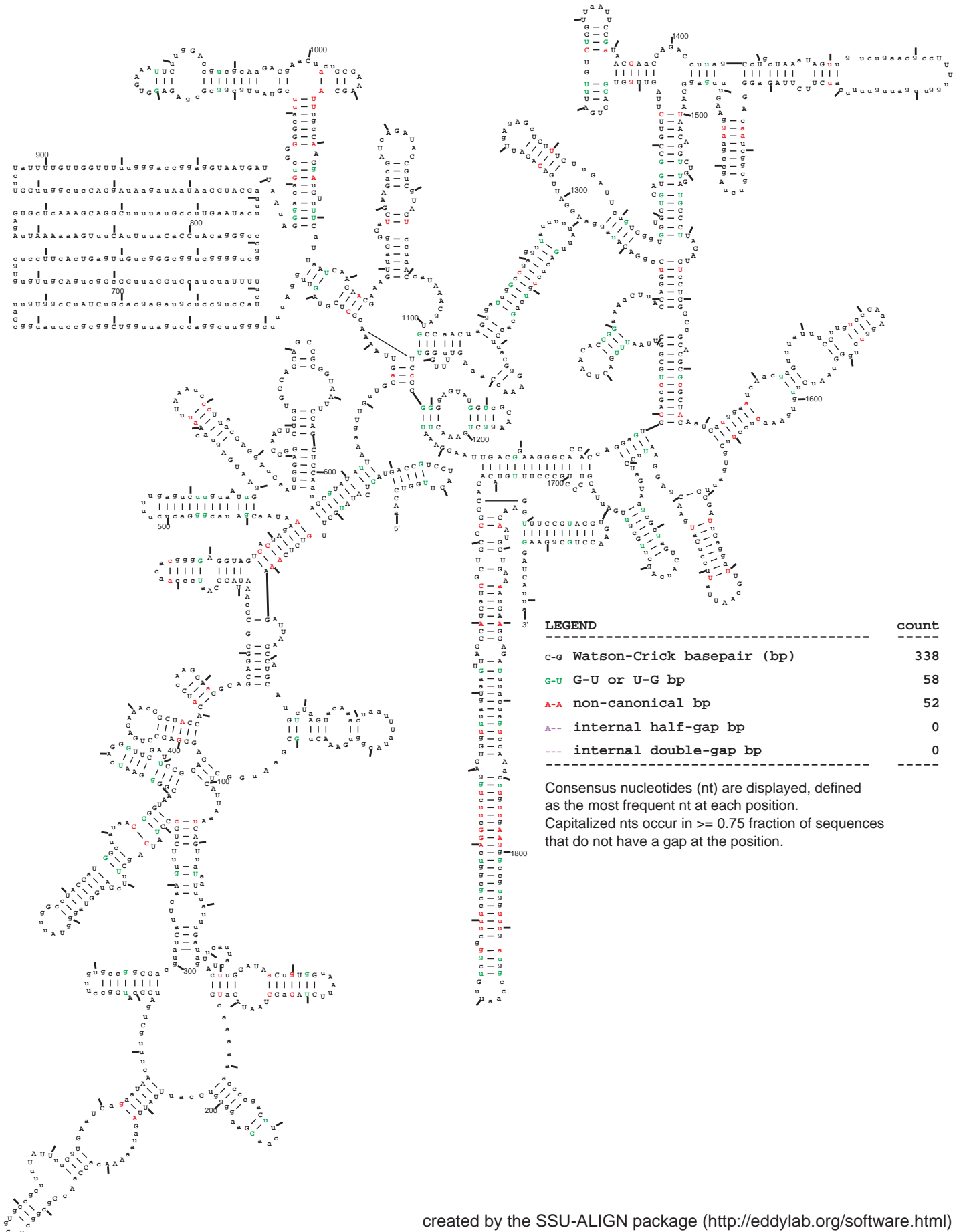
