30. MYCOPHLYXIN CAPRILICOL
31. MYCOPHLYXIN CAPRILICOL
32. MYCOPHLYXIN CAPRILICOL

Eubacteria 1 5S RNA sequences

Nr	Species	Specification	Taxonomic position		Reference
17	SPYROPLASMA SP.	Strain BC3	mucopolasata		30
18	MYCOPLASMA CAPRICOLUM	ATCC 27243			31
19	MYCOPLASMA NICOTIANES SSP. CAPRI	Strain P63			30
20	MICROCOCCUS LUTEUS(ATCC 9341)	ATCC 9341	gram-positives	actinomycetes	29
21	MICROCOCCUS LUTEUS(ATCC 4498)	ATCC 4498			29(32)
22	STREPTOMYCES GRISEUS	Strain 45-H			33
23	THERMUS THERMOPHILUS	Strain 51	purple photosynthetic bacteria and relatives	uncertain affiliation	34(35)
24	THERMUS AQUATICUS	ATCC 25104			25(36)
25	PARACOCCLUS NITRIFICANS	ATCC 13543		subdivision alpha-2	37
26	RHODOSPIRILLUM RUBRUM	Strain 81		subdivision alpha-1	38
27	PSEUDOMONAS FLUORESCENS	ATCC 13525		subdivision gamma-3	39
28	PSEUDOMONAS AERUGINOSA	CCEB 481	from still-tissue of C. asenifica from still-tissue of S. velum trochosome/trunk wall of R. pachytrula		39
29	AZOTOBACTER VINELANDII	NCIB 8789			39
30	"CALYPTOGENA" SYMBIONT	from still-tissue of C. asenifica			40
31	"SOLERIA" SYMBIONT	from still-tissue of S. velum			40
32	"RIFFIA" SYMBIONT	trochosome/trunk wall of R. pachytrula			40

Eubacterial 5S RNA sequences

10	20	30	40	50	60	70	80	90		
33	ESCHERICHIA COLI MEGAO (1) 1	10	20	30	40	50	60	70	80	90
34	ESCHERICHIA COLI MEGAO (2) 1	10	20	30	40	50	60	70	80	90
35	ESCHERICHIA COLI MEGAO (2) 2	10	20	30	40	50	60	70	80	90
36	ESCHERICHIA COLI M9 1	10	20	30	40	50	60	70	80	90
37	ESCHERICHIA COLI M9 2	10	20	30	40	50	60	70	80	90
38	ESCHERICHIA COLI OX45(1)	10	20	30	40	50	60	70	80	90
39	ESCHERICHIA COLI OX45(2)	10	20	30	40	50	60	70	80	90
40	PROTEUS VULGARIS	10	20	30	40	50	60	70	80	90
41	PHOTOBACTERIUM PHOSPHOREUM	10	20	30	40	50	60	70	80	90
42	LACTICACIDUS MARI	10	20	30	40	50	60	70	80	90
43	VIBRIO SP. (IMPROVISED)	10	20	30	40	50	60	70	80	90
44	VIBRIO MARI	10	20	30	40	50	60	70	80	90
45	VIBRIO CHLORAE	10	20	30	40	50	60	70	80	90
46	VIBRIO VULNIFICUS	10	20	30	40	50	60	70	80	90
47	VIBRIO ANITILLARUM	10	20	30	40	50	60	70	80	90
48	AEROMONAS HYDROPHILA	10	20	30	40	50	60	70	80	90
49	AMNISTIS MIBILANS	10	20	30	40	50	60	70	80	90
50	STREPTOCOCCUS LIVINGS 111	10	20	30	40	50	60	70	80	90
51	PROBACILLUM SP.	10	20	30	40	50	60	70	80	90

100	110	120	130	140		
33	ESCHERICHIA COLI MEGAO (1) 1	100	110	120	130	140
34	ESCHERICHIA COLI MEGAO (2) 1	100	110	120	130	140
35	ESCHERICHIA COLI MEGAO (2) 2	100	110	120	130	140
36	ESCHERICHIA COLI M9 1	100	110	120	130	140
37	ESCHERICHIA COLI M9 2	100	110	120	130	140
38	ESCHERICHIA COLI OX45(1)	100	110	120	130	140
39	ESCHERICHIA COLI OX45(2)	100	110	120	130	140
40	PROTEUS VULGARIS	100	110	120	130	140
41	PHOTOBACTERIUM PHOSPHOREUM	100	110	120	130	140
42	LACTICACIDUS MARI	100	110	120	130	140
43	VIBRIO SP. (IMPROVISED)	100	110	120	130	140
44	VIBRIO MARI	100	110	120	130	140
45	VIBRIO CHLORAE	100	110	120	130	140
46	VIBRIO VULNIFICUS	100	110	120	130	140
47	VIBRIO ANITILLARUM	100	110	120	130	140
48	AEROMONAS HYDROPHILA	100	110	120	130	140
49	AMNISTIS MIBILANS	100	110	120	130	140
50	STREPTOCOCCUS LIVINGS 111	100	110	120	130	140
51	PROBACILLUM SP.	100	110	120	130	140

Eubacteria 1 5S RNA sequences

Nr	Species	Specification	Taxonomic position		Reference
			Purple photosynthetic bacteria and relatives	subdivision samaa-3	
33	ESCHERICHIA COLI HRE600 (1) 1	HRE 600			41
34	ESCHERICHIA COLI HRE600 (2) 1	HRE 600			41
35	ESCHERICHIA COLI HRE600 2	HRE 600			42
36	ESCHERICHIA COLI A19 1	HRE 600			43
37	ESCHERICHIA COLI A19 2	A19			44
38	ESCHERICHIA COLI CA2AS(1)	CA2AS			45
39	ESCHERICHIA COLI CA2AS(2)	CA2AS			45
40	PROTEUS VULGARIS				42
41	PHOTOBACTERIUM PHOSPHOREUM	Strain B2AS			44
42	LUCIFACTERIUM MARVELI	Strain 392			47
43	VIBRIO SP. (MAGPHILIC)	Strains UM40,M145	cyanobacteria	cocconesae	48
44	VIBRIO MARINUS	ATCC 15381			49
45	VIBRIO CHLORAE				50
46	VIBRIO VULNIFICUS				50
47	VIBRIO ANGULLARUM				50
48	AERONAS HYDROPHILA				50
49	ANACTYSIS NITULANS	Strain 1405/1 kratz/allen			51
50	STREPTOCOCCUS LIVINUS III				52
51	PROCHLORON SP.	Lissoclinum patellarhost		uncertain affiliation	37

Plastidial and Mitochondrial 5S RNA sequences

52 EMBLEMA GRACILIS CHL.	10	20	30	40	50	60	70	80
53 MARCHANTIA POLYTRICHA CHL.	10	20	30	40	50	60	70	80
54 MARCHANTIA SIMULATA CHL.	10	20	30	40	50	60	70	80
55 BRIDOPTERIS ACROSTICHA CHL.	10	20	30	40	50	60	70	80
56 ZEA MAYS CHL.	10	20	30	40	50	60	70	80
57 LEMNA MINOR CHL.	10	20	30	40	50	60	70	80
58 NICOTIANA GLANDULA CHL.	10	20	30	40	50	60	70	80
59 SPINACIA OLERACEA CHL.	10	20	30	40	50	60	70	80
60 ELYCINE MAX INT.	10	20	30	40	50	60	70	80
61 TRITICUM AESTIVUM INT.	10	20	30	40	50	60	70	80
62 ZEA MAYS INT.	10	20	30	40	50	60	70	80
63 EMBLEMA GRACILIS CHL.	90	100	110	120	130	140	150	160
64 MARCHANTIA POLYTRICHA CHL.	90	100	110	120	130	140	150	160
65 MARCHANTIA SIMULATA CHL.	90	100	110	120	130	140	150	160
66 BRIDOPTERIS ACROSTICHA CHL.	90	100	110	120	130	140	150	160
67 ZEA MAYS CHL.	90	100	110	120	130	140	150	160
68 LEMNA MINOR CHL.	90	100	110	120	130	140	150	160
69 NICOTIANA GLANDULA CHL.	90	100	110	120	130	140	150	160
70 ELYCINE MAX INT.	90	100	110	120	130	140	150	160
71 TRITICUM AESTIVUM INT.	90	100	110	120	130	140	150	160
72 ZEA MAYS INT.	90	100	110	120	130	140	150	160

Plastidial 5S RNA sequences

Nr	Species	Specification	Tecnonomic position	Reference
52	EMBLEMA GRACILIS CHL.	Strain Z	chloroplasts	53
53	MACRANTHA POLYTRICHA CHL.			54
54	JUNCEMANA SULCATA CHL.			54
55	CRYPTOPTERIS ACUMINATA CHL.			55
56	ZEA MAYS CHL.			56
57	LEPNA MINOR CHL.	Clone #Zac134	chloroplasts	57
58	SPINDELIA OLIGORHIZA CHL.	Clone #Br-c18H		58
59	MICOTTIANA TAMARINI CHL.	var. Bright Yellow		59(40)
		Clone #TC7		41

Mitochondrial 5S RNA sequences

40	OLYCEME MAX MIT.	var. Thatcher Clone Zant MS42	mitochondria	42
41	TRITICUM AESTIVUM MIT.			43
42	ZEA MAYS MIT.			44

Archaeobacterial 5S RNA sequences

43 HALOBACTERIUM CUTTIBIUM	10	20	30	40	50	60	70	80
44 HALODICUS NUBIAE	10	20	30	40	50	60	70	80
45 METHANOSPIRILLUM MARIANUM	10	20	30	40	50	60	70	80
46 METHANOSPIRILLUM MARIANUM	10	20	30	40	50	60	70	80
47 METHANOCoccus VARIETII 1	10	20	30	40	50	60	70	80
48 METHANOCoccus VARIETII 2	10	20	30	40	50	60	70	80
49 SULFOLOBUS ACETICOLACTUS	10	20	30	40	50	60	70	80
50 THERMOPLASMA ACETICUM	10	20	30	40	50	60	70	80
43 HALOBACTERIUM CUTTIBIUM	90	100	110	120	130	140	150	160
44 HALODICUS NUBIAE	90	100	110	120	130	140	150	160
45 METHANOSPIRILLUM MARIANUM	90	100	110	120	130	140	150	160
46 METHANOSPIRILLUM MARIANUM	90	100	110	120	130	140	150	160
47 METHANOCoccus VARIETII 1	90	100	110	120	130	140	150	160
48 METHANOCoccus VARIETII 2	90	100	110	120	130	140	150	160
49 SULFOLOBUS ACETICOLACTUS	90	100	110	120	130	140	150	160
50 THERMOPLASMA ACETICUM	90	100	110	120	130	140	150	160

Archaeobacterial 5S RNA sequences

Nr	Species	Specification	Taxonomic position	Reference
63	HALODACTYLOPHILUS CUTIRUBRUM	MRC 34001	halobacteriales	65(66)
	HALODACTYLOPHILUS HALOBIVUM	Strain R1		67
64	HALODACTYLOPHILUS MORRHUAE ^a	ATCC 17082	Methanobacteriales	68
65	METHANOBREVIBACTER RUMINANTIIUM	Strain PS		65
66	METHANOSPIRILLUM HUNGATEI		Methanomicrobiales	65
67	METHANOCOCCUS VANNIELII 1		Methanococcales	69
68	METHANOCOCCUS VANNIELII 2			65
69	SULFOLOBUS ACIDICOLORATUS ^b		Sulfolobales	70
	SULFOLOBUS SOLFATARICUS ^b			25
70	THERMOPLASMA ACIDOPHILUM	MT 4 Strain 122-182 or 122-183	Thermoplasmatales	71

