

cDNA sequence of a new *ras*-related gene (*rap2b*) isolated from human platelets with sequence homology to *rap2*

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The existence of several low molecular weight GTP-binding proteins in platelets has been documented (1, 2). We have shown these proteins can be phosphorylated and translocated by agonists that increase cAMP levels in human platelets (1, 2) and human erythroleukemia cells (3). For this reason, we have initiated studies to characterize the genes which encode these proteins. A human platelet cDNA library was screened for *ras*-related proteins with a monoclonal antibody (M90) specific for amino acids 107–130 of *ras*-encoded p21 proteins (4). A partial cDNA clone was isolated which shared strong sequence homology with the previously described rap2 cDNA isolated from a human Burkitt lymphoma cell line (5). A 750 bp *Aval* fragment from the isolated clone was used to rescreen the library to obtain a longer cDNA insert. Upon rescreening, a longer cDNA insert containing an open reading frame of 552 bp was obtained. This open reading frame shares 84.2% nucleotide and 89.6% amino acid homology with rap2 with the greatest divergence in the C-terminal region. The isolated clone exhibits the characteristic Cys-A-A-X C-terminal region of *ras* proteins, where A is an aliphatic amino acid and X the C-terminal amino acid of the protein, yet

the isolated clone and rap2 differ in that our clone contains the amino acid sequence CVIL whereas rap2 terminates with CNIQ. Recently, we have expressed the cDNA in *E. coli* and show that it encodes a 22 kDa protein which specifically bound GTP (6). In conclusion we report the isolation of a new rap protein sharing homology with rap2 whereas known as rap2b.

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ggaaagagaagtccagccgccaagccccagccttcc
 ccggcgccgcaccccgacggccgcaggcgccggcgagagcgctgacggagcc
 ATGAGAGAGTACAAGTGGTGGCTGGGCTCGGGCGGCTGGGCAAGTC 50
 M R E Y K V V V L G S G G V G K S
 CGCGCTCACCGTGCAGTTCGTGACGGGCTCCTCATCGAGAAGTACGACC
 A L T V Q F V T G S F I E K Y D 100
 CGACCATCGAAGACTTTACCGCAAGGAGATTGAGGTTGACTCGTCGCCG
 P T I E D F Y R K E I E V D S S P 150
 TCGGTGCTGGAGATCTGGATAACGGCGGGCACCGAGCAGTCGGTCCAT
 S V L E I L D T A G T E Q F A S M 200
 GCGGGACCTGTACATCAAGAACGGCAGGGCTTCATCTGGTCTACAGCC
 R D L Y I K N G Q G F I L V Y S 250
 TCGTCAACCAGCAGAGCTCCAGGACATCAAGCCCATGCGGGACAGATC
 L V N Q Q S S Q D I K P M R D Q I 300
 ATCCCGTGAAGCGGTACGAGCGCGTGCCCATGATCCTGGTGGCAACAA
 I R V K R Y E R V P M I L V G N K 350
 GGTGGACCTGGAGGGTGAGCGCGAGGTCTCGTACGGGGAGGGCAAGGCC
 V D L E G E R E V S Y G E G K A 400
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 L A E E W S C P F M E T S A K N K 450
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 A S V D E L R A E I V R Q M N Y A 500
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 A Q S N G D E G C C S A C V I L 550
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