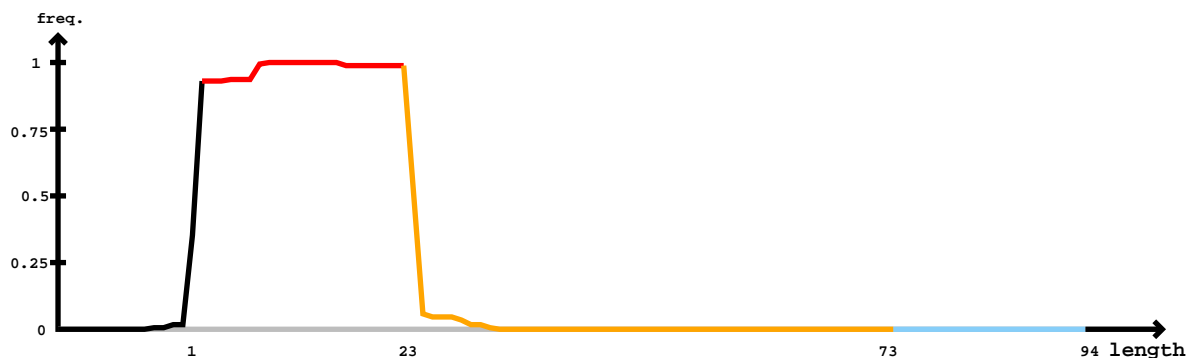


| | | |
|------------------------|---|--|
| Provisional ID | : | NW_025322676.1_Acropora_millepora_isolate_JS-1_unplaced_genomic_scaffold_Amil_v2.1_Sc0000184_whole_genome_shotgun_sequen |
| Score total | : | 1.5 |
| Score for star read(s) | : | -1.3 |
| Score for read counts | : | 0 |
| Score for mfe | : | -0.1 |
| Score for randfold | : | 0 |
| Score for cons. seed | : | 3 |
| Total read count | : | 164 |
| Mature read count | : | 164 |
| Loop read count | : | 0 |
| Star read count | : | 0 |

The secondary structure diagram illustrates the predicted folding of the RNA sequence. It features a mix of Watson-Crick base pairs (A-C, U-G) and non-canonical pairs (G-A). The structure includes multiple stem-loops and internal loops, particularly visible in the middle and right portions of the sequence.



Mature

[illegible]