(a) The chain length of the complete 5S RNA is 231 nucleotides. The following sequence has to be inserted between positions 123 and 127: GCCUGGCAAGAGGGGCCAAGUGUGAGCCGAGGAGCGCAUUCGGUAGUACAG CGGAGUCCGUCGGGGAACCGAGACCGGCUCCGUUACACGGCUCUAUACUAGU

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

Eukaryotic 5S RNA sequences

- 71 HOMO SAPIENS
- 72 RATUS NORVIGI
- 73 GALLUS GALLUS(1)
- 74 GALLUS GALLUS(11)
- 75 XENOPUS LAEVIS(40)
- 76 XENOPUS LAEVIS(40)
- 77 XENOPUS LAEVIS(40-2)
- 78 XENOPUS LAEVIS(40-3)
- 79 XENOPUS LAEVIS(40-3)
- 80 XENOPUS LAEVIS(40-3)
- 81 XENOPUS LAEVIS(40-3)
- 82 XENOPUS LAEVIS(40-3)
- 83 XENOPUS LAEVIS(40-3)
- 84 TIGRA TIGRA(40)
- 85 TIGRA TIGRA(40)
- 86 TIGRA TIGRA(40)
- 87 TIGRA TIGRA(40)
- 88 TIGRA TIGRA(40)

- 71 HOMO SAPIENS
- 72 RATUS NORVIGI
- 73 GALLUS GALLUS(1)
- 74 GALLUS GALLUS(11)
- 75 XENOPUS LAEVIS(40)
- 76 XENOPUS LAEVIS(40)
- 77 XENOPUS LAEVIS(40-2)
- 78 XENOPUS LAEVIS(40-3)
- 79 XENOPUS LAEVIS(40-3)
- 80 XENOPUS LAEVIS(40-3)
- 81 XENOPUS LAEVIS(40-3)
- 82 XENOPUS LAEVIS(40-3)
- 83 TIGRA TIGRA(40)
- 84 TIGRA TIGRA(40)
- 85 TIGRA TIGRA(40)
- 86 TIGRA TIGRA(40)
- 87 TIGRA TIGRA(40)
- 88 TIGRA TIGRA(40)

Eukaryotic 5S RNA sequences

nr	Species	Specification	Taxonomic position		Reference
71	HOMO SAPIENS	KB cells	Chordata(Ph.)	Mammalia(Cl.)	72
72	RATTUS NATTUS	Liver			73
73	GALLUS GALLUS(1)	Liver and brain cells			74
74	GALLUS GALLUS(II)	Liver and brain cells			74
75	XEROPUS LAEVIS(0)	Oocytes	Amphibia(Cl.)		75
76	XEROPUS BOREALIS(0-1)	Oocytes/clones p/bool			76
77	XEROPUS BOREALIS(0-2)	Oocytes/clones p/bool			76
78	XEROPUS BOREALIS(0-3)	Oocytes/clones p/bool			76
79	MITOPHTALMUS VIRIDESCENS	Clone P55 10	Osteichthyes(Cl.)		77
80	SALMO GALTHERII	Liver			78
81	KLONOBUS FOSILIS(5)	Oocytes			79
82	KLONOBUS FOSILIS(0)	Liver			79
83	TINCA TINCA(5)	Oocytes	Tunicata(SPh.)		80
84	TINCA TINCA(0)	Branchial pouches			80
85	HALCYNTHIA ROSETZI	Gonads			81
86	HALCYNTHIA ROSETZI	Whole organism			82
87	SACCORHINUS KOMALEVSKII(1)	Whole organism	Hemichordata(Ph.)		83
88	SACCORHINUS KOMALEVSKII(2)	Whole tissue			83
89	ACTYNOTRIPHTER MARULIAE	Whole tissue	Arthropoda(Ph.)	Hexapoda(Cl.)	84

89 *BROSIPHILLA HELANDGASTER*(11)
90 *BROSIPHILLA HELANDGASTER*(12)
91 *BROSIPHILLA HELANDGASTER*(3)
92 *CALLIPHORA ERYTHROCEPHALA*
93 *PHYLLOSTOMA CYNTHIA-RICINI*
94 *MONETA MORI*
95 *ARTEDIA SALINA*
96 *LITHECHINUS VARIEGATUS*
97 *HEINICENTROTUS PULCHERRIMUS*
98 *ASTERIAS VULGARIS*
99 *ASTERIAS PECTINIFERA*
00 *STICHOMUS OSHIMAE*
01 *LIMBULA ANTHIA*
02 *BUGULA ANTHIA*
03 *HELIOPOMA*
04 *ARTON RUFIUS*

Figure 1 shows the sequence of the 1000 bp DNA fragment. The sequence is presented in a grid format, with columns labeled A, B, C, C', and B' at the top. The rows are numbered 1 to 1000 on the left side. The sequence is composed of nucleotides (A, C, G, T) and dashes representing gaps. The sequence is divided into five segments: A (1-1000), B (1-1000), C (1-1000), C' (1-1000), and B' (1-1000). The sequence is presented in a grid format, with columns labeled A, B, C, C', and B' at the top. The rows are numbered 1 to 1000 on the left side. The sequence is composed of nucleotides (A, C, G, T) and dashes representing gaps. The sequence is divided into five segments: A (1-1000), B (1-1000), C (1-1000), C' (1-1000), and B' (1-1000).

89 *BROSOPHILLA MELANGASTER*(11)
90 *BROSOPHILLA MELANGASTER*(2)
91 *BROSOPHILLA MELANGASTER*(3)
92 *CALLITRIPODA EXTINCTOPHALLA*
93 *PHILLAGASTRA CYNTHIA-RICINI*
94 *BONNYI* ROKI
95 *ARTENIA SALINA*
96 *LYTECHINUS VARIEGATUS*
97 *HEMICEINOTRIPS PULCHERRIMUS*
98 *ASTERIAS VULGARIS*
99 *ASTERIAS PECTINIFERA*
00 *STICHOPUS OSMINE*
01 *LIMBULA AMANTIA*
02 *BUBULA MERTINIA*
03 *HELYX PONTICA*
04 *ARTION REFUS*

[illegible]

Eukaryotic 5S RNA sequences

Nr	Species	Specification	Taxonomic position		Reference
89	BRASOPHILLA MELANOGASTER(1)	Clone pBcSSI	Arthropoda(Ph.)	Hexapoda(Cl.)	85(84, 87)
	BRASOPHILLA SIMILANS	Strain 204-1			88
	BRASOPHILLA TEISSIERI	Strain 201-5			88
90	BRASOPHILLA MELANOGASTER(2)	Clone pBcSSII			85
91	BRASOPHILLA MELANOGASTER(3)	Clone pBcSSIII			85
92	CALLIPHORA ERYTHROCEPHALA	Clone pLR1	Echinodermata(Ph.)	Crustacea(Cl.)	89
93	PHILODONTIA CYNTHIA-RICINI	Posterior silklands			90
94	BOMBYX MORI	Silkland			91
95	ARTERIA SALINA	Cysts			92
96	LYTECHINUS VARIEGATUS	Clone pLul03			Echinoides(Cl.)
97	HEMICENTROTUS PULCHERRIMUS	Ovaries	Lophophorata(Ph.)	Asteroidea(Cl.)	94
98	ASTERIAS VULGARIS	Ovaries			95
99	ASTERINA PECTINIFERA	Ovaries			94
100	STICHOPUS OSHTIME	Waterlands			94
101	LIMBULA ANATIMA	Whole tissue			Holothuroidea(Cl.)
102	BUGULA NERITIMA	Whole organism	Lophophorata(Ph.)	Phoronidea(Cl.)	96
103	HELIX POMATIA	Whole tissue		Bryozoa(Cl.)	83
104	ARTON RUFUS	Whole tissue	Mollusca(Ph.)	Gastropoda(Cl.)	97

r126

r126

Eukaryotic 5S RNA sequences

Nr	Species	Specification	Taxonomic position		Reference
105	MYTILUS EDULIS	Whole tissue	Mollusca(Ph.)	Bivalvia(Cl.)	97
106	SOLENTIA VELUM	Gill tissue			40
107	CALYPTOSENA MAGNIFICA	Gill tissue			98
108	OCTOPUS VULGARIS	Liver cells		Cephalopoda(Cl.)	83
109	ILLEX ILLECEBRUSUS	Digestive gland	Cnidaria(Ph.)	Anthozoa(Cl.)	95
110	ANTHOPELURA JAPONICA	Whole tissue			99
111	SPINOCCORON SALTATRIX	Ovaries			Hydrozoa(Cl.)
112	NEROPSIS DOFLEINI	Ovaries		Scyphozoa(Cl.)	100
113	AURELIA AURITA 1	Ovaries	100		
114	AURELIA AURITA 2	Ovaries	95		
115	CHYTOSARA QUINTOLECTRONA	Whole tissue	Porifera(Ph.)		100
116	HALICOLA OCLATA	Whole tissue			101
117	HALICORNIA PAVICEA	Whole tissue			101
118	HYDRIACIDON SAMBUIKEA	Whole tissue			101
	HALICORNIA JAPONICA	Whole tissue	Plathelminthes(Ph.)	Polycladida(Cl.)	81
119	PLANOCERA RETICULATA	Whole tissue			102
120	BUESIA JAPONICA (FURUYU)	Whole tissue			Seriata(Cl.)
121	BUESIA JAPONICA (SAMRGE)	Whole tissue			102

Eukaryotic 5S RNA sequences

122 RIFTA PACHYPTILA	10	20	30	40	50	60	70	80
123 LINEUS GENTILIATUS	10	20	30	40	50	60	70	80
124 EPIPECTENUM BRACILE (L)	10	20	30	40	50	60	70	80
125 EPIPECTENUM BRACILE (S)	10	20	30	40	50	60	70	80
126 CAEROPHANTIS ELEGANS	10	20	30	40	50	60	70	80
127 PANDORITIS TOKAI	10	20	30	40	50	60	70	80
128 MACHIMUS PLEATILIS	10	20	30	40	50	60	70	80
129 PERIDORETIS BREVICORNIS	10	20	30	40	50	60	70	80
130 SABELLASTARTE JAPONICA	10	20	30	40	50	60	70	80
131 URECHIS UNICINCTUS	10	20	30	40	50	60	70	80
132 PHASCOLOPSIS GOLIATH	10	20	30	40	50	60	70	80
133 BICTERA VISAINTERSE	10	20	30	40	50	60	70	80
134 EUREMA BRACILIS 1	10	20	30	40	50	60	70	80
135 EUREMA BRACILIS 2	10	20	30	40	50	60	70	80
136 CRYPTHECIDIUM COMITI	10	20	30	40	50	60	70	80
137 OCTIDIUM FASCICULATA	10	20	30	40	50	60	70	80

