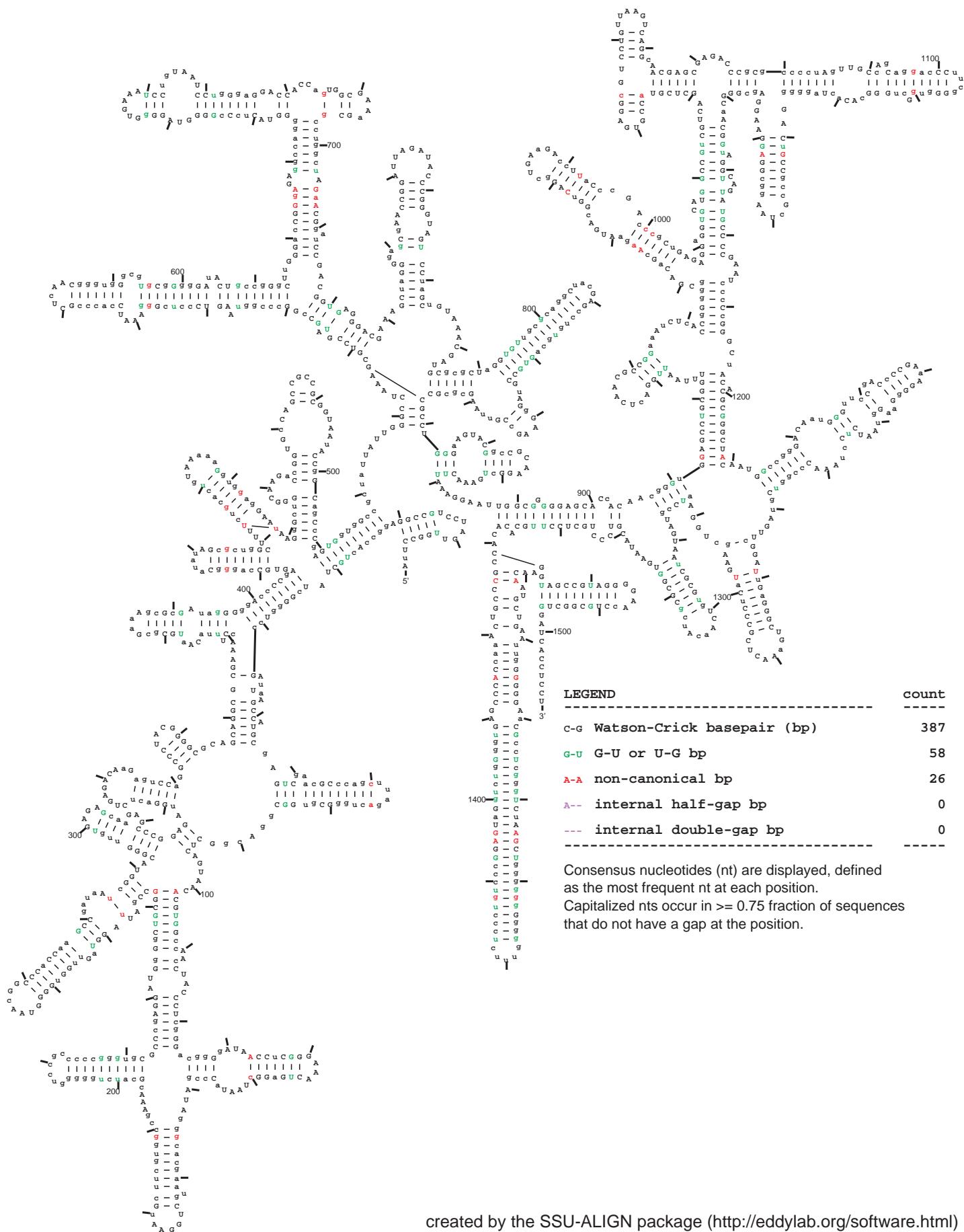


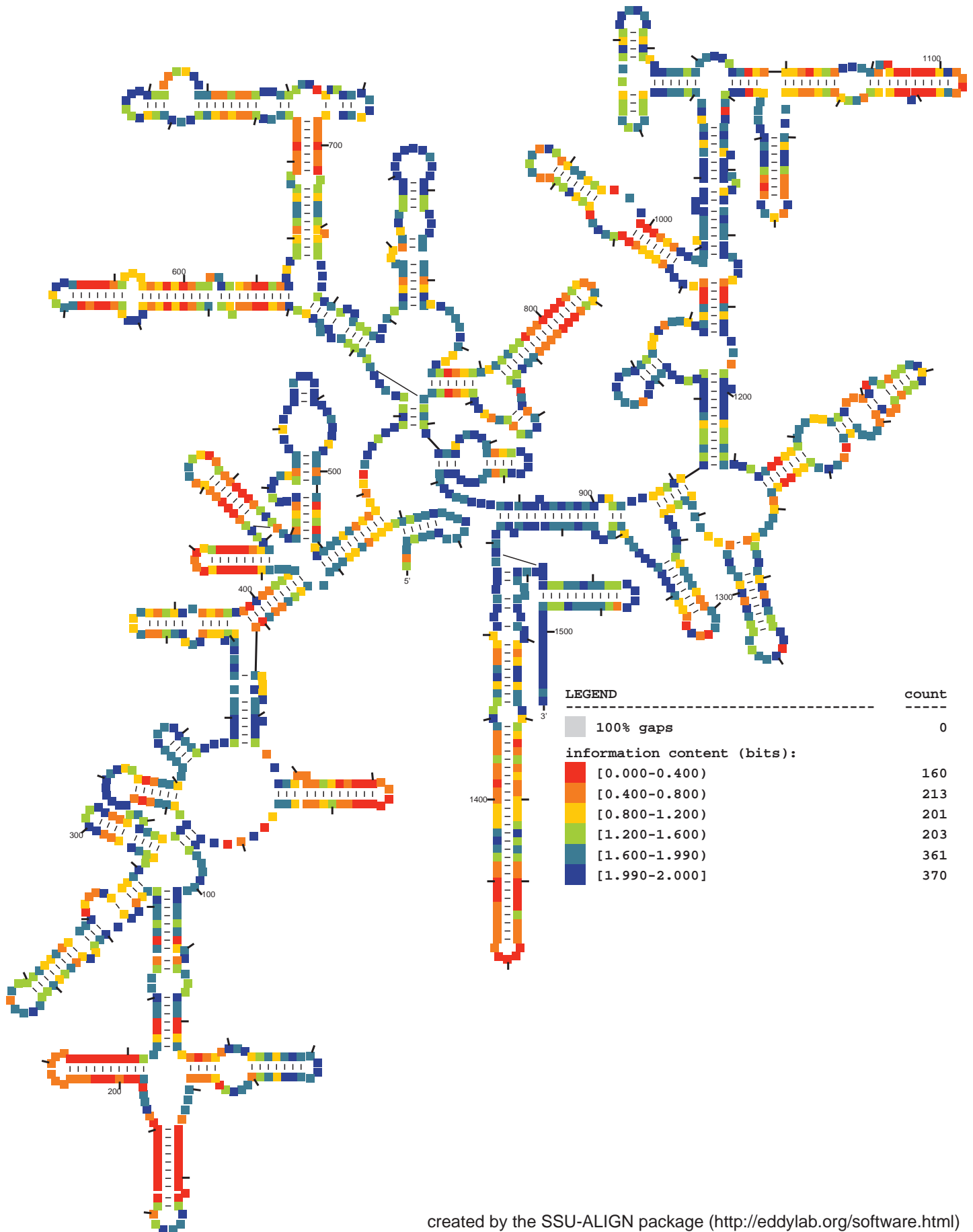
model	#pos	#bps
-----	-----	-----
archaea	1508	471

