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SRPDB: Signal Recognition Particle Database

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ABSTRACT

The Signal Recognition Particle Database (SRPDB) at http://psyche.uthct.edu/dbs/SRPDB/SRPDB.html and http://bio.lundberg.gu.se/dbs/SRPDB/SRPDB.html assists in the better understanding of the structure and function of the signal recognition particle (SRP), a ribonucleoprotein complex that recognizes signal sequences as they emerge from the ribosome. SRPDB provides alphabetically and phylogenetically ordered lists of SRP RNA and SRP protein sequences. The SRP RNA alignment emphasizes base pairs supported by comparative sequence analysis to derive accurate SRP RNA secondary structures for each species. This release includes a total of 181 SRP RNA sequences, 7 protein SRP9, 11 SRP14, 31 SRP19, 113 SRP54 (Ffh), 9 SRP68 and 12 SRP72 sequences. There are 44 new sequences of the SRP receptor alpha subunit and its FtsY homolog (a total of 99 entries). Additional data are provided for polypeptides with established or potential roles in SRP-mediated protein targeting, such as the beta subunit of SRP receptor, Flhf, Hbsu and cpSRP43. Also available are motifs for the identification of new SRP RNA sequences, 2D representations, three-dimensional models in PDB format, and links to the high-resolution structures of several SRP components. New to this version of SRPDB is the introduction of a relational database system and a SRP RNA prediction server (SRP-Scan) which allows the identification of SRP RNAs within genome sequences and also generates secondary structure diagrams.

SRPDB TABLE OF CONTENTS

About SRP. About SRPRDB. What's New?

SRP RNA — In alphabetical or phylogenetic order, alignment, 2D, 3D, search motif, SRP-Scan.

SRP protein — SRP9, SRP14, SRP19, Yeast SRP21, SRP54, SRP68, SRP72.

More protein — SRP receptor alpha subunit (FtsY), SRP receptor beta subunit, Flhf, Hbsu, CaM kinase II, cpSRP43.

Links. Disclaimer.

SRP FUNCTION

Signal recognition particle (SRP) is a ribonucleoprotein complex which interacts with signal sequences as they appear on the surface of translating ribosomes. Subsequent to signal peptide recognition, SRP binds to membrane receptors and assures the proper delivery of secretory proteins. Significant advances have been made recently in understanding this essential biological process on the molecular level. (For reviews, see refs 1–3.)

SRP COMPONENTS

SRP is composed of an RNA molecule and at least one polypeptide, named SRP54 or Ffh. In most bacteria, Ffh binds to a small 4.5S SRP RNA. The SRPs of eukaryotes contain not only SRP54 but also the SRP9/14 heterodimer and proteins SRP19, SRP68 and SRP72. However, different compositions have been observed in some of the yeast complexes. Although the secondary structures of archaeal and eukaryotic SRP RNAs were found to be very similar, only the homologues SRP19 and SRP54 could be identified in the genomes of the archaea (3). Proteins that were shown or are suspected to function in SRP-mediated targeting include the alpha (FtsY) and beta subunits of the SRP receptor, as well as Flhf, Hbsu and cpSRP43.

SRPDB DESCRIPTION

SRPDB provides aligned, annotated and phylogenetically ordered sequences of the SRP components, organized for SRP RNA, SRP proteins and additional proteins that play a role in SRP-mediated protein transport or are related to SRP components.

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SRP RNAs

Forty-four new SRP RNAs for a total of 181 sequences were identified using SRP-Scan as described recently by Regalia *et al.* (4). In this method, a heuristic search for the highly conserved helix 8 is carried out first by using the motif finder RNABOB (available at http://www.genetics.wustl.edu/eddy/software/#rnabob). Subsequently, the results of the scan are analyzed using covariance models (5) that were based on the previous sequences and alignments (6). New to this release is a web interface to this method at http://bio.lundberg.gu.se/srpscan where a nucleotide sequence can be submitted to predict SRP RNA genes and generate a matching SRP RNA secondary structure. The sequences and their corresponding annotations are maintained in a relational database with an improved user interface. Interestingly, a 266 nt sequence of *Thermotoga maritima* was discovered which, unlike all other non-grampositive eubacteria, contained an Alu-like domain. An UGAC tetranucleotide loop in helix 8 (usually a conserved GNRA-loop) was found in the SRP RNAs of *Lactococcus* and *Staphylococcus*. Analysis of the human genome revealed only two likely genes on chromosome 14. Several new SRP RNAs were identified by screening of the recently sequenced yeast genomes, including those available at http://www.genome.wustl.edu/blast/yeast_client.cgi. The yeast sequences reveal a highly conserved Alu-like motif near the 5′-terminus. With the addition of a significant number of yeast SRP RNA sequences, it should be finally possible to generate phylogenetically supported secondary structures of these larger yeast SRP RNAs.

The sequences were aligned using the previously described rules (7) and the multiple sequence alignment editors Genedoc (available at http://www.psc.edu/biomed/genedoc/) or BioEdit (http://www.mbio.ncsu.edu/RNaseP/info/programs/BIOEDIT/bioedit.html). Secondary structure information is included for each of the aligned SRP RNA sequences. In addition, secondary structure predicted by SRP-Scan is available for all RNAs. Base pairing consistencies, phylogenetic support and possible helix extensions were checked using RNAdbtools (8) available at http://www.bioinf.au.dk/rnadbtool. The previously determined secondary structure features were confirmed. Three-dimensional SRP RNA models in PDB format were generated with ERNA-3D (9) and refined by energy minimization with VCMD (10). A 3D model of human SRP, excluding proteins SRP68 and SRP72, has been made available which incorporates the recent advances. Links were provided to the coordinates of structures solved by X-ray diffraction or NMR.

SRP proteins

Known SRP protein sequences were used as queries for BLASTP or PSI-BLAST (11). Multiple alignments of the top-scoring entries from PSI-BLAST shown at http://bio.lundberg.gu.se/srpdb were generated with CLUSTALW (12). The number of homologs of SRP9, SRP14, SRP19, SRP68 and SRP72 increased for a total of 7, 11, 31, 9 and 12 sequences, respectively. In September, 2002, SRPDB contained 99 SRalpha/FtsY proteins (44 new sequences) and 21 (8 new) Flhf protein sequences.

ACCESS

The data are freely accessible for research purposes at the URL http://psyche.uthct.edu/dbs/SRPDB/SRPDB.html and the European mirror site at http://bio.lundberg.gu.se/dbs/SRPDB/SRPDB.html. Suggestions should be directed to C.Z. at zwieb@uthct.edu. The first and last authors can be reached at the email addresses magnus.alm@medkem.gu.se and tore.samuelsson@medkem.gu.se, respectively. J.G. and B.K. can be reached at gorodkin@bioinf.kvl.dk and bk@bioinf.au.dk, respectively. This article should be cited in research projects assisted by the use of the SRPDB.

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