

A comprehensive database of mirtrons knowledge

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MicroRNAs (miRNAs) are one class of small non-coding RNAs (ncRNAs) that occurs in several eukaryotic genomes. They are responsible for post-transcriptional control of mRNA levels in cells. Recently, mirtrons were discovered as an alternative miRNA class, whose biogenesis is based on the splicing process as the first cleavage step in miRNA maturation. Up to now, most public data in mirtrons are restricted to few model organisms: *Arabidopsis thaliana*, *Oryza sativa*, *Homo sapiens*, *Mus musculus*, *Drosophila melanogaster*, and *Caenorhabditis elegans*. These data are available in many different sources and structures. To our knowledge, there is no central repository or integrated web resource for mirtron research. In order to fill this gap, we describe mirtronDB, a public repository for mirtrons. This database has as major contributions: (i) integration of all public data available in literature under a unique and structured database and system, and (ii) become the first friendly central repository about mitrons. Among the functionalities, we highlight: (a) general search (e.g. names, identification); (b) similarity search; (c) graphic visualization; (d) conservational analysis among organisms; and (e) comparative analysis between mirtrons and canonical miRNA. This web application will be built using PHP language, with Chado scheme, in a MySQL database. For that, we: (i) analyzed and extracted all public data in the literature about mirtrons; (ii) organized and structured all data for these organisms; and (iii) we will built a web application. We think that this repository will allow and facilitate the scientific communities apply methods and computational techniques in bioinformatics in this data.

Support: CNPq (#454505/2014-0).