sequence name

alignment consensus sequence

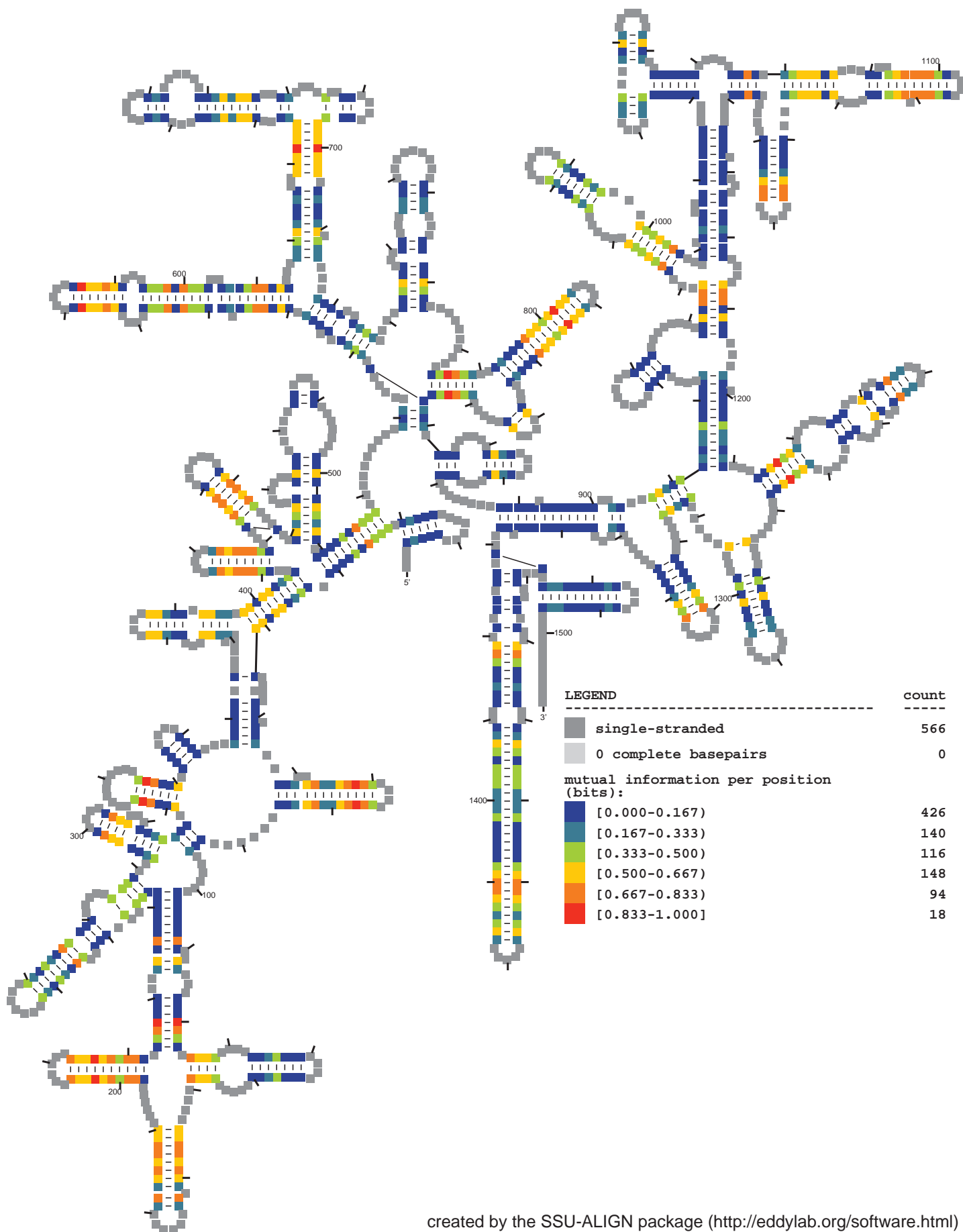


model	#pos	#bps	#seqs	description
archaea	1508	471	86	information content per position



