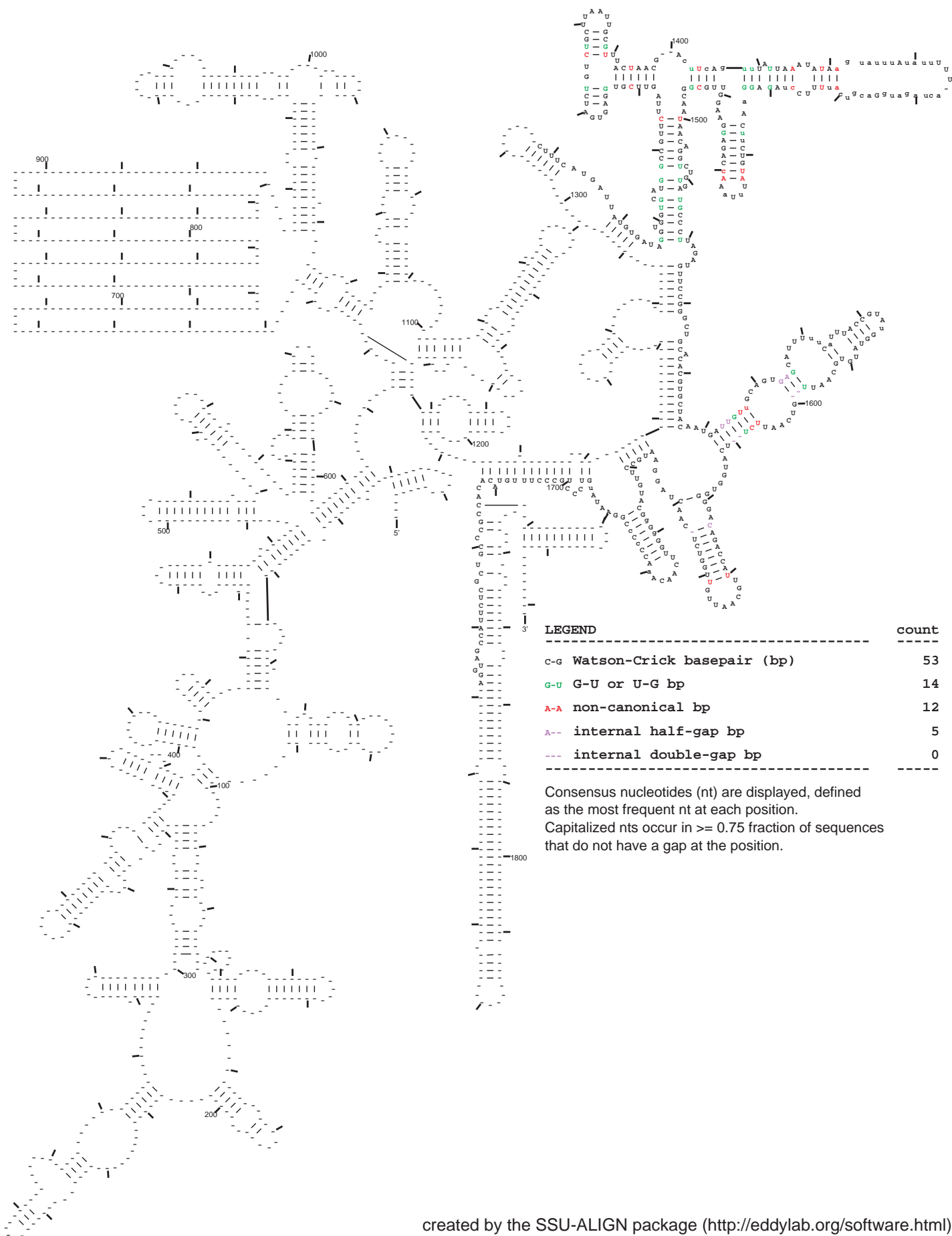
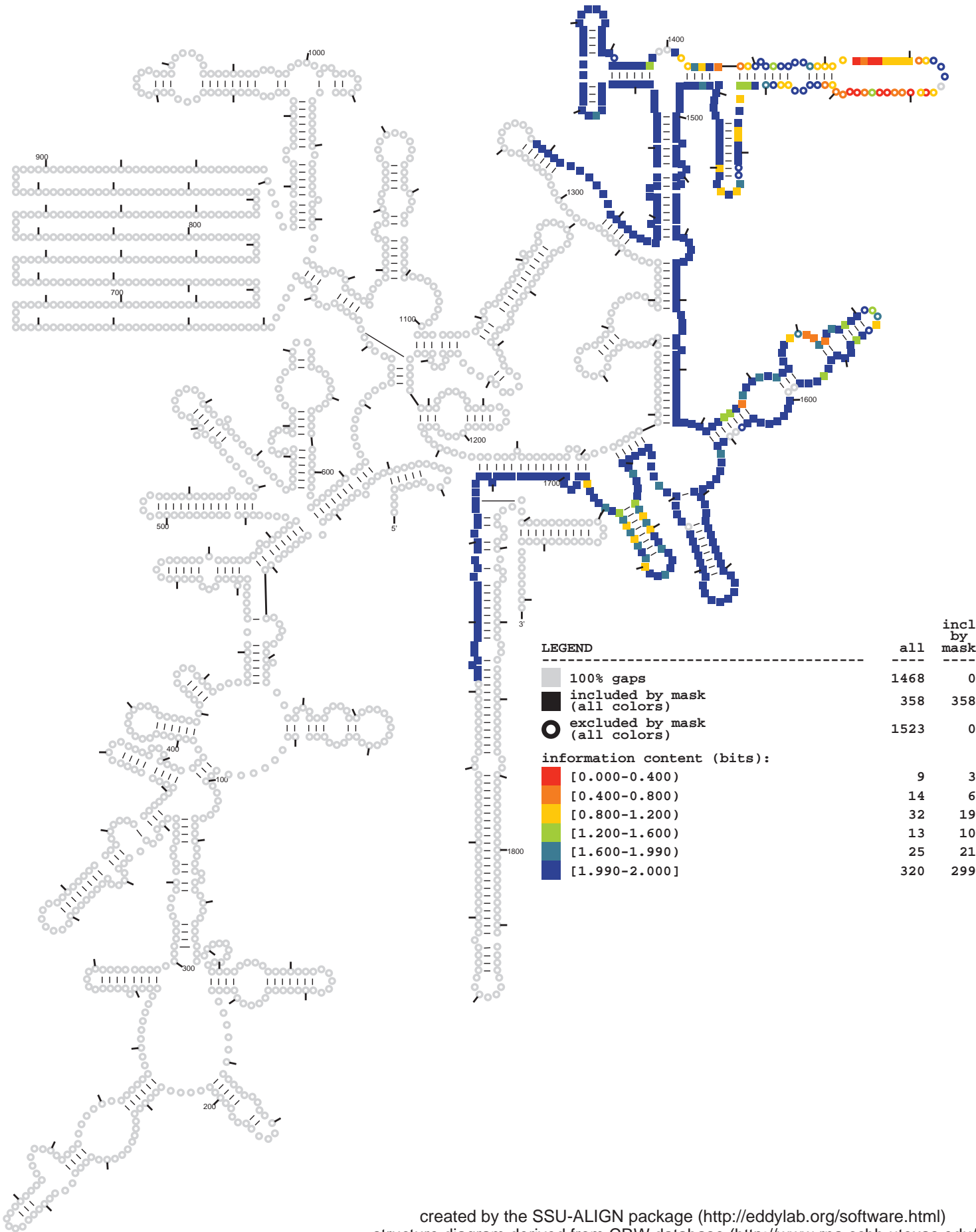


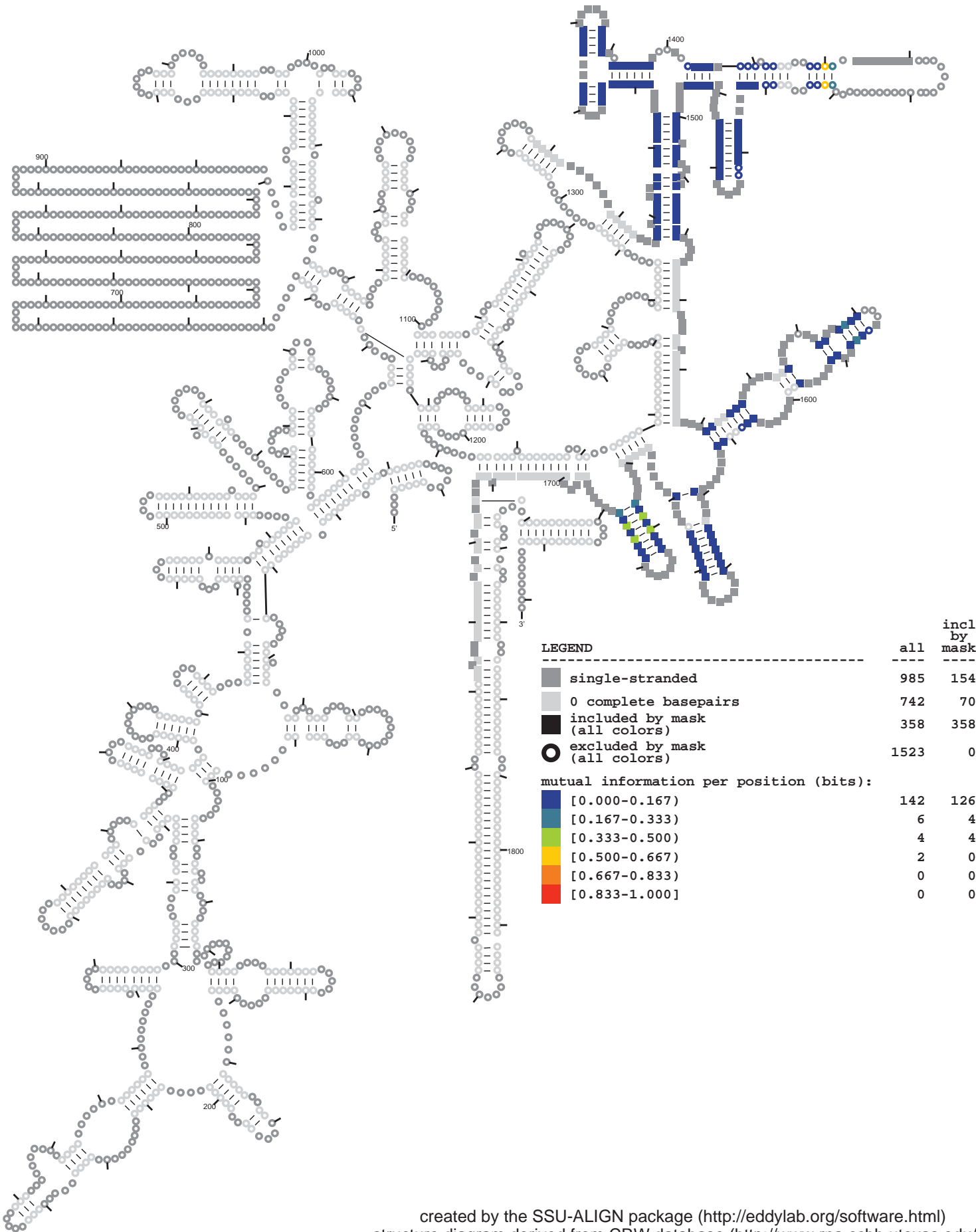
model	#pos	#bps
eukarya	1881	448