122 RIFTA PACHYPTILA	100	110	120	130	140	150	160	170	180
123 LINEUS GENTILIATUS	100	110	120	130	140	150	160	170	180
124 EPIPECTENUM BRACILE (L)	100	110	120	130	140	150	160	170	180
125 EPIPECTENUM BRACILE (S)	100	110	120	130	140	150	160	170	180
126 CAEROPHANTIS ELEGANS	100	110	120	130	140	150	160	170	180
127 PANDORITIS TOKAI	100	110	120	130	140	150	160	170	180
128 MACHIMUS PLEATILIS	100	110	120	130	140	150	160	170	180
129 PERIDORETIS BREVICORNIS	100	110	120	130	140	150	160	170	180
130 SABELLASTARTE JAPONICA	100	110	120	130	140	150	160	170	180
131 URECHIS UNICINCTUS	100	110	120	130	140	150	160	170	180
132 PHASCOLOPSIS GOLIATH	100	110	120	130	140	150	160	170	180
133 BICTERA VISAINTERSE	100	110	120	130	140	150	160	170	180
134 EUREMA BRACILIS 1	100	110	120	130	140	150	160	170	180
135 EUREMA BRACILIS 2	100	110	120	130	140	150	160	170	180
136 CRYPTHECIDIUM COMITI	100	110	120	130	140	150	160	170	180
137 OCTIDIUM FASCICULATA	100	110	120	130	140	150	160	170	180

Eukaryotic 5S RNA sequences

Mr	Species	Specification	Taxonomic position		Reference
122	RIFTIA PACHYPTILA	Trunk wall-Trophosome	Podocophora(Ph.)	Affrenulata(Cl.)	98
123	LINELUS GERICULATUS	Whole tissue	Neemertini(Ph.)	Neemertini(Cl.)	103
124	EUPLECTONEMA GRACILE (L)	Whole tissue		Neemertini(Cl.)	103
125	EUPLECTONEMA GRACILE (S)	Whole tissue			103
126	CACIDIORHABDITIS ELEGANS	Var. Bristol strain #2	Neemertinae(Ph.)	Neemertoda(Cl.)	104
127	CACIDIORHABDITIS BRIGGSIAE				104
128	RHABDITIS TOKAI	Whole cells			105
129	BRACHIONUS PLEURALIS	Whole cells		Rotatoria(Cl.)	105
129	PERIMETIS BREVICIRRIS	Whole tissue			106
130	SABELLASTARTE JAPONICA	Whole tissue	Annelida(Ph.)	Polychaeta(Cl.)	106
131	URECHIS UNICINCTUS	Ovaries	Echiurida(Ph.)		106
132	PHASCOLOPSIS GOULDI	Coelomic fluid	Sipunculida(Ph.)		95
133	DICTYEA NISAKIENSE	from renal appendages Octopus vulgaris	Nesozoa(Ph.)		83
134	EURELEA GRACILIS 1	Strain Z	Eulampropheta(Ph.)		107
135	EURELEA GRACILIS 2 a	Strain ZACHSOO			108
136	CRYPTHOCODONUM COMBII		Binocheta(Ph.)		109
137	CITRINIDIA FASCICULATA		Flebotellata(Ph.)	Protomonadina(Cl.)	110

(a) The U residue at position 47 stands for pseudouridine

[illegible]

 

Eukaryotic 5S RNA sequences

Nr	Species	Specification	Taxonomic position	Reference
138	TETRAHYENA THERIOPHILA 1	Strain B	Ciliata(Ph.)	111
139	TETRAHYENA THERIOPHILA 2	Notated type IV		112
140	BLEPHARISMA JAPONICUM	R 13		112
141	PARAMECIUM TETRAURELIA	Notated type VIII		112
142	BRESSLAHA VORAX	Whole cells	Haptotricha(Cl.)	113
143	EUPLOTES VODRUFFI	Whole cells		113
144	CHILONIMAS PARAMECIUM	Whole tissue	Ceratophrya(Ph.)	114
145	ETISENTA BICYCLIS	Whole tissue		115
146	SARMASSUM FULVELLUM	Whole tissue	Phaeothrix(Ph.)	115
147	ACANTHAMEBA CASTELLANII	ATCC 30010		116
148	PHYSAUM POLYCEPHALUM	Strain MC-4	Rhizopoda(Ph.)	117
149	DICTYOSTELIUM DISCOIDEUM		Homoniscetes(Cl.)	118
150	PHYCOMYCES BLAKESLEEANUS		Acrosomycetes(Cl.)	119
151	BLASTOCADIAELLA SIMPLEX		Zooecocetes(Cl.)	120
152	PHLYCTOCYTRIDIUM IRREGULARE	ATCC 32046	Nestisomycota(Ph.)	120
153	THRAUSTICOTRIDIUM VISURGENSE			121
154	SCHIZOTRIDIUM AGGREGATUM			121

Eukaryotic 5S RNA sequences

135	SAPROLENTIA FENAX	U	10	20	30	40	50	60	70	80
136	PTILINOTRITHUSPUDIN	U	10	20	30	40	50	60	70	80
137	PUCETIA PUMON	U	10	20	30	40	50	60	70	80
138	EMPHYLLINUS SEPIVITI	U	10	20	30	40	50	60	70	80
139	ALICISTOTRITHUS JULIANIS	U	10	20	30	40	50	60	70	80
140	ARTICULATA ARTICULATA-JUNE	U	10	20	30	40	50	60	70	80
141	TREPETELLA RESETERICA	U	10	20	30	40	50	60	70	80
142	AMARITUS EMILIS	U	10	20	30	40	50	60	70	80
143	MUSCULA CYMBANTHIA	U	10	20	30	40	50	60	70	80
144	PLEURONOTUS OSTREATUS	U	10	20	30	40	50	60	70	80
145	COPIRINUS RABATUS	U	10	20	30	40	50	60	70	80
146	ALLENHAMIA ANUSTA	U	10	20	30	40	50	60	70	80
147	SCHIZOPHYLLINUS COMANE	U	10	20	30	40	50	60	70	80
148	MACYTICES BELINSESCUS	U	10	20	30	40	50	60	70	80
149	EXOSTRITUM VACILLANTI	U	10	20	30	40	50	60	70	80
150	EXOSTRITUM VACILLANTI	U	10	20	30	40	50	60	70	80
151	TILLETIA TILLETIA	U	10	20	30	40	50	60	70	80
152	AMARITUS EMILIS	U	10	20	30	40	50	60	70	80
153	MUSCULA CYMBANTHIA	U	10	20	30	40	50	60	70	80
154	PLEURONOTUS OSTREATUS	U	10	20	30	40	50	60	70	80
155	COPIRINUS RABATUS	U	10	20	30	40	50	60	70	80
156	EMPHYLLINUS SEPIVITI	U	10	20	30	40	50	60	70	80
157	PUCETIA PUMON	U	10	20	30	40	50	60	70	80
158	EMPHYLLINUS SEPIVITI	U	10	20	30	40	50	60	70	80
159	ALICISTOTRITHUS JULIANIS	U	10	20	30	40	50	60	70	80
160	ARTICULATA ARTICULATA-JUNE	U	10	20	30	40	50	60	70	80
161	TREPETELLA RESETERICA	U	10	20	30	40	50	60	70	80
162	AMARITUS EMILIS	U	10	20	30	40	50	60	70	80
163	MUSCULA CYMBANTHIA	U	10	20	30	40	50	60	70	80
164	PLEURONOTUS OSTREATUS	U	10	20	30	40	50	60	70	80
165	COPIRINUS RABATUS	U	10	20	30	40	50	60	70	80
166	ALLENHAMIA ANUSTA	U	10	20	30	40	50	60	70	80
167	SCHIZOPHYLLINUS COMANE	U	10	20	30	40	50	60	70	80
168	MACYTICES BELINSESCUS	U	10	20	30	40	50	60	70	80
169	EXOSTRITUM VACILLANTI	U	10	20	30	40	50	60	70	80
170	EXOSTRITUM VACILLANTI	U	10	20	30	40	50	60	70	80
171	TILLETIA TILLETIA	U	10	20	30	40	50	60	70	80

Eukaryotic 5S RNA sequences

Nr	Species	Specification	Taxonomic position		Reference
155	SAPROLENTIA FEDAX	ATCC 26116	Mastidiomycota (Ph.)	Oomycetes (Cl.)	120
156	PHYLLUM HYMNOSPORUM	ATCC 26929			120
157	PUCINIA POMUM	Strain #630 (R. Bauer)	Basidiomycetes (Cl.)	Uredinales (O.)	122
	COLEOPHORUM TUSSILAGINIS	Strain #776 (R. Bauer)			122
	GYNOPODANGIUM CLAVARIIFORME	Strain #655 (R. Bauer)			122
158	EMUPHYLLUM SEMPERVIVI	Strain #778 (R. Bauer)			122
159	MICROSTROMA JUBLANDIS	Strain PB 4142			122
160	AURICULARIA MURICULA-JURNE	Fruibody			123
161	TREVELLA NESENERICA	Yeast phase	Tremellales (O.)	Adaricales (O.)	124
162	AGARICUS EDULIS	Fruibody			123
163	RUSSULA CYANOGANTHA	Fruibody			123
164	PLEUROTUS OSTREATUS	Fruibody			123
165	COPRINUS RADIATUS	ATCC 26538			125
	COPRINUS CINEREUS	Mucella			126
166	BJERKANDERA ANUSTA	Mucella		Arhulenhomales (O.)	124
167	SCHIZOPHYLLUM COMMUNE	Mucella			124
168	BACKTRICES BELIOUESCENS	ATCC 13292		Bacromycetes (O.)	125
169	EXOMASTIDIUM VACCINI	ATCC 24312			125
170	TILLETIA CONTRAVERSA				125
171	TILLETARIA ANOMALA	ATCC 24038	Ustilomycetes (Cl.)	Ustilaginales (O.)	125

372 USTILAGO VIOLACEA
373 AESSPORUM SALICINICOLOR
374 RHODOSPORIUM TONILLITES
375 PACHYTICTE FERRUGINEA
376 AGARICOTILIA PANICULIUM
377 CLOPHOSPORUM APOHYSPALES
378 TRICHOSPORUM KENDRUMALIS
379 RHIZELLA ACETABULUS
380 STEPHANOTRYPTIS PESTICILLATUS
381 MILLERA ALMA
382 CRYPTOCOCUS ALUTIS
383 TERESBILIA PELEGRINA
384 PHOTIA RHODOTIZA
385 FLOMOSIDORIUM CAPSULIGERUM
386 FLOMOSIDORIUM FLORIDORUM
387 TRICHOMYCES ARIZAE
388 TRICHOTOMA HYEMALIS

[illegible]

772 USTILAGO VITIDOLICA
773 AECOSPORIUM SALICINICOLOR
774 AECOSPORIUM TOMATIDIS
775 PACHYTICHA FENESTRAE
776 AMARICOSTILUM PALLIDUM
777 CLONOSPORUM APICINASTES
778 TRICHOSPORIDIOSIS KNEZEPHALIS
779 PHILIELLA ACETABULUM
780 STEPHANOMYCES PESTICILLATUS
781 MILLERA ALBA
782 CRYPTOCODON ALBUS
783 TRICHOTILIA PEXIPLEXANS
784 PHOTIA INDOXYNA
785 FILONASTRUM CAPSULEORUM
786 FILONASTRUM FLORIDORUM
787 TRICHOSPORUM ORYZAE
788 MICROTICHTIA NIENHANSI

	99	100	110	120	130	140
D	C	U	C	C	U	C
E	A	U	C	C	U	C
F'	A	U	C	C	U	C
D'	A	U	C	C	U	C
E'	A	U	C	C	U	C
F	A	U	C	C	U	C
G	A	U	C	C	U	C
H	A	U	C	C	U	C
I	A	U	C	C	U	C
J	A	U	C	C	U	C
K	A	U	C	C	U	C
L	A	U	C	C	U	C
M	A	U	C	C	U	C
N	A	U	C	C	U	C
O	A	U	C	C	U	C
P	A	U	C	C	U	C
Q	A	U	C	C	U	C
R	A	U	C	C	U	C
S	A	U	C	C	U	C
T	A	U	C	C	U	C
U	A	U	C	C	U	C
V	A	U	C	C	U	C
W	A	U	C	C	U	C
X	A	U	C	C	U	C
Y	A	U	C	C	U	C
Z	A	U	C	C	U	C