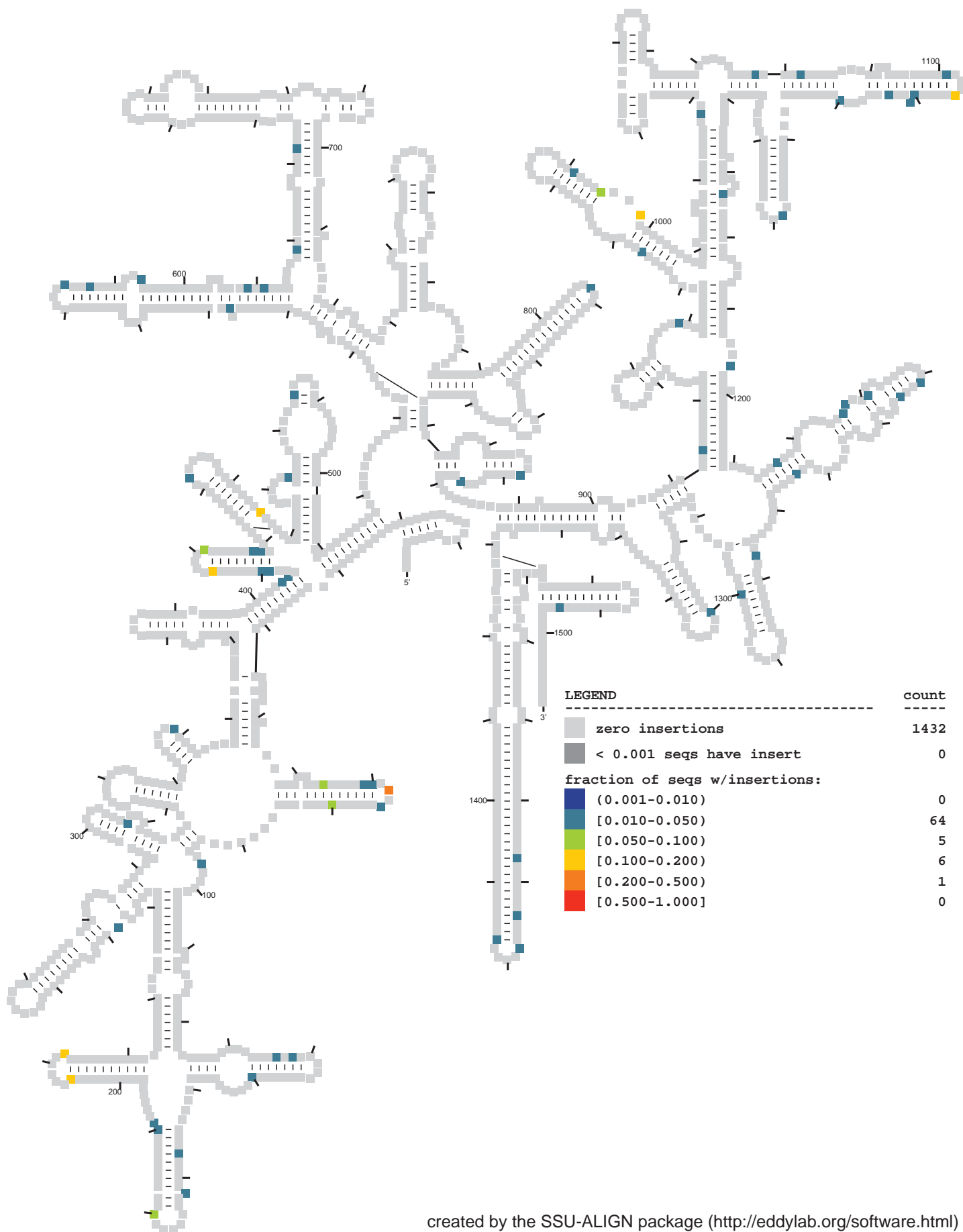
created by the SSU-ALIGN package (<http://eddylib.org/software.html>)
structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

model	#pos	#bps	#seqs	description
archaea	1508	471	86	mutual information per basepaired position



