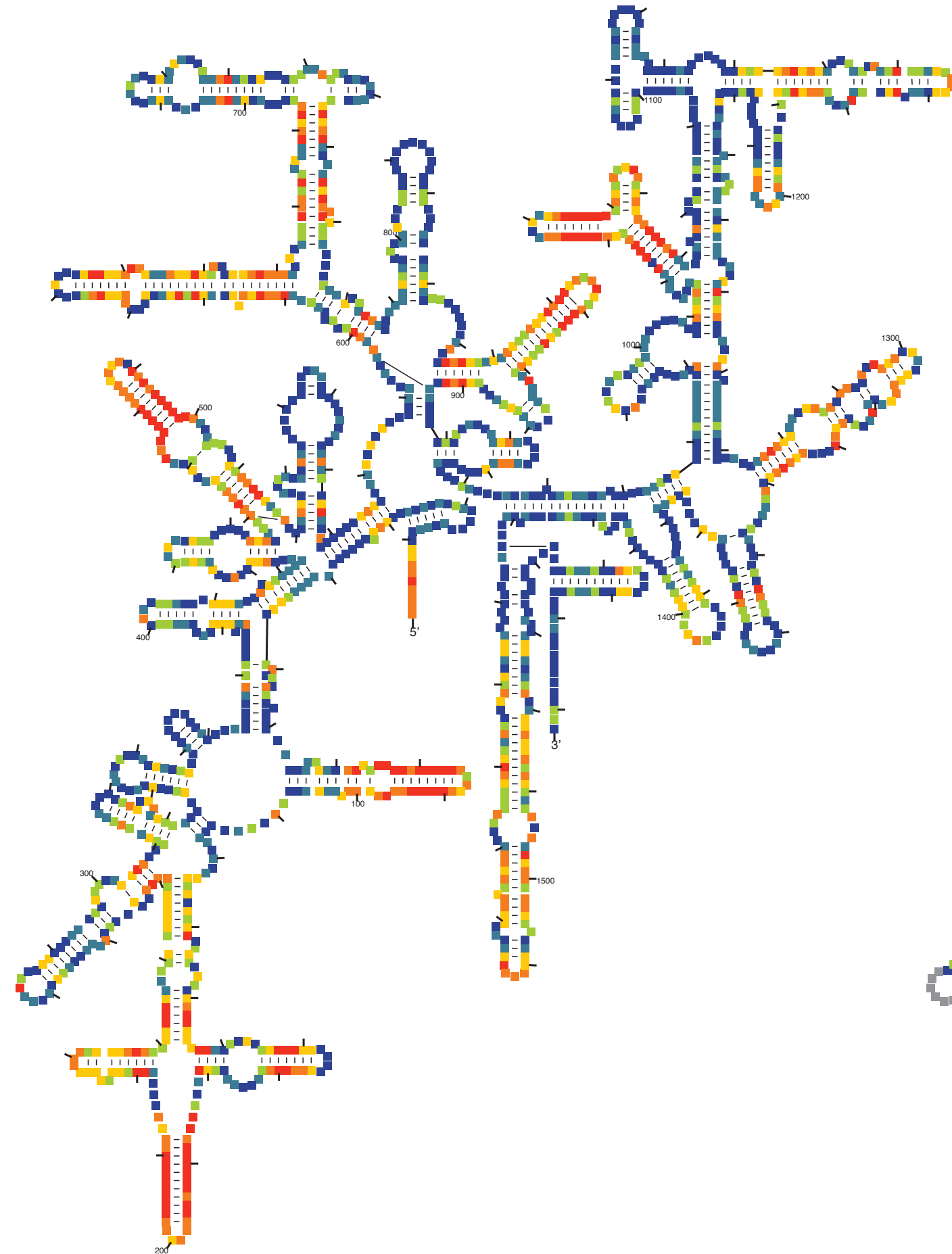


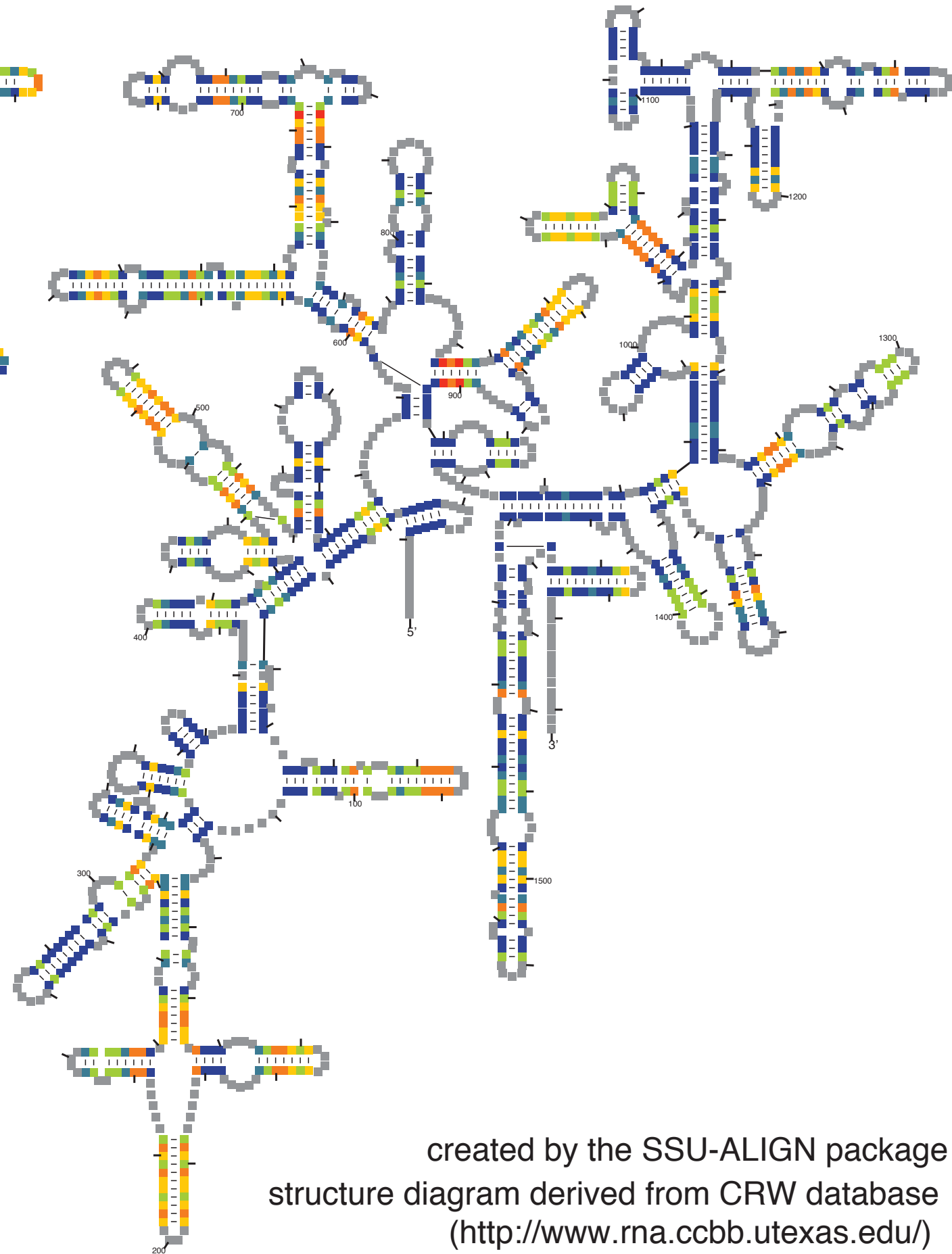
Sequence conservation per position

blue: highly conserved red: highly variable



Secondary structure (mutual) information per position

blue: low information red: high information



created by the SSU-ALIGN package
structure diagram derived from CRW database
(<http://www.rna.ccbb.utexas.edu/>)