Eukaryotic 5S RNA sequences

Nr	Species	Specification	Taxonomic position		Reference
			Ustilaceales(Cl.)	Ustilaginales(O.)	
172	USTILAGO VIOLACEA	Yeast phase			124
173	AESSOSPORUM SALMONICOLOR	Yeast phase			124
174	INDOSPORIDIUM TORULOIDES	Yeast phase			124
175	PACHYDICTYE FERUGINEA	mycelia	deuteromycetes	basidiomycetous herbariocyte	127
176	AGARICOSTILBUM PALNICOLUM	yeast phase			127
177	CHIONOSPHERA APOMASIDIALES	yeast phase			127
178	TRICHOSPORONIUM DEMOCEPHALIS	ATCC 16988			127
179	NOBILIELLA ACETABULUM	ATCC 18455			127
180	STERIGMATONYCES PERICILLATUS	ATCC 32127		basidiomycetous yeast	127
181	MULLERA ALMA	ATCC 18548			127
182	CRYPTOCOCCUS ALBIDUS	ATCC 10466			127
183	ITEROBULLIA PERPLEXANS	ATCC 15495			127
184	PHAFFIA RHODOLYTICA	ATCC 24202			127
185	FILOMASIDIUM CAPSULIGENUM	Yeast phase			124
186	FILOMASIDIUM FLORIFORME	Yeast phase			124
187	TRICHOSPORUM ORYZAE	ATCC 26323			125
188	BLIZOCTONIA NIENHALIS	ATCC 14016		basidiomycetous herbariocyte	125

89 INITIATIONIA DROGUM	AUCU	G666CAUA	C6	AAC6C	EAUAUA	C	66CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA	U6	CA
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	99	100	110	120	130	140
89 RHIZOCTONIA CROCINUM	G C C C - A G U	- A G U A	U G G G G G G C	C A C C G C G C	A C U	G C C C - A G U
90 RHIZOCTONIA EMBLIIANS	G C C C - A G U	- A G U A C	U G G G G G G C	C A C C G C G C	A C U	G C C C - A G U
91 SACCHAROMYCES CEREVISIAE 1	G C C C - A G U	- A G U A C	U G G G G G G C	C A C C G C G C	A C U	G C C C - A G U
92 SACCHAROMYCES CEREVISIAE (1) 2	G C C C - A G U	- A G U A C	U G G G G G G C	C A C C G C G C	A C U	G C C C - A G U
93 SACCHAROMYCES CEREVISIAE (2) 1	G C C C - A G U	- A G U A C	U G G G G G G C	C A C C G C G C	A C U	G C C C - A G U
94 SACCHAROMYCES CEREVISIAE (2) 2	G C C C - A G U	- A G U A C	U G G G G G G C	C A C C G C G C	A C U	G C C C - A G U
95 RHIZOCTONIA CROCINUM	G C C C - A G U	- A G U A C	U G G G G G G C	C A C C G C G C	A C U	G C C C - A G U
 

Eukaryotic 5S RNA sequences

Nr	Species	Specification	Taxonomic position		Reference
			deuteromycetes	basidiomycetes herbariocyte	
189	RHIZOCTONIA CRUCIARIA	ATCC 11070			125
190	RHIZOCTONIA BLOUARIIS	ATCC 14015			127
191	SACCHAROMYCES CEREVISIAE 1	Clone pMB 25	Ascomycota (Ph.)	Neolascocetes (Cl.)	128
192	SACCHAROMYCES CEREVISIAE (1) 2	Clone pYef9			129
193	SACCHAROMYCES CEREVISIAE (2) 2	Clones pYef83, pYef147			129
194	SACCHAROMYCES CARLSBERGENSIS				130
195	SCHIZOSACCHAROMYCES POMBE	IFO 6345			131
196	CANDIDA ALBICANS	NCBI C001	deuteromycetes	ascocytous yeast	132
197	TORULOPSIS UTILIS	Clone pTU 824			133(134)
198	NEUROSPORA CRASSA (ALPHA)	Clone pKD 51 and pKD 52	Ascomycota (Ph.)	Puronomycetes (Cl.)	135(136)
199	NEUROSPORA CRASSA (BETA)	Clone pKD 51 and pKD 52			135
200	ACHERONITUM CHRYSOGENUM	ATCC 14553	deuteromycetes	ascocytous herbariocyte	132
201	ACHERONITUM PERSICINUM (1)	CBS 169.45			132
202	ACHERONITUM PERSICINUM (2)	CBS 169.45			132
203	ACHERONITUM PERSICINUM (3)	CBS 169.45			132
204	ASPERGILLUS NIDULANS (1)	NCBI A007	Ascomycota (Ph.)	Plectonomycetes (Cl.)	132(136)
205	ASPERGILLUS NIDULANS (2)	NCBI A007			132
206	ASPERGILLUS NIDULANS (3)	NCBI A007			132

Eukaryotic 5S RNA sequences

206 ASPERGILLUS FLAVUS	10	20	30	40	50	60
207 ASPERGILLUS NIGER	10	20	30	40	50	60
208 PENICILLIUM CHrysogenum	10	20	30	40	50	60
209 PENICILLIUM PATULUM	10	20	30	40	50	60
210 TRICHOMYCES LAMPROSPORUS (1)	10	20	30	40	50	60
211 TRICHOMYCES LAMPROSPORUS (2)	10	20	30	40	50	60
212 TRITICUM AESTIVUM	10	20	30	40	50	60
213 SECALE CEREALE	10	20	30	40	50	60
214 LEMNA MINOR	10	20	30	40	50	60
215 LUNIA ISTATIATISSIMUM	10	20	30	40	50	60
216 LUPINUS LUTIDUS(1)	10	20	30	40	50	60
217 LUPINUS LUTIDUS(2)	10	20	30	40	50	60
218 LYCOPESIDIUM ESCULENTUM	10	20	30	40	50	60
219 HELIANTHUS ANNUUS	10	20	30	40	50	60
220 PHASEOLUS VILLOSPUS	10	20	30	40	50	60
221 VICIA FABA	10	20	30	40	50	60
222 SPINACIA OLERACEA	10	20	30	40	50	60

206 ASPERGILLUS FLAVUS	70	80	90	100	110	120	130	140
207 ASPERGILLUS NIGER	70	80	90	100	110	120	130	140
208 PENICILLIUM CHrysogenum	70	80	90	100	110	120	130	140
209 PENICILLIUM PATULUM	70	80	90	100	110	120	130	140
210 TRICHOMYCES LAMPROSPORUS (1)	70	80	90	100	110	120	130	140
211 TRICHOMYCES LAMPROSPORUS (2)	70	80	90	100	110	120	130	140
212 TRITICUM AESTIVUM	70	80	90	100	110	120	130	140
213 SECALE CEREALE	70	80	90	100	110	120	130	140
214 LEMNA MINOR	70	80	90	100	110	120	130	140
215 LUNIA ISTATIATISSIMUM	70	80	90	100	110	120	130	140
216 LUPINUS LUTIDUS(1)	70	80	90	100	110	120	130	140
217 LUPINUS LUTIDUS(2)	70	80	90	100	110	120	130	140
218 LYCOPESIDIUM ESCULENTUM	70	80	90	100	110	120	130	140
219 HELIANTHUS ANNUUS	70	80	90	100	110	120	130	140
220 PHASEOLUS VILLOSPUS	70	80	90	100	110	120	130	140
221 VICIA FABA	70	80	90	100	110	120	130	140
222 SPINACIA OLERACEA	70	80	90	100	110	120	130	140

Eukaryotic 5S RNA sequences

Nr	Species	Specification	Taxonomic position		Reference
206	ASPERGILLUS FLAVUS	NCRI 4003	Ascomycota (Ph.)	Plectomycetes (Cl.)	132
207	ASPERGILLUS NIGER	HB115 (Dechae pharma.)			132
208	PENICILLIUM CHRYSOGENUM	ATCC 10002			132
209	PENICILLIUM PATULUM	NCRI P931	deuteromycetes	ascomycetous heteromycete	132
210	THEWYMYCES LAMBINGUS (1)	ATCC 16455			137
211	THEWYMYCES LAMBINGUS (2)	ATCC 16455			137
212	TRITICUM AESTIVUM	Embryo	Spermatophyta (Ph.)	Liliopsida (Cl.)	138 (139)
213	SECALE CEREALE	cv. Somro			140 (141)
214	LENA NIMOR				140
215	LINUM USITATISSIMUM	Clones p864, p8613	Mammaliopsida (Cl.)		142
216	LUPINUS LUTEUS (1)	Clone p481			143
217	LUPINUS LUTEUS (2)	Clone p484			143
218	LYCOPERSICON ESCULENTUM	cv. Heronde			140
219	HELIANTHUS ANNUUS	cv. sisanleus			140
220	PHASEOLUS VULGARIS	cv. Limbus			140
221	VICIA FABA	var. 424			140
222	SPINACIA OLERACEA				144

Eukaryotic 5S RNA sequences

223	INTROTERIS ACHILANTA	10	20	30	40	50	60	70	80
224	EMISESTIN ANERE	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
225	MACHANTIA POLYORPHA	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
226	LUPHOCLEA HETEROPHYLLA	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
227	PLATONOTUM TRICHOMES	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
228	ANTHOCERUS PUNCTATUS	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
229	DALYMPHOMAS BEINMARTII(11)	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
230	DALYMPHOMAS BEINMARTII(11)	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
231	DALYMPHOMAS SP.	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
232	DALYMPHOMAS SP.	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
233	SCYRUS GAMBICARNA	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
234	SCYRUS GAMBICARNA	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
235	ILYX PECTUS	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
236	PORPHYRA TETRACIS	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
237	PORPHYRA TETRACIS	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
238	BACTILANTIA COMPRESSA	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC

223	INTROTERIS ACHILANTA	100	110	120	130	140
224	EMISESTIN ANERE	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
225	MACHANTIA POLYORPHA	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
226	LUPHOCLEA HETEROPHYLLA	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
227	PLATONOTUM TRICHOMES	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
228	ANTHOCERUS PUNCTATUS	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
229	DALYMPHOMAS BEINMARTII(11)	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
230	DALYMPHOMAS BEINMARTII(11)	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
231	DALYMPHOMAS SP.	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
232	DALYMPHOMAS SP.	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
233	SCYRUS GAMBICARNA	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
234	SCYRUS GAMBICARNA	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
235	ILYX PECTUS	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
236	PORPHYRA TETRACIS	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
237	PORPHYRA TETRACIS	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC
238	BACTILANTIA COMPRESSA	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC	6536U-6C66UUAAC

