COMPUTATIONAL IDENTIFICATION OF BEST RNAi TARGETS BASED ON FREE ENERGY FEATURES

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RNA interference is a recent technology that promotes potent and specific gene silencing through dsRNAs; (Fire, 1998). In mammals, dsRNAs trigger antiviral responses and cell death ensues. In these models, small interfering RNAs (siRNAs) are the molecules of choice for RNAi studies once they are too small to trigger such responses. It is interesting to note that siRNAs directed to different regions of a specific transcript display widely different silencing efficacies (Holen, 2002). Here we present **Strand Analysis** (SA) a free on line software for identification of best RNAi targets based on thermodynamical features (Khvorova, 2003,). SA computes dG in such a way that, the greater this value, more preferentially will the antisense strand be kept in slicer, thus resulting in better efficiency. The software was implemented in a Linux platform, is web based and written in Perl language which is widely used in bioinformatics. With a small source code – 7,9 Kb – it has a good performance taking only 2.3 seconds to run a sequence of 20,000 bases and can be used along with other bioinformatics tools developed in our laboratory (http://lgm.fcm.unicamp.br:9001). It is important to note that SA must be used in combination with other computational tools for siRNA design (Tuschl's rules), and not alone.

Key words: RNAi, siRNA, software, design