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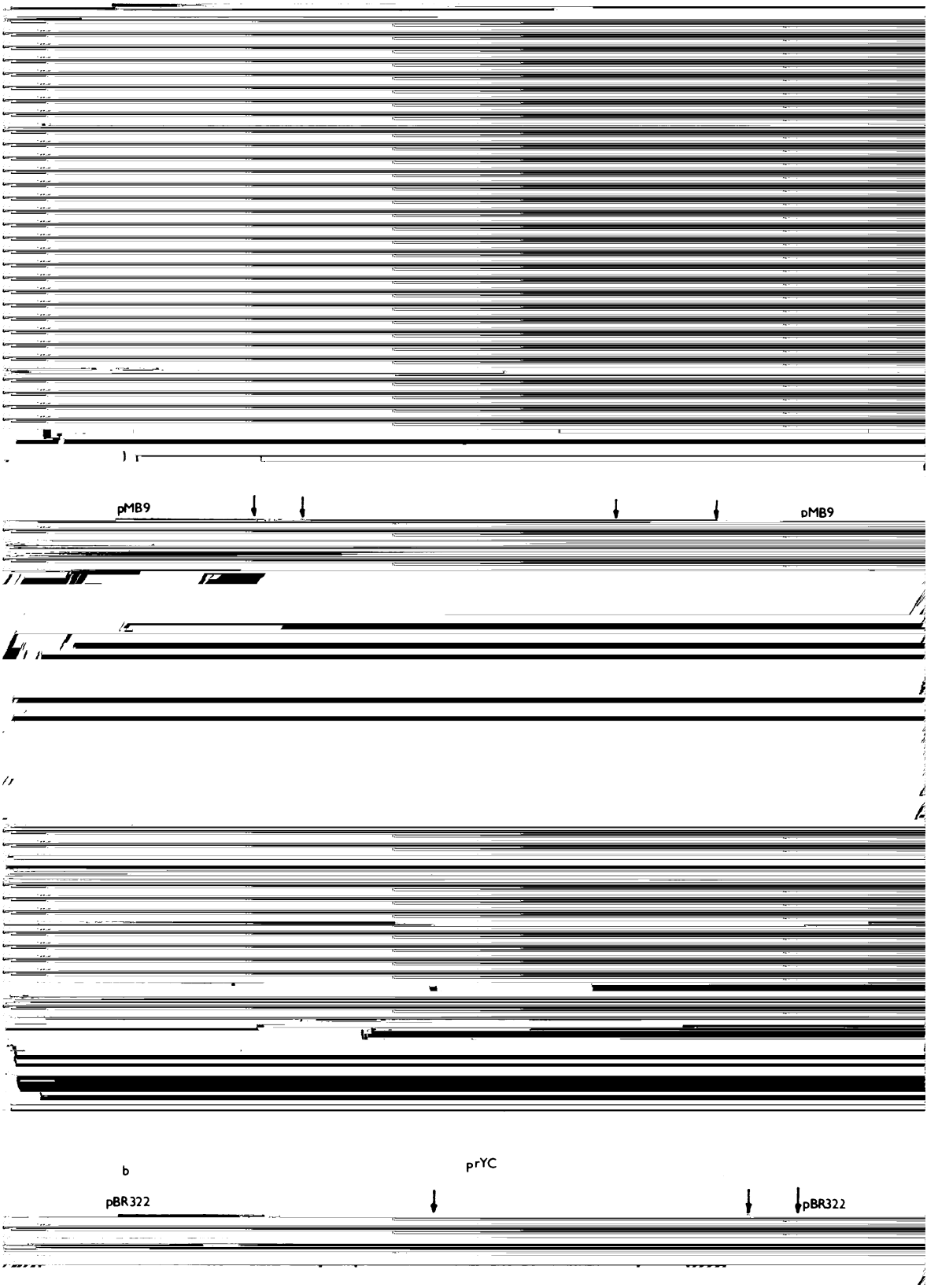
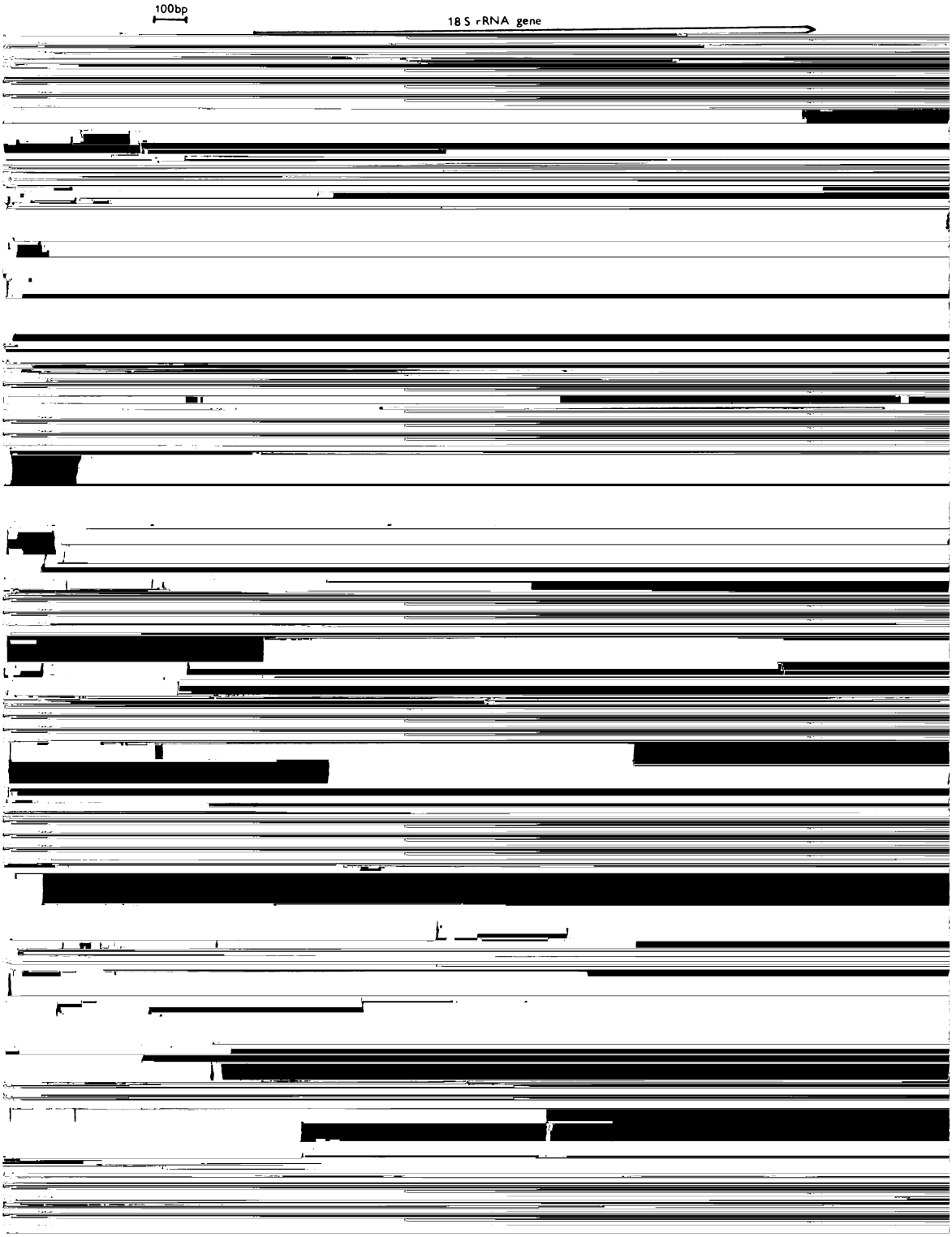
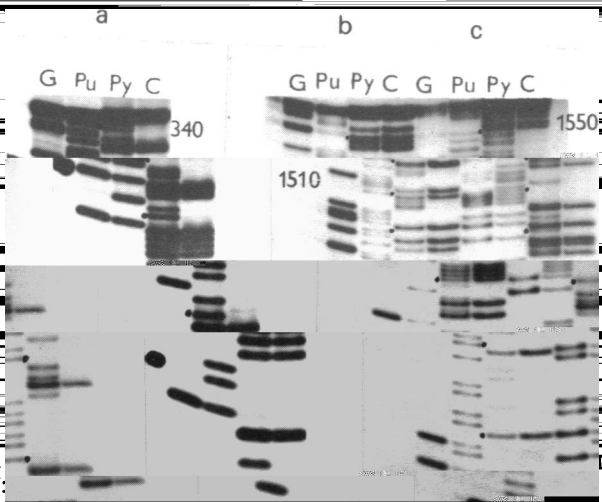
and the identification of evolutionary divergence of different