Eukaryotic 5S RNA sequences

Nr	Species	Specification	Taxonomic position	Reference
223	DRYopteris adiantum		Pleridophyta(Ph.)	145
224	Equisetum arvense		Pteropsida(Cl.)	145
225	Machonia polynoria		Equisetopsida(Cl.)	146
226	Lophocolea heterophylla	Cultured cells	Heraticopsida(Cl.)	146
227	Platoniun trichomanes	Cultured cells		146
228	Antrodia punctatus	Whole tissue	Brucopsida(Cl.)	146
229	Clanthidias reinhardtii(I)	Cultured cells	Anthocerosida(Cl.)	146
230	Clanthidias reinhardtii(II)	Cell wall deficient mutant(CW 15)	Anthocerosida(Cl.)	147
231	Clanthidias sp.	Cell wall deficient mutant(CW 15)	Anthocerosida(Cl.)	147
232	Chlorella pyrenoidosa		Chlorophyta(Ph.)	113
233	Scenedesmus quadricauda	ATCC 11469		148
234	Scenedesmus obliquus	ATCC 11460	Chlorophyceae(Cl.)	148
235	Ulva pertusa			149
236	Porphyra yezoensis	Whole tissue	Sarothecae(Cl.)	115
237	Porphyra tenera			150
238	Gracilaria compressa		Banidiorhaceae(Cl.)	151
			Floriidiorhaceae(Cl.)	151

SEQUENCES OF THE 4.5S-SUBDOMAIN OF LARGE SUBUNIT RIBOSOMAL RNA

10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400	3410	3420	3430	3440	3450	3460	3470	3480	3490	3500	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600	3610	3620	3630	3640	3650	3660	3670	3680	3690	3700	3710	3720	3730	3740	3750	3760	3770	3780	3790	3800	3810	3820	3830	3840	3850	3860	3870	3880	3890	3900	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000	4010	4020	4030	4040	4050	4060	4070	4080	4090	4100	4110	4120	4130	4140	4150	4160	4170	4180	4190	4200	4210	4220	4230	4240	4250	4260	4270	4280	4290	4300	4310	4320	4330	4340	4350	4360	4370	4380	4390	4400	4410	4420	4430	4440	4450	4460	4470	4480	4490	4500	4510	4520	4530	4540	4550	4560	4570	4580	4590	4600	4610	4620	4630	4640	4650	4660	4670	4680	4690	4700	4710	4720	4730	4740	4750	4760	4770	4780	4790	4800	4810	4820	4830	4840	4850	4860	4870	4880	4890	4900	4910	4920	4930	4940	4950	4960	4970	4980	4990	5000	5010	5020	5030	5040	5050	5060	5070	5080	5090	5100	5110	5120	5130	5140	5150	5160	5170	5180	5190	5200	5210	5220	5230	5240	5250	5260	5270	5280	5290	5300	5310	5320	5330	5340	5350	5360	5370	5380	5390	5400	5410	5420	5430	5440	5450	5460	5470	5480	5490	5500	5510	5520	5530	5540	5550	5560	5570	5580	5590	5600	5610	5620	5630	5640	5650	5660	5670	5680	5690	5700	5710	5720	5730	5740	5750	5760	5770	5780	5790	5800	5810	5820	5830	5840	5850	5860	5870	5880	5890	5900	5910	5920	5930	5940	5950	5960	5970	5980	5990	6000	6010	6020	6030	6040	6050	6060	6070	6080	6090	6100	6110	6120	6130	6140	6150	6160	6170	6180	6190	6200	6210	6220	6230	6240	6250	6260	6270	6280	6290	6300	6310	6320	6330	6340	6350	6360	6370	6380	6390	6400	6410	6420	6430	6440	6450	6460	6470	6480	6490	6500	6510	6520	6530	6540	6550	6560	6570	6580	6590	6600	6610	6620	6630	6640	6650	6660	6670	6680	6690	6700	6710	6720	6730	6740	6750	6760	6770	6780	6790	6800	6810	6820	6830	6840	6850	6860	6870	6880	6890	6900	6910	6920	6930	6940	6950	6960	6970	6980	6990	7000	7010	7020	7030	7040	7050	7060	7070	7080	7090	7100	7110	7120	7130	7140	7150	7160	7170	7180	7190	7200	7210	7220	7230	7240	7250	7260	7270	7280	7290	7300	7310	7320	7330	7340	7350	7360	7370	7380	7390	7400	7410	7420	7430	7440	7450	7460	7470	7480	7490	7500	7510	7520	7530	7540	7550	7560	7570	7580	7590	7600	7610	7620	7630	7640	7650	7660	7670	7680	7690	7700	7710	7720	7730	7740	7750	7760	7770	7780	7790	7800	7810	7820	7830	7840	7850	7860	7870	7880	7890	7900	7910	7920	7930	7940	7950	7960	7970	7980	7990	8000	8010	8020	8030	8040	8050	8060	8070	8080	8090	8100	8110	8120	8130	8140	8150	8160	8170	8180	8190	8200	8210	8220	8230	8240	8250	8260	8270	8280	8290	8300	8310	8320	8330	8340	8350	8360	8370	8380	8390	8400	8410	8420	8430	8440	8450	8460	8470	8480	8490	8500	8510	8520	8530	8540	8550	8560	8570	8580	8590	8600	8610	8620	8630	8640	8650	8660	8670	8680	8690	8700	8710	8720	8730	8740	8750	8760	8770	8780	8790	8800	8810	8820	8830	8840	8850	8860	8870	8880	8890	8900	8910	8920	8930	8940	8950	8960	8970	8980	8990	9000	9010	9020	9030	9040	9050	9060	9070	9080	9090	9100	9110	9120	9130	9140	9150	9160	9170	9180	9190	9200	9210	9220	9230	9240	9250	9260	9270	9280	9290	9300	9310	9320	9330	9340	9350	9360	9370	9380	9390	9400	9410	9420	9430	9440	9450	9460	9470	9480	9490	9500	9510	9520	9530	9540	9550	9560	9570	9580	9590	9600	9610	9620	9630	9640	9650	9660	9670	9680	9690	9700	9710	9720	9730	9740	9750	9760	9770	9780	9790	9800	9810	9820	9830	9840	9850	9860	9870	9880	9890	9900	9910	9920	9930	9940	9950	9960	9970	9980	9990	10000	10010	10020	10030	10040	10050	10060	10070	10080	10090	10100	10110	10120	10130	10140	10150	10160	10170	10180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SPECIES SPECIFICATION AND REMARKS

4.5S rRNA SEQUENCE REFERENCES

- ZEA MAYS (MAIZE, MAIS, MAIS) ; CLONE PZMC134
 4501 EDWARDS K., BEDBROOK J., DYER T., KOESSEL H.†
 BIOCHEM. INT. 2:533-38(1981).
 EDWARDS K., KOESSEL H.†
 NUCL. ACIDS RES. 9:2853-69(1981).
 WILDEMAN A.G., NAZAR R.N.†
 J. BIOL. CHEM. 255:11896-11900(1980).
 4502 KEUS R.J.A., ROEVERS D.J., DEKKER A.F., GROOT G.S.F.†
 NUCL. ACIDS RES. 11:3405-10(1983).
 4503 TAKAIWA F., SUGIURA M.†
 NUCL. ACIDS RES. 8:4125-29(1980).
 TAKAIWA F., SUGIURA M.†
 MOL. GEN. GENET. 182:385-89(1981).
 4504 KUMAGAI I., PIELER T., SUBRAMANIAN A.R., ERDMANN V.A.†
 J. BIOL. CHEM. 257:12724-28(1982).
 KUMAGAI I., BARTSCH M., SUBRAMANIAN A.R., ERDMANN V.A.†
 NUCL. ACIDS RES. 11:961-70(1983).
 4505 TAKAIWA F., KUSUDA M., SUGIURA M.†
 NUCL. ACIDS RES. 10:2257-60(1982).
 4506 TROITSKY A.V., BOBROVA V.K., FONDOMAREV A.G., ANTONOV A.S.†
 FEBS LETT. 176:105-08(1984).
 4507 KARAPIN G.D., NARITA J.O., DODD J.R., HALLICK R.B.†
 J. BIOL. CHEM. 258:14790-96(1983).
 4508 KUMANO M., TOMIOKA N., SUGIURA M.†
 GENE 24:219-25(1983).
 DOUGLAS S.E., DOOLITTLE W.F.†
 FEBS LETT. 166:307-10(1984).
 DOUGLAS S.E., DOOLITTLE W.F.†
 NUCL. ACIDS RES. 12:13373-86(1984).
 4509 MACHATT M.A., EBEL J.-F., BRANLANT C.†
 NUCL. ACIDS RES. 9:1533-49(1981).
 4510 SEE 4509
 4511 SEE 4509
 4512 GREEN C.J., VOLD B.S.†
 NUCL. ACIDS RES. 11:5763-74(1983).
 4513 KOP J., WHEATON V., GUPTA R., WOESE C.R., NOLLER H.F.†
 DNA 3:347-57(1984).
 4514 DALE R.H.K., MENDU N., GINSBURG H., KRIDL J.C.†
 PLASMID 11:141-50(1984).
 4515 SEILHAMER J.J., GUTELL R.R., CUMMINGS D.J.†
 J. BIOL. CHEM. 259:5173-81(1984).
 4516 SEE 4515
- TRITICUM AESTIVUM (WHEAT, BLE, WEIZEN) ; LEAVES
 IDENTICAL TO ZEA EXCEPT ADD G AFTER FOS 6
 SPIRODELA OLIGORHIZA (DUCK'S NEAT, SPIRODELE, TEICHILINSE)
 CLONE P5POC18M
 NICOTIANA TABACUM (TOBACCO, TABAC, TABAK)
 69 70 AG [DNA] IS GA IN [RNA]
 UNSURE
 SPINACIA OLERACEA (SPINACH, EPINARD, SPINAT)
 DRYOPTERIS ACUMINATA (WOOD FERN, , WURMFARN) ; LEAVES
 MNIMUM RUGICUM (, ,)
 EUGLENA GRACILIS 2 (, , AUGENTIERCHEN)
 ANACYSTIS NIDULANS [1] 6301 ; [1] CLONE PAN4 [2,3] CLONES
 ESCHERICHIA COLI MRE600
 PROTEUS VULGARIS
 AEROMONAS PUNCTATA INST.PASTEUR 67.12
 BACILLUS SUBTILIS [RRNB] ; CLONE PEC204
 BACILLUS STEAROTHEROPHILUS 1054 ; CLONES PKW223 AND PKW382
 ZEA MAYS A188 N (MAIZE, MAIS, MAIS) ; CLONES
 PARAMECIUM PRIMAURELIA (SLIPPER ANIMALCULE,
 PANTOFELTIERCHEN) ; CLONES
 PARAMECIUM TETRAURELIA (SLIPPER ANIMALCULE,
 PANTOFELTIERCHEN) ; CLONES

1144

[illegible]

[illegible]