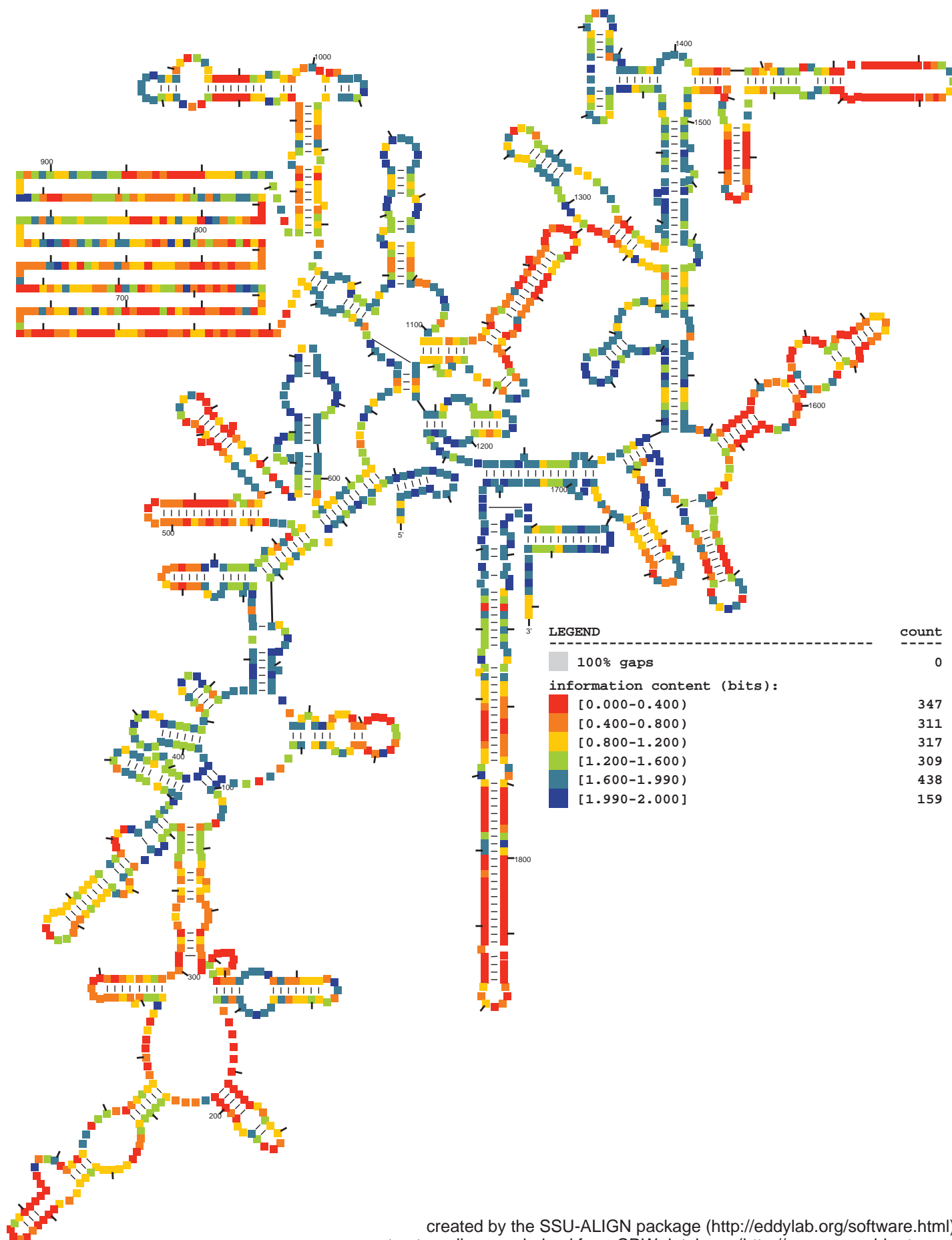