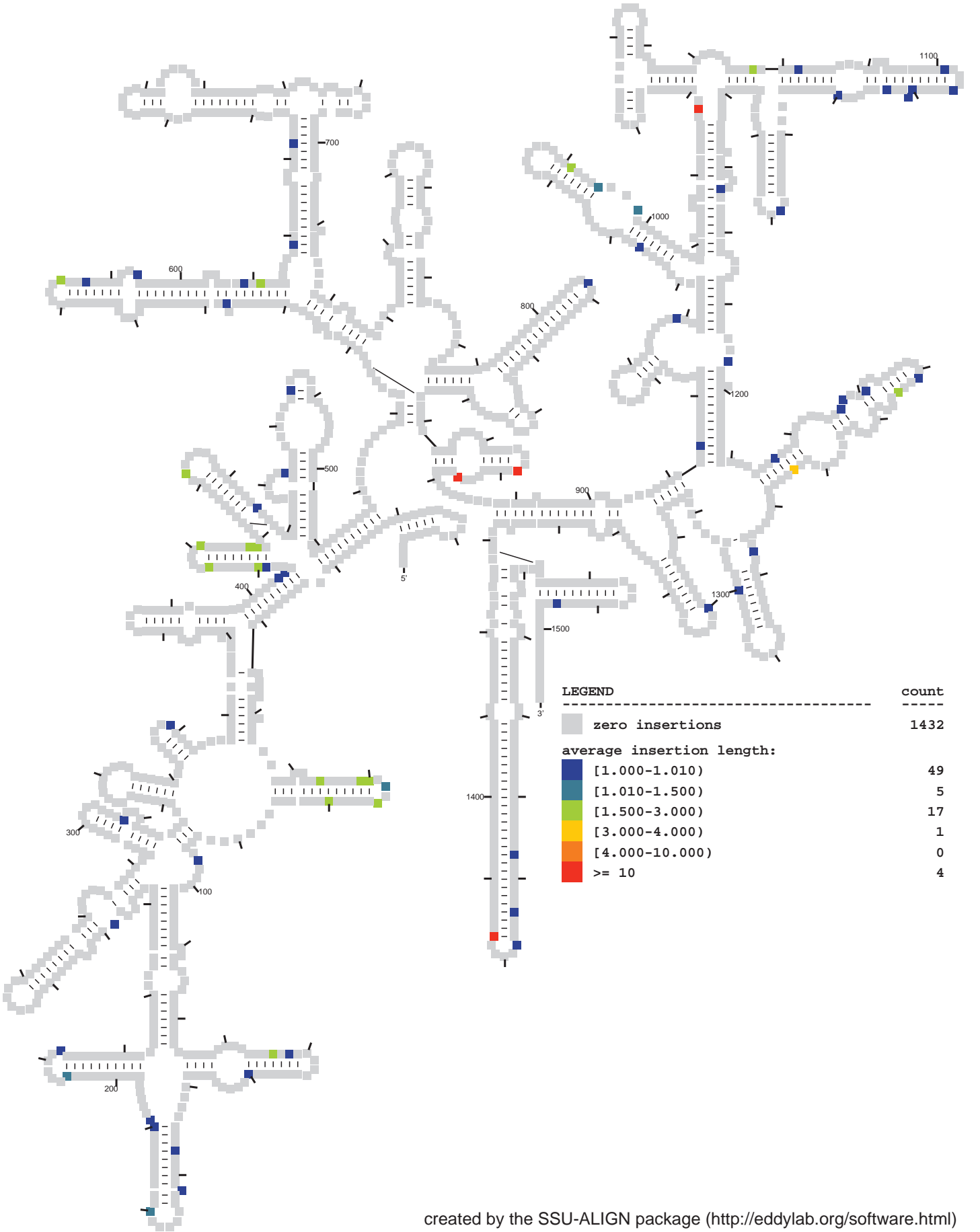
created by the SSU-ALIGN package (<http://eddylib.org/software.html>)
structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

model	#pos	#bps	#seqs	description
archaea	1508	471	86	frequency of insertions after each position

