# Coding sequence of the precursor of the  $\beta$  subunit of rat propionyl-CoA carboxylase

(mitochondrial enzyme/leader peptide structure/propionic acidemia)

Jan P. Kraus\*, Frank Firgaira\*, Jiří Novotný†, František Kalousek\*, Kenneth R. Williams‡, CYNTHIA WILLIAMSON\*, TOSHIHIRO OHURA\*, AND LEON E. ROSENBERG\*

Departments of \*Human Genetics and \*Molecular Biophysics and Biochemistry, Yale University School of Medicine, <sup>333</sup> Cedar Street, P.O. Box 3333, New Haven, CT 06510; and tMassachusetts General Hospital and Harvard Medical School, Molecular and Cellular Research Laboratory, Boston, MA <sup>02114</sup>

Contributed by Leon E. Rosenberg, July 14, 1986

ABSTRACT A cDNA encoding the cytoplasmic precursor of the  $\beta$  subunit of the mitochondrial enzyme propionyl-CoA carboxylase (EC 6.4.1.3) was cloned and sequenced. The DNA sequence of 2070 nucleotides is almost identical in size to the major hybridizing mRNA from rat liver (2000  $\pm$  50 nucleotides), suggesting that the cloned DNA represents nearly all of the mRNA sequence. A polypeptide expressed in vitro from an mRNA transcript of this cDNA is indistinguishable in size from the  $\beta$  subunit precursor (58,500 Da). An open reading frame of 1623 nucleotides, flanked by stop codons, encodes a polypeptide of 541 amino acids; the predicted amino acid sequence was confirmed as that of the  $\beta$  subunit of propionyl-CoA carboxylase by matching it to the amino acid sequences of five peptides derived from pure mature rat enzyme. Although the exact length of the cleavable,  $NH_2$ -terminal leader peptide has not been determined because the NH<sub>2</sub>-terminal residue of the mature subunit is blocked, the leader is most likely 40-42 amino acids in length and is highly positively charged. Computer-aided analysis of secondary structure suggests that the leader peptide consists of two  $\alpha$ -helical segments, with the two most NH2-terminal arginine residues occupying opposite sites of the first helix; this helix has no apparent hydrophobic moment.

Propionyl-CoA carboxylase [PCCase; propanoyl-CoA: carbon-dioxide ligase (ADP-forming), EC 6.4.1.3], a biotindependent mitochondrial enzyme, is a key enzyme in the catabolic pathway for odd-chain fatty acids, isoleucine, threonine, methionine, and valine. In humans, propionic acidemia due to recessively inherited deficiency of PCCase activity often causes life-threatening ketosis and acidosis (1). The native enzyme is probably a dodecamer (2) composed of six biotin-containing  $\alpha$  subunits ( $M_r = 70,000-72,000$ ) and six  $\beta$  subunits ( $M_r = 54,000-56,000$ ) (3). The  $\alpha$  and  $\beta$  subunits are each synthesized initially as larger precursors on cytoplasmic polyribosomes. These precursors, containing NH2-terminal leader sequences, are subsequently transported across both mitochondrial membranes, cleaved to their mature size, and assembled (4). To facilitate investigation of PCCase biogenesis and the nature of mutations in the various complementation groups of inherited PCCase deficiency (5), we have isolated cDNA clones for the  $\beta$  subunit ( $\beta$ PCCase) (6). In this communication we present the entire amino acid sequence of the  $\beta$ PCCase precursor as deduced from the cDNA sequence. This primary structure is supported by amino acid sequences of five peptides isolated from homogeneous rat liver PCCase.

## EXPERIMENTAL PROCEDURES

cDNA Cloning. We have previously described the isolation and identification of  $\beta$ PCCase cDNA clones from a cDNA library prepared from a highly enriched, immunopurified  $\beta$ PCCase mRNA (6, 7). A restriction map of the clones has also been published (6).