model	#pos	#bps
eukarya	1881	448

sequence name
alignment consensus sequence

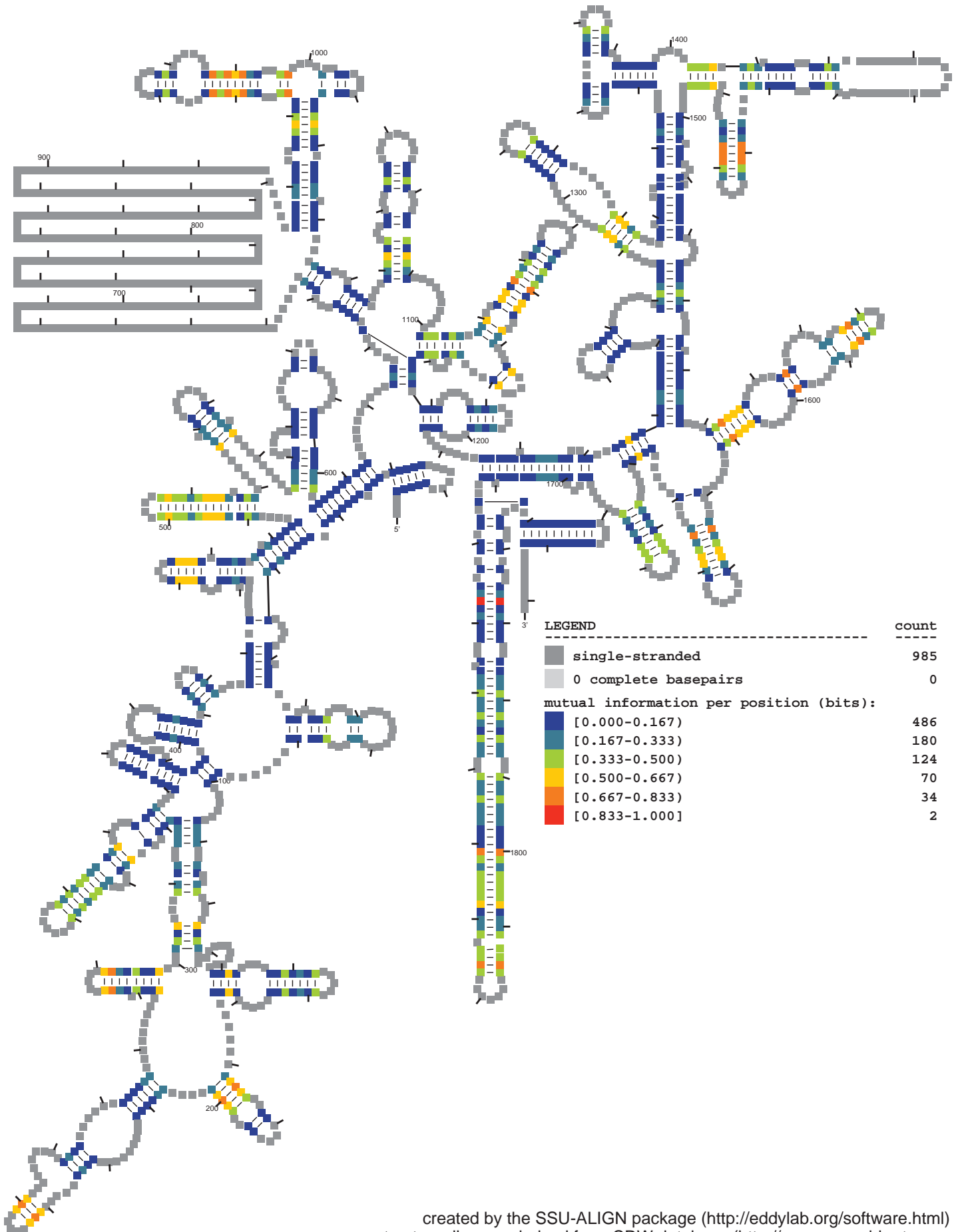


model	#pos	#bps	#seqs	description
eukarya	1881	448	91	information content per position



