

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

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