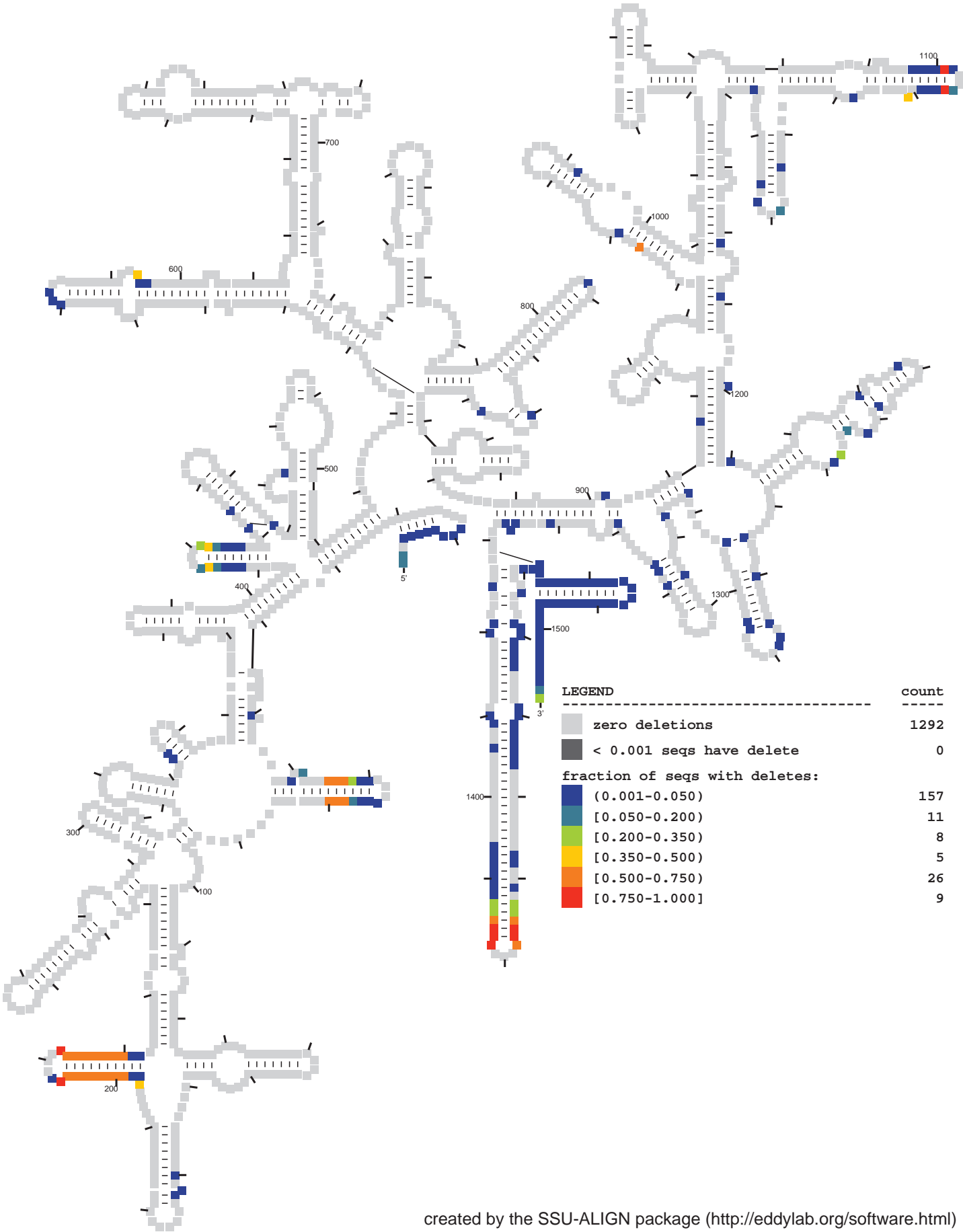


created by the SSU-ALIGN package (<http://eddylib.org/software.html>)
structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

