

CGCACGGCTCTTAACCGTGTGGTCGTGGGTTCGAGCCCCACGG

CAATCGGCT--TAACCGATTGGTCGCAGGTTCGAATCCTGCCT

CAGAGGACTGCAAATCCTTTA-TCCCCAGTTCAAATCTGGGTG

Multiple sequence alignment

((( ((( (.....) )))) )) .. ((( ((( (.....) )))) )) .. -20.2

((( ((( (.....) )))) )) .. ((( ((( (.....) )))) )) .. -16.3

. ((( ((( (.....) )))) )) .. ((( ((( (.....) )))) )) .. -11.7

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((( ((( ((( ((( ((( (.....) )))) )) )) )) )) .. ((( ((( (.....) )))) )) .. -18.9

RNAfold: single sequence MFEs

RNAalifold: Consensus MFE

$$\text{SCI} = \frac{\text{Consensus MFE}}{\text{Mean single MFEs}}$$