In Vitro Transcription and Translation. Plasmid DNA containing the T7 promoter joined with the  $\beta$ PCCase coding sequence was prepared for transcription by restriction cleavage at a unique Pvu II site downstream from the coding sequence. The product was extracted with phenol and precipitated with ethanol, and  $1 \mu g$  of linearized DNA was then used in a 50- $\mu$ l transcription reaction mixture containing nucleoside triphosphates at 0.5 mM each, 10  $\mu$ Ci (1 Ci = 37 GBq) of  $\left[\alpha^{-32}P\right]$ GTP, 40 mM Tris-HCl at pH 7.5, 6 mM MgCl<sub>2</sub>, <sup>2</sup> mM spermidine, <sup>10</sup> mM NaCl, <sup>10</sup> mM dithiothreitol, <sup>70</sup> units of RNasin (Promega Biotec, Madison, WI), and 125 units of T7 RNA polymerase. The reaction was carried out for 90 min at 40°C. The products were extracted with phenol and precipitated with ethanol from <sup>2</sup> M ammonium acetate to remove the unincorporated nucleotides. Cell-free translation in rabbit reticulocyte lysate followed by immunoprecipitation was carried out as previously described (7).

Blot Hybridization Analysis. Total RNA from rat and human liver or from human skin fibroblasts were prepared as described (8). Polyadenylylated RNA was isolated by oligo(dT)-cellulose chromatography according to the supplier's instructions (Collaborative Research, Waltham, MA). Blot hybridization analysis was performed after electrophoresis of the RNAs through a 1% agarose gel containing formaldehyde (9).

DNA Sequencing. DNA was sequenced according to Maxam and Gilbert (10). Restriction endonuclease fragments were sequenced on both strands by radiolabeling at their <sup>5</sup>' termini using T4 polynucleotide kinase (Bethesda Research Laboratories) and  $[\gamma^{32}P]ATP$  (Amersham) or at their 3' termini by using the Klenow fragment of Escherichia coli DNA polymerase <sup>I</sup> (Boehringer Mannheim) and the appropriate  $\lceil \alpha^{-32}P \rceil dNTP$  (Amersham).

Succinylation, Isolation, and Sequencing of Arginine Peptides from PCCase. Rat liver PCCase was purified to homogeneity by using affinity chromatography on avidin (11). To obtain arginine peptides, 30 nmol of PCCase was dialyzed against <sup>5</sup> M guanidine hydrochloride (pH 8.5) for <sup>36</sup> hr. The sample (20 ml) was then succinylated (12) with 150 mg of succinic anhydride while the pH was maintained at 8.5. When succinylation was complete (5 min), solid NH<sub>2</sub>OH·HCl was added to <sup>a</sup> final concentration of <sup>1</sup> M, <sup>5</sup> M NaOH was used to adjust the pH to 10, and the mixture was stirred for <sup>1</sup> hr.

The publication costs of this article were defrayed in part by page charge payment. This article must therefore be hereby marked "advertisement" in accordance with 18 U.S.C. §1734 solely to indicate this fact.

Abbreviations: PCCase, propionyl-CoA carboxylase;  $\beta$ PCCase,  $\beta$ subunit of PCCase; bp, base pair(s).

After dialysis against  $0.25$  mM NaHCO<sub>3</sub> and drying, the succinylated PCCase was dissolved in 1 ml of 0.2 M NaHCO<sub>3</sub> and digested with tosylphenylalanyl chloromethyl ketone (TPCK)-treated trypsin at 1:20 (wt/wt) ratio at 37 $\degree$ C for 8 hr. The resulting peptides were separated on a Vydac  $C_4$  reversephase column (0.45  $\times$  25 cm) equilibrated with 0.05% trifluoroacetic acid and then eluted as described previously with increasing concentrations of acetonitrile (13). Aliquots were taken from the peak fractions for hydrolysis in 6 M HCl  $(115^{\circ}C, 16 \text{ hr})$ , followed by analysis on a Beckman 121 M amino acid analyzer. Several selected peptides were either coupled to aminopolystyrene and then subjected to solidphase sequencing on a Sequemat mini 15 sequenator or were dried under reduced pressure and then loaded onto an Applied Biosystems gas phase sequencer in 0.1 ml of trifluoroacetic acid. The resulting phenylthiohydantoin amino acids were identified by reverse-phase HPLC (13).