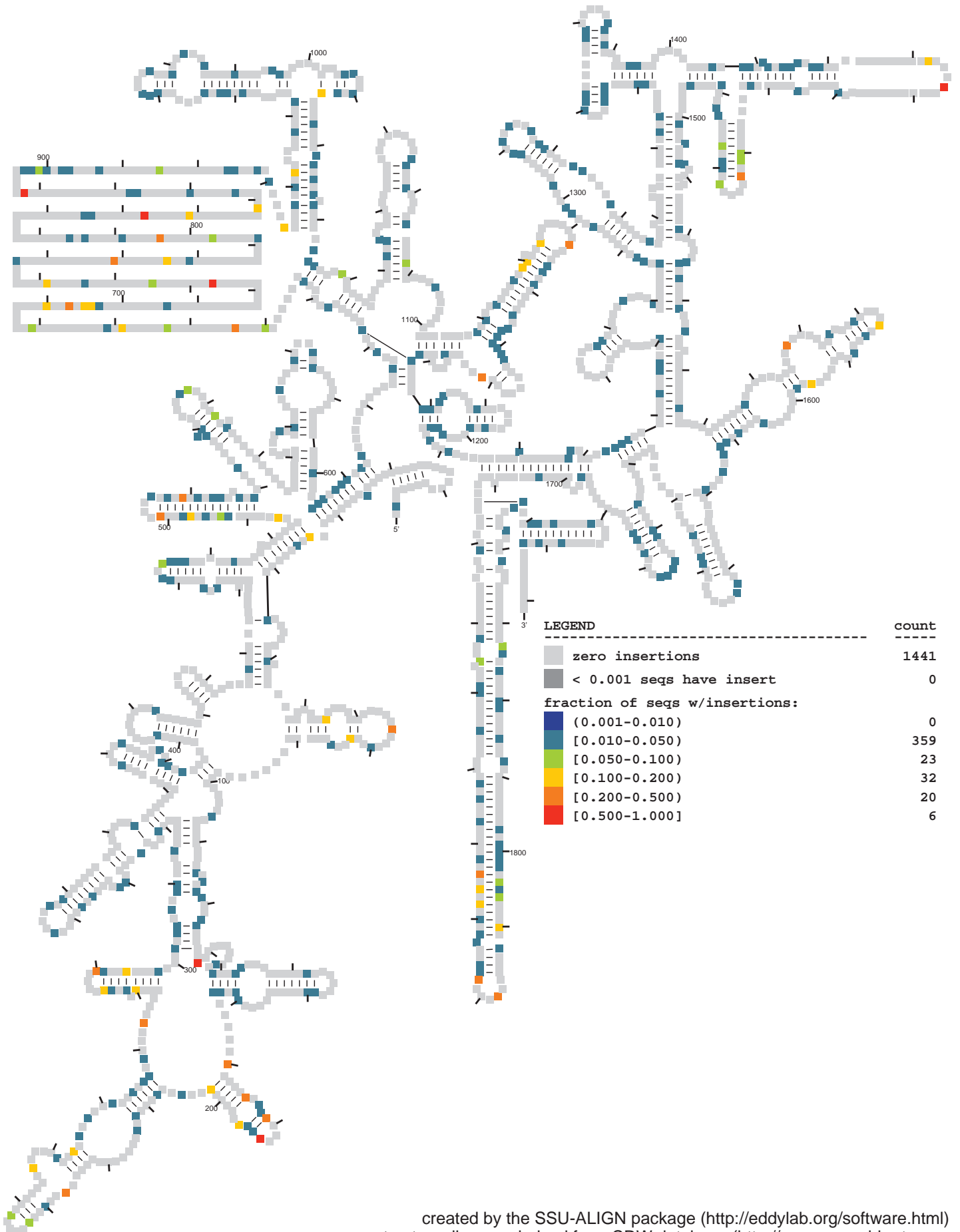
created by the SSU-ALIGN package (<http://eddylib.org/software.html>)  
 structure diagram derived from CRW database (<http://www.rna.cccb.utexas.edu/>)

model	#pos	#bps	#seqs	description
eukarya	1881	448	91	mutual information per basepaired position



