

Complete sequence of mouse S6 ribosomal protein

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Submitted May 14, 1987

Accession no. Y00348

We report the nucleotide (and deduced aminoacid) sequence of mouse S6 ribosomal protein. This sequence was determined on both strands of full length cDNA clones isolated from a library made from T2D4 cells (1) poly(A)+ RNA. The protein was identified by computer analysis of NBRF data bank using CIT12 software (2) due to its homology (60% overall - identical aminoacids are shown below in uppercase letter) with yeast S10 ribosomal protein (3); it fits published partial aminoacid sequences of rat S6, which cover respectively the NH2-terminus (4), and the sites of phosphorylation by cAMP-dependent protein kinases (5) located at the COOH-terminus. Since S6 is a substrate for several kinases (4), this sequence could help to locate phosphorylated aminoacids.

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                                     M K L N I S f P a t
TGACGCCCTCCAGGCGCTCGGCTGTGTCAAGATGAAGCTGAACATCTCCTTCCCCGCCAC 60
  G c Q K l i E v D D E r k l R t F y e K
CGGCTGTCAAGCTCATCGAGGTGGATGACGAGCGCAAGCTCCGCACCTTCTATGAGAA 120
  R m a t E V a a d A l G e E w K G Y U v
GCGCATGGCCAGGAAGTAGCCGCTGATGCTCTTGGTGAAGAGTGGAAAGGGTTATGTGGT 180
  r I S G G N D K Q G F P M K Q G V L t h
CCGGATCAGCGGTGGGAATGACAAAGCAAGGTTTTCCCATGAAGCAAGGTGTTCTGACCCA 240
  g R v r L L L s K g h S C Y R P R R t G
TGCCAGAGTGCGCCTGCTGTTGAGTAAGGGGCATTCTGTTACAGGCCAAGGAGAACTGG 300
  E R K R K S U R G c I U d a n L s U L n
AGAGAGGAAGCGCAAGTCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
  L V I V K K G E k d i p G L T D T T U P
CTTGGTCATTGTAAAGAAAGGAGAGAAAGGATATTCTGACTGACAGACACTACTGTGCC 420
  r R L G P K R A s r I R K l F n L S K E
TCGTCGGTTGGGACCTAAAAGGGCTAGTAGAATCCGCAAGCTTTTTAATCTCTCCAAAGA 480
  D D U R q y U v R k p l n K e G k K p r
AGATGATGTCCGCAGTATGTTGTGTCAGGAAGCCCTTAAACAAGAAAGGTAAGAAAGCCAG 540
  T K A P K I Q R L V T p r v L Q h K R r
GACCAAGCACCCCAAGATTCAGCGACTTGTTACTCCTCGTGTCCGCAACACAAACGCCG 600
  r i A L K k q r t k k n k E e A A E Y A
ACGTATTGCTCTGAAGAACCAACGCACTAAGAAAGCAAGGAGGAGGCTGCAGAAATACGC 660
  k L L A K R m k E a K e k r q E q i a k
TAACTTTTGGCCAAGGAAATGAAGGAAGCCAAAGAAAGCGCCAGGAAACAGATTGCCAA 720
  r R R l S S L r A s t s k s e s s q k
GAGACGTAGGCTGTCTCACTGAGAGCTTCTACTTCTAAGTCTGAGTCCAGTCAAAATG 780
  AGTCTTTAAGAGCAACAATAAATGACCTTGAATCTTT(A)n 821

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