cDNA and deduced amino acid sequence of murine Cu-Zn superoxide dismutase

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Cu-Zn superoxide dismutase (EC 1.15.1.1) is a eukaryotic cytoplasmic enzyme involved in the antioxidant defense against the toxic effects of superoxide anion-induced cellular damage (1). We have isolated cDNA clones from a murine SWR/J liver cDNA library (2) using the human cDNA clone pS61-10 as a heterologous probe (3). The nucleotide and deduced amino acid sequence of one of these clones containing the entire coding region is shown below. The murine enzyme is coded for by 459 nt after ATG followed by a single stop codon. The deduced amino acid sequence exhibits 83.7% identity to the human enzyme (3) and 96.7% identity to the rat enzyme (4). The 3'-non-coding end following TAA is 66 nt in length and contains an uncommon polyadenylation signal, ATTAAA, 16 nt upstream of the poly(A) tail. This clone hybridizes to a single band of RNA isolated from mouse liver with a molecular size between 0.5-0.6 kb.

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      1      10      20      30      40      50      60
      *      *      *      *      *      *      *
A AGC ATG GCG ATG AAA GCG GTG TGC GTG CTG AAG GGC GAC GGT CCG GTG CAG GGA ACC ATC CAC TTC GAG CAG
Met Ala Met Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln Gly Thr Ile His Phe Glu Gln

      70      80      90      100      110      120      130      140
      *      *      *      *      *      *      *      *
AAG GCA AGC GGT GAA CCA GTT GTG TTG TCA GGA CAA ATT ACA GGA TTA ACT GAA GGC CAG CAT GGG TTC CAC GTC
Lys Ala Ser Gly Glu Pro Val Val Leu Ser Gly Gln Ile Thr Gly Leu Thr Glu Gly Gln His Gly Phe His Val

      150      160      170      180      190      200      210
      *      *      *      *      *      *      *
CAT CAG TAT GGG GAC AAT ACA CAA GGC TGT ACC AGT GCA GGA CCT CAT TTT AAT CCT CAC TCT AAG AAA CAT GGT
His Gln Tyr Gly Asp Asn Thr Gln Gly Cys Thr Ser Ala Gly Pro His Phe Asn Pro His Ser Lys Lys His Gly

      220      230      240      250      260      270      280      290
      *      *      *      *      *      *      *      *
GGC CCG GCG GAT GAA GAG AGG CAT GTT GGA GAC CTG GGC AAT GTG ACT GCT GGA AAG GAC GGT GTG GCC AAT GTG
Gly Pro Ala Asp Glu Glu Arg His Val Gly Asp Leu Gly Asn Val Thr Ala Gly Lys Asp Gly Val Ala Asn Val

      300      310      320      330      340      350      360
      *      *      *      *      *      *      *
TCC ATT GAA CAT CGT GTG ATC TCA CTC TCA GGA GAG CAT TCC ATC ATT GGC CGT ACA ATG GTG GTC CAT GAG AAA
Ser Ile Glu Asp Arg Val Ile Ser Leu Ser Gly Glu His Ser Ile Ile Gly Arg Thr Met Val Val His Glu Lys

      370      380      390      400      410      420      430      440
      *      *      *      *      *      *      *      *
CAA GAT GAC TTG GGC AAA GGT GGA AAT GAA GAA AGT ACA AAG ACT GGA AAT GCT GGG AGC CGC TTG GCC TGT GGA
Gln Asp Asp Leu Gly Lys Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg Leu Ala Cys Gly

      450      460      470      480      490      500      510
      *      *      *      *      *      *      *
GTG ATT GGG ATT GCG CAG TAA ACA TTC CCT GTG TGG TCT GAA GTC TCA GAC TCA ACT GCT ACC CTC AAA CCA TTA
Val Ile Gly Ile Ala Gln -

      520      530      540
      *      *      *
AAC TGT AAT CTG AAA AAA AAA

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