

Nucleotide sequence of V1, a ribosomal protein gene from *Dictyostelium discoideum*

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 Submitted August 28, 1989 EMBL accession no. X15710

The sequence of the cDNA corresponding to the vegetative specific gene V1 (Dev. Biol. 119, 433-441) is presented. A single intron of at least 700 bp exists between residues 32 and 33, or within the sixth codon. The start and stop codons of the open reading frame are underlined. Data base searches suggest V1 encodes a protein homologous to the ribosomal protein L2 of *E. coli* (28.1% identity), common tobacco chloroplast (27%), and liverwort (27.1%). These percent identities are consonant with those found between two other ribosomal proteins from *Dictyostelium* and their *E. coli* counterpart (L. Steel, personal communication; CKS, unpublished). The predicted amino acid sequence is shown and compared to that of the *E. coli* protein. Bold letters show identical amino acids, and conservative amino acid changes are indicated by underlines. (accession No. x15710; supported by NSF grant DCB 8809026).

TATCAAAAACGCCAAATGGGTAGAATAATCAGAGCTCAAAGAAAAAGGTAA 50
 AGCCGGTTTCAGTTTCGGTGCACACACTCACCCACCGTAAGGTACCCCAC 100
 GTTCCGTGCTTAGATTATGCCAACGTCAGGTAAAGGTAAAGGTGTT 150
 GTCAGGAGATCATCCACGATCAGTAGAGGTGCTCATTAGCCCGTGT 200
 TGTTTCAAAGGCTTAACCCAATCAAATTAGACAAACAATTATCATCG 250
 CCCCAGAAGGTATGCACACTGGTCAATTGTTTGCTGGTAAAAAGCC 300
 ACCCTCACCATTCGTCACATCCTCCAAATTGGTAAACTCCCAAAGGTAC 350
 CATCTTGCACAGTTGAAGAAAAACTGGTATTGTTGCTGCTGTC 400
 GTTGTTCAGGTAACTATGCTACCACATCGTCTCACACAAACCCAGATGAAGGT 450
 GTTACCCGTATCAAATTACCATCAGGTTAAAGAAGAACGGTTCTCATT 500
 AGCTCGTGTATGATCGGTATTGTTGCGGGTGGTGGTGTATCGATAAAC 550
 CAATGCTCAAAGCTGGTCGTCTTCCACAAATACAGAGTTAAGAAGAAT 600
 AACTGGCCAAGGTTAGGGTGTGCTATGAATCAGTAGAACATCACAC 650
 GGTGGTGGTAAATCATCAACATGGTGTGCTACCAACTACAACCCAGAGAGA 700
 CGATCCAGCTGGTAAGAAAGTTGGTTAAATGGCTGCCGTCGGTACTGGTC 750
 GTTAGAGGAACTAAAACATTAGAATAAACTGCATTCAAAACCTTT 800
 AT

D_d MGR II RAQRKKGKAGSYFGAHTGGR
E_c AVVKCKPTSPQRHVVNPELHKGPFA PL L EKNSKSGRRNNNGRIT R H IGGG
 KGT PRERALDYAEROGYYKGVYKEI I HDPGRGRAPLARVYFKGLQFKLDKOLEI
 H- KQAYRI VDFKRNKDGPA VVERLEYDPR RS ANIALVLYK- ---- DGERRYIL
 APEGMHTGOFYFAGKKAILTRH I LP I GK I PEGT I JC NVEE KLGDCGAVARC
 APKGLKAGDQIQ SGVD AAICPGNTLPMRNI PVGSTVHNVEMKPGKGGQLARS
 SCNYATIVSHNPDEGVTLYQIT I R F KEERSLARAMIGI VAGGGRJDKPMLKAG
 AGTYVQIWARD-GAYVTLRLRSGEMRKVEAD-CRATLGEVNA EHMLRVLGKAG
 RAPHKYRVKJNNWPKVRGYAMNPVEHHTV VV I INMLVMPL QPRET I QLVRK
 AA - RWRGVR - PTVRGATMNPVDIHPGG GHEGRIN PGKHPVTPWGQTKG

LV
 KKTRSNKRTDKFIVRRSK