pMB9
pMB9
b
pBR322
prYC
pBR322

mixture, to which "stop-solution" has already been added.

method of Glynn and Chappel (17). The 18 S rRNA from the


100bp
18 S rRNA gene



a
f
I.7-

(fig. 4). T
the

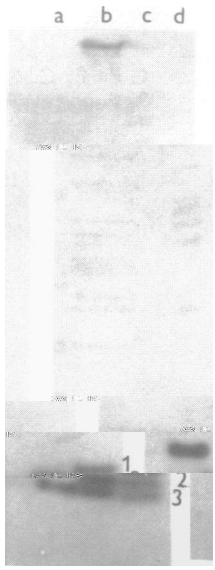


Figure 4. Autoradiograph of 10% non-denaturing acrylamide

strand.
a. appr. 0.05 µg the 5'end labelled DNA fragment was denaturated in 5XSSC and 50% formamide in

3'-end of eucaryotic 18 S RNAs is a strikingly conserved region.

The 3'-end of the 16 S rRNA molecule: as pointed out by Shine-Dalgarno model, is involved in a complex with an mRNA that is indispensable for effective translation, the interaction do occurring via the sequence CCUCC (27). All

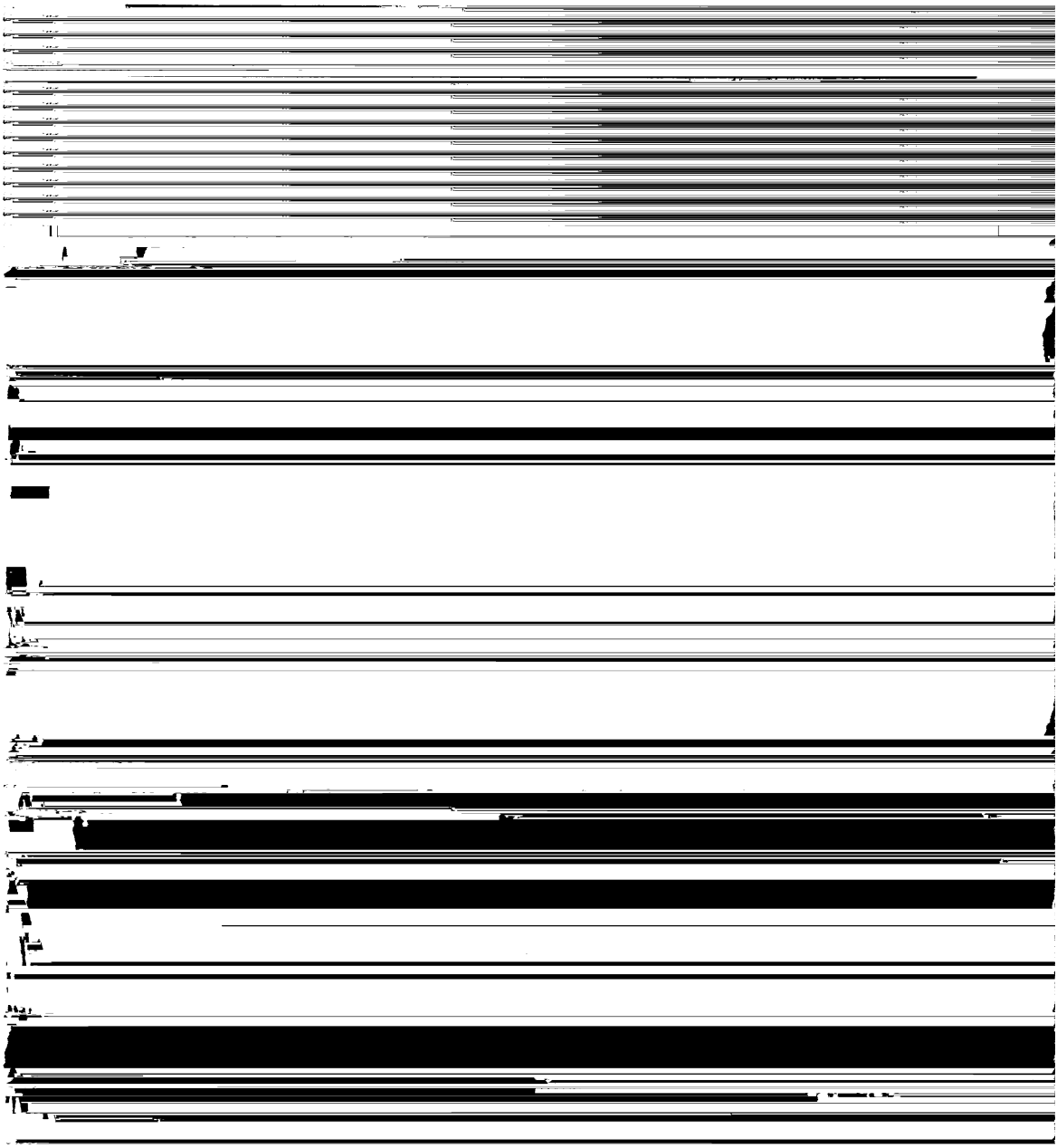
cular sequence (28). So does the *S.cerevisiae* rRNA, though it shows striking homology with adjacent region of 16 S

```
      100
   90 GAAACUGC GAAUGGCUCA
      200
  190 UCUCGACC CUUUGGAAGA
      300
  290 UGGCGAUG GUUCAUUCAA
      400
  390 GGAGAGGG AGCCUGAGAA
      500
  490 ACAGGGCC CAUUCGGGUC
      600
  590 CCCAGCUCC AAUAGCGUAU
      700
  690 CCAACGGG CCUUUCCUUC
      800
  790 GCUCGAAU AUAUUAGCAU
      900
  890 CGGUAUUC AAUUGUCGAG
     1000
  990 GAGGGAUCU GAUACCGUCG
```

