

**A *Caenorhabditis elegans* cDNA that encodes a product resembling the rat glutathione S-transferase P subunit**

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Part of a *Caenorhabditis elegans* gene capable of encoding a glutathione S-transferase subunit was present on a genomic clone that also contains part of the *lin-12* gene (1). The genes are oppositely oriented, and their 3' ends lie within 40 base pairs of each other. In order to further determine the relationship of the nematode gene, which we propose to name *gst-1*, to the vertebrate members of the glutathione S-transferase gene family, we analyzed cDNA clones isolated from a library prepared with mRNA from a mixed-stage population of wild-type N2 worms. The predicted product is 40% identical to the P subunit (2), 30% identical to the Y<sub>B</sub> and Y<sub>C</sub> subunits (3,4), and 28% identical to the Y<sub>A</sub> subunit (5), all from rat. The Figure contains a comparison of the *C. elegans* sequence with that predicted for the rat P subunit. Comparison of the cDNA sequence with the available genomic DNA sequence indicates that an intron greater than 138 base pairs separates positions 276 and 277 of the cDNA and that a single exon comprises the cDNA from 277 to the end. A splice site is found at a corresponding position in the rat P subunit gene (2). Genomic sequence data are not available for determination of exon structure further 5'.

	zxc	M P P Y T I V Y F P V R G R C E A T R M L L L A	23
		. . . . .	22
	<i>C. elegans</i>	H T L K L T Y F D I H G L A E F I R L L L A	22
TCGAGGGTGGTGAAGAGTAATGTTCAAGGGTGGTAATTA	CTCAACTTGGTTC	CAATATAGCCCTCAAGCTCAGCTACGCTACGACATCCAGCGGACTCGGTGAGCCAAATCCGCTTCTCTCCGGC	120
D O G Q S M K E E V V T I D V W L G S L R K S T C L Y G Q L P K F E D G D L T L Y Q		. . . . .	65
I . . . . .		. . . . .	64
D K Q V A Y E D H R V T Y E Q W - - A D I K P K M I F G O V P C L L S G D E E I V O		. . . . .	62
GACAAGCAAGTGGCTACGAGGATCATCGTGAACCTATGAACAAATGGGCTGATATTAACCAAAGATGATCTTCGGCCAGGTTC	CCATGCTTCTATCCGGAGACGAGGAGATTGTTCAA		240
S N A I L R H L G R S L G L Y G K D O K E A A L V D H V N D G V E D L R C K Y G		. . . . .	105
I . . . . .		. . . . .	104
S G A I I R H L A R L N G L N G S N E T E T T F I D M F Y E G L R D L H T R K Y T		. . . . .	102
TCTGGAGCTATCATCGCTCATCTCGCTTAAATGGGCTCAATGGGCTCCAACGAGACAGAGACAAC	TTTCATCGACATGTTCTACGAAAGACTTTCGTGATTGACACCAAGTACAC		360
1 -> 3' exon			
T L I Y T N Y E N G K D D Y V K - - A L P G H L K P P F E T L L S Q N Q G G K A F I		. . . . .	144
I . . . . .		. . . . .	143
T H I Y R N Y E D G R A P Y I E D V L P G E L A R L E K L F P H T Y K N G E H Y V		. . . . .	142
ACTATGATCTACGAAAGCTACGAAGCGGCAAGGCTCGGTACATCAAGAGAGCTTCTTCCAGGAGAGCTCGCTGCTCGGAGAGCTTTCCATAC	CTACAGAAACGGAGAGCAGCTACGTT		480
V G N Q I S F A D Y N L L D L L L V H Q V L A P G C L D N F P L L S A Y V A R L		. . . . .	184
. . . . .		. . . . .	183
I G D K E S Y A D Y V L F E E L D I H L I L T P N A L D G V P A L K K F H E R F		. . . . .	182
ATTGGAGACAAGAAAGCTATGCGGATATGTGCTGTCGAGAGCTCGACATTCATTGATTCACACCCAAATGCTCTTGATGGTTC	CCAGCACTCAAGAGTTCACGAGAGATTCC		600
S A R P K I K A F L S S P D H L N R P I N G N G K O		. . . . .	210
. . . . .		. . . . .	209
A E R P N I K A Y L N K R A A I N P P V N G N G K O *		. . . . .	208
GCTGAGCGTCCAAACATCAAGGCATATCTCAACAGAGAGCTGCTATCAACCCACAGATAAGTGGAAA	TGGAAAACAAATAAGCTAAATCAATTTTTCTCTATTTTGCATCTCAAAAAT		720
TCGAGTTGATATAATTTATTGTCTTCCCTAAAGCTTCCAAATGAATCTCTGCTTCCCATAAAAA			779

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