

**Rat porphobilinogen deaminase cDNA: nucleotide sequence of the erythropoietic form**

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Porphobilinogen deaminase (PBG-D, E.C.4.3.1.8) is the third enzyme of the heme biosynthetic pathway. Inherited deficiency of this enzyme is associated, in man with the autosomal dominant disease acute intermittent porphyria. The PBG-D gene gives rise to two different mRNAs, one of which is only present in erythropoietic cells, the other being ubiquitous (1). From the human mRNAs sequences it was deduced that an additional stretch of 17 amino acid residues at the NH2 terminus of the protein was encoded by the ubiquitous form of mRNA as compared to the erythropoietic form (1,2). We previously cloned a cDNA from erythropoietic spleen of phenylhydrazine-treated rats (3) and we present here its sequence which contains the complete coding information. The nucleotide and amino acid sequence homology between human (2) and rat erythropoietic PBG-D are 75% and 91% respectively. The availability of the rat cDNA will facilitate the study of the expression of the PBG-D gene in various cell types. The initiation and termination codons as well as the polyadenylation signal are underlined.

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TGGTCTCTGC TTCTCTGGAT CCCGAAGGAG GGCAGAAGGA AGAAAACGGC TCAATGATGA 60
GGGTGATTCC AGTGGGACC CGGAAGAGTC AGCTGGCTCG CATAAGACC GACACTGTGG 120
TAGCGATGCT GAAAACCTTG TACCCTGGCA TACAGTTTGA AATCATTGCT ATGTCCACCA 180
CAGGGGACAA GATTCTTGAT ACTGCACTCT CTAAGATTGG AGAGAAGAGC CTGTTTACCA 240
AGGAGCTAGA AAACGCCCTG GAAAAAATG AAGTGGACCT GGTGTTTCC TCCCTGAAGG 300
ATGTGCCTAC CATACTACCT CCTGGCTTTA CCATTGGAGC CATCTGCAA C6GGAAAACC 360
CTTGTGATGC TGTGTTTTT GAGGGAAAGT TTATTGGAAA GACCCCTGGAA ACCTTGCCAG 420
AGAAAAGTGC CGTGGGGACC AGTCCTCTGA GGAGAGTGGC GCAGTACAG AGAAAAGTTC 480
CTCACCTGGA ATCAAGAGT ATTCGGGGAA ACCTCAACAC CCGCTACGG AAGCTGGATG 540
AGCAGCTGGA GTTCAGTGCC ATTATCCTGG CTGTGGCTGG CCTACAGCGC ATGGGCTGGC 600
AGAACC6GGT GGGCCAGATC TTGCACCCA6 AGGAATGCAT GTATGCTGTG GGTACAGGGAG 660
CCCTGGCGGT GGAGGTCCGA GCCAAGGACC AGGATATCTT GGACCTAGTG GGTGTGTGTC 720
ATGATCCTGA AACTCTGCTT CGCTGCATTG CTGAAAGGGA TTTTCTGAGG CACCTGGAGG 780
GAGGCTGTAG CGTGCCAGTA GCAGTGCATA CAGTGATGAA GGATGGGCAA CTGTACCTGA 840
CTGGTGGAGT CTGGAGTCTA GATGGCTCAG ATAGCATGCA AGAGACCATG CAGGCCACCA 900
TCCAGGTCCC TGTTACGCAA GAAGATGGTC CAGAGGATGA CCCACAGTTG GTTGGAAATCA 960
CTGCCCGGAA CATTCCAAGA GGAGCCAGC TAGCTGCTGA GAACCTGGGC ATCAGCCTGG 1020
CAAGCTTGTT GCTCAACAAA GGAGCTAAGA ACATCCTAGA TGTTGCACGG CAGCTTAATG 1080
ATGTGCGCTA ACTGGCGACG TCGGCACAGG AACCGAACCC CAGCTGTAC TCCAGTGCCT 1140
ATGTCTGGCT GTCAGTGCC CTGTGCTCCT TAACAAGGGGG AATGATTATC CCAAGGAGATT 1200
GAACAGAGTT GTTGAGACT CGGCCCTTGA AGATATGCCT CAACTGGGG CCTCCATGAC 1260
TGCCCTTCCC TCAGTAGTTT GTGGGCTTCA TCTCTTAGA GAAAGTCCAT GCCAATCTTT 1320
TATGTAACCA ATGCCACTAA TCAGTTGAGA ATGTGGTTCT CCTGGAGTTG GGGGAAGATA 1380
TGAATAAAC CAAAGCCCTT TAACCGTAAA AA

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