

CGCACGGCTCTTAACCGTGTGGTCGTGGGTTTCGAGCCCCACGG

CAATCGGCT--TAACCGATTGGTCGCAGGTTCTGAATCCTGCCT

CAGAGGACTGCAAATCCTTTA-TCCCCAGTTCAAATCTGGGTG

Multiple sequence alignment

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

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

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

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

RNAfold: single sequence MFEs

RNAalifold: Consensus MFE

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