

cDNA and deduced amino acid sequences of a male dominant P-450M_d mRNA in rats

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A λ gt11 library constructed from hepatic mRNA of a 10 week-old male rat was screened with P-450-male specific antibody (1) and a new cDNA designated P-450M_d cDNA, was isolated and sequenced. The deduced amino acid sequence of P-450M_d cDNA displayed the highest similarity (60%) to those of P-450 (M-1) (2) or P-450f (3). The cysteine residue that attached to haem iron with the enzyme active site and the polyadenylation signal are underlined. The mRNA hybridized with a specific oligonucleotide probe displayed a male dominant expression in adult rats.

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GTGAGCCAATGGCCCTCTTCATTTTTCTGGGGATTGGCTTTCTGTTTGGTTTTCTTTTTCTATGGAATCAGCACCATGTCAGAAGGAAGCTCCCACCTGGTCCCCTCTCTACCAA 120
MetAlaLeuPheIlePheLeuGlyIleTrpLeuSerCysLeuValPheLeuPheLeuTrpAsnGlnHisHisValArgArgLysLeuProProGlyProThrProLeuProI 38

TTTTTGGCAATATTTTGGCAAGTGGGTGTTAAAAATATCAGCAATCTATGTGCATGTAGCAAAAAGTACGGGCTGTGTTCCACATGTATCTGGGCATGAAGCCCACTGTGGTGTCTGT 240
lePheGlyAsnIleLeuGlnValGlyValLysAsnIleSerLysSerMetCysMetLeuAlaLysGluTyrGlyProValPheThrMetTyrLeuGlyMetLysProThrValValLeuT 78

ATGGATATGAAGTATTGAAAGAAGCTCTGATTGACCCGGGAGAAGAGTTTTCTGATAAAATGCATTGCTCAATGCTCAGTAAAGTCAGCAAGGGTTAGGCATTGTCTCAGCAATGGAG 360
yrGlyTyrGluValLeuLysGluAlaLeuIleAspArgGlyGluGluPheSerAspLysMetHisSerSerMetLeuSerLysValSerGlnGlyLeuGlyIleValPheSerAsnGlyG 118

AAATATGGAACAAACACGGCCTTCTCCCTCATGGTCTTAAGTCTATGGGGATGGGAAAGAGAATTTGAAACCGAATTCAGGAGGAAGTGTATTATCTGCTGGAAGCACTGAGAA 480
luIleTrpLysGlnThrArgArgPheSerLeuMetValLeuArgSerMetGlyMetGlyLysArgThrIleGluAsnArgIleGlnGluGluValValTyrLeuLeuGluAlaLeuArgL 158

AAACCAATGGGTCCCGTGTGACCCAGCTTCTCTCTGGCCTGTGTTCCCTGCAATGTGATCTCCAGTGTCAATTTCCAGCACCCTTTTGACTACAGTGTAGAAATTCAAAAATTC 600
ysThrAsnGlySerProCysAspProSerPheLeuLeuAlaCysValProCysAsnValIleSerSerValIlePheGlnHisArgPheAspTyrSerAspGluLysPheGlnLysPheI 198

TAGAGAATTTCCATACAAAAATTGAAATTTTAGCATCTCCTTGGGCCAGTTGTGCAGTGCCATCTCTGTTCTATACTATCTCCCGGAATCCATAACAAATTTTAAAAAGATGTGACTG 720
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AGTCTGAATTTACCATGGACAACCTGATAGTACCATAGGTGATCTTTTGGAGCAGGAACAGAGACAACGAGTCCACCATAAAATATGGGCTTTTGCTCTTGCTGAAGTACCCAGAGG 960
ysSerGluPheThrMetAspAsnLeuIleValThrIleGlyAspLeuPheGlyAlaGlyThrGluThrThrSerSerThrIleLysTyrGlyLeuLeuLeuLeuLysTyrProGluV 318

TCACAGCTAAAATTCAGGAAGAAATTAATCGCGTATTGGTAGACACCGGAGACCTGCATGCAGGACAGGAACACATGCCCTATACGGATGCTGTGCTGCATGAGATCCAGAGATACA 1080
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TTGATTTTGTCCCATTCCTTGCCTCGTAAGACAACGCAGGATGTGGAGTTCCAGAGGATACCACATTCACAAAGGGCACAAGCGTAATGGCATGTCTGACTTCTGCCCTGCACGATGACA 1200
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AAGAAATTTCCCAACCCAGAGAAGTTCGACCCCTGGCCACTTTCTCGATGAGAAAGGCAACTTCAAGAAGAGTGACTACTTCATGGCTTTCTCAGCAGGAAGAAGCCTGTATTGGAGAAG 1320
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GTTTAGCCCGCATGGAGATGTTCTTAATCCTGACCAGCATTTCACAGCATTACTTTAAAACTCTGTCAATCCAGAGGACATCGACACAACCCAGTTCACCTGGTTTATTGTCTG 1440
lyLeuAlaArgMetGluMetPheLeuIleLeuThrSerIleLeuGlnHisPheThrLeuLysProLeuValAsnProGluAspIleAspThrThrProValGlnProGlyLeuLeuSerV 478

TGCCCCACCCCTTTGAGCTCTGTTTCATTCCAGCTGAAGCGGCATAGTCTTTCACACAGATGACTGAGACCCTGCTTCTACTGTGAGCAACAGGTCCTCTGTCTGTGTACTCTGTA 1560
alProProProPheGluLeuCysPheIleProVal 489

ACTGGCAGTCTCTGAAATGGCAGGGATGCTACTCTGAACTGTCTACATTTTTTTCAATCTTTGTGAACAGTCCAATTTTTTCATATGTGAAAAAACTTCACTGTTTTAGCACTA 1680
ATAAAGTTTTTTGTAGTGTATGTGAGAAAAAAA 1715