



**Figure 5-figure supplement 1. Workflow for predicting ribozyme activity.** Workflow detailing how the CNN model predicts the individual basal gene-regulatory activity level of each ribozyme in a set of ribozyme sequences. The library of training sequences is divided into groups based on the structure of the computationally-folded ribozymes. The set of ribozymes to be predicted is also divided into groups based on the structure of computationally-folded ribozymes. Only the ribozymes in the training with similar enough structures to the test set are used to predict ribozymes in the test set. Initially, only sequences in the training set that have an identical structure to those in the test set are considered, but the training set is incrementally increased by considering ribozymes with increasing differences in structure until at least 1,000 ribozymes are in the training set.