**Abstract:**

Phylogenetic databases of functional, non-coding RNAs (ncRNAs) such as Rfam sort sequences into families according to homology to single structural profiles. Supposing that some of the myriad alternative foldings of these families will be present in vivo and seeing no prior reason to rule out the biological importance of RNAs in alternative conformations, this paper attempts a systematic investigation of the likelihood that evolution acts to conserve structural alternates in 1493 RNA such families from Rfam. By a combination of thermodynamic and phylogenetic methods using novel and published algorithms, this paper supposes that