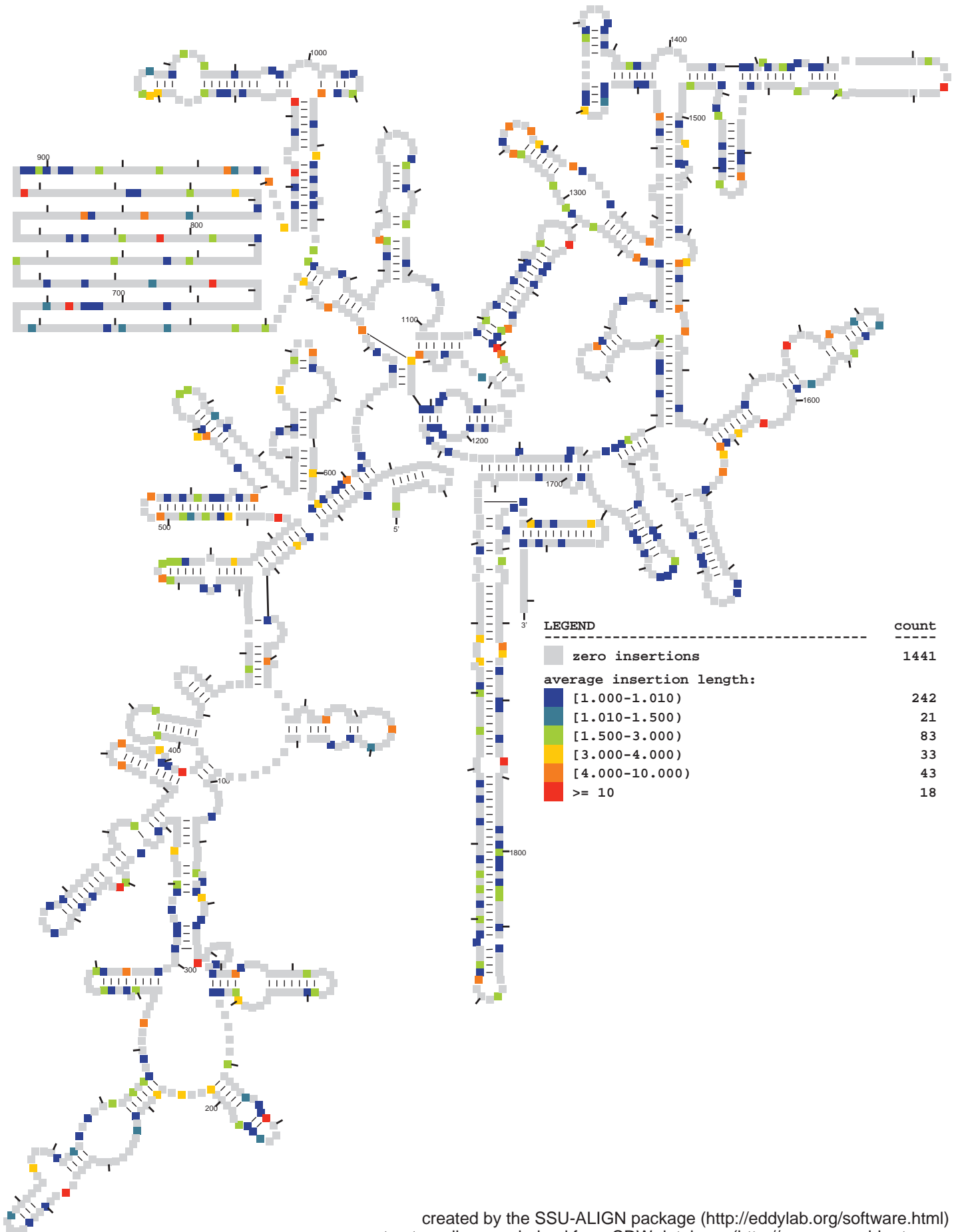
created by the SSU-ALIGN package (<http://eddylab.org/software.html>)  
structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

model	#pos	#bps	#seqs	description
eukarya	1881	448	91	frequency of insertions after each position

