

Rat uroporphyrinogen decarboxylase cDNA: nucleotide sequence and comparison to human uroporphyrinogen decarboxylase

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Uroporphyrinogen decarboxylase (URO-D, E.C. 4.1.1.31) is a cytosolic enzyme involved in the heme biosynthetic pathway. In humans, a dominantly inherited disorder, Porphyrria Cutanea Tarda (P.C.T.) is caused by a partial deficiency of URO-D activity (1) and a recent report (2) has shown a correlation between an amino acid substitution and the decrease in URO-D activity in a patient homozygous for the disease. However, this substitution was not found in unrelated heterozygous patients. We previously cloned the rat cDNA coding for uroporphyrinogen decarboxylase (3) and we present here its complete sequence. The nucleotide and amino acid sequence homologies between human (4) and rat uroporphyrinogen decarboxylase are 85% and 90% respectively. The amino acid substitutions are shown in Table I and indicate the protein regions which are not good candidates for the search for mutations in patients with PCT.

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CGAACGGCTTGGGACTCCAGAAATTTCCCGGAGCTGAAGAATGACACGTTCTTGAGAGCAG 60
CCTGGGAGAGGAAACAGACTATACTCTCTGTTTGGTGCATGAGACAAGCAGGCCGCTACT 120
TACCAGAGTTTAGGGAAACAGGGCTGCCAGGACTTCTTCCAGCCTGTCCATCTCTTG 180
AGGCTTGTCTGTAAGTACTGACTCTGGAGCCTAGTGCAGAGGTTTCTTTGGATGCTGCTATAA 240
TTTTCTCTGACATCTCTGTTGTATCCCGAGGACTTGGCTATGAGAGTGAACCATGGTACTCTG 300
GCAAGGAGCCAGCTTTCCAGAGCCATTAGAGAGAGAGCAGGACTTGAAGCTCTACAGGG 360
ATCCAGCAGCAGTGGCTTCAGAGTATAGGCTATGTGTTCCAAGCCATCACCCTTACCAGC 420
AACAGCTGGCTGGAGCTGTGCCACTGATTGGCTTGGCTGGTGGCTCCGTGGACCCGTATGA 480
CGTACATGGTGAAGCAGCAGTTCAGAGCCATGGCTCAGGCCAAGCAGTGGCTCATC 540
AGAAAGCAGTGGCCAGTCCAGAGCTGCTTGGCATACTCACTCATGCTGTGGTCCATATC 600
TAATAGGACAATAGCTGCTGGTGGCTCAGGCAATACAGCTCTTGGAGTCCAGCAGGAG 660
ATCTTGGCTCCGAGCTCTTCCAGAAATTTGCACTGGCTTACATCCGTGATGTGGCCAAAC 720
GAGTGAAGGCTGGGTTGCAGAAAGCCGGGCTGACCAAGATGCCATGATCATCTTTGCCA 780
AGATGGACATTTTGGCTGGAGAGCTGGCCAGGCTGGCTATGAGGTAATTTGGCTT 840
ACTGGACAGTGGCTCCAAAGAAAGCCGGGAACTGTTGGAAAGCAGTGAATCTGCAAG 900
GGGAAGTGGATCCCTGTGCCCTGTATGCATCTGAGGAAAGATTTGGTGGCTGGTGGCAGC 960
AGATGCTGATGACTTTGGGCCACAGGCTACATTGCTAAGCTAGGGCATGGGCTTTACC 1020
CTGACATGGAGCCAGAACAGTAGGAGGCTTTTGGATGCAATACACAAACACTCACGCC 1080
TGCTTCGACAGAAATTTGATATGTGCTTTTCTGCTCAAGTACCACCGACAGATTTGTTCC 1140
CAGGAAATAGAACTCCAGAAACTTCCA 1200
    
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A. A. POSITION	7	9	23	72	84	102	115	124	125	143	169	170	171	183	185	189	192		
HUMAN	P	G	W	L	G	S	Q	E	V	Q	G	S	S	R	Q	Q	R		
RAT	L	N	T	V	A	G	R	A	A	R	S	F	K	K	V	K	G		
186	203	207	225	229	242	246	248	249	253	254	255	293	303	318	321	325	330	353	
D	V	V	P	Q	H	Q	R	R	E	A	P	V	K	N	Q	K	D	H	V
H	I	A	S	E	S	R	G	Q	K	T	R	N	P	E	R	Q	N	Q	L

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