DIANA-TarBase v7: indexing hundreds of thousands experimentally supported miRNA:mRNA interactions

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microRNAs are short non-coding RNAs which act as potent post-transcriptional regulators. Accurate identification and cataloging of miRNA targets is crucial to understanding their function. Currently, hundreds of thousands of miRNA:gene interactions have been experimentally identified. Numerous wet lab methodologies have been developed, enabling the validation of predicted miRNA interactions or the high-throughput screening and identification of novel miRNA targets. However, this wealth of information is fragmented and hidden in thousands of manuscripts and raw next generation sequencing data sets.

DIANA-TarBase v7.0[1] aims to provide for the first time hundreds of thousands of high-quality manually curated experimentally validated miRNA:gene interactions. A text-mining pipeline has been implemented for the identification of all the advanced in experimental methodologies articles which have been subjected to manual curation.

DIANA-TarBase v7.0 has been significantly extended with richer meta-data and detailed information for each interaction, while the interface now supports advanced real-time queering and result filtering. The database enables users to easily identify positive or negative experimental results, the utilised experimental methodology, experimental conditions including cell/tissue type and treatment. The new interface provides also advanced information ranging from the binding site location, as identified experimentally as well as in silico, to the primer sequences used for cloning experiments.

DIANA-TarBase v7.0 is the first relevant database which breaks the barrier of hundreds of thousands entries by indexing more than half a million interactions in 24 species, 9–250 times more than any other manually curated database. This wealth of information can be utilised for exploratory studies and can significantly boost the understanding of miRNA:mRNA collaboration.

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References

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1 www.microrna.gr/tarbase