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Collection of published 5S and 5.8S ribosomal RNA sequences

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On the following pages the published sequences for the prokaryotic 5S RNAs (1-18), eukaryotic 5S (19-38) and 5.8S RNAs (39-43) including their precursors are listed in alphabetical order. The strains of the organisms used were not always sufficiently defined by the authors. It is therefore recommended that more care is taken in this respect in future, since there sometimes appear to be sequence differences between different strains of the same organism.

In addition I would like to point out that there are thorough collections of oligonucleotide compositions published for Proteus mirabilis P1, Salmonella typhimurium, Erwinia aroideae NRRL B-138, Aerobacter aerogenes, Serratia marcescens, Alcaligenes faecalis, Clostridium perfringens, Pseudomonas aeruginosa (44) and Yersinia (Pasteurella) pestis 1122 (45). Since partial ribonuclease hydrolysis of these prokaryotic 5S RNAs was not performed the absolute primary structure could not be deduced with certainty.

Mammalian eukaryotic 5S RNAs seem to be more strongly conserved. It was therefore concluded from oligonucleotide composition studies that mouse Landschütz cell (46), mouse LS cell (46), mouse ascites hepatoma MH 134 (47), marsupial (Protorous tridactylis, rat kangaroo ATCCCR CCL35) (48), Chinese hamster V79 (49), dolphin kidney (Stenella plagiodon ATCCCR CCL78) (50) and embryonic bovine trachea (Bos taurus ATCCCR CCL44) (50) 5S RNAs are similar in primary structure to KB cell (27,28) 5S RNA. Labrie (as cited in ref. 46) came to a similar conclusion for rat pituitary and rabbit reticulocyte 5S RNAs.

There has been only one report on eukaryotic precursor 5S RNA, in which extensive heterogeneity at the 3' end of Xenopus Laevis oocyte 5S RNA was observed (51).

## Nucleic Acids Research

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Mammalian 5.8S RNAs seem also highly conserved and it was therefore concluded from oligonucleotide products that mouse cells L5178Y (52), mouse myeloma MPC-11 cells (53) and HeLa cells contain 5.8S RNAs with identical sequences to that of Novikoff hepatoma.

The following papers are recommended for those readers interested in evolution (44,48,49) and structures and functions of 5S and 5.8S RNAs (56,57).

PROKARYOTIC 5S RNA SEQUENCES

	1	10	20	30	40	50	60	70	80	90	100	110	120
A.N.	pUCCUGGUCUAUGGGCGUAUGGAACACACUCUGACCCCAUCCCGAAUCAGUUGUGAAACUACCUUGCGGAACCAUAGCUCCCGGUAAGCCGGUCUAAAAUAGCUCCAGCCAGGUC, <sup>OH</sup>												
B.L.	PUUUGGCGCAUAGCGAAGGUCACACCGGUCCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGCUUCCCGCUUGCAGAGUAGGACGCCGCCAAAG, <sup>OH</sup>												
B.M.	PUCUGGCGCAUAGCGAAGGUCACACCGGUCCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGCUUCCCGCUUGCAGAGUAGGACGCCGCCAAAG, <sup>OH</sup>												
B.S. (a)	PCCUAGUCACAAUAGCGGAGAAACACCGGUCCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGCACGCCCGUCCGUAAGUAGGUCUUGCGG, <sup>OH</sup>												
B.S. (b)	PCCUAGUGUCUAGCGGAGAAACACCGGUCCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGCACGCCCGUCCGUAAGUAGGUCUUGCGG, <sup>OH</sup>												
B.Su.	PUUUGGCGCAUAGCGAAGGUCACACCGGUCCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGCUUCCCGCUUGCAGAGUAGGACGCCGCCAAAG, <sup>OH</sup>												
C.P.	PUCCAGUCUUAUAGCUUAGAGUAACACUCCUUCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGAAAGCCUUGGGGAAAGUAGGUCGACGCCCGGAAAG, <sup>OH</sup>												
E.C. (a)	PUCCUGGCGCGUAGCGGAGAAACACCGGUCCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGCACGCCCGUCCGUAAGUAGGUCUUGCGG, <sup>OH</sup>												
E.C. (b)	PUCCUGGCGCGUAGCGGAGAAACACCGGUCCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGCACGCCCGUCCGUAAGUAGGUCUUGCGG, <sup>OH</sup>												
P.V.	PUCUCUGGCGCAUAGCGGAGAAACACCGGUCCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGAAAGCCUUGGGGAAAGUAGGUCGACGCCCGGAAAG, <sup>OH</sup>												
P.	PUCCUGGCGCGUAGCGGAGAAACACCGGUCCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGCACGCCCGUCCGUAAGUAGGUCUUGCGG, <sup>OH</sup>												
P.F.	PUCUCUGUCACGAGUAGCGGAGAAACACCGGUCCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGAAAGCCUUGGGGAAAGUAGGUCGACGCCCGGAAAG, <sup>OH</sup>												
T.A.	PAUCCCGCGCUUAGCGGAGAAACACCGGUCCGUAUCGGCGAAGUAAGUCUUCACGCGCGGATGGUACUUGGGGGCACGCCCGUCCGUAAGUAGGUCUUGCGG, <sup>OH</sup>												