sequence name
alignment consensus sequence



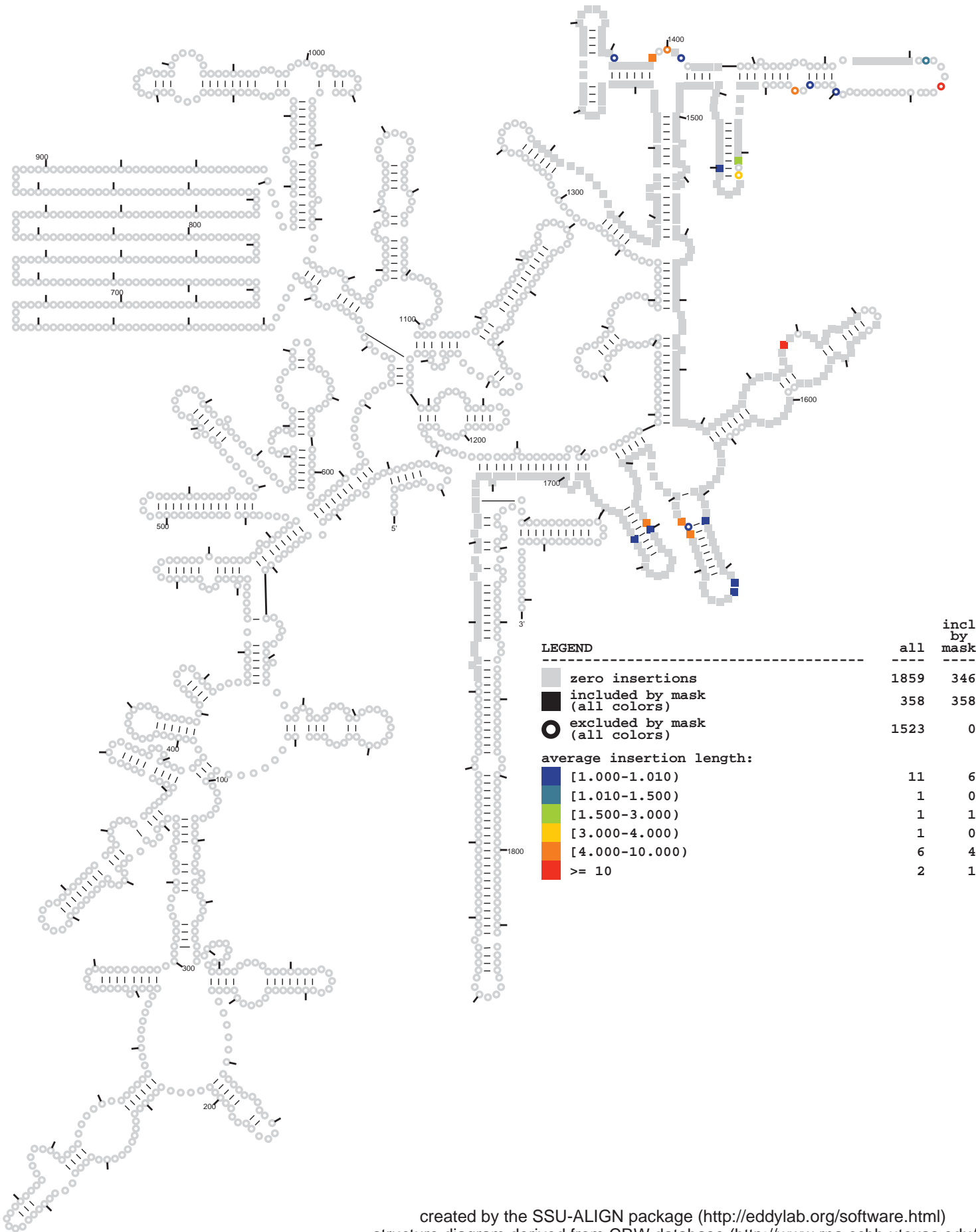


model	#pos	#bps	#seqs	description
eukarya	1881	448	67	mutual