## RESULTS AND DISCUSSION

BPCCase cDNA Clones. We had previously isolated and identified two overlapping  $\beta$ PCCase cDNA clones from a rat liver cDNA library highly enriched for  $\beta$ PCCase sequences (6). The unique portions [2070 base pairs (bp)] of these two clones were joined and inserted into a plasmid, pGEM2 (Promega Biotec, Madison, WI), bearing <sup>a</sup> T7 RNA polymerase promoter. The  $\beta$ PCCase cDNA was transcribed in vitro, and the transcript was translated by using a reticulocyte lysate-programmed system. Fig. 1 shows that the translated polypeptide (58.5 kDa) is indistinguishable in size from the  $\beta$ PCCase precursor immunoprecipitated from a translation mixture of total rat liver mRNA.

RNA Analysis. Blot hybridization analysis ofrat and human liver and human skin fibroblast mRNA with the  $\beta$ PCCase cDNA probe just described yielded <sup>a</sup> major hybridizing species of  $2000 \pm 50$  nucleotides in both rat and human mRNA (Fig. 2). In addition, minor bands were observed at <sup>2600</sup> and <sup>4500</sup> nucleotides in rat mRNA and at <sup>450</sup> and <sup>4500</sup> nucleotides in human mRNA. The 2600-nucleotide rat transcript may represent <sup>a</sup> minor mRNA species elongated at the <sup>3</sup>' end. The existence of such an elongated species has been shown to account for the two mRNAs found for the  $\alpha$  chain



FIG. 1. NaDodSO<sub>4</sub>/polyacrylamide gel analysis of  $\beta$ PCCase polypeptides translated from transcribed 8PCCase cDNA and from total rat liver mRNA. A plasmid containing the T7 RNA polymerase promoter joined with the  $\beta$ PCCase cDNA sequence was transcribed in vitro and the product was used to direct a reticulocyte lysateprogrammed translation mixture containing [35S]methionine. After translation, an aliquot  $(1 \mu I)$  of the mixture was applied to the gel (lane 1). The  $\beta$ PCCase band in lane 1 is, in fact, a doublet produced by initiation at both the initiator methionine codon and at the first internal methionine (residue 10). Total rat liver mRNA was translated in 100  $\mu$ l of translation mixture and the precursor of  $\beta$ PCCase ( $p\beta$ CCase) was immunoprecipitated with anti- $\beta$ PCCase antiserum (lane 2). The radioactive bands were visualized by fluorography for 10 hr.



FIG. 2. Blot hybridization analysis of  $\beta$ PCCase mRNA from rat liver, human liver, and human skin fibroblasts. mRNA samples were denatured with formaldehyde and formamide and electrophoresed in <sup>a</sup> 1% agarose gel (9). The separated mRNAs were transferred to nitrocellulose, and the blot was probed with radiolabeled rat  $\beta$ PCCase cDNA. Lane 1, rat liver mRNA, 5  $\mu$ g; lane 2, human liver mRNA, 5  $\mu$ g; lane 3, human skin fibroblast mRNA, 10  $\mu$ g. The sizes of ribosomal RNA markers are as follows: 16S, <sup>1541</sup> nucleotides; 18S, 1740 nucleotides; 23S, 3000 nucleotides; and 28S, 4850 nucleotides.

of  $\beta$ -hexosaminidase (14). The 4500-nucleotide species probably represent nuclear precursors. The nature of the 450 nucleotide species, particularly prominent in human fibroblast mRNA, is unknown.

