

CGCACGGCTCTTAACCGTGTGGTCGTGGGTTTCGAGCCCCACGG

CAATCGGCT--TAACCGATTGGTCGCAGGTTCTGAATCCTGCCT

CAGAGGACTGCAAATCCTTTA-TCCCCAGTTCAAATCTGGGTG

Multiple sequence alignment

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

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

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

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

RNAfold: single sequence MFES

RNAalifold: Consensus MFE

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