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Genomic sequence encoding a heat shock-induced, RNA polymerase III-transcribed RNA from *Tetrahymena thermophila*

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A heat shock administered to *Tetrahymena thermophila* cells elicits the rapid accumulation of a small, RNA polymerase III-transcribed, cytoplasmic RNA (G8), a partial cDNA copy of which had been previously cloned and sequenced (1, 2). We have now cloned and sequenced the single haploid genomic copy (data not shown) of the *T. thermophila* G8 gene (the transcribed region begins at +1 and terminates at +300) and some of its 5′-flanking sequences. The 5′ terminus of the stable cytoplasmic form of the G8 molecule was determined by primer extension of RNA isolated from heat shocked cells (2). The transcription termination site was inferred from the sequence of the cloned cDNA (1) and the fact that RNA polymerase III transcribed genes terminate in runs of T. The 5′-flanking region contains two putative heat shock motifs (3) at −149 to −140 and at −130 to −121 relative to the transcription start site (underlined with the consensus sequences above). In addition, there are also two sequences which may be homologous to known 5′ control regions of some snRNA genes. The first, at −56 to −42, is a 12 out of 15 base match with the proximal sequence element (PSE) of the human U6 gene (4). The second, from −23 to −15, contains an 8 out of 9 base match with the T/A-rich element of the human U6 gene (4). In both cases the locations of these sequences (shown underlined with the human U6 gene sequence (4) given above) are at almost the same positions relative to the transcription initiation site as are the comparable U6 gene control elements. Whether any of these G8-flanking sequences exhibit any functional homology is unknown at this time.

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                 -gaa--ttc-         -gaa--ttc-                     -97
TAAATACGTCAATAATAAGAAATCTCTAGTGTGTTTTGAAATTTCCTCTATTCTAAATTTTATAATCATC
                                        cttaccgtaacttga            -27
TTATCTTAGAGTAAATATCATTACATTTAACATAGGCCTCCTTACTTTAAATTGACTCAACAAATTTACT
   tttatatat             +1                                        +44
AAATTTATAGATAATAATTAAATTAAAATAAAAAAAAAAATAAATAAACTTAATAAAAAAACAACTGCTA
                                                                  +114
AAAACTAAAATGGGTGGAAAGAAAGATCAAGGAAAGAAACAAGAACAAGCTAAGACCAAGGATGAAGCTC
                                                                  +184
CCAAGTAAGAGCAACATGCTGATGGTAAAGAAGCTAACAAGAAGGCTGACAAGAAGAAGAAGTGATAGTC
                                                                  +254
ATTTTCTAAAATGACAACTCATTCTTTATAAACTGATTAACTTTATAATAAAATAATAAAGAATATAAAT
                                          +300
CTTGTCAATAGCAATTTATATTACTACTTTATATTTGTATTATTTT
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