Nucleotide Sequence. The cloned  $\beta$ PCCase cDNA sequence is 2070 bp long (Fig. 3). Comparison of the estimated size of the  $\beta$ PCCase mRNA with that of the cloned cDNA suggests that very little mRNA information is missing from the cDNA. The open reading frame of 1623 bp is flanked by stop codons at positions 1 and 1630. The putative translation initiation codon beginning at position 7 within the sequence AAAAAAUGG differs somewhat from the optimal context for initiation, CCACCAUGG, derived from surveys of eukaryotic mRNAs (15). However, the two most highly conserved residues, an A at position  $-3$  and a G at position  $+4$ , are present in the  $\beta$ PCCase mRNA. The 3' untranslated region of 441 bp does not contain a poly(A) tail. Codon usage in the  $\beta$ PCCase mRNA is summarized in Table 1. Of all the possible <sup>61</sup> codons, only <sup>57</sup> are utilized in the sequence. CUA (Leu), GUA (Val), and UCG (Ser) are not used. UUA is used only once in 39 leucine codons, and all 15 Gln residues are coded for by CAG rather than CAA.

Peptide Sequence Analysis of Mature  $\beta$ PCCase. The homogeneous rat PCCase was modified at lysine residues by succinylation, and the modified protein was cleaved with trypsin. Thus, the protein was cleaved only at arginine residues. The resulting peptides were separated by HPLC and their sequences were determined on a solid-phase sequenator or gas-phase sequencer. Out of eight sequenced peptides, five matched the  $\beta$ PCCase DNA sequence, while the other three were later found to match the human  $\alpha$ PCCase chain (16). The NH<sub>2</sub> termini of both the  $\alpha$  and the  $\beta$ PCCase mature subunits were found to be blocked, as evidenced by the lack of any identifiable sequence when 900 pmol of the succinylated subunits was loaded onto the gas-phase sequencer. With the exception of a steadily decreasing background of glycine, cycles 2-10 contained less than 10 pmol of any individual phenylthiohydantoin derivative.

Amino Acid Sequence of  $\beta$ PCCase and a Predicted Secondary Structure of Its Leader. The open reading frame of 1623 nucleotides in the cDNA sequence (Fig. 3) encodes <sup>a</sup> poly-

### Biochemistry: Kraus et al.

1 TAAAAAATGGCGGCGGTGATTCGGATTCGGCCATGGCAGCTGGAACGAGGCTCAGAGTTTTGAACTGCGGCCTCGGCACCACAATCCGC  $\mathbf{1}$ MetAlaAlaValIleArgIleArgAlaMetAlaAlaGlyThrArgLeuArgValLeuAsnCysGlyLeuGlyThrThrIleArg

91 AGCCTTTGCAGCCAGCCGGTCTCAGTTAATGAGCGCATCGAAAACAAGCGCCATGCCGCGCTGCTGGGAGGAGGCCAGCGACGCATCGAC 29 SerLeuCysSerG1nProVa1SerVa1AsnG1uArgI1eG1uAsnLysArgHisA1aA1aLeuLeuG1yG1yG1yG1nArgArgI1eAsp

181 GCACAGCACAAGCGAGGAAAGCTGACAGCCAGGGAGCGGATCAGTCTCCTGCTGGATCCTGGAGAGCTTCCTGGAGAGCGACATGTTTGTG 59 AlaGlnHisLysArgGlyLysLeuThrAlaArgGluArgIleSerLeuLeuLeuAspProGlySerPheLeuGluSerAspMetPheVal

271 GAACACAGGTGTGCCGACTTCGGAATGGCTGCCGAGAAGAATAAGTTTCCTGGAGATAGTGTGGTCACTGGACGGGGCAGAATCAACGGA 89 GluHisArgCysAlaAspPheGlyMetAlaAlaGluLysAsnLysPheProGlyAspSerValValThrGlyArgGlyArgIleAsnGly

