Query executed in 0.032 s

```
mcff -s ggacacccagcuaggaccauuacugcc -sd ggcagugucuuagcugguugu -t 2 -v
ggacacccagcuaggaccauuacugcc  ggcagugucuuagcugguugu
..((((((((((((((....((((((  )))))))))))))))))))) -54.002  7-mer-A1
(..((((((((((((((....((((((  ))))))))))))))))))))  +1.732  7-mer-A1
..((((((((((((((....(((((((  )))))))))))))))))))))  +1.765  8-mer
.(.((((((((((((((....((((((  )))))))))))))))))))).  +1.813  7-mer-A1
```

Duplex structure	Target Guide	Seed type	Efficiency	Source
5' ...CCAGCUAGGACCAUUACUGCCAG... ||||||| |||||| 3' UGUUGGUCGAUUCUG----UGACGGU	Sirt1 miR-34a-5p	7-mer-A1	< 0.1	Targetscan 7.2
5'-ggacacccagcuaggaccauuacugccA-3' |||:|||||||!||| |||||| 3'---uguugGUCGAUucuG----UGACGGU-5'	Sirt1 miR-34a-5p	7-mer-A1	0.52	RISCulate
5'-ggacacccagcuaggaccauuacugccA-3' |||:|||||||!|| !|||||| 3'---uguugGUCGAUucu----GUGACGGU-5'	Sirt1 miR-34a-5p	8-mer	0.83	RISCulate

| Watson-Crick base pair
! GU base pair
: non-canonical base pair (mismatch)