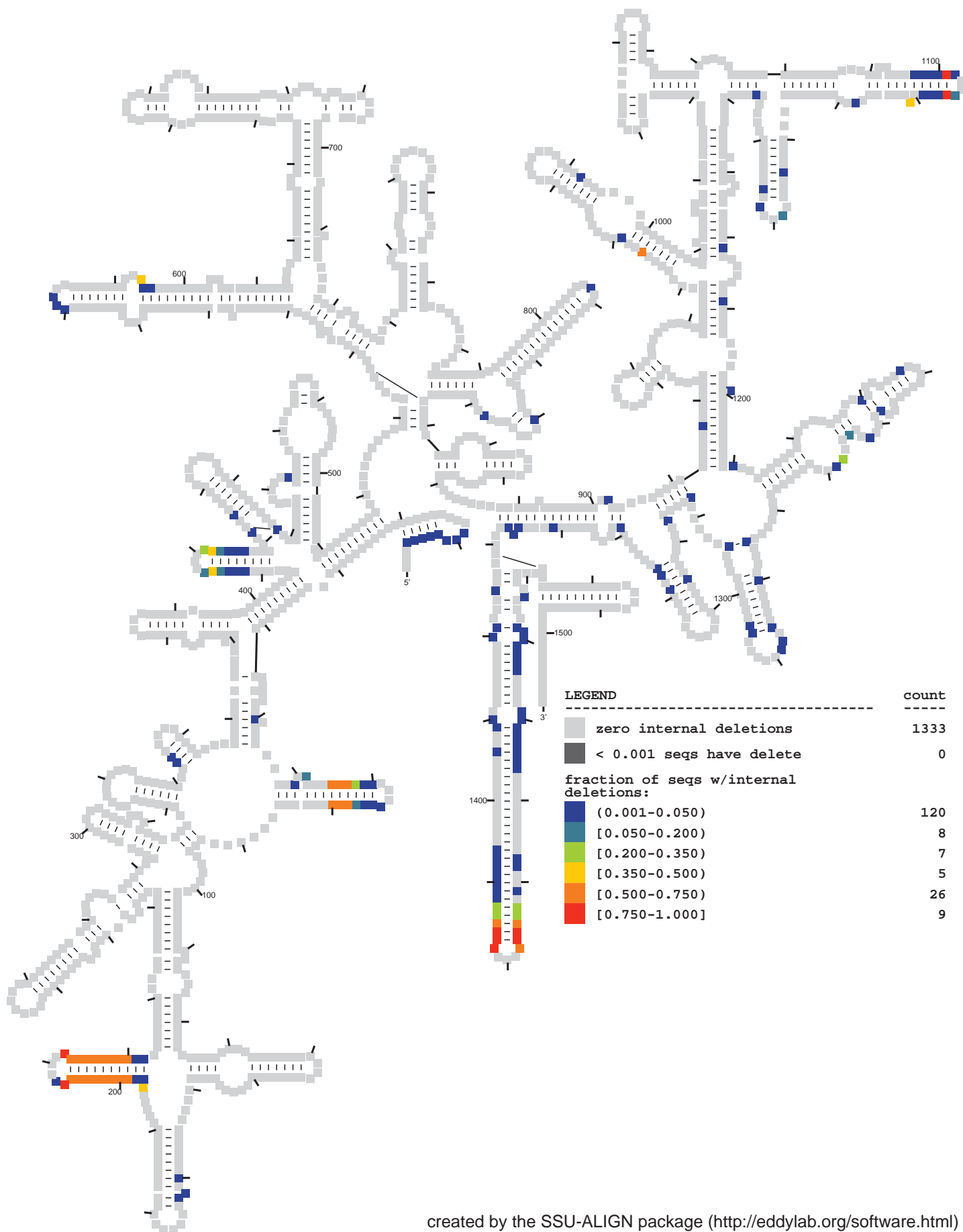
model	#pos	#bps	#seqs	description
archaea	1508	471	86	average insertion length after each position



model	#pos	#bps	#seqs	description
archaea	1508	471	86	frequency of deletions at each position