361 CGATTGGTTTATGTCTTCAGTCAGGACTTTACAGTTTTTGGAGGCAGTCTGTCAGGCGCACATGCTCAGAAGATCTGCAAAATCATGGAC 119 ArgLeuValTyrValPheSerGlnAspPheThrValPheGlyGlySerLeuSerGlyAlaHisAlaGlnLysIleCysLysIleMetAsp

451 CAGGCCATAACAGTGGGGCCTCCAGTGATCGGACTCAATGACTCCGGGGGCCCAGAATCCAGGAGGGGTGGAGTCCTTGGCTGCTAT 149 GlnAlaileThrValGlyAlaProValIleGlyLeuAsnAspSerGlyGlyAlaArgIleGlnGluGlyValGluSerLeuAlaGlyTyr

541 GCAGACATCTTCCTGAGGAATGTCACAGCGTCCGGAGTCATCCCTCAGATTTCTCTGATCATGGGCCCATGCGCTGGTGGGGCCGTCTAC 179 AlaAspIlePheLeuArgAsnValThrAlaSerGlyValIleProGlnIleSerLeuIleMetGlyProCysAlaGlyGlyAlaValTyr

631 TCCCCCGCCCTGACAGACTTCACATTCATGGTGAAGGACACGTCCTACCTGTTTATCACTGGCCCTGAATTTGTGAAGTCTGTTACCAAT 209 SerProAlaLeuThrAspPheThrPheMetValLysAspThrSerTyrLeuPheIleThrGlyProGluPheValLysSerValThrAsn

721 GAAGACGTGACTCAGGAGCAGCTGGGTGGTGCCAAGACCCACACCACTGTGTCAGGTGTGGCCCACAGAGCTTTCGACAATGACGTCGAT 239 GluAspValThrGlnGluGlnLeuGlyGlyAlaLysThrHisThrThrValSerGlyValAlaHisArgAlaPheAspAsnAspValAsp

811 GCTCTGTGTAACCTGCGTGAATTCTTAAACTTTCTGCCCCTCAGCAACCAGGACCCGGCTTCCATCCGAGAGTGCCATGACCCCAGTGAC 269 AlaLeuCysAsnLeuArgGluPheLeuAsnPheLeuProLeuSerAsnGlnAspProAlaSerIleArgGluCysHisAspProSerAsp

901 CGTCTGGTTCCTGAGCTGGATACAGTTGTCCCTTTGGAGTCAAGCAAAGCCTATAACATGCTGGACATCATACATGCAGTGATTGACGAG 299 ArgLeuValProGluLeuAspThrValValProLeuGluSerSerLysAlaTyrAsnMetLeuAspI1eI1eH1sAlaValI1eAspGlu

329 ArgGluPhePheGluIleMetProAsnTyrAlaLysAsnIleValIleGlyPheAlaArgMetAsnGlyArgThrValGlyIleValGly

1081 AACCAGCCCAACGTGGCTTCAGGGTGCCTGGACATTAATTCATCTGTGAAGGGGCTCGCTTTGTCAGATTCTGTGATGCTTTCAGCATT 359 AsnG1nProAsnVa1A1aSerG1yCysLeuAspI1eAsnSerSerVa1LysG1yA1aArgPheVa1ArgPheCysAspA1aPheSerI1e

389 ProLeuIleThrPheValAspValProGlyPheLeuProGlyThrAlaGlnGluTyrGlyGlyIleIleArgHisGlyAlaLysLeuLeu

1261 TACGCCTTTGCCGAGGCCACCGTGCCCAAAATCACGGTCATCACCAGGAAGGCCTATGGAGGTGCCTATGATGTCATGAGCTCCAAACAC 419 TyrA1aPheA1aG1uA1aThrVa1ProLysI1eThrVa1I1eThrArgLysA1aTyrG1yG1yA1aTyrAspVa1MetSerSerLysH1s