SPECIES SPECIFICATION AND REMARKS

5.8S rRNA SEQUENCE REFERENCES

- MUS MUSCULUS (HOUSE MOUSE, SOURIS DOMESTIQUE, HAUSHAUS)
 HOMO SAPIENS (MAN, HOMME, MENSCH)
 RATIUS RATTUS (RAT, RAT, WANDERHÄRTE)
 [1] [4] NOVICKOFF HEPATOMA ASCITES, [2] CLONE P59 OF CHR-04 IN FBR322,
 [3] LIVER [5] MFC-11 AND HELA, [7] L-929, [8] CLONE PHEB3 IN FBR322
 HETS 1
 2
 MODBASE 14 U PARTIALLY (20/100 IN HELA)
 CONFLICT 50 ADDITIONAL GC IS PRESENT IN [3]
 MODBASE 55 P PARTIALLY
 SITE 157 U NOT PRESENT IN RATTUS
- TERRAPENE CAROLINA (, AMERIKANISCHE DRENSCHILDKRÖTZE)
 1 HEART CELLS CCL50
 MODBASE 14 U 50/100
 GALLUS GALLUS (CHICK, POULE, HAUSHAHN) ; EMBRYO FIBROBLASTS
 HETS 1
 2
 MODBASE 14 U 70-90/100
 MODBASE 55 P PARTIALLY
 XENOPUS LAEVIS (CLAMMED TOAD, XENOPE, KHALLENFROSCH)
 [1] [2] TRANSFORMED KIDNEY CELLS, [3] CLONE PAL212 IN FOR1,
 [4] CLONE PAL101 IN FBR9
 HETS 1 40/100
 HETS 2 20/100
 HETS 3 40/100
 MODBASE 15 U 30-40/100 (EXCLUDING MODBASE 19)
 MODBASE 19 P 50/100 (EXCLUDING MODBASE 15)
 VARIANT 140 C MAYBE U LESS THAN 1/100
 HETS 159 55/100
 HETS 160 34/100
 XENOPUS BOREALIS (CLAMMED TOAD, XENOPE, KHALLENFROSCH)
 1 TRANSFORMED KIDNEY CELLS
 HETS 1 40/100
 HETS 2 20/100
 HETS 3 40/100
 MODBASE 15 U 30-40/100 (EXCLUDING MODBASE 19)
 SALMO GAIARDNERI (RAINBOW TROUT, TRUTTE ARC-EN-CIEL,
 REGENBOGENFORELLE) ; FIBROBLAST CELL LINE R10-2
 HETS 1 40/100
 HETS 2 60/100
 MODBASE 14 U PARTIALLY
 MODBASE 55 P PARTIALLY
 LYTECHINUS VARIEGATUS (SEA URCHIN, SEEIGEL)
 1 CLONE PLV134 IN PACYC184, CLONE FBR06
 HETS 1 33/100
 HETS 2 66/100
- 5801 NAZAR R.N., SITZ T.O., BUSCH H.:
 J. BIOL. CHEM. 250:8591-97(1975).
 SUBRAMANYAM C.S., CASSIDY E., BUSCH H., ROTHBLUM L.I.:
 NUCL. ACIDS RES. 10:13667-80(1982).
 LIU W., LO A.C., NAZAR R.N.:
 J. MOL. BIOL. 171:217-24(1983).
 NAZAR R.N., SITZ T.O., BUSCH H.:
 BIOCHEM. BIOPHYS. RES. COMM. 62:736-43(1975).
 NAZAR R.N., SITZ T.O., BUSCH H.:
 BIOCHEMISTRY 15:505-08(1976).
 KELLY J.M., MADEN E.E.H.:
 NUCL. ACIDS RES. 8:4521-34(1980).
 WALKER T.A., JOHNSON K.D., OLSEN G.J., PETERS M.A., FACE N.R.:
 BIOCHEMISTRY 21:2320-29(1982).
 MICHOT B., BACHELLERIE J.-F., RAYNAL F.:
 NUCL. ACIDS RES. 10:5273-83(1982).
 NAZAR R.N., ROY K.L.:
 FEBS LETT. 72:111-116(1976).
- 5802
- 5803 KHAN M.S.N., MADEN E.E.H.:
 NUCL. ACIDS RES. 4:2495-2505(1977).
- 5804 SEE 5803
 FORD F.J., MATHIESON T.:
 EUR. J. BIOCHEM. 87:199-214(1978).
 ROSELEY P.G., TUYNIS A., BIRNSTIEL M.L.:
 NUCL. ACIDS RES. 5:1121-37(1978).
 HALL L.M.C., MADEN E.E.H.:
 NUCL. ACIDS RES. 8:5993-6005(1980).
- 5805 SEE 5804 [2]
 SEE 5804 [4]
- 5806 NAZAR R.N., ROY K.L.:
 J. BIOL. CHEM. 253:395-99(1978).
- 5807 HINDENACH B.R., STAFFORD D.W.:
 NUCL. ACIDS RES. 12:1737-47(1984).

- DROSOPHILA MELANOGASTER OREGON R (FRUIT FLY, , FRUCHTFLIEGE)
WHOLE TISSUE
RNA 1 123 MS-BS RNA
RNA 124 153 2S RNA
SCLARA COPROPHILA (GNAT, , TRAUEMUECKE) ; CLONE PBC2
RNA 1 123 MS-BS RNA
RNA 124 153 2S RNA
BOMBAY MORI (SILKWORM, , SEIDENSPIINNER)
; POSTERIOR SILKGLAND OF SILKWORM
PHILIDANIA CYNTHIA RICINI (SILKWORM, , SEIDENSPIINNER)
; FOSTERIOR SILKGLAND OF SILKWORM
ACTYDUSIPON MAGNOLIAE (ELDER APHID, , HOLUNDERBLATTLAUS)
WHOLE TISSUE
ARTERIA SALINA (ERINE SHRIMP, , SALINENKREBS) ; CYSTS
HETS -2 -1 5/100 PROBABLY GU
HETS 1 25/100
HETS 2 25/100
HETS 3 45/100
MOUSE
ARION RUFUS (SNAIL, , WEGSCHNECKE)
; WHOLE TISSUE
HYMENTACIDON SANGUINEA (SPONGE, EFONGE, SCHWAMM) ; WHOLE TISSUE
HETS 1 LESS THAN 50/100
HETS 2 MORE THAN 50/100
THERMOMYCES LANUGINOSUS
NEUROSPORA CRASSA
; CLONE PMF2 IN PBR322
SACCHAROMYCES CEREVISIAE (BAKERS YEAST, LEVURE, BAECKERHEFE)
; [1] ATCC 22244 (A364A), [2] 528BC HAPLOID
HETS 1 5/100
HETS 2 5/100
HETS 8 90/100
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST, LEVURE, SPALTHEFE)
; CLONE PYS32 AND PYS3 IN PBR322
HETS 1
HETS 2 MOST ABUNDANT
HETS 3
HETS 4
HETS 5
HETS 6
HETS 7 MOST ABUNDANT
HETS 9
- 5808 PAVLAKIS G.N., JORDAN B.R., WURST R.M., VOURNAKIS J.N.;
NUCL. ACIDS RES. 7:2213-38(1979).
5809 JORDAN B.R., LATIL-DAHOTTE M., JOURDAN R.;
NUCL. ACIDS RES. 8:3565-73(1980).
5810 FUJIMURA H., KAWATA Y., ISHIKAWA H.;
NUCL. ACIDS RES. 10:2415-18(1982).
5811 FENG Y.-X., KRUFP G., GROSS H.J.;
NUCL. ACIDS RES. 10:16383-87(1982).
5812 FUJIMURA H., ISHIKAWA H.;
NUCL. ACIDS RES. 10:5173-82(1982).
5813 URSI D., VANDENBERGHE A., DE WACHTER R.;
NUCL. ACIDS RES. 10:3517-30(1982).
5814 URSI D., VANDENBERGHE A., DE WACHTER R.;
NUCL. ACIDS RES. 11:8111-20(1983).
5815 SEE 5814
5816 WILDEMAN A.G., NAZAR R.N.;
J. BIOL. CHEM. 256:15675-82(1981).
5817 SELKER E., YANOFSKY C.;
NUCL. ACIDS RES. 6:12561-67(1979).
5818 RUBIN G.M.;
J. BIOL. CHEM. 248:13860-75(1973).
RUBIN G.M.;
EUR. J. BIOCHEM. 41:197-202(1974).
DONIS-KELLER H., MAXAM A.M., OILBERT W.;
NUCL. ACIDS RES. 4:12527-38(1977).
FEATIE D.A.;
PROC. NATL. ACAD. SCI. USA 76:1760-64(1979).
5819 SCHIAK J., MAD J., SOELL D.;
NUCL. ACIDS RES. 10:2851-64(1982).

SPECIES SPECIFICATION AND REMARKS

- DICTYOSTELIUM DISCOIDEUM AX3 (CELLULAR SLIME MOLD, , ZELLULAERER SCHLEIMPILZ)
 PHYSARUM POLYCEPHALUM (PLASMODIAL SLIME MOLD, , FLASCHODIALER SCHLEIMPILZ) ; CLONE PRD4
 ACANTHAMEBA CASTELLANII ATCC 30010
 UNISURE 162 U MAYBE NOT PRESENT
 CRITHIDIA FASCICULATA (TRYPANOSOMATIDIAN, TRYPANOSOME, TRYPANOSOM) MOUSSE 7 U 80/100
 HET3 171 34/100
 HET3 172 63/100
 CRYPTOCODINIUM COHNII (DINOFLAGELLATE, , DINOFLAGELLAT) MOUSSE NOT DETERMINED
 TETRAHYENA PYRIFORMIS W
 CHLAMYDOMONAS REINHARDII CW15
 TRITICUM AESTIVUM (WHEAT, BLE, WEITZEN) ; EMBRYO HET5 1 79/100
 HET5 2 16/100
 UNISURE 117 C MAYBE NOT PRESENT
 UNISURE 125 A MAYBE NOT PRESENT
 LUPINUS LUTEUS (YELLOW LUPINE, GELBE LUPINE) ; CLONES PAR6 AND PAR12 IN LAMBDA07
 VARIANT 1 C IS A IN 15/100
 VICIA FABA (BROAD BEAN, , SAUBOHNE) ; LEAVES.
 NICOTIANA TABACUM BRIGHT YELLOW 4 (TODACCO, TABAC, TABAK) ; CLONE PTC243
 ZEA MAYS (MAIZE, MAIS, MAIS) ; CLONE PZNC134
 CHLAMYDOMONAS REINHARDII
 ; CLONES
 EUGLENA GRACILIS Z (, AUGENTIERCHEN) ; [1] CLONE PEGC11 [2] CLONES
 ANACYSTIS NIDULANS [1] 6301
 ; [1] CLONE PAN4 [2] CLONES
 ESCHERICHIA COLI (RNB3)
 ; CLONE PER18
 BACILLUS STEAROTHEROPHILUS 1054
 ; CLONES PKW223 AND PKW382

5.8S rRNA SEQUENCE REFERENCES

- 5820 OLSEN G.J., SOGIN M.L.: BIOCHEMISTRY 21:2335-43(1982).
 5821 OBUKA T., MORIYAMA H., SAKAKI Y., TAKAGI Y.: NUCL. ACIDS RES. 10:2379-85(1982).
 5822 MACKAY R.M., DOOLITTLE M.F.: NUCL. ACIDS RES. 9:3321-34(1981).
 5823 SCHNARE M.N., GRAY M.W.: NUCL. ACIDS RES. 10:2085-92(1982).
 5824 HINNEBUSCH A.G., KLOTZ L.C., BLANKEN R.L., LOEDLICH A.R.: J. MOL. EVOL. 17:334-47(1981).
 5825 FUJIMURA H., ISHIKAWA H.: NUCL. ACIDS RES. 10:5173-82(1982).
 5826 DARLIX J.-L., ROCHAIX J.-D.: NUCL. ACIDS RES. 9:1291-99(1981).
 5827 MACKAY R.M., SPENCER D.F., DOOLITTLE M.F., GRAY M.W.: EUR. J. BIOCHEM. 112:561-76(1980).
 5828 RAFALSKI J.A., WIEMURSKI M., SOELL D.: FEBS LETT. 152:241-46(1983).
 5829 TANAKA Y., DYER T.A., ROGNLEE G.B.: NUCL. ACIDS RES. 8:1259-72(1980).
 NAZAR R.N., WILDEMAN A.G.: NUCL. ACIDS RES. 9:5345-58(1981).
 5830 TAKAIWA F., SUGIURA H.: EUR. J. BIOCHEM. 124:113-19(1982).
 5831 EDWARDS K., KOESSEL H.: NUCL. ACIDS RES. 9:2853-69(1981).
 5832 ROCHAIX J.-D., DARLIX J.-L.: J. MOL. BIOL. 159:383-95(1982).
 5833 GRAF L., KOESSEL H., STUIZ E.: NATURE 286:908-10(1980).
 DROZDO E.H.: PH.D. THESIS, UNIV. OF COLORADO (1981).
 5834 KUMANO H., TOMIOKA N., SUGIURA H.: GENE 24:219-25(1983).
 DOUGLAS S.E., DOOLITTLE M.F.: NUCL. ACIDS RES. 12:3373-86(1984).
 5835 BROSTIUS J., DULL T.J., NOLLER H.F.: PROC. NATL. ACAD. SCI. USA 77:201-04(1980).
 5836 KOP J., WHEATON V., GUPTA R., WOESE C.R., NOLLER H.F.: DNA 3:347-57(1984).