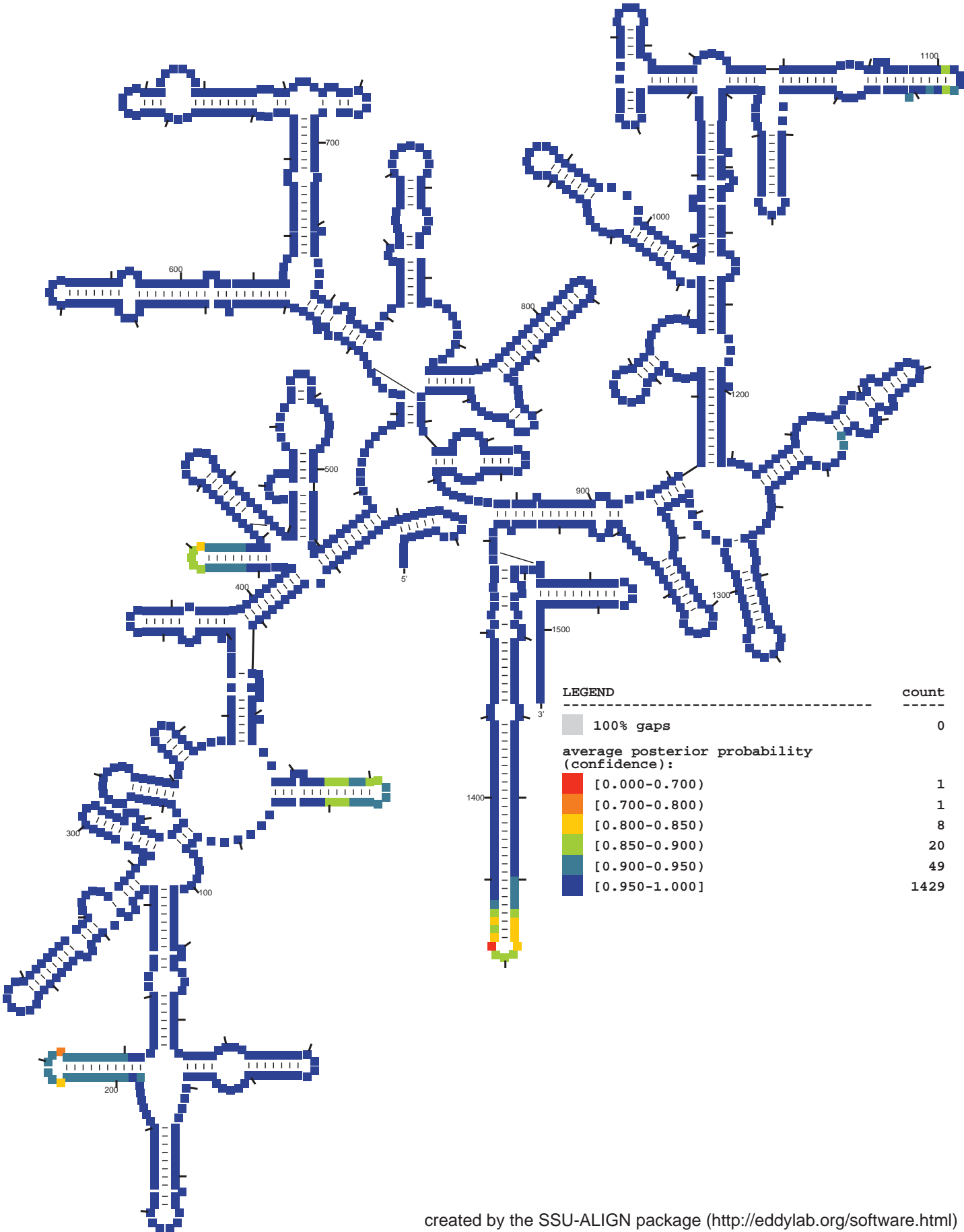


model	#pos	#bps	#seqs	description
archaea	1508	471	86	frequency of internal deletions in each position



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

model	#pos	#bps	#seqs	description
archaea	1508	471	86	average posterior probability per position



model	#pos	#bps	#seqs	description
archaea	1508	471	86	fraction of sequences that span each position

