



Prediction and extraction of microRNA2target interactions associated with leukemia

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ABSTRACT. MicroRNAs are small, non-coding RNAs that regulate gene expression by suppressing mRNA translation or inducing mRNA degradation, and have been implicated in a growing number of diseases. To understand microRNAs' function, it is vital to identify microRNA2target interactions. This work explores the prediction and extraction of leukemia-associated microRNA2target interactions, based on text mining. We extracted 371 interactions of microRNA2targets that, from prior knowledge, could be related to leukemia. By measuring similarities between unknown and known targets, the study could also predict some interactions of microRNA2targets. To analyze the prioritized data, the proposed approach identified some microRNA2target interactions, 17 of which were validated by other evidences. The remaining unconfirmed interactions provide a resource for leukemia researchers. Experimental results show the work has promise for predicting and extracting interactions of microRNA2targets

related to leukemia.

Key words: MicroRNA; Target genes; Interactions of microRNA2target; Leukemia