

Run Infernal and TransTermHP to identify location of aptamer- and expression platform-like motifs in RefSeq data



Co-localize aptamers and expression platforms to generate pool of candidate riboswitches



Coarse-grained filtering of candidate pool based on sequence and structural characteristics



Fold candidates into on- and off-conformations using RNAfold with literature-derived constraint mask



Fine-grained filtering using Foldalign against xpt as well as pairwise global sequence alignment to find xpt-related dissimilar hits