1351 CTTCTTGGTGATACCAACTATGCCTGGCCCACAGCTGAGATTGCAGTGCATGGGTGCAAAGGGTGCCGTGGAGATCATCTTCAAAGGACAC 449 LeuLeuGlyAspThrAsnTyrAlaTrpProThrAlaGluIleAlaVa1MetGlyAlaLysGlyAlaVa1GluIleIlePheLysGlyHis

1441 GAAGACGTGGAAGCCGCCCAGGCAGAGTATGTGGAGAAGTTTGCCAATCCTTTCCCTGCAGCCGTGAGAGGGTTCGTGGATGACATCATC 479 GluAspValGluA1aA1aGlnA1aGluTyrValGluLysPheA1aAsnProPheProA1aA1aVa1ArgGlyPheVa1AspAspI1eI1e

1531 CAGCCGTCCTCTACTCGTGCTCGGATATGCTGTGACCTGGAAGTCCTGGCCAGCAAGAAGGTCCATCGTCCTTGGAGGAAGCATGCCAAT 509 G1nProSerSerThrArgA1aArgI1eCysCysAspLeuG1uVa1LeuA1aSerLysLysVa1H1sArgProTrpArgLysH1sA1aAsn

1621 GTCCCACTGTGAAGAGATCAAAAGAAGAGAGCAACAGTGAGAAGCTGGCCTTTTGCAGCCTACCCCTGCCTTCTACAATCATGAAAGAAC 539 ValProLeuEnd

1711 GGATCTACATACCTTGGACACTGATTGAATTGCATAAAGAGTTCCTGTGCTTGGAGAAAAATTATGTGCTCTATTAAAATCTTCACTGGT

1891 GTTGCCTTGTATCTGGTTCTGGCTGACAGTAATGTGGTTAGGATTCATTGGCCTAGAGGTCACGTGTGGGAACTTGGATTCCGTGTGGAG

1981 TGGTGAGAGGGAAGATATAGTGGGAAGGTGCTGAGGTCAGCTGGGCTGGGATCTGTGCTACCCAAGAGGCTGAGGTCTTTCCTCAGCTGCT

FIG. 3. Nucleotide and amino acid sequences of the rat  $\beta$ PCCase precursor. The first nucleotide of the 5' untranslated region and the first amino acid residue of  $\beta$ PCCase are denoted no. 1. The five sequenced peptides derived from homogeneous mature rat  $\beta$ PCCase are underlined; the broken line indicates those amino acid residues in the fourth peptide that were not determined.

peptide of 541 amino acids with a molecular mass of 58,626 Da—in excellent agreement with the estimate of 58,500 Da determined for the cytosolic precursor of  $\beta$ PCCase by NaDodSO<sub>4</sub>/polyacrylamide gel electrophoresis (Fig. 1). Two isolated arginine peptides match the predicted amino acid sequence from His-46 to Arg-63. Furthermore, the COOHterminal sequences from Gly-502 to Arg-514 and from Ile-517 to Leu-541 were found in the other three sequenced  $\beta$ PCCase peptides. Comparison of the rat  $\beta$ PCCase sequence to the cloned COOH-terminal half of human  $\beta$ PCCase (16) reveals a high degree of homology (94%); there are only 16 differences in 251 amino acid residues compared.

We have shown previously that  $\beta$ PCCase is synthesized on cytoplasmic polysomes as a larger precursor with an NH<sub>2</sub>terminal leader sequence that is cleaved off concomitant with the transport of the precursor to the mitochondrial matrix (4). The estimated mass of the mature subunit is 54,000 Da (4). This would predict the mass of the precursor segment to be approximately 4500 daltons—i.e., 40–42 amino acids. If this

