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SRPDB (Signal Recognition Particle Database)

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ABSTRACT

The signal recognition particle database (SRPDB) is maintained at the University of Texas Health Science Center at Tyler, Texas, and organizes SRP-related information about SRP RNA, SRP proteins and the SRP receptor. SRPDB is accessible on the WWW at the URL http://psyche.uthct.edu/dbs/SRPDB/SRPDB.html . A mirror site of the SRPDB is located in Europe at the University of Göteborg, Sweden (http://www.medkem.gu.se/dbs/SRPDB/SRPDB.html). This release of SRPDB adds 10 new SRP RNA sequences (a total of 117 SRP RNAs), four protein SRP19 sequences (a total of 15), seven new SRP54 (ffh) sequences (a total of 52), and eight sequences of the SRP receptor alpha subunit (FtsY) (total of 36). Sequences are arranged in alphabetical and phylogenetic order and alignments are provided which highlight base paired and conserved regions. SPRDB also provides motifs to find new sequences, a brief introduction to SRP function in protein secretion, numerous SRP RNA secondary structure diagrams, 3-D SRP RNA models, and recently obtained crystal structure PDB coordinates of the human SRP54m domain.

SRPDB TABLE OF CONTENTS

- SRP RNA sequences listed in alphabetical or phylogenetic order
- SRP RNA alignment in html, text (94 columns), text (wide), postscript, pdf, EMBL, GenBank, msf or nbrf format
- Representative SRP RNA secondary structures in postscript or gif format
- SRP RNA 3-D models in pdb format
- SRP RNA search motifs: universal or bacterial
- SRP proteins: SRP9, SRP14, SRP19, SRP21, SRP54, SRP68, SRP72
- SRP receptor proteins: SR-alpha (FtsY)
- About SRPDB
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SRP FUNCTION

The signal recognition particle (SRP) associates with ribosomes which translate mRNA of secretory proteins. As implied, SRP recognizes the signal of the newly-synthesized protein typically close to the N-terminus of the nascent protein. Ribosome- and signal-bound SRP then interacts with the SRP-receptor, a component of the ER membrane. Finally, SRP is released from the ribosome and translation continues with the protein transversing the membrane. The molecular details of this important biological process are the subject of ongoing research (for reviews see 1–3).

SRP COMPONENTS

SRP consists of both RNA and protein. In the secondary structure of SRP RNA, supported by comparative sequence analysis (4), helices are numbered according to the nomenclature of Larsen and Zwieb (5) and define the two domains of the SRP: a small domain (helices 2, 3 and 4, and a portion of helix 5), and a larger domain (a portion of helix 5, and helices 6, 7 and 8). Helix 1 is present only in archaeal SRP and certain bacteria and extends the ends of the RNA (5). The six proteins in mammalian SRP (6) are named according to their approximate molecular weight in kDa (see Table of Contents, above). Protein SRP54 or its bacterial homologue (ffh) is present in every SRP (7) and binds the signal peptide of the nascent secretory protein (8). SRPDB provides detailed information about the various components, including the alpha subunit of the SRP receptor (called FtsY in the bacteria).

SRP RNAs

A representative subset of 45 SRP RNA sequences was used as input for searching the primary databases with BLASTN (9). Also, the PatScan algorithm (http://www-unix.mcs.anl.gov/compbio/PatScan/) was used with an improved helix 8 motif. By comparison with the established aligned sequences in SRPDB, candidates were either rejected or identified as positives. Ten new sequences (all of bacterial origin) were identified from the following species: *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Helicobacter pylori* (strains J99 and 26695), *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Synechocystis sp*., *Thermotoga maritima* and *Yersinia pestis*. The alignment was updated manually with the SeqPup editor (see http://ftp.sunet.se/pub/molbio/seqapp/seqpup/) and is available in popular formats (see Table of Contents, above). SRP RNA secondary structure features determined previously (5,7) were confirmed. As

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sequences were derived from genome projects, the RNA termini are ambiguous. Available at SRPDB are tentative 3-D SRP RNA models in PDB format generated with ERNA-3D (10) for the human SRP RNA and the SRP RNAs of *Methanococcus jannaschii*, *Bacillus subtilits*, *Escherichia coli* and *Mycoplasma mycoides*. Additional structural information about portions of SRP RNA is available via the links section (see Table of Contents, above).

SRP proteins

Sequences of known SRP proteins were used as queries with BLAST (9) to identify new SRP proteins in the primary databases. No new SRP9 or SRP14 proteins were found. The *Schizosaccharomyces pombe* protein (accession no. 3183357, annotated as a hypothetical protein) may be a candidate for SRP9. The total count for SRP9 and SRP14 is five and eight, respectively. There are four new SRP19 sequences from *Aeropyrum pernix*, *Caenorhabditis elegans*, *Pyrococcus abysii* and *S.pombe* for a total of 15 SRP19 entries. No homologues to yeast SRP21 (accession no. P32342) were found. Seven more SRP54 sequences (total of 52) were from *A.pernix*, *C.pneumoniae*, *Drosophila melanogaster*, *Pisum sativum* (chloroplast), *P.abyssi*, *Rickettsia prowazekii*, and *T.maritima*. No new SRP68 or SRP72 sequences were identified. The protein alignments can be viewed directly or downloaded as concatenated entries in the most popular formats. SRPDB also distributes the recently obtained crystal structure of human SRP54m (SRP54m structure, PDB accession no. 1QB2) as well as additional structural information about other SRP proteins through the links section.

SRP receptor proteins

Homologues to SRalpha (FtsY) were identified with TFASTA (11) by a search of individual bacterial genomes or by TBLASTN and BLASTP at NCBI (12). Seven new bacterial sequences were from *A.pernix*, *C.pneumoniae*, *H.pylori* J99, *N.meningitidis*, *P.abyssi*, *Streptomyces coelicolor* and *T.maritima*. Included is the recently discovered FtsY homologue of *Arabidopsis thaliana* chloroplast for a total of 36 SRalpha sequences.

The G domains of the protein encoded by the *B.subtilis* flhf gene (13) are closely related to Ffh and FtsY, and details of this relationship are provided. Flhf homologues were identified in *Aquifex aeolicus*, *Borrelia burgdorferi*, *H.pylori*, *Pseudomonas putida* and *Treponema pallidum*. However, it needs to be investigated whether the flhf protein is related functionally to SRP.

ACCESS

The data are accessible freely for research purpose at the URL http://psyche.uthct.edu/dbs/SRPDB/SRPDB.html and the SRPDB mirror site (http://www.medkem.gu.se/dbs/SRPDB/SRPDB.html). Hardcopies of the alignments are available by Email request to the first author at zwieb@uthct.edu or through written contact. The second author can be contacted by Email at tore.samuelsson@medkem.gu.se . Please cite this article in research projects assisted by the use of SRPDB.

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