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Complete cDNA sequence of rat phosphoribosylpyrophosphate synthetase subunit I (PRS I)

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Rat phosphoribosylpyrophosphate synthetase (EC 2.7.6.1) has two distinct types of subunit, referred to as PRS I and PRS II (1), and the coding sequences of the cDNAs for the two subunits were reported (1). We now report a full cDNA sequence for rat PRS I. The sequence contains a 5' untranslated region of 111 bp, a protein coding region of 954 bp, a 3' untranslated region of 916 bp and a 78 base poly(A) tract. The initiation and termination codons and the putative poly(A) signal are boxed. In the following paper (2), we report a cDNA sequence for rat PRS II. While the deduced amino acid sequences of rat PRS I and PRS II are highly homologous (96% identical)(1), the number of synonymous substitutions per site was calculated to be 0.735, according to Miyata and Yasunaga (3). This value is comparable to 0.75, a value expected for completely random codon choice, suggesting that there is a long evolutionary distance between the two subunits, with highly selective functional constraints operating on the amino acid sequences.

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   1 CAACGCGGTTCTGTTGGTGT TCAGGTTCCCTACTGACTTC CCTTCCAGTGGCAGCGGCGG AGGCGGCAGTGGCAGCGGCA AGCACTGAGCACGTTTGGGT
 101 AGTTGTCCAAGATGCCGAAT ATCAAAATCTTCAGCGGGAG CTCCCACCAGGACTTATCCC AGAAAATTGCTGACCGCCTG GGCCTGGAGCTAGGCAAGGT
 201 GGTGACTAAGAAATTCAGCA ACCAGGAGACCTGTGTGGAA ATTGGGGAGAGTGTTCGTGG AGAGGATGTCTACATTGTTC AGAGTGGCTGCGGTGAGATA
 301 AATGACAATCTAATGGAGCT TTTGATCATGATCAATGCTT GCAAGATCGCTTCTGCCAGC CGGGTTACTGCGGTCATCCC ATGCTTCCCTTATGCCCGGC
 401 AGGATAAGAAGGATAAGAGC CGGGCTCCAATCTCAGCTAA GCTTGTTGCAAATATGCTAT CTGTAGCAGGTGCGGATCAT ATTATCACCATGGATCTACA
 501 TGCATCTCAGATTCAGGGCT TCTTTGATATCCCAGTGGAC AATTTATACGCAGAGCCAGC TGTCCTGAAGTGGATTCGGG AGAACATATCTGAGTGGAGA
 601 AACTGTACTATTGTCTCACC TGACGCTGGCGGAGCCAAGA GAGTGACCTCCATTGCAGAC CGATTGAATGTGGATTTTGC TTTGATTCACAAAGAACGGA
 701 AGAAGGCCAATGAAGTGGAC CGCATGGTACTAGTAGGAGA TGTGAAGGATCGTGTGGCTA TACTTGTGGATGACATGGCT GACACTTGTGGTACAATTTG
 801 TCATGCTGCTGACAAACTTC TCTCAGCTGGAGCTACCAGA GTTTATGCCATTTTGACGCA TGGGATCTTTTCTGGTCCAG CCATTTCTCGCATCAACAAT
 901 GCATGCTTTGAAGCAGTAGT AGTTACCAATACCATACCTC AGGAGGACAAGATGAAACAC TGCTCCAAAATCCAGGTGAT CGACATCTCTATGATCCTTG
1001 CAGAAGCCATCAGGAGAACC CACAATGGAGAATCTGTCTC CTACCTGTTCAGCCATGTTC CTCTATAATATCATAAATTC TGAAGCGTTTTCAAAATGAA
1101 ACCACCCCCACCCCTTGTTT TTCTTGTATTTGGTGAGTTG GGCAGAAGAGCCAGCTTGCT TCAGTGTAGCTTTTTACAGC CCACATTAGCTACATTAGGA
1201 TTTATCCTAATTGGAGAAAG ACAGACTGCTATTAACTGCT AGGACACCCTACGTGCATTG TTGCAGCCTGGCTTTCTTGT TTATTTTGTGATCCTTGCAG
1301 CTTTAAATTGAGTTCCACTG TTGAAAGCTGCATAGACTGT TAAAAGAGAGAGTATTCCCC AAGGTCCTTAGGATGGAATT GTGGAGCTCATACTCCATTG
1401 CATGTGAAGGCTTTGGAGTT TCCTTCATTCAGAATAACTA GCGACAAAGCCAGCCCTCGT GTGATACATTTTCAGAGGTG TATGCTACACTGCAGCAAGT
1501 TCCCTGTGCATCCTTAAACA GAGTTCGCCTGCTGAGCACC CTGTACGGCAGGGGCGGGTA GCTCAATGCAGTAATCAATT TTTGGGAGGAAGAAGCCTGA
1601 TCTATTATCATCTGTTTAAT TCTCTGTAGCTTGGATTCTC TATGCCTATTCCTTTCCTGT TGGCTTCACCTTCAGCTATC TCGACCCTTTCCTGGACAAA
1701 TATCTTGAACTCAGTGATCA TTGTTTGTGACAAAATTTTC TGTAAGACAGACTTGCTTCT TGCTATGTAACTGCTAACGT TGACATTAGGTAACTTGCTA
1801 TAGCACAATCTTCCTTAGCC CGCTCTCTCTGAGTTAGTGG GTTTTAGGTGGTGTGTGTGT CGTAGTGCCTTTTGATTAAT TTAAGTATTTAATTTTTATC
1901 TTCCTTCGATCTGTTTGGCT TAACAATTTGATCTTATTGT CTCATGTAGAAGAAACTTAA TAAAATGTCTGTCATGTGTA CA_78
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