prediction is correct, the leader peptide would contain 6 arginines and 1 or 2 glutamates, and would carry a net positive charge. Alternatively, the blocked NH<sub>2</sub> terminus of the mature polypeptide could be a pyroglutamic acid residue derived from the glutamine at position 33. This would predict a leader peptide of 32 amino acids, cleavage between serine and glutamine residues, and the presence in the leader of 5 arginines and no acidic residues. It is of interest, in this regard, that position 34 is occupied by proline, because the propensity for the pyrrolidine ring to form is enhanced when glutamine is followed by proline (17). In fact, this sequence situation has already been reported for another mitochondrial matrix enzyme with a blocked mature NH<sub>2</sub> terminus, ornithine aminotransferase (18). Regardless of overall length, the leader peptide is particularly rich in nonpolar amino acid residues such as alanine, valine, isoleucine, and leucine, and in the polar, uncharged residues serine and threonine.

The preponderance of positively charged arginines and of nonpolar and polar uncharged residues in  $p\beta$ PCCase are





AA, amino acid residue (standard one-letter code); No., number of times the given codon is used in fPCCase; \*, stop codon.

features that are shared with the other dozen known mitochondrial leaders that target cytoplasmic precursors to the mitochondrial matrix, suggesting that a common structural motif is responsible for the targeting role of these sequences. Although there is little conservation of amino acid sequence among the leader segments, recent analyses have suggested the presence of  $\alpha$ -helical domains in these leader peptides (19, 20). von Heijne, in particular, has emphasized the possible importance of the amphipathic character of these  $\alpha$ -helices (20). Profiles of secondary structure propensity and of hydrophobicity (21) of the  $\beta$ PCCase leader sequence (Fig. 4 Upper) strongly predict three to four turns of an  $\alpha$ -helix



FIG. 4. Amino acid sequence profiles of the first 32 amino acid residues of the leader peptide of the  $\beta$ PCCase precursor and a helical-wheel analysis. (Upper) From top to bottom, the amino acid sequence (one-letter code) used to compute the profiles; reverse-turn propensity (T);  $\alpha$ -helix (thin line) and  $\beta$ -sheet (heavy line) propensities (B, A); profile of charged residues (+ or -); and hydrophobicity (HB). The most NH<sub>2</sub>-terminal a-helical region predicted is represented by the horizontal box below the panel. (Lower) Helical-wheel analysis of amino acid residues 1-12. Residues are numbered consecutively from the NH<sub>2</sub> terminus of the helix. The residues are plotted circularly with a successive angular displacement of 100°. Such a plot corresponds to angular periodicity of residues in the ideal  $\alpha$ -helix with 3.7 residues per helical turn (22). Note the perfect distribution of hydrophobic residues (boldface letters) in the helix, indicating that the whole helix with the exception of the two arginines is hydrophobic.

#### Biochemistry: Kraus et al.

between positions <sup>1</sup> and 12 and also give a weaker, more ambiguous, prediction of  $\alpha$ -helix for residues 17 to 28. The strong prediction for an NH<sub>2</sub>-terminal  $\alpha$ -helical segment is supported by use of the helical wheel (Fig. 4 Lower). Although the  $NH_2$ -terminal  $\alpha$ -helix is exceptionally hydrophobic, its overall hydrophobic moment (23) is virtually nil because its two pairs of methionine and isoleucine residues, as well as its two charged arginine side chains, occupy opposite faces of the helix. Unlike the NH2-terminal segment, the second  $\alpha$ -helix (residues 17-28), if it exists, is likely to be amphipathic. Clearly, more experimental and theoretical work is needed to define more precisely the putative role of amphipathicity in mitochondrial transport.

The authors thank the following people: Anne-Marie Lamhonwah and Roy Gravel for sharing with us the unpublished partial cDNA sequences of both subunits of human PCCase; Peter Hodges for many helpful suggestions; Wayne Fenton for his help with computerassisted analysis of nucleotide sequences; Manju Swaroop and Kathy Stone for their expert technical help with DNA and protein sequencing, respectively; and Connie Woznick for secretarial assistance. This work was supported by Grants AM09527, AM12579, and GM31359 from the National Institutes of Health.

