Sequence of the cDNA for one acidic ribosomal protein of Schizosaccharomyces pombe

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We have sequenced a λ gtl1 clone from a Schizosaccharomyces pombe cDNA library (provided by Dr. Paul Nurse, ICRF Laboratories, London). The open reading frames were translated into aminoacid sequences and compared to the NBRF protein data bank: one of them proved to be strikingly similar to acidic ribosomal proteins from several organisms. Additional literature searches revealed that the first 40 amino-terminal residues of this open reading frame are identical to the sequence obtained by Edman degradation from one of the purified cytoplasmic ribosomal proteins of S. pombe, the one indicated by the authors as SP-L40c (1). Moreover, the deduced aminoacid composition matches exactly that determined by the same authors. These data allowed us to identify the sequence reported below as the S. pombe SP-L40c ribosomal protein. It is composed of 110 aminoacids (mw 11 158), has a high alanine content and a net charge of -17. These are hallmarks of the A-type ribosomal protein family, the eukaryotic counterpart of Escherichia coli L7/L12 ribosomal protein (2).

1
GTCAAAATGAAGTACCTTGCAGCTTATTTACTCTTGACCGTTGGTGGAAAGGACTCCCCTTCCGCTTCTGATATC
MetLysTyrLeuAlaAlaTyrLeuLeuLeuThrValGlyGlyLysAspSerProSerAlaSerAspIle

GAGTCTGTTTTGTCTACTGTCGGTATTGAAGCTGAATCTGAGCGCATTGAAACTTTGATCAACGAGCTTAACGGT GluSerValLeuSerThrValGlyIleGluAlaGluSerGluArgIleGluThrLeuIleAsnGluLeuAsnGly

 ${\tt GAATCTGATGAAGACATGGGTTTCGGTCTTTTCGACTAAACCAAATGATCCCTTGTTTTCATTACGCTTTCATAACGUSerAspGluAspMetGlyPheGlyLeuPheAsp***$

376 AAATAAATCGCCGTGTTGGTTTATTTTACCA₁₅

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