Nucleotide sequence of a cDNA coding for mouse cyclophilin

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Cyclophilin is an abundant cytosolic protein that is expressed in most tissues and is found in all eukaryotic species examined, including yeast and man (1, 2). The immunosuppressive drug Cyclosporin A has been shown to bind cyclophilin with high affinity (1). The porcine enzyme peptidyl-prolyl cis-trans isomerase, which is inhibited by Cyclosporin A, is identical to the bovine cyclophilin (3, 4). Cyclophilin may represent the intracellular target for Cyclosporin A-mediated immunosuppression. Reported here is the nucleotide sequence of a clone of cyclophilin derived from a cDNA library made from mouse thymus mRNA. The sequence, as determined by primer extension and direct RNA sequencing methods, represents a full-length mRNA except the first nucleotide. The deduced mouse protein sequence shows extremely high identity to all mammalian cyclophilins of known sequence: 96.3%, 95.7%, 95.7%, 97.6%, and 98.8% amino acid identity with the human (5), bovine (2), porcine (3, 4), rat (6), and hamster (7) sequences, respectively.

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TTTGCAGACGCCACTGTCGCTTTTCGCCGCTTGCTGCAGCCATGGTCAACCCCACCGTGTTCTTCGACATC  71
                                                METValAsnProThrValPhePheAspIle  10

ACGGCCGATGACGAGCCCTTGGGCCGCGTCTCCTTCGAGCTGTTTGCAGACAAAGTTCCAAAGACAGCAGAA 143
ThrAlaAspAspGluProLeuGlyArgValSerPheGluLeuPheAlaAspLysValProLysThrAlaGlu  34

AACTTTCGAGCTCTGAGCACTGGAGAGAAAGGATTTGGCTATAAGGGTTCCTCCTTTCACAGAATTATTCCA 215
AsnPheArgAlaLeuSerThrGlyGluLysGlyPheGlyTyrLysGlySerSerPheHisArgIleIlePro  58

GGATTCATGTGCCAGGGTGGTGACTTTACACGCCATAATGGCACTGGCGGCAGGTCCATCTACGGAGAGAAA 287
GlyPheMetCysGlnGlyGlyAspPheThrArgHisAsnGlyThrGlyGlyArgSerIleTyrGlyGluLys  82

TTTGAGGATGAGAACTTCATCCTAAAGCATACAGGTCCTGGCATCTTGTCCATGGCAAATGCTGGACCAAAC 359
PheGluAspGluAsnPheIleLeuLysHisThrGlyProGlyIleLeuSerMetAlaAsnAlaGlyProAsn 106

ACAAACGGTTCCCAGTTTTTTATCTGCACTGCCAAGACTGAATGGCTGGATGGCAAGCATGTGGTCTTTGGG 431
ThrAsnGlySerGlnPhePheIleCysThrAlaLysThrGluTrpLeuAspGlyLysHisValValPheGly 130

AAGGTGAAAGAAGGCATGAACATTGTGGAAGCCATGGAGCGTTTTGGGTCCAGGAATGGCAAGACCAGCAAG 503
LysValLysGluGlyMetAsnIleValGluAlaMetGluArgPheGlySerArgAsnGlyLysThrSerLys 154

AAGATCACCATTTCCGACTGTGGACAGCTCTAATTTCTTTTGACTTGCGGGCATTTTACCCATCAAACCATT 575
LysIleThrIleSerAspCysGlyGlnLeu***                                        164

CCTTCTGTAGCTCAGGAGAGCGTCCCTACCCCATCTGCTCGCAATGTCCTGTAATCTCTGCTCTCACTGAAG 647
TTCTTTGGGTTCCATATTTTCCTCATTCCCCTTCAAGTCTAGCTGGATTGCAAAGTTAAGTTTATGATTATG 719
AATAAAAACTAAATAAGAAAAAAAAAAAAAAAAAA                                      736
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