- 1. Rosenberg, L. E. (1983) in The Metabolic Basis of Inherited Disease, eds. Stanbury, J. B., Wyngaarden, J. B., Fredrickson, D. S., Goldstein, J. L. & Brown, M. S. (McGraw-Hill, New York), 5th Ed., pp. 474-497.
- 2. Haase, F. C., Beegen, H. & Allen, S. H. G. (1984) Eur. J. Biachem. 140, 147-151.
- 3. Kalousek, F., Darigo, M. D. & Rosenberg, L. E. (1980) J. Biol. Cbem. 245, 60-65.
- 4. Kraus, J. P., Kalousek, F. & Rosenberg, L. E. (1983) J. Biol. Chem. 258, 7245-7248.
- 5. Gravel, R. A., Lam, F. K., Scully, K. J. & Hsia, Y. E. (1977) Am. J. Hum. Genet. 29, 378-388.
- 6. Kraus, J. P., Williamson, C. L., Firgaira, F. A., Yang-Feng, T. L., Munke, M., Francke, U. & Rosenberg, L. E. (1986) Proc. Natl. Acad. Sci. USA 83, 2047-2051.
- 7. Kraus, J. P. & Rosenberg, L. E. (1982) Proc. Natl. Acad. Sci. USA 79, 4015-4019.
- 8. Chirgwin, J. M., Przybyla, A. E., MacDonald, R. J. & Rutter, W. J. (1970) Biochemistry 18, 5294-5299.
- 9. Maniatis, T., Fritsch, E. F. & Sambrook, J. (1982) Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY), pp. 202-203.
- 10. Maxam, A. M. & Gilbert, W. (1980) Methods Enzymol. 65, 499-560.
- 11. Gravel, R. A., Lam, K. F., Mahuran, D. & Kronis, A. (1980) Arch. Biochem. Biophys. 201, 669-673.
- 12. Williams, K. R., LoPresti, M. D., Setoguchi, M. & Konigsberg, W. H. (1980) Proc. Natl. Acad. Sci. USA 77, 4614-4617.
- 13. Williams, K. R., Hemmings, H. C., LoPresti, M. B., Kopigsberg, W. H. & Greengard, P. (1986) J. Biol. Chem. 261,
- 14. Myerowitz, R., Piekarz, R., Neufeld, E. F., Shows, T. B. & Suzuki, K. (1985) Proc. Natl. Acad. Sci. USA 82, 7830-7834.
- 15. Kozak, M. (1986) Cell 44, 283-292.
- Lamhonwah, A.-M., Barankiewicz, T. J., Willard, H. F., Mahuran, D. J., Quan, F. & Gravel, R. A. (1986) Proc. Natl. Acad. Sci. USA 83, 4864-4868.
- 17. <sup>O</sup>'Donnell, I. J. & Inglis, A. S. (1974) Aust. J. Biol. Sci. 27, 369-382.
- 18. Mueckler, M. M. & Pitot, H. C. (1985) J. Biol. Chem. 260, 12993-12997.
- 19. Horwich, A. L., Kalousek, F., Fenton, W. A., Pollock, R. A. & Rosenberg, L. E. (1986) Cell 44, 451-459.
- 20. von Heijne, G. (1986) *EMBO J. 5*, 1335–1342.<br>21. Novotný, J. & Auffray, C. (1984) *Nucleic*
- Novotný, J. & Auffray, C. (1984) Nucleic Acids Res. 12, 243-255.
- 22. Schiffer, M. & Edmundson, A. B. (1968) Biophys. J. 8, 29–39.<br>23. Eisenberg. D., Weiss. R. M. & Terwilliger. T. S. (1982) Nature
- Eisenberg, D., Weiss, R. M. & Terwilliger, T. S. (1982) Nature (London) 299, 371-374.