

# A cDNA sequence coding a class pi glutathione S-transferase of mouse

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Glutathione S-transferases (GSTs) are a family of dimeric enzymes that catalyze the conjugation of glutathione with a number of electrophilic compounds (1). The mammalian cytosolic GSTs have been classified into three groups (Alpha, Mu, and Pi) according to their enzymatic, immunological and physicochemical properties (2). Attention has been focused on the class pi GSTs, because rat GST-P (7-7) and human GST- $\pi$  are specifically elevated in (pre)neoplastic tissues (1). Expression of the equivalent mouse GST-II is selectively regulated by androgen (3). The present report concerns the nucleotide and deduced amino acid sequences of the gene encoding mouse GST-II. We screened a mouse liver cDNA library in  $\lambda$ gt10 using rat GST-P cDNA as a probe, and obtained a clone (pGM211) containing 630 nucleotides of an open reading frame encoding 210 amino acids including the initiator methionine. In the 3'-noncoding region, a poly (A) addition signal, AATAAA, was found located 17 nucleotides upstream from the poly (A) stretch. The molecular weight of GST-II omitting the initiator methionine was calculated to be 23,536, which is close to values for GST-P (23,307) and GST- $\pi$  (23,224). In addition, the deduced amino

acid sequence shared 92% and 85% identity with GST-P and GST- $\pi$ , respectively.

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                                                    TTCGCAGC   8
ATGCCACCATACACCATTGTCTACTTCCCAGTTCGAGGGCGGTGTGAGGCCATGCCAATGCTGCTGGCT   77
M P P Y T I V Y F P V R G R C E A M R M L L A   23
GACCAGGGCCAGAGCTGGAAGGAGGAGGTGGTTACCATAGATACCTGGATGCAAGGCTTGCTCAAGCCC 146
D Q G Q S W K E E V V T I D T W M Q G L L K P   46
ACTTGTCTGTATGGGCAGCTCCCAAGTTTGAGGATGGAGACCTCACCCTTTACCAATCTAATGCCATC 215
T C L Y G Q L P K F E D G D L T L Y Q S N A I   69
TTGAGACACCTTGGCCGCTCTTTGGGGCTTTATGGGAAAACCAGAGGGAGGCCGCCAGATGGATATG 284
L R H L G R S L G L Y G K N Q R E A A Q M D M   92
GTGAATGATGGGGTGGAGGACCTTCGCGGCAAATATGTCACCCTCATCTACACCAACTATGAGAATGGT 353
V N D G V E D L R G K Y V T L I Y T N Y E N G 115
AAGAATGACTACGTGAAGCCCTGCCTGGGCATCTGAAGCCTTTTGAGACCCTGCTGTCCCAGAACCAG 422
K N D Y V K A L P G H L K P F E T L L S Q N Q 138
GGAGCAAAGCTTTCATCGTGGGTGACCAGATCTCCTTTGCGGATTACAACCTTGCTGGACCTGCTGCTG 491
G G K A F I V G D Q I S F A D Y N L L D L L L 161
ATCCACCAAGTCTGGCCCTGGCTGCCTGGACAACCTCCCCCTGCTCTCTGCCTATGTGGCTCGCCTC 560
I H Q V L A P G C L D N F P L L S A Y V A R L 184
AGTGCCCGGCCAAGATCAAGGCCTTCTGTCTCCCGGAACATGTGAACCGTCCCATCAATGGCAAT 629
S A R P K I K A F L S S P E H V N R P I N G N 207
GGCAAACAGTAGTGACTGAAGAGACAAGAGCTTCTGTCCCGCTTTTCCAGCACTAATAAAGTTTGT 698
G K Q *
AAGAC (A) n
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