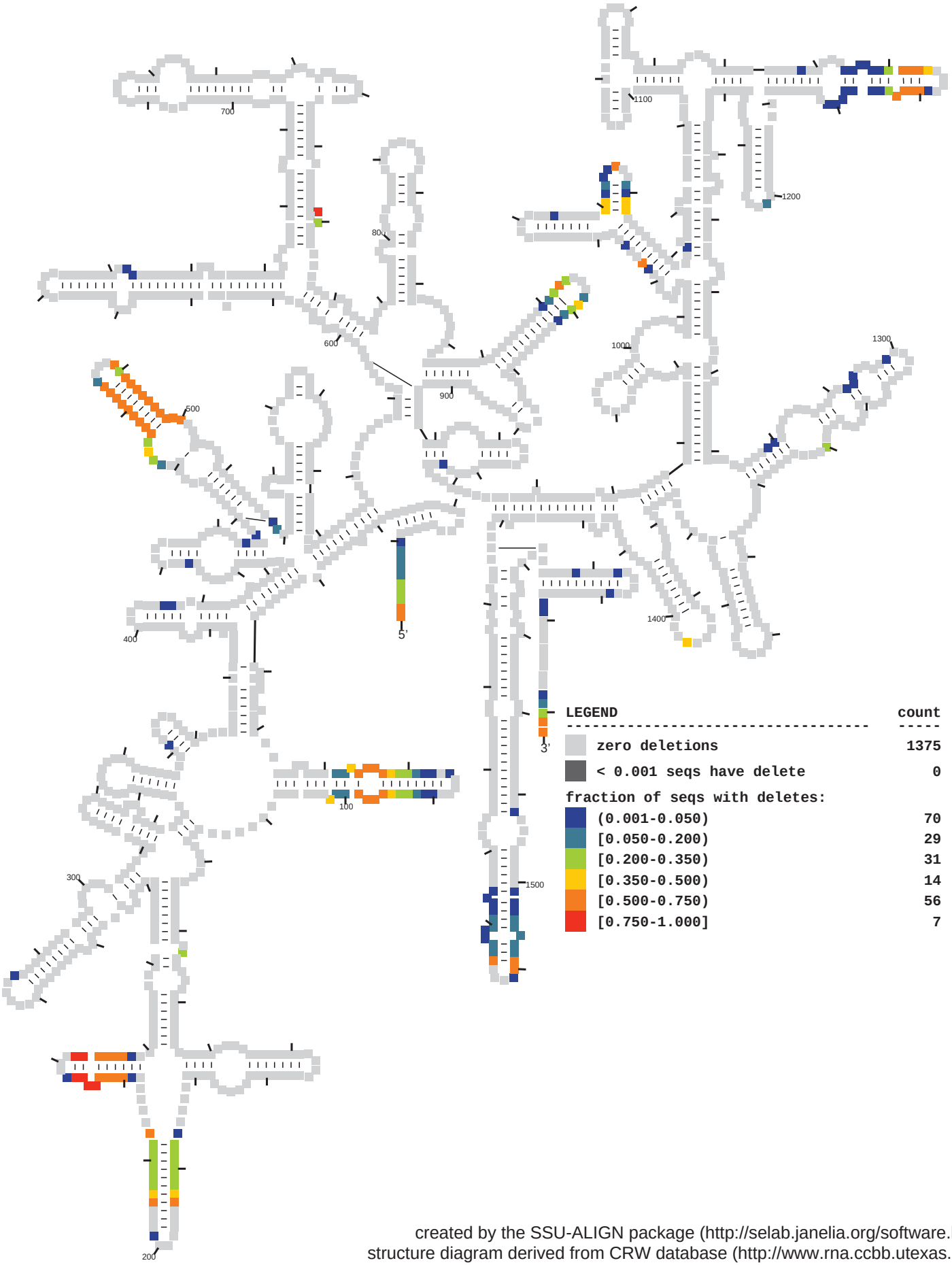
model	#pos	#bps	#seqs	description
bacteria	1582	480	93	frequency of deletions at each position



created by the SSU-ALIGN package (http://selab.janelia.org/software.html)
structure diagram derived from CRW database (http://www.rna.ccbb.utexas.edu/)