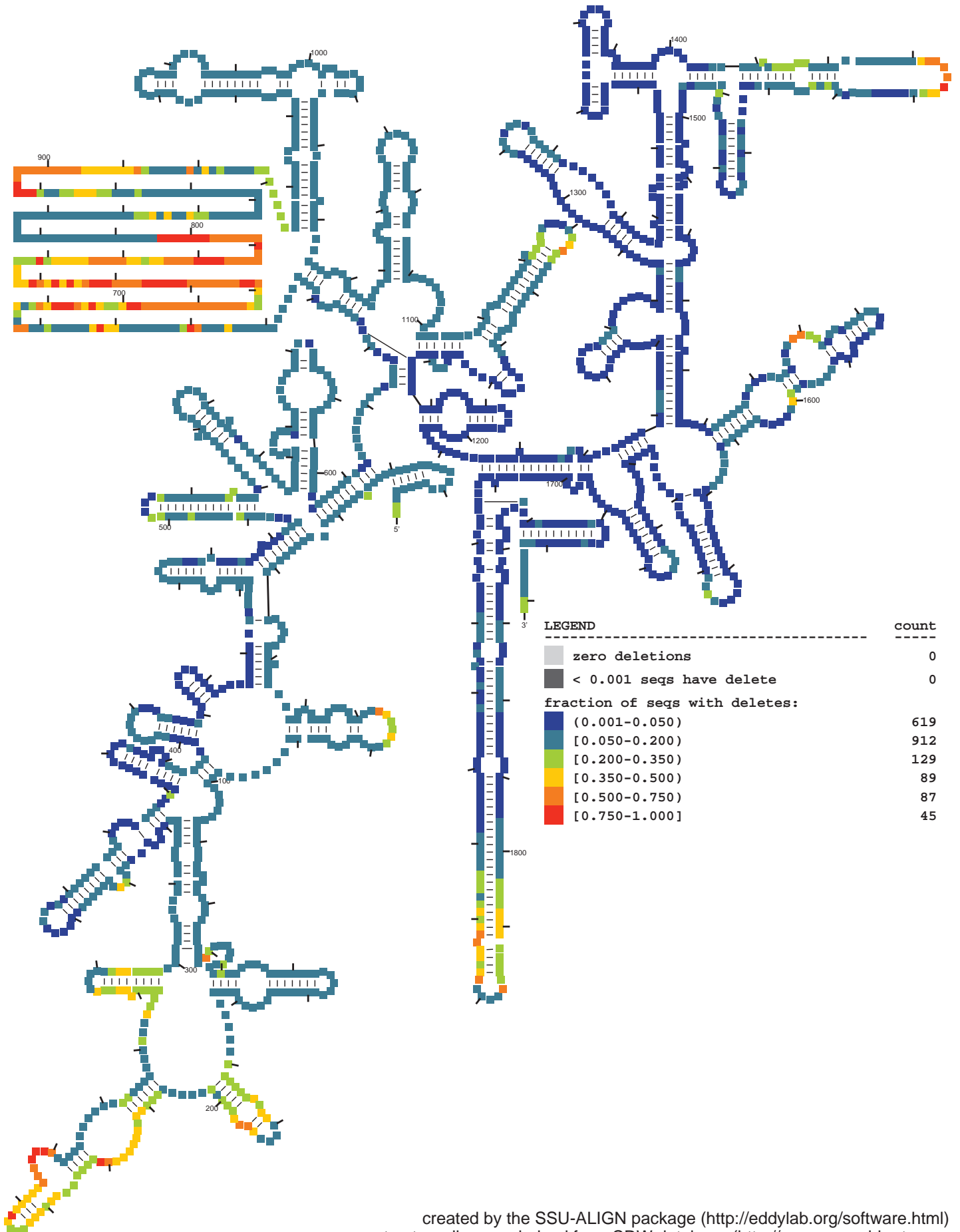


created by the SSU-ALIGN package (<http://eddylib.org/software.html>)  
 structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

