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Sequence and genomic locus of a Leishmania protein homologous to rat ribosomal protein S8

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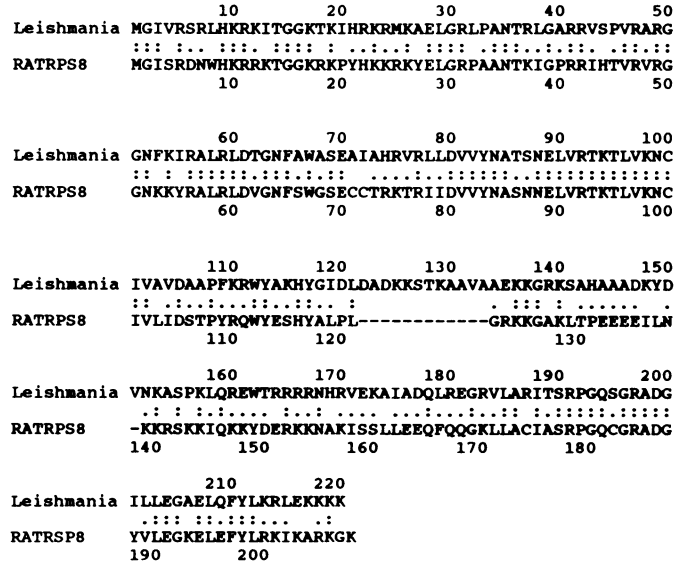
A genomic clone, E1, containing the locus of a Leishmania protein homologous to rat ribosomal protein S8 was identified in a EMBL3 phage library, ELT, prepared by cloning Leishmania major LT252 (LT252) DNA partially digested with Sau3A in the BamHI site. ELT was screened with a cDNA (pLT6) from LT252 promastigotes that was identified while screening a pUC8 library with a monoclonal antibody (F2B4) in search of a stage specific membrane protein. Apparently both proteins share an epitope recognized by F2B4.

The sequence of pLT6 cDNA was published (with minor errors) (1), it contains part of the spliced leader (SL), 30 nt of genomic 5′ untranslated region (5′UTR), and 474 nt coding for 158 aa. The coding sequence is interrupted by an internal HindIII site that also corresponds to the linker used for cloning. The gene is conserved in a chromosome of about 850 kbp in all species of Leishmania tested: arabica, brasiliens, major, mexicana, panamiensis and tropica (2). Restriction analysis and Southern blots showed an identical pattern in those and two other Leishmania species tested: donovani and enriettii.

We have sequenced 4353 bp of the genomic locus contained in two adjacent SalI and one overlapping HindIII fragments of E1. The gene is present in two copies as a tandem repeat (at least 715 nt each) and the ORFs are separated by 900 nt. pLT6 cDNA was transcribed from the second (downstream) gene because the 5′ nucleotide of the UTR is adjacent to the AG splicing acceptor site for the SL, and there is no AG at that position in the upstream gene.

We scanned the GenBank (3) using the FASTA program (4) and found one sequence (5), GenBank accession number X06423, which showed 49.5% identity in 212 aa overlap. The Leishmania protein contains 220 aa while the rat protein has 208 aa. The protein is highly conserved between the two species that are very distant in the evolution tree.



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