REFERENCES

1. Erdmann, V.A., Wolters, J., Huysmans, E., Vandenberghe, A., De Wachter, R. (1984) *Nucl. Acids Res.* 12, r133-r166.
2. Erdmann, V.A. (1978) *Nucl. Acids Res.* 5, r1-r13.
3. De Wachter, R., Chen, M.-W., Vandenberghe, A. (1982) *Biochimie* 64, 311-329.
4. Kaestner, A. (1969) *Lehrbuch der Speziellen Zoologie*, Gustaf Fisher Verlag, Stuttgart.
5. Ainsworth, G.C., Sparrow, F.K., Sussman, A.S. (1973) *The Fungi, an Advanced Treatise*, Academic Press, New York.
6. Oberwinkler, F. (1982) in *Basidium and Basidiocarp, Evolution, Cytology, Function and Development*, Wells, K., and Wells, E.K., Eds., pp. 9-35, Springer Verlag, New York, Heidelberg, Berlin.
7. Moore, R.T. (1972) *Antonie van Leeuwenhoek* 38, 567-584.
8. Fritsch, F.E. (1971) *The Structure and Reproduction of the Algae*, University Press, Cambridge.
9. Engler, A. (1954) *Syllabus der Pflanzenfamilien*, Gebrüder Borntraeger, Berlin.
10. Balch, W.E., Fox, G.E., Magrum, L.J., Woese, C.R., Wolfe, R.S. (1979) *Microbiol. Rev.* 43, 260-296.
11. Schnabel, R., Huet, J., Thomur, M., Zillig, W., Sentenac, A., Stetter, K.O. (1983) in *Endocytobiology*, vol. 2, pp. 895-912, De Gruyter, Berlin, New York.
12. Stackebrandt, E., Woese, C.R. (1984) *Microbiol. Sci.* 1, 117-122.
13. Woese, C.R., Stackebrandt, E., Weisburg, W.G., Paster, B.J., Madigan, M.T., Fowler, V.J., Hahn, C.M., Blanz, P., Gupta, R., Nealson, K.K., Fox, G.E. (1984) *System. Appl. Microbiol.* 5, 315-326.
14. Woese, C.R., Weisburg, W.G., Paster, B.J., Hahn, C.M., Tanner, R.S., Krieg, N.R., Koops, H.P., Harms, H., Stackebrandt, E. (1984) *System. Appl. Microbiol.* 5, 327-336.
15. Woese, C.R., Weisburg, W.G., Hahn, C.M., Paster, B., Zablen, L.B., Lewis, B.J., Macke, T.J., Ludwig, W., Stackebrandt, E. (1985) *System. Appl. Microbiol.*, in press.
16. Monier, R. (1974) in *Ribosomes*, Nomura, M., Tissières, A. and Lengyel, P., Eds., pp. 141-168, Cold Spring Harbor Laboratory, New York.
17. Erdmann, V.A. (1976) in *Progress in Nucleic Acids Research and Molecular Biology*, Cohn, W.E., Ed., Vol. 18, pp 45-90, Academic Press, New York.
18. Studnicka, G.M., Eiserling, F.A., Lake, J.A. (1981) *Nucl. Acids Res.* 9, 1885-1904.
19. Böhm, S., Fabian, H., Welfle, H. (1982) *Acta biol. med. germ.* 41, 1-16.
20. Delihias, N., Andersen, J. (1982) *Nucl. Acids Res.* 10, 7323-7344.
21. Pribula, C.D., Fox, G.E., Woese, C.R. (1976) *FEBS Lett.* 64, 350-352.
22. Marotta, C.A., Varricchio, F., Smith, I., Weissman, S.M., Sogin, M.L., Pace, N.R. (1976) *J. Biol. Chem.* 251, 3122-3127.
23. Raué, H.A., Stoof, T.J., Planta, R.J. (1975) *Eur. J. Biochem.* 59, 35-42.
24. Woese, C.R., Luehrsen, K.R., Pribula, C.D., Fox, G.E. (1976) *J. Mol. Evol.* 8, 143-153.
25. Dams, E., Londei, P., Cammarano, P., Vandenberghe, A., De Wachter, R. (1983) *Nucl. Acids Res.* 11, 4667-4676.
26. Alexander, L.J., Stewart, T.S. (1980) *Nucl. Acids Res.* 8, 979-987.
27. Alexander, L.J., Stewart, T.S. (1981) *FEBS Lett.* 135, 151-154.
28. Neimark, H., Andersen, J., Delihias, N. (1983) *Nucl. Acids Res.* 11, 7569-7577.
29. Dekio, S., Yamasaki, R., Jidoi, J., Hori, H., Osawa, S. (1984) *J. Bacteriol.* 159, 233-237.
30. Walker, R.T., Chelton, E.T.J., Kilpatrick, M.W., Rogers, M.J., Simmons, J. (1982) *Nucl. Acids Res.* 10, 6363-6367.

31. Hori, H., Sawada, M., Osawa, S., Murao, K., Ishikura, H. (1981) *Nucl. Acids Res.* 9, 5407-5410.
32. Hori, H., Osawa, S., Murao, K., Ishikura, H. (1980) *Nucl. Acids Res.* 8, 5423-5426.
33. Simoncsits, A. (1980) *Nucl. Acids Res.* 8, 4111-4124.
34. Komiya, H., Kawakami, M., Takemura, S., Kumagai, I., Erdmann, V.A. (1983) *Nucl. Acids Res.* 11, 913-916.
35. Kumagai, T., Digweed, M., Erdmann, V.A., Watanabe, K., Oshima, T. (1981) *Nucl. Acids Res.* 9, 5159-5162.
36. Nazar, R.N., Matheson, A.T. (1977) *J. Biol. Chem.* 252, 4256-4261.
37. MacKay, R.M., Salgado, D., Bonen, L., Stackebrandt, E., Doolittle, W.F. (1982) *Nucl. Acids Res.* 10, 2963-2970.
38. Newhouse, N., Nicoghoshian, K., Cedergren, R.J. (1981) *Can. J. Biochem.* 59, 921-932.
39. Dams, E., Vandenbergh, A., De Wachter, R. (1983) *Nucl. Acids Res.* 11, 1245-1252.
40. Stahl, D.A., Lane, D.J., Olsen, G.J., Pace, N.R. (1984) *Science* 224, 409-411.
41. Brownlee, G.G., Sanger, F., Barrell, B.G. (1968) *J. Mol. Biol.* 34, 379-412.
42. Fischel, J.-L., Ebel, J.-P. (1975) *Biochimie* 57, 899-904.
43. Zimmerman, J., Erdmann, V.A. (1978) *Mol. Gen. Genet.* 160, 247-257.
44. Digweed, M., Kumagai, I., Pieler, T., Erdmann, V.A. (1982) *Eur. J. Biochem.* 127, 531-537.
45. Brownlee, G.G., Sanger, F., Barrell, B.G. (1968) *J. Mol. Biol.* 34, 379-412.
46. Woese, C.R., Pribula, C.D., Fox, G.E., Zablen, L.B. (1975) *J. Mol. Evol.* 5, 35-46.
47. Luehrsen, K.R., Fox, G.E. (1981) *J. Mol. Evol.* 17, 52-55.
48. Deming, J.W., Hada, H., Colwell, R.R., Luehrsen, K.R., Fox, G.E. (1984) *J. Gen. Microbiol.* 130, 1911-1920.
49. MacDonell, M.T., Colwell, R.R. (1984) *Microbiol. Sci.* 1, 229-231.
50. MacDonell, M.T., Colwell, R.R. (1984) *FEBS Lett.* 175, 183-188.
51. Corry, M.J., Payne, P.I., Dyer, T.A. (1974) *FEBS Lett.* 46, 63-66.
52. Delihias, N., Andresini, W., Andersen, J., Berns, D. (1982) *J. Mol. Biol.* 162, 721-727.
53. Karabin, G.D., Narita, J.O., Dodd, J.R., Hallick, R.B. (1983) *J. Biol. Chem.* 258, 14790-14796.
54. Yamano, Y., Ohyama, K., Komano, T. (1984) *Nucl. Acids Res.* 12, 4621-4624.
55. Takaiwa, F., Sugiura, M. (1982) *Nucl. Acids Res.* 10, 5369-5373.
56. Strittmatter, G., Kössel, H. (1984) *Nucl. Acids Res.* 12, 7633-7647.
57. Dyer, T.A., Bowman, C.M. (1979) *Biochem. J.* 183, 595-604.
58. Keus, R.J.A., Roovers, D.J., Dekker, A.F., Groot, G.S.P. (1983) *Nucl. Acids Res.* 11, 3405-3410.
59. Takaiwa, F., Sugiura, M. (1980) *Mol. Gen. Genet.* 180, 1-4.
60. Takaiwa, F., Sugiura, M. (1981) *Mol. Gen. Genet.* 182, 385-389.
61. Delihias, N., Andersen, J., Sprouse, H.M., Dudock, B. (1981) *Nucl. Acids Res.* 9, 2801-2805.
62. Morgens, P.N., Graban, E.A., Gesteland, R.F. (1984) *Nucl. Acids Res.* 12, 5665-5684.
63. Spencer, D.F., Bonen, L., Gray, M.W. (1981) *Biochemistry* 20, 4022-4029.
64. Chao, S., Sederoff, R.R., Levings, C.S. (1983) *Plant. Physiol.* 71, 190-193.
65. Fox, G.E., Luehrsen, K.R., Woese, C.R. (1982) *Zbl. Bakt. Hyg. 1 Abt. Orig. C3*, 330-345.
66. Nazar, R., Matheson, A.T., Bellemare, G. (1978) *J. Biol. Chem.* 253, 5464-5469.
67. Mankin, A.S., Kagramanova, V.K., Belova, E.N., Teterina, N.L., Baratova, L.A., Bogdanov, A. (1983) *Biochem. Int.* 5, 719-726.