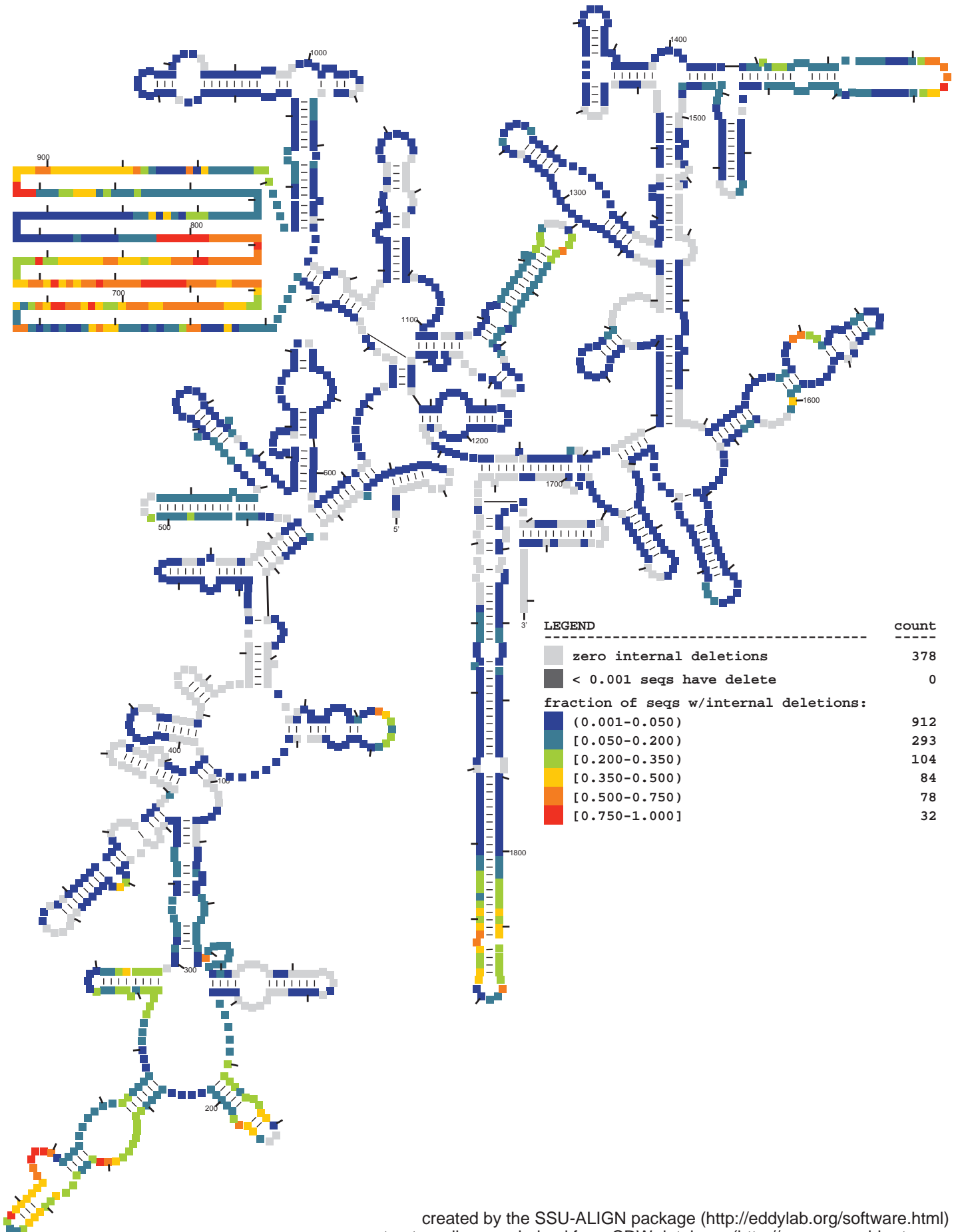
model	#pos	#bps	#seqs	description
eukarya	1881	448	91	average insertion length after each position