PROKARYOTIC 5S RNA PRECURSORS

	1	10	20	140	150	160	170	179
P.B.Su.	pUGAGAACACUCUCAAUUUG.....B. subtilis 5S RNA.....AAGCUAAACCGCAGGCUAAUGAGGUGGUUUUUUUUUUUUG, <sup>OH</sup>							
P.E.C.	pAUU , pUU and pU have been found at the 5' end of <u>E. coli</u> 5S RNA							

The single underlined sequences are tentative. The double underlined nucleotides occur in less than one mole per mole 5S RNA. Nucleotide written directly under another nucleotide in the sequence indicates that it may also be found in this position. For abbreviation of organisms and literature references see opposite page.

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 Prokaryotic 5S RNA Sequences
 

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Abbreviation	RNA Source	Reference Number
A.N.	<u>Anacystis nidulans</u> 1405/1 Katz/Allen (Blue-green Alga)	1
B.L.	<u>Bacillus licheniformis</u> S 244	2
B.M.	<u>Bacillus megaterium</u> KM	3
B.S.(a)	<u>Bacillus stearothermophilus</u> 1439 FV	4
B.S.(b)	<u>Bacillus stearothermophilus</u> (strain not given)	5
B.S.(b)	<u>Bacillus stearothermophilus</u> 799	6
B.Su.	<u>Bacillus subtilis</u> 168	4
C.P.	<u>Clostridium pasteurianum</u> ATCC 6013	7
E.C.(a)	<u>Escherichia coli</u> MRE600	8-12
E.C.(b)	<u>Escherichia coli</u> CA265	8-11
P.V.	<u>Proteus vulgaris</u> (strain not given)	12
P	<u>Photobacter</u> 8265	13
P.F.	<u>Pseudomonas fluorescens</u> ATCC 13430	14
T.A.	<u>Thermus aquaticus</u> ATCC 25104	15
<hr/> Prokaryotic 5S RNA Precursors <hr/>		
P.B.Su.	<u>Bacillus subtilis</u> 168	16,17
P.E.C.	<u>Escherichia coli</u> 217 (sud-1)	18

EUKARYOTIC 5S RNA SEQUENCES

Table with columns 1-120 and rows B.B., C. (a), C. (b), C.P., D.M., D.B., H.L., K.B., Re., Ry., S., To., Tu., X.L.S., X.L.O., X.M.S., X.M.O., Y.S.Ca. (a), Y.S.Ca. (b), Y.S.Ce., Y.K.L., Y.P.M., Y.T.U. containing nucleotide sequences with underlined and double underlined regions.

Single underlined sequences are tentative. Double underlined nucleotides or 5' phosphates occur in less than one mole per mole 5S RNA. ? underneath the 3' terminal U of the D.B. sequence indicates that it has not been clearly identified as uridine. For abbreviations of organisms and literature references see opposite page.

## Eukaryotic 5S RNA Sequences

Abbreviation	Source	Reference Number
B.B.	Broad bean ( <u>Vicia faba</u> )	19,20
C (a)	Chicken ( <u>Gallus gallus</u> ), embryo fibroblast culture	21
C (b)	Chicken, embryo fibroblast culture	22
C.P.	<u>Chlorella pyrenoidosa</u> 211/8b	23
D.M.	<u>Drosophila melanogaster</u> F6 of KC	24
D.B.	Dwarf bean ( <u>Phaseolus vulgaris</u> )	19,20
H.L.	HeLa cells	25,26
K.B.	KB cells	27,28
Re.	Reptile ( <u>Iguana iguana</u> )	29
Ry.	Rye ( <u>Secale cereale</u> c.v. Lovaszpatonai)	19,20
S.	Sunflower ( <u>Helianthus annuus</u> )	19,20
To.	Tomato ( <u>Lycopersicum esculentum</u> )	19,20
Tu.	Turtle ( <u>Terrapene carolina</u> , TH-I line of heart cells)	30
X.L.S.	<u>Xenopus laevis</u> (somatic from kidney)	31-33
X.L.O.	<u>Xenopus laevis</u> (oocytes)	31-33
X.M.S.	<u>Xenopus mulleri</u> (somatic)	34
X.M.O.	<u>Xenopus mulleri</u> (oocytes)	34
Y.S.Ca. (a)	Yeast ( <u>Saccharomyces carlsbergensis</u> )	35
Y.S.Ca. (b)	Yeast ( <u>Saccharomyces carlsbergensis</u> )	36
Y.S.Ce.	Yeast ( <u>Saccharomyces cerevisiae</u> )	36,37
Y.K.L.	Yeast ( <u>Kluyveromyces lactis</u> )	36
Y.P.M.	Yeast ( <u>Pichia membranaefaciens</u> )	36
Y.T.U.	Yeast ( <u>Torulopsis utilis</u> )	38

