

Nucleotide and deduced amino acid sequence of human liver microsomal epoxide hydrolase

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A partial length human liver microsomal epoxide hydrolase (mEH) cDNA (1) was used to screen a human liver λ gt11 cDNA library. The longest mEH cDNA isolated, was sequenced by the dideoxy method. Comparison of the protein sequence deduced by translation of the cDNA, with the amino terminal sequence of the purified human liver enzyme (2) showed an identical 19 amino acid sequence. The translated protein is 455 residues long and is 82% homologous to rat mEH (3).

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GTTCCTCAAGGAGTAATCAGAGGGTGGAGCGTGGAGCCTGGTGGACAGGTGAAGCACTGGGATCTTTCTGCC 73
10
CAGAAAGGGGAAAGTGCACATTTATATCTCTAGAGGGAAGCCAGCAGGTCCTCTCCCTGTGCTGAGGTACAGGAGCC 182
Met Trp Leu Glu Ile Leu Leu Thr Ser Val
20 30
CTG GGC TTT GCC ATC TAC TGG TTC ATC TCC CGG GAC AAA GAG GAA ACT TTG CCA CTT GAA GAT GGG TGG TGG GCG CCA GGC ACG AGG TCC 272
Leu Gly Phe Ala Ile Tyr Trp Phe Ile Ser Arg Asp Lys Glu Glu Thr Leu Pro Leu Glu Asp Gly Trp Trp Gly Pro Gly Thr Arg Ser
50 60
GCA GCC AGG GAG GAC GAC AGC ATC CCG CCT TTC ANG GTG GAA AGC TCA GAT GAG CAC ATC CAC GAC TTA CAC CAC AGG ATC GAT ANG TTC 362
Ala Ala Arg Glu Asp Asp Ser Ile Arg Pro Phe Lys Val Glu Thr Ser Asp Glu Glu Ile His Asp Leu His Gln Arg Ile Asp Lys Phe
80 90
CGT TTC ACC CCA CTT TTT GAG GAC AGC TGC TTC CAC TAT GGC TTC ACC TCC ANG TAC CTG AAG AAA CTC ATC TCC TAC TGG GCG AAT GAA 452
Arg Phe Thr Pro Pro Leu Glu Asp Ser Lys Phe His Tyr Gly Phe Asn Ser Asn Tyr Leu Lys Lys Val Ile Ser Tyr Trp Arg Asn Glu
110 120
TTT GAC TGG AAG ANG CAG GTG GAG ATT CTC AAC AGA TAC CCT CAC TTC AAG ACT AAA ATT GAA GGG CTG GAC ATC CAC TTC ATC CAC GTG 542
Phe Asp Trp Lys Lys Gln Val Glu Ile Leu Asn Arg Tyr Pro His Phe Lys Thr Lys Ile Glu Gly Leu Asp Ile His Phe Ile His Val
140 150
AAG CCC CCC CAG CTG CCC GCA GGC CAT ACC CCG AAG CCC TTG CTG ATG GTG AAC GGC TGG CCC GGC TCT TTC TAC GAG TTT TAT ANG ATC 632
Lys Pro Pro Gln Leu Pro Ala Gly His Thr Pro Lys Pro Leu Leu Met Val Asn Gly Trp Pro Gly Ser Phe Tyr Glu Phe Tyr Lys Ile
170 180
ATC CCA CTC CTG ACT GAC CCC ANG AAC CAT GGC CTG AGC GAT GAG CAC GTT TTT GAA CTC ATC TCC CCT TCC ATC CCT GGC TAT GGC TTC 722
Ile Pro Leu Leu Thr Asp Pro Lys Asn His Gly Leu Ser Asp Glu His Val Phe Glu Val Ile Cys Pro Ser Ile Pro Gly Tyr Gly Phe
200 210
