



Figure 3-figure supplement 2. Workflow for encoding of a ribozyme sequence into numerical features with a linear regression algorithm. A) The RNA sequence is computationally-folded to obtain a predicted secondary structure. B) The predicted structure is converted into a one-dimensional set of features, where each feature is a binary recording of whether a specific base exists in a specific position close to the stem. As an example, the first nucleotide of the loop is a U, so the feature Loop1 +1 A is given a value of 0, while Loop1 +1 U is given a value of 1. The encoding of a nucleotide as a set of binary features is repeated for the two bases closest to the stem on the 5' and 3' part of the loop.