information per basepaired position

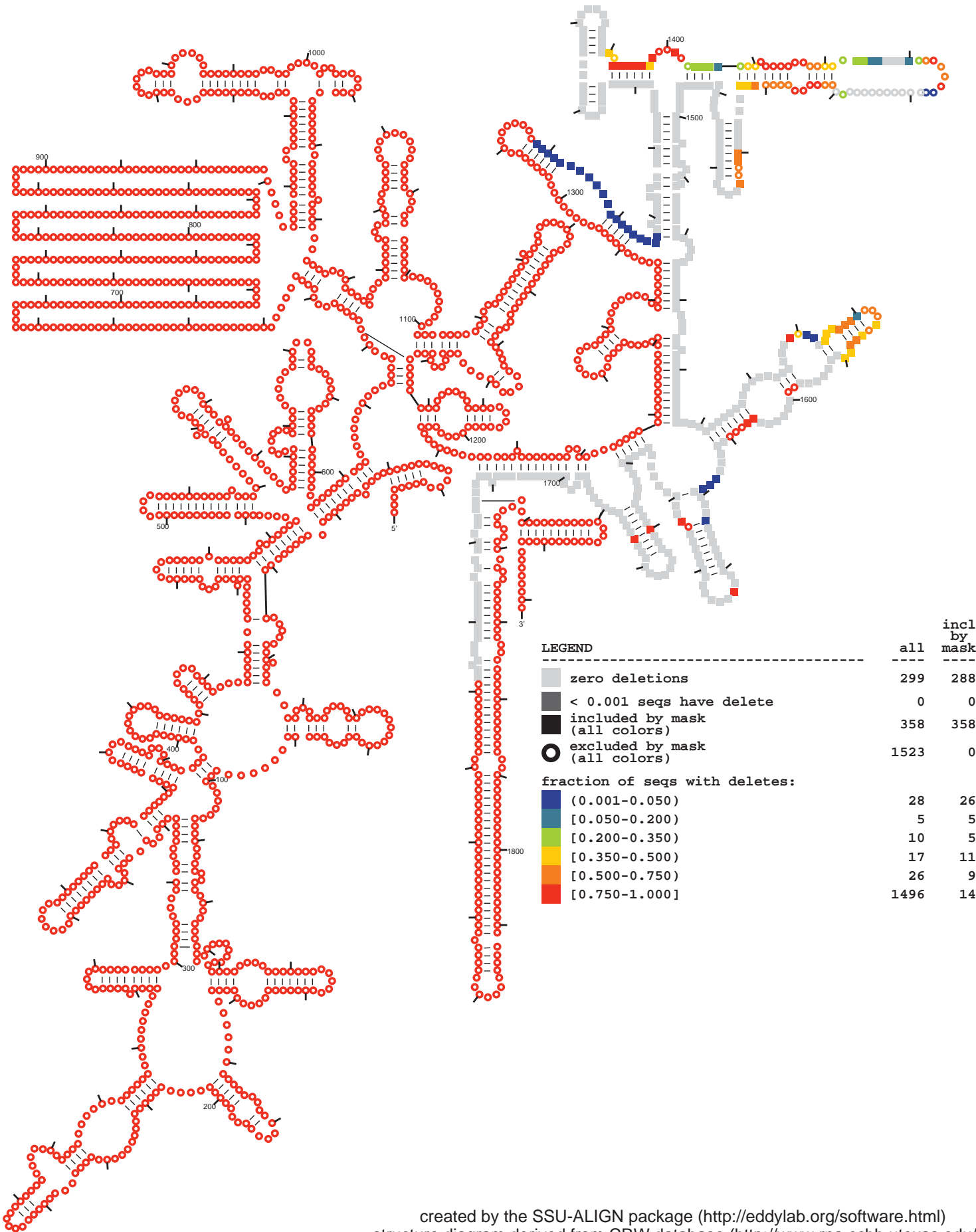




model	#pos	#bps	#seqs	description
eukarya	1881	448	67	average insertion length after each position

