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A second cyclophilin-related gene in *Saccharomyces cerevisiae*

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Cyclophilin (CyP) is a cyclosporin A (CsA) binding protein of ∼ 18,000 daltons originally isolated from bovine thymus (1) and subsequently found in organisms of a broad phylogenetic distribution (2). CyP has been shown to be identical to peptidyl-prolyl *cis-trans* isomerase, the inhibition of which appears to be responsible for the immunosuppressive action of CsA (3, 4). A recent report (5) describes the cloning of a *Saccharomyces cerevisiae* gene encoding a protein sharing 65% sequence homology with a human CyP protein. Here we show the nucleotide and deduced amino acid sequence of a second *S. cerevisiae* CyP-related gene. This gene was isolated from a λZAP *S. cerevisiae* genomic library using a human CyP cDNA as a hybridization probe. The genomic sequence has an open reading frame of 615 bp encoding a protein of 205 amino acids. This protein shares 52% and 56% identity with, and is 40 and 43 amino acid residues larger than, the reported human (6) and yeast CyP proteins, respectively. In contrast to the reported yeast CyP, this protein contains a hydrophobic 34 amino acid N-terminal extension which may function as a signal sequence for subcellular compartmentalization. Positions of amino acid homology with human CyP are underlined.

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                                                           -315
                                                            TCAACCACAAATGTC -301
AACATGACAGTCAACACTATGGGTACAGGAGGACAAACTATAGACAACGGTACCGGTCGTACTGGCAACGGTAAC -226
ATGGGTATAACTACAGAGATGTTGGACAAATTAATGGTCACAAGCATTCGATCCACCCCAAACTACATATGAGAA -151
CTGCCATGGCAATTGCATATATCTTTGTACTATATTATAAAACCCCGCGAAATCAACTTTTCAGTTTTCTTCAAA  -76
AATCGATGTACCCATCATAAGAAGTTCCCCCAAAAGGAAAGAAATGAGAGGAAAAAGACACGAAGGGAAAACAAA   -1
 M  K  F  S  G  L  W  C  W  L  L  L  F  L  S  V  N  V  I  A  S  D  V  G  E    25
ATGAAATTCAGTGGCTTGTGGTGTTGGTTGTTATTATTCCTTAGCGTTAATGTTATTGCATCTGATGTGGGTGAG   75
 L  I  D  Q  D  D  E  V  I  T  Q  K  V  F  F  D  I  E  H  G  E  E  K  V  G    50
TTGATTGATCAGGACGACGAAGTAATTACACAAAAGGTGTTTTTCGATATTGAACATGGTGAAGAGAAAGTTGGC  150
 R  I  V  I  G  L  Y  G  K  V  C  P  K  T  A  K  N  F  Y  K  L  S  T  T  T    75
AGAATCGTTATTGGGTTGTACGGAAAGGTATGTCCTAAGACGGCGAAGAACTTCTACAAGTTAAGCACCACCACT  225
 N  S  K  K  G  F  I  G  S  T  F  H  R  V  I  P  N  F  M  V  Q  G  G  D  F   100
AATTCCAAAAAGGGGTTCATCGGGTCCACTTTCCATAGGGTGATTCCCAACTTCATGGTACAGGGAGGGGACTTC  300
 T  D  G  T  G  V  G  G  K  S  I  Y  G  D  T  F  P  D  E  N  F  T  L  K  H   125
ACAGACGGCACTGGCGTTGGTGGCAAATCCATCTATGGAGATACTTTCCCTGACGAAAACTTTACTTTGAAGCAT  375
 D  R  K  G  R  L  S  M  A  N  R  G  K  D  T  N  G  S  Q  F  F  I  T  T  T   150
GATCGCAAGGGCAGACTATCGATGGCTAATCGTGGTAAAGATACCAATGGATCTCAGTTCTTCATCACCACTACG  450
 E  E  A  S  W  L  D  G  K  H  V  V  F  G  Q  V  V  D  G  M  D  V  V  N  Y   175
GAAGAAGCGTCGTGGCTCGATGGAAAGCATGTGGTATTTGGACAGGTTGTGGACGGCATGGATGTGGTGAACTAC  525
 I  Q  H  V  S  R  D  A  N  D  K  P  L  E  A  V  K  I  A  K  C  G  E  W  T   200
ATACAGCACGTGTCCAGAGATGCGAATGACAAACCTCTCGAGGCGGTCAAGATCGCAAAATGCGGTGAGTGGACG  600
 P  E  L  S  S  *                                                             205
CCTGAGCTCTCTTCTTGAGTATATGCAATATTTCATACTATATACATAGATATCAATTTCAGTATGTATAGTTAA  675
AGGTAAATTAACTAGAGAACGTGGGAACAGTTCCGCACTGTGACCACCGGAACGT                      728
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