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5'-Flanking sequence of mouse glutathione S-transferase Ya gene

Violet Daniel, Yehuda Tichauer and Ronit Sharon

Biochemistry Department, The Weizmann Institute of Science, Rehovot 76100, Israel

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We have recently reported the complete sequence of a mouse glutathione S-transferase Ya subunit gene, including a small portion of the 5'-flanking sequence with the transcription initiation site (1). The 5'-flanking region of this gene, 1594 base pairs upstream the initiation of transcription site, has now been determined. Promoter elements such as modified TATA and CCAAT sequences, TACTAAA and CCTAT, are located in the Ya gene 32 and 70 nucleotides upstream the cap site. Between nucleotides -136 to -141 we observed a potential half recognition site for a TGGCA-binding protein or NF-1 (consensus: 5'-TGG(A/C)N_5 GCCAA-3') (2,3). A similar sequence in the liver-specific promoter to the albumin gene was found to bind the NF-1 protein (4).

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CTTCACTCAGGGCTTCACTCCATCTAGAAAGGGACTGGTGGAGGCAGTGCAGCCCAGAGGATAGAGAGGA -1524
TGCAGAGGAAAAGGATGGAGAGGATGCAGAGAAGGAGGGCCAGCTGAAGAAACATGAGTGTGGAGTCTGG -1454
ACTTCAGAGAAAGGCTAAAGTGCAGGCAGGCTTGAAGAACAGGGCCTCCACATGACCACAGGCAAATGGC -1384
ACAGAACAGGCAGGCAGCTGAGTGCTTCCTTTCAGGGAGGGACAATGCACTCAGCTCTAAGGCAAAGGCA -1314
GTCCTCAGCAGTACTCCTGAATCAGCCCTTGCTGTGCACTGTAGATCTCCCAGTTGTCTCTGCTGGGTCT -1244
TGGCATTGCTCTCTGGGACATCTCCTTTCACCACGGGTTTCCTTCCCTCCTCTGCCATAGGCTGTCAGGC -1174
TGTGACAAGGACTCTTTCATGAGCAGTGCTCAAACACAACTCATCCCTGTGGCTGAGACCCTGTGCTGGT -1104
GCCATGTGTGTACCTTGAAATGCGGAATGGCTAGGTTGTCATCTGTTTTTAGCAAAGTGAAGGGCCCTTG -1034
AAGAATGAAATTCTATAGCTGAAGAGAAATTAGCAGTGGACATTAAGATAAAAAGAGGCCAGCCCTGCTC  -964
TCTGGTAGGGTATACAGCCTTAGGCATGTGACAGGCATCTCGGAGGCCAGCCAGATCATCAGGTAATGAT  -894
TAATAACCAAGACCCATGAACCAAGGATTAACTAAAATCATGAATCAGCTTGTGGGTGTGTGAGTGAGGT  -824
CAGCAAGAATGACCATGTTGTGGATAAGAGCCATGTCTGAACTTGGCAGGAAGGATCAGTAATTCTCATT  -754
AGCTTGGAAATGACATTGCTAATGGTGACAAAGCAACTTTCCCACAGGAGTAACTGCAGGGACTCACAGG  -684
CTGCACTGAGACCTAGAGCAGGCTGGACAGAATGTGTCTGGTCATCCAGGATAAAGTTAAGTGTGAGCTG  -614
TGTCCCTCCTTTCTGCCCTCTGGCTCTTGAGTTTTTTGAATCAAAGCGGGACAAAGATTAAGATGGATAT  -544
CATGCTATGGCAGGATTTTAATATTGACGTGCTTCACCAGAGAAAACGAGGAGGGAGCAGTGTGACCTGT  -474
TGTGTTTGACTTAGTCTTGAATTTGAGACAATGCATTAATTCTGCAATTTAGGGCTACTTAACAAGCCAT  -404
CCCTGAAATCCAATAGTTCAATGTCACATTGTTGCATAGCTGAGGGTTCCCAAGGTTGACTCTGTGGTAT  -334
TATTTCTGCTCCTAGTGCAGTTTTCCCTCCTTCCTTTCTTCCCTTCTTAGCCAAGATGTCTCTTTCAGGT  -264
TACTCACAGGATCATGGAGAGGAGAGGTGACTTAGAGGCCCATAAACATGACACCAAGAACTTCATGAAT  -194
GGAGCCAGATCTTCAGGGAAAGGTGGTGGCTTGTCAGCCCCTCCCGATGATTTGGCACCTTTCTAGTCTA  -124
TCATGAAACTCTGGAATCTTGGACTCTGTGTGTGTCTGTGGGAGGGGCTGTTCCCTATTTGTCCCCACAC   -54
CCTAGGTAAGAATTGTCACCTTACTAAAGTAGCGTGCACACTCCTCTGGAGCTGGACTGGGAGCTGAGTG
GAGAAGAAGCCAGGACTCTCACTAGGTCAGTGTTCTCTCTTATAACCTGTGGAACCTCTTCCCAGGTCTG
CAGCACTGCAAACTAGTTTTTCAGCGTTTTATTTAGTTAGCATGCACTGATTGCATAAGATAATTAGATT
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