EUKARYOTIC 5.8S RNA SEQUENCES

1 10 20 30 40 50 60 70 80 90 100  
 C. pGAACUCUUAGGGGUGGAUCACUCUGCCUCUGCCGUCGAUGAAGAACGCAGCGUAGCCGAGAUAUAAUGGAAUUGCAGGCACACAUUGAUCAUCGACAC  
 H.L. pCGACUCUUAGGGGUGGAUCACUCUGCCUCUGCCGUCGAUGAAGAACCGCAGCGUAGCCGCGAGAAUUAAGUGGAAUUGCAGGCACACAUUGAUCAUCGACAC  
 N. pCGACUCUUAGGGGUGGAUCACUCUGCCUCUGCCGUCGAUGAAGAACCGCAGCGUAGCCGCGAGAAUUAAGUGGAAUUGCAGGCACACAUUGAUCAUCGACAC  
 T. pGAACUCUUAGGGGUGGAUCACUCUGCCUCUGCCGUCGAUGAAGAACCGCAGCGUAGCCGCGAGAAUUAAGUGGAAUUGCAGGCACACAUUGAUCAUCGACAC  
 X.L. pCGACUCUUAGGGGUGGAUCACUCUGCCUCUGCCGUCGAUGAAGAACCGCAGCGUAGCCGCGAGAAUUAAGUGGAAUUGCAGGCACACAUUGAUCAUCGACAC  
 Y.S.Ce. pAAACUUCAACACGGAUCUCUUGGUAUCUGGCAUGGAUGAAGAACGCGAGAAUUGCGAAUUGGUAUGGAAUUGCGAGAAUUCGCCUGAAUUCGAAUCU

101 110 120 130 140 150  
 C. UUGGAAAGCCACUUGGGCCCGGGUUCUCCCGGGGCUACGCCUUGCCUGAGCGUCGCUU<sub>OH</sub>  
 H.L. UUGGAAAGCCACUUGGGCCCGGGUUCUCCCGGGGCUACGCCUUGCCUGAGCGUCGCUU<sub>OH</sub>  
 N. UUGGAAAGCCACUUGGGCCCGGGUUCUCCCGGGGCUACGCCUUGCCUGAGCGUCGCUU<sub>OH</sub>  
 T. UUGGAAAGCCACUUGGGCCCGGGUUCUCCCGGGGCUACGCCUUGCCUGAGCGUCGCUU<sub>OH</sub>  
 X.L. UUGGAAAGCCACUUGGGCCCGGGUUCUCCCGGGGCUACGCCUUGCCUGAGCGUCGCUU<sub>OH</sub>  
 Y.S.Ce. UUGAAGCGACAUUUGCGCCCUUUGUAUUCGAGGGGCUAGCCUUGUUGAGCGUCAUU<sub>OH</sub>

EUKARYOTIC 5.8S RNA PRECURSORS

p.Y.S.Ce. pUAUUA and pUAUUA have been found at the 5' end of YEAST 5.8S RNA.

The double underlined nucleotides occur in less than one mole per mole 5.8S RNA. Nucleotide written directly under another nucleotide in the sequence indicates that it may also be found in this position. m indicates that the nucleotide is methylated. For abbreviations of organisms and literature references see opposite page.

<u>Eukaryotic 5.8S RNA Sequences</u>		
Abbreviation	RNA Source	Reference Number
C.	Chicken (embryonic cells)	39
H.L.	HeLa cells	39
N.	Novikoff hepatoma ascites cells	40
T.	Turtle (heart cells CCL 50)	41
X.L.	<u>Xenopus leavis</u> (somatic)	39
Y.S.Ce.	Yeast ( <u>Saccharomyces cerevisiae</u> A364A gal-1 ade-1 ade-2 ura-1 his-7 lys-2 tyr-1 (ATCC 22 244))	42
<u>Eukaryotic 5.8S RNA Precursors</u>		
p.Y.S.Ce.	Yeast ( <u>Saccharomyces cerevisiae</u> S288 $\alpha$ mal gal-2)	43



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