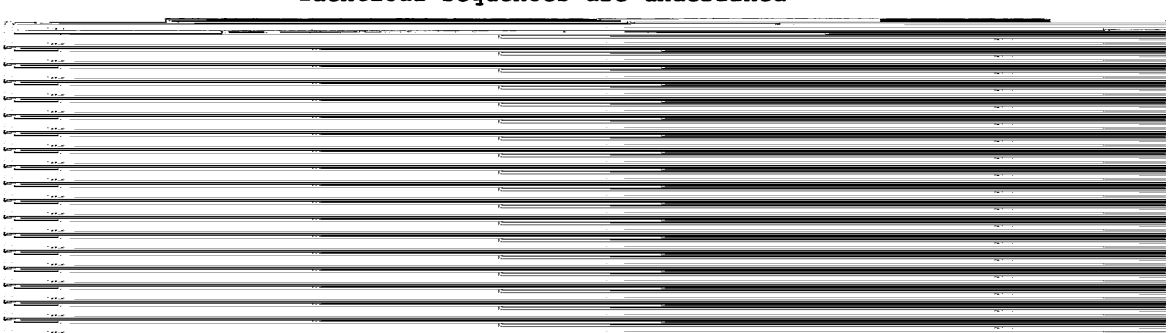
0 G 0 G 0 U 0 A 0 U 0 G A U 0

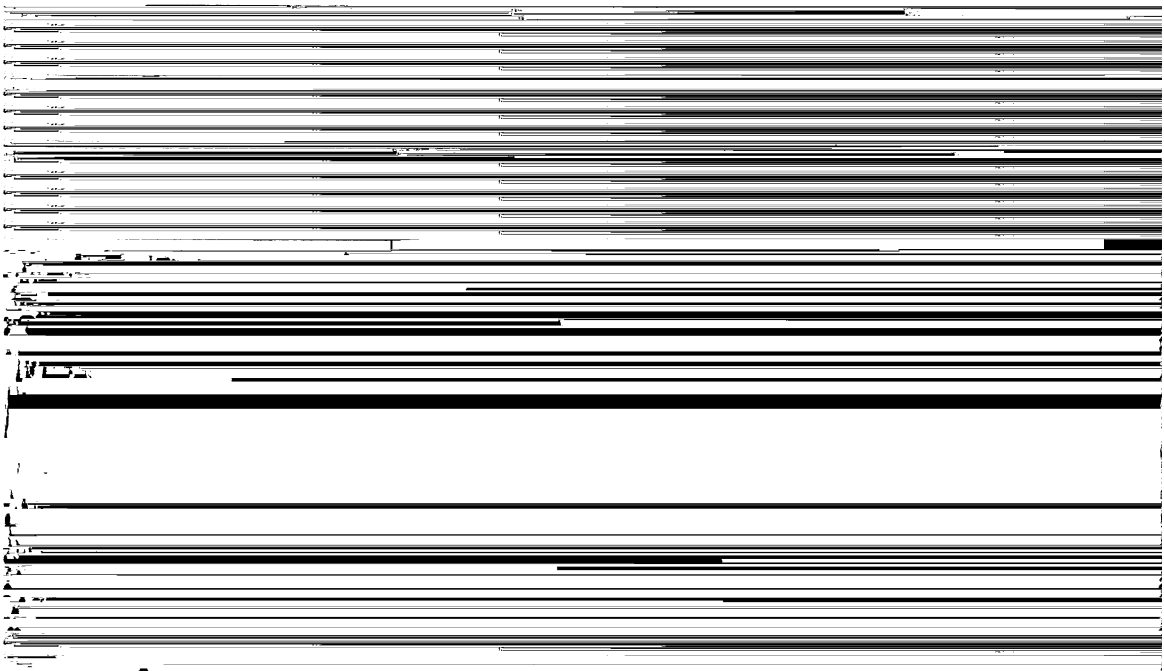
UGG UCA UCU GAU GAG UGC UCC

1090 UUGGGU 1190 GGGGAA 1290 GUGAUU 1390 UUCAAG 1490 UUGGCC 1590 CAUCAG 1690 GGGGCA 1790 CAUUA



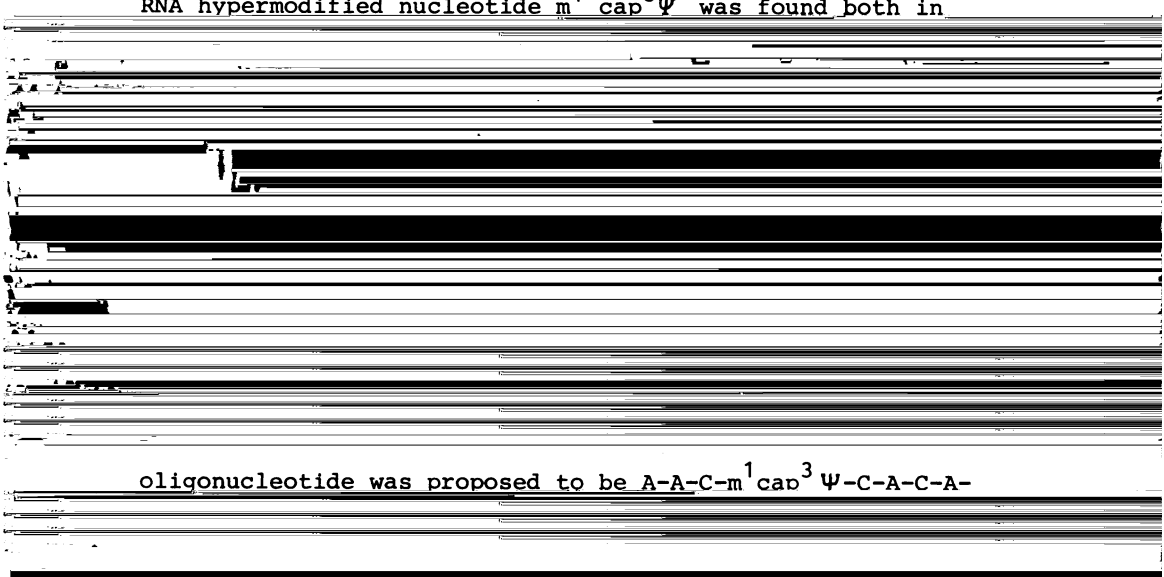
Identical sequences are underlined





RNA gene of *X.laevis* (31), *D.melanogaster* (32);

(d) The T1 oligonucleotide possessing the unique 18 S RNA hypermodified nucleotide m^1 cap$^3\Psi$ was found both in



oligonucleotide was proposed to be A-A-C-m^1cap$^3\Psi$-C-A-C-A-C-Gp.

We could not find such oligonucleotide within *S.cerevisiae* 18 S RNA sequence. The only appropriate T1 oligonucleotide which could be deduced was A-C-U-C-A-A-C-A-C-Gp.

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