-
68. Luehrsen, K.R., Nicholson, D.E., Eubanks, D.C., Fox, G.E. (1981) *Nature* 293, 755-756.
 69. Wich, G., Jarsch, M., Bock, A. (1984) *Mol. Gen. Genet.* 196, 146-151.
 70. Stahl, D.A., Luehrsen, K.R., Woese, C.R., Pace, N.R. (1981) *Nucl. Acids Res.* 9, 6129-6137.
 71. Luehrsen, K.R., Fox, G.E., KilPatrick, M.W., Walker, R.T., Domdey, H., Krupp, G., Gross, H.J. (1981) *Nucl. Acids Res.* 9, 965-970.
 72. Forget, B.G., Weissman, S.M. (1969) *J. Mol. Biol.* 244, 3148-3165.
 73. Aoyama, K., Hidaka, S., Tanaka, T., Ishikawa, K. (1982) *J. Biochem.* 91, 363-367.
 74. Lazar, E., Haendler, B., Jacob, M. (1983) *Nucl. Acids Res.* 11, 7735-7741.
 75. Fedoroff, N.V., Brown, D.D. (1977) *C.S.H.S. Quant. Biol.* 42, 1195-1200.
 76. Korn, L.J., Brown, D.D. (1978) *Cell* 15, 1145-1156.
 77. Kay, B.K., Gall, J.G. (1981) *Nucl. Acids Res.* 9, 6457-6469.
 78. Komiya, H., Takemura, S. (1979) *J. Biochem.* 86, 1067-1080.
 79. Mashkova, T.D., Serenkova, T.I., Mazo, A.M., Avdonina, T.A., Timofeyeva, M. Ya., Kisselev, L.L. (1981) *Nucl. Acids Res.* 9, 2141-2151.
 80. Denis, H., Wegnez, M. (1977) *Develop. Biol.* 59, 228-236.
 81. Komiya, H., Hasegawa, M., Takemura, S. (1983) *Nucl. Acids Res.* 11, 1969-1974.
 82. Kumazaki, T., Hori, H., Osawa, S. (1983) *FEBS Lett.* 155, 81-84.
 83. Ohama, T., Kumazaki, T., Hori, H., Osawa, S. (1984) *Nucl. Acids Res.* 12, 5101-5108.
 84. Kawata, Y., Ishikawa, H. (1982) *Nucl. Acids Res.* 10, 1833-1840.
 85. Sharp, S., Garcia, A., Cooley, L., Soll, D. (1984) *Nucl. Acids Res.* 12, 7617-7632.
 86. Tschudi, C., Pirrotta, V. (1980) *Nucl. Acids Res.* 8, 441-451.
 87. Benhamou, J., Jourdan, R., Jordan, B.R. (1977) *J. Mol. Evol.* 9, 279-298.
 88. Samson, M.L., Wegnez, M. (1984) *Nucl. Acids Res.* 12, 1003-1014.
 89. Rubacha, A., Sumner, W., Richter, L., Beckingham, K. (1984) *Nucl. Acids Res.* 12, 8193-8207.
 90. Gu, X.-R., Nicoghossian, K., Cedergren, R.J. (1982) *Nucl. Acids Res.* 10, 5711-5716.
 91. Komiya, H., Kawakami, M., Shimizu, N., Takemura, S. (1980) *Nucl. Acids Res. Symp. Ser. No. 8*, 119-122.
 92. Diels, L., De Baere, R., Vandenberghe, A., De Wachter, R. (1981) *Nucl. Acids Res.* 9, 5141-5144.
 93. Lu, A.L., Steege, D.A., Stafford, D.W. (1980) *Nucl. Acids Res.* 8, 1839-1853.
 94. Ohama, T., Hori, H., Osawa, S. (1983) *Nucl. Acids Res.* 11, 5181-5184.
 95. Walker, W.F., Doolittle, W.F. (1983) *Nucl. Acids Res.* 11, 5159-5164.
 96. Komiya, H., Shimizu, N., Kawakami, M., Takemura, S. (1980) *J. Biochem.* 88, 1449-1456.
 97. Fang, B.-L., De Baere, R., Vandenberghe, A., De Wachter, R. (1982) *Nucl. Acids Res.* 10, 4679-4685.
 98. Stahl, D.A., Lane, D.J., Olsen, G.J., Pace, N.R. (1984) *Science* 214, 409-411.
 99. Kumazaki, T., Hori, H., Osawa, S. (1982) *FEBS Lett.* 146, 307-310.
 100. Hori, H., Ohama, T., Kumazaki, T., Osawa, S. (1982) *Nucl. Acids Res.* 10, 7405-7408.
 101. Dams, E., Vandenberghe, A., De Wachter, R. (1982) *Nucl. Acids Res.* 10, 5297-5302.
 102. Ohama, T., Kumazaki, T., Hori, H., Osawa, S., Takai, M. (1983) *Nucl. Acids Res.* 11, 473-476.
 103. Kumazaki, T., Hori, H., Osawa, S. (1983) *Nucl. Acids Res.* 11, 7141-7144.
 104. Butler, M.H., Wall, S.M., Luehrsen, K.R., Fox, G.E., Hecht, R.M. (1981) *J. Mol. Evol.* 18, 18-23.
-

105. Kumazaki, T., Hori, H., Osawa, S., Ishii, N., Suzuki, K. (1982) Nucl. Acids Res. 10, 7001-7004.
106. Kumazaki, T., Hori, H., Osawa, S. (1983) Nucl. Acids Res. 11, 3347-3350.
107. Delihás, N., Andersen, J., Andresini, W., Kaufman, L., Lyman, H. (1981) Nucl. Acids Res. 9, 6627-6633.
108. Kumazaki, T., Hori, H., Osawa, S. (1982) J. Mol. Evol. 18, 293-296.
109. Hinnebusch, A.G., Klotz, L.C., Blanken, R.L., Loeblich, A.R. (1981) J. Mol. Evol. 17, 334-347.
110. MacKay, R.M., Gray, M.W., Doolittle, W.F. (1980) Nucl. Acids Res. 8, 4911-4917.
111. Luehrsen, K.R., Fox, G.E., Woese, C.R. (1980) Curr. Microbiol. 4, 123-126.
112. Kumazaki, T., Hori, H., Osawa, S., Mita, T., Higashinakagawa, T. (1982) Nucl. Acids Res. 10, 4409-4412.
113. Kumazaki, T., Hori, H., Osawa, S. (1983) J. Mol. Evol. 19, 411-419.
114. Kumazaki, T., Hori, H., Osawa, S. (1982) FEBS Lett. 149, 281-284.
115. Lim, B.-L., Hori, H., Osawa, S. (1983) Nucl. Acids Res. 11, 1909-1912.
116. MacKay, R.M., Doolittle, W.F. (1981) Nucl. Acids Res. 9, 3321-3334.
117. Komiya, H., Takemura, S. (1981) J. Biochem. 90, 1577-1581.
118. Hori, H., Osawa, S., Iwabuchi, M. (1980) Nucl. Acids Res. 8, 5535-5539.
119. Andersen, J., Andresini, W., Delihás, N. (1982) J. Biol. Chem. 257, 9114-9118.
120. Walker, W.F., Doolittle, W.F. (1982) Nucl. Acids Res. 10, 5717-5721.
121. MacKay, R.M., Doolittle, W.F. (1982) Nucl. Acids Res. 10, 8307-8310.
122. Gottschalk, M., Blanz, P.A. (1984) Nucl. Acids Res. 12, 3951-3958.
123. Huysmans, E., Dams, E., Vandenberghe, A., De Wachter, R. (1983) Nucl. Acids Res. 11, 2871-2880.
124. Walker, W.F., Doolittle, W.F. (1982) Nature 299, 723-724.
125. Walker, W.F., Doolittle, W.F. (1983) Nucl. Acids Res. 11, 7625-7630.
126. Liu, W., Nazar, R.N. (1983) Biochem. Biophys. Res. Commun. 116, 148-153.
127. Walker, W.F. (1984) System. Appl. Microbiol. 5, 352-359.
128. Valenzuela, P., Bell, G.I., Masiari, F.R., Degennaro, L.J., Rutter, W.J. (1977) Nature 267, 641-642.
129. Piper, P.W., Lockhaert, A., Patel, N. (1984) Nucl. Acids Res. 12, 4083-4096.
130. Hindley, J., Page, S.M. (1972) FEBS Lett. 26, 157-160.
131. Komiya, H., Miyazaki, M., Takemura, S. (1981) J. Biochem. 89, 1663-1666.
132. Chen, M.-W., Anné, J., Volckaert, G., Huysmans, E., Vandenberghe, A., De Wachter, R. (1984) Nucl. Acids Res. 12, 4881-4892.
133. Tabata, S. (1980) Eur. J. Biochem. 110, 107-114.
134. Nishikawa, K., Takemura, S. (1974) J. Biochem. 76, 935-947.
135. Selker, E.U., Yanofsky, C., Driftmier, K., Metzenberg, R.L., Alzner-Deweerd, B., Rajbhandary, U.L. (1981) Cell 24, 819-828.
136. Piechulla, B., Hahn, U., McLaughlin, L.W., Kuntzel, H. (1981) Nucl. Acids Res. 9, 1445-1450.
137. Wildeman, A.G., Nazar, R.N. (1982) J. Biol. Chem. 257, 11395-11404.
138. MacKay, R.M., Spencer, D.F., Doolittle, W.F., Gray, M.W. (1980) Eur. J. Biochem. 112, 561-576.
139. Gerlach, W.L., Dyer, T.A. (1980) Nucl. Acids Res. 8, 4851-4865.
140. Vandenberghe, A., Chen, M.-W., Dams, E., De Baere, R., De Roeck, E., Huysmans, E., De Wachter, R. (1984) FEBS Lett. 171, 17-23.
141. Payne, P.I., Dyer, T.A. (1976) Eur. J. Biochem. 71, 33-38.
142. Goldsbrough, P.B., Ellis, T.H.N., Lomonosoff, G.P. (1982) Nucl. Acids Res. 10, 4501-4514.
143. Rafalsky, J.A., Wiewiorowski, M., Soll, D. (1982) Nucl. Acids Res. 10, 7635-7642.
144. Delihás, N., Andersen, J., Sprouse, H.M., Kashdan, M., Dudock, B. (1981) J. Biol. Chem. 256, 7515-7517.

145. Hori, H., Osawa, S., Takaiwa, F., Sugiura, M.L. (1984) Nucl. Acids Res. 12, 1573-1576.
146. Katoh, K., Hori, H., Osawa, S. (1983) Nucl. Acids Res. 11, 5671-5674.
147. Darlix, J.-L., Rochaix, J.-D. (1981) Nucl. Acids Res. 9, 1291-1299.
148. Luehrsen, K.R., Fox, G.E. (1981) Proc. Natl. Acad. Sci. USA 78, 2150-2154.
149. Green, G.A., McCoy, J.M., Jones, D.S. (1982) Nucl. Acids Res. 10, 6389-6392.
150. Takaiwa, F., Kusuda, M., Saga, N., Sugiura, M. (1982) Nucl. Acids Res. 10, 6037-6040.
151. Lim, B.-L., Hori, H., Osawa, S. (1983) Nucl. Acids Res. 11, 5185-5188.
152. Pieler, T., Kumagai, I., Erdmann, V.A. (1983) Endocytobiology II, 881-894.
153. Wolters, J., Erdmann, V.A. (1984) Endocyt. C. Res. 1, 1-23.
154. Sor, F., Fukuhara, H. (1983) Nucl. Acids Res. 11, 339-348.
155. Köchel, H.G., Küntzel, H. (1982) Nucl. Acids Res. 10, 4795-4801.
156. Luoma, G.A., Marshall, A.G. (1978) Proc. Natl. Acad. Sci. U.S.A. 75, 4901-4905.
157. Walker, T.A., Pace, N.R. (1983) Cell 33, 320-322.
158. Vaughn, J.C., Sperbeck, S.J. (1984) Nucl. Acids Res. 12, 7479-7502.
159. Krüger, M., Osterburg, G. (1983) Comp. Progr. Biomed. 16, 68-70.
160. Maly, P., Brimacombe, R. (1983) Nucl. Acids Res. 11, 7263-7286.