

RNA22 v2 results

Results have been computed and are shown below. If there are no results shown, it means your chosen parameters yielded no results. Note: The p-value represents the likelihood that the target site loci is random. That is, a lower p-value represents a greater chance that the loci contains a valid MRE.

miR Name	transcript name	leftmost position of predicted target site	folding energy (in-Kcal/mol)	heteroduplex	p value
hsa_miR_154_5p MIMAT0000452	hsa_SMURF1	985	-18.40	CAA TGG TGA --AA GGA TAA CCT C GCT TCC GTT GTG CCT ATT GGA T	9.15E-2

miR Name	transcript name	leftmost position of predicted target site	folding energy (in-Kcal/mol)	heteroduplex	p value
rno_miR_154_5p MIMAT0000856	rno_SMURF1	72	-18.30	CGC ATG GCG G--G CCG A--G GCC TG GC-- TTC CGT TGT GCC TAT TGGAT	1.69E-1
rno_miR_154_5p MIMAT0000856	rno_SMURF1	327	-16.70	CGA GGG T--T TGC G---- TGG CCT C GCT TCC GTT GTG CCT ATT GGA T	3.45E-2
rno_miR_154_5p MIMAT0000856	rno_SMURF1	1715	-17.10	AAA AGG CG-- CAA GGA --AG CCT G GCT TCC GTT GTG CCT ATT GGA T	3.06E-1