TCA GAG GCA TCC TCC AAG ANG GGC TTC AAC TGG GTG GGC ACC GGC AGG ATC TTT TAC AAG CTG ATG CTG GCG CTG GGC TTC CAG GAA TTC 812
Ser Glu Ala Ser Ser Lys Lys Gly Phe Asn Ser Val Ala Thr Ala Arg Ile Phe Tyr Lys Leu Met Leu Arg Leu Gly Phe Gln Glu Phe
230 240
TAC ATT CAA GGA GGG GAC TGG GGG TCC CTC ATC TCC ACT AAT ATG GGC CAG CTG GTG GGC ACC CAC GTG AAA GGC CTG CAC TTG AAC ATG 902
Ile Gln Gly Gly Asp Trp Gly Ser Leu Ile Cys Thr Asn Met Ala Gln Leu Val Pro Ser His Lys Gly Leu His Leu Asn Met
260 270
GCT TTG GTT TTA ACC AAC TTC TCT ACC CTC ACC CTC CTC CTG GGA CAG CGT TTC GGG AGG TTT CTT GGC CTC ACT GAG AGG GAT GTG GAG 982
Ala Leu Val Leu Ser Asn Phe Ser Thr Leu Thr Leu Leu Leu Gly Gln Arg Phe Gly Arg Phe Leu Gly Leu Thr Glu Arg Asp Val Glu
290 300
CTG CTG TAC CDE GTC AAG CAG ANG GTA TTC TAC ACC CTG ATG AGG GAG ACC GGC TAC ATG CAC TGC ACC AAC CDE GAC ACC GTA 1082
Leu Leu Tyr Pro Val Lys Glu Lys Val Phe Tyr Ser Leu Met Arg Glu Ser Gly Tyr Met His Ile Gln Cys Thr Lys Pro Asp Thr Val
320 330
GGC TCT GCT CTG AAT GAC TCT CDT GTG GGT CTG GCT GCT TAT ATT CTA GAG ANG TTT TCC ACC TGG ACC AAT ACG GAA TTC CGA TAC CTG 1172
Gly Ser Ala Leu Asn Asp Ser Pro Val Gly Leu Ala Ala Tyr Ile Leu Glu Lys Phe Ser Thr Trp Thr Asn Thr Glu Phe Arg Tyr Leu
350 360
GAG GAT GGA GGC CTG GAA AGA AGC TTC CTC GTC GAC GAC CTG CTG ACC AAT GTC ATG CTC TAC TGG ACA ACA GGC ACC ATC ATC TCC TCC 1262
Glu Asp Gly Gly Leu Glu Arg Ser Phe Ser Leu Asp Asp Leu Leu Thr Asn Val Met Leu Tyr Trp Thr Thr Thr Gly Thr Ile Ile Ser Ser
380 390
CAG CDE TTC TAC ANG CAG AAC CTG GGA CAG GGC TGG ATG ACC CAG ANG CAT GAG CCG ATG ANG GTC TAT GTG CCG ACT GGC TTC TCT GGC 1352
Gln Arg Phe Tyr Lys Glu Asn Leu Gly Gln Gly Trp Met Thr Gln Lys His Glu Arg Met Lys Val Tyr Val Pro Thr Gly Phe Ser Ala
410 420
TTC CDT TTT GAG CTA TTC CAC ACC CDT GAA ANG TGG GTG AGG TTT ANG TAC CDE ARA GTC ATC TCC TAT TCC TAC ATG GTT CDT GGG GGC 1442
Pro Phe Glu Leu Leu His Thr Pro Glu Lys Trp Val Arg Phe Lys Tyr Pro Lys Val Ile Ser Arg Tyr Met Val Arg Gly Gly
440 450
CAC TTT GCG GGC TTT GAG GAG CCG GAC CTC CDE CAG GAC ATC CCG AAG TTC CTG TCG GTC CAG CCG GAA TGA CCGACCCCTCTCCDC 1535
His Phe Ala Ala Phe Glu Glu Pro Glu Leu Leu Ala Gln Asp Arg Lys Phe Leu Ser Val Leu Glu Arg Gln
CCGCTTCCACCTCCCCCAACGTCGCCCTCCAGCCCTTTCTGGGAGAGTACCCCTTTCTGAGGAATGAGTTGGCTCCCTCCCTGCGCATCGGAGCCCAACCGTCCGCCCTG 1654
ACCCCTCAAGCTCACTCCCAACCCCACTCCGTTGGTAGGACACATGGCTTTGATGATAAAGCACTTTACTCTAAAAAAMAAAAA 1743
    
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