miRecords: a new integrated resource for microRNA target interactions

The miRecords Database is made up of Validated Targets and Predicted Targets.

Validated Targets

The validated targets component of this resource hosts a large, high-quality manually curated database of experimentally validated miRNA–target interactions with systematic documentation of experimental support for each interaction.

The current release of this database includes 1135 records of validated miRNA–target interactions between 301 miRNAs and 902 target genes in seven animal species.

The database makes a clear distinction between endogenous miRNA experiments and exogenous miRNA experiments. Since many miRNA-target interactions were performed by exogenous experiments and concerns have been raised over how many of these interactions actually take place in endogenous, physiological conditions, a brief summary about the rationale of exogenous experiments is provided, as well as an explanation of the results.

Experimental evidence about miRNA-target interactions is also classified into one of three levels: target gene level (entire gene, mRNA or protein), target region level (shorter than full length transcript) and target site level (length comparable to that of miRNA).

Predicted Targets

While much progress has been made in computational target prediction of miRNAs in recent years and miRNA target prediction programs have proliferated, the prediction of miRNA targets remains a challenging task. These programs make predictions based on principles of known miRNA-target interactions:

1. Near-perfect complementarity in the 6-8 nt region close to the 5' end of the miRNA (seed- region) with the 3' UTR of the target sequence.
2. Evolutionary conservation of the target sequences between species.
4. Cooperativity between multiple sites in close proximity.
5. Existence of a central non-matched region (forming a loop or bulge).
6. Favorable energetic hybridizations.

http://mirecords.biolead.org/

The miRecords Database is made up of two components: Validated Targets and Predicted Targets.
Recent comparative studies conducted of early target prediction methods has shown that none is significantly superior than another and it has become common to look at predictions from multiple target prediction programs and concentrate where the results intersect.

The Predicted Targets component of miRecords is in integration of predicted miRNA targets produced by 11 established miRNA target prediction programs making it the most complete integration of predicted miRNA targets to date.

Established miRNA prediction programs:

DIANA-microT
MicroInspector
miRanda
MirTarget2
miTarget
NBmiRTar
PicTar
PITA
RNA22
RNAhybrid
TargetScanS

For more information see the publication below:


http://nar.oxfordjournals.org/content/37/suppl_1/D105.full