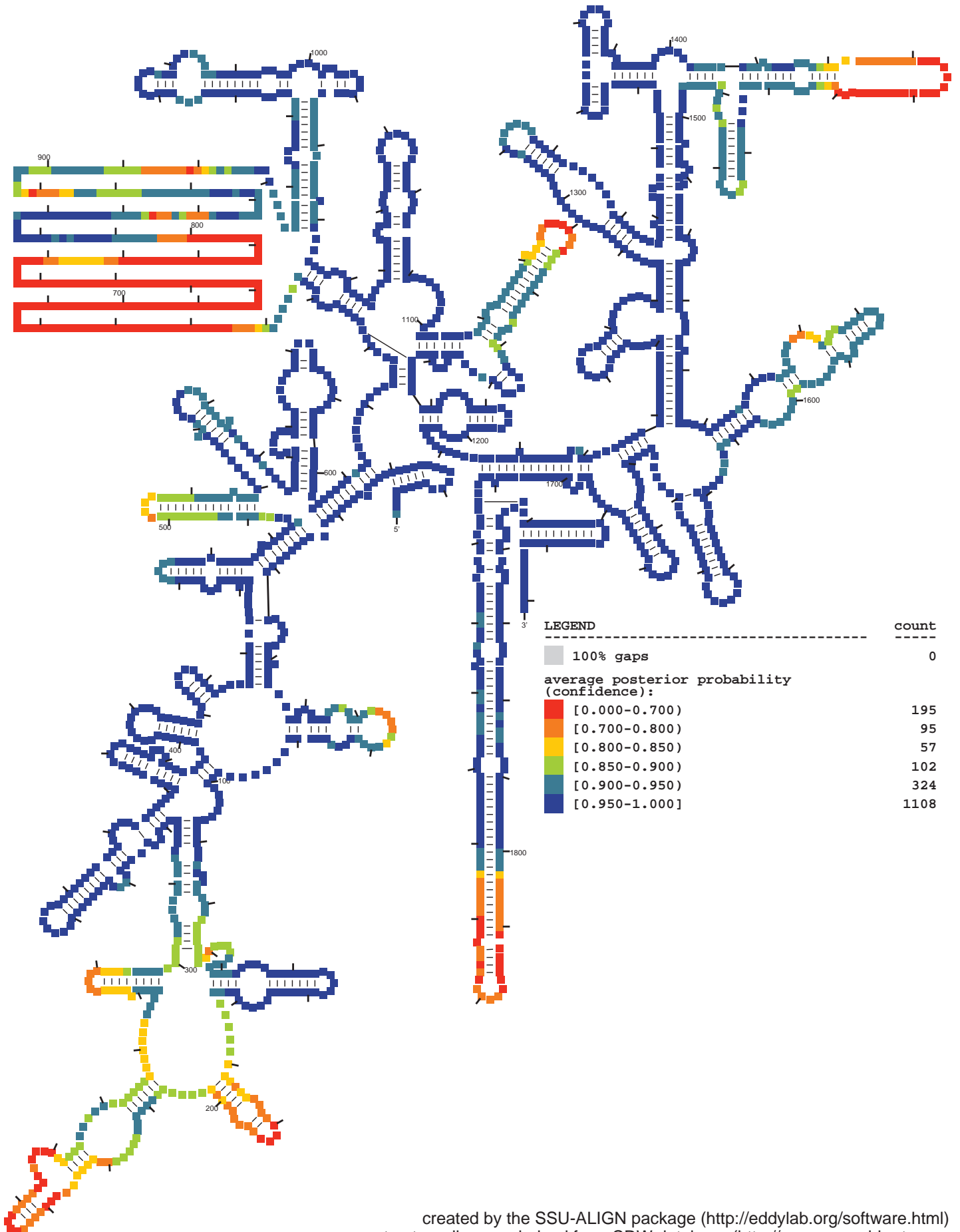
model	#pos	#bps	#seqs	description
eukarya	1881	448	91	frequency of deletions at each position



model	#pos	#bps	#seqs	description
eukarya	1881	448	91	frequency of internal deletions in each position



model	#pos	#bps	#seqs	description
eukarya	1881	448	91	average posterior probability per position





model	#pos	#bps	#seqs	description
eukarya	1881	448	91	fraction of sequences that span each position