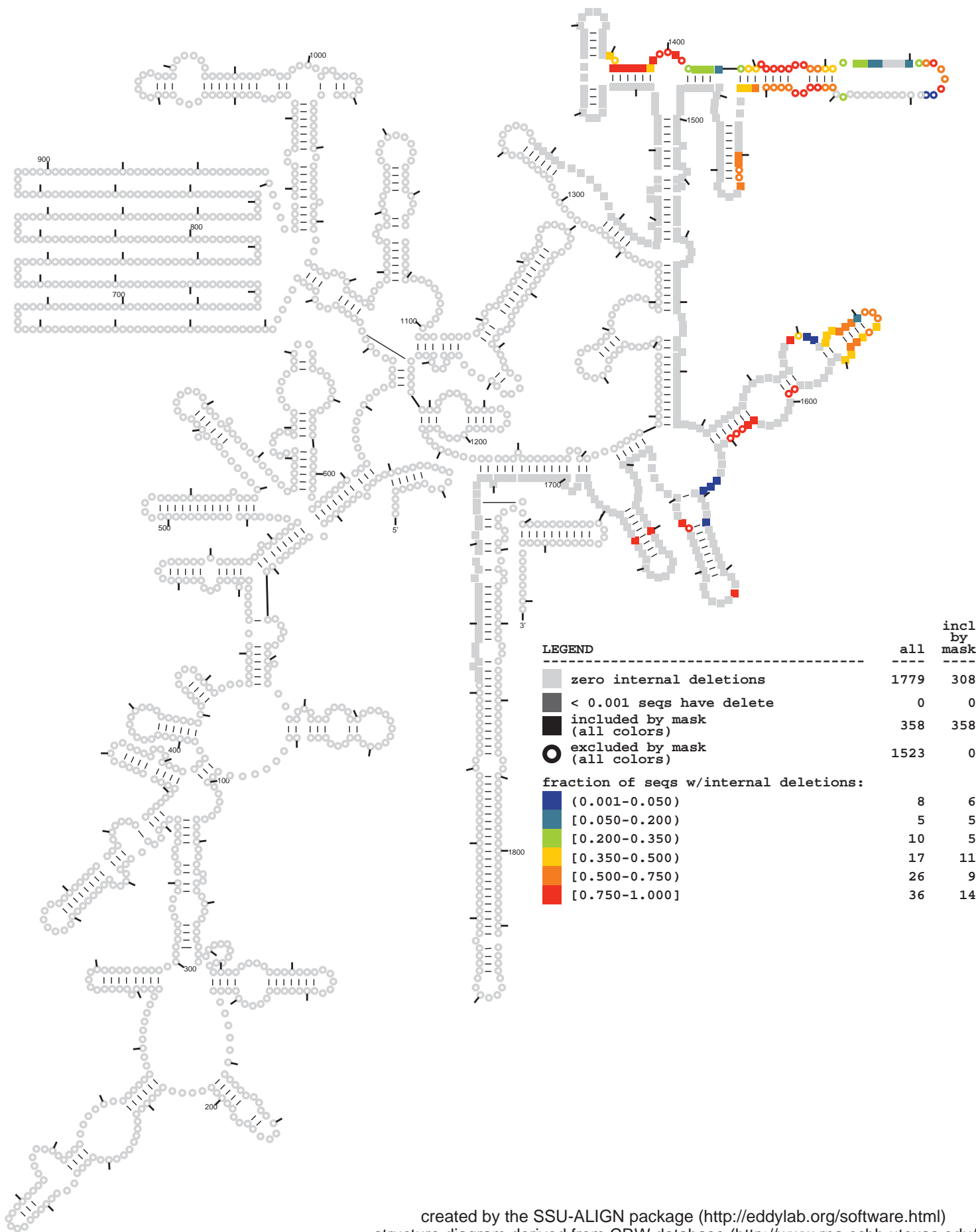


model	#pos	#bps	#seqs	description
eukarya	1881	448	67	frequency of deletions at each position



	all	incl by mask
LEGEND		
zero deletions	299	288
< 0.001 seqs have delete	0	0
included by mask (all colors)	358	358
excluded by mask (all colors)	1523	0
fraction of seqs with deletes:		
(0.001-0.050)	28	26
[0.050-0.200]	5	5
[0.200-0.350]	10	5
[0.350-0.500]	17	11
[0.500-0.750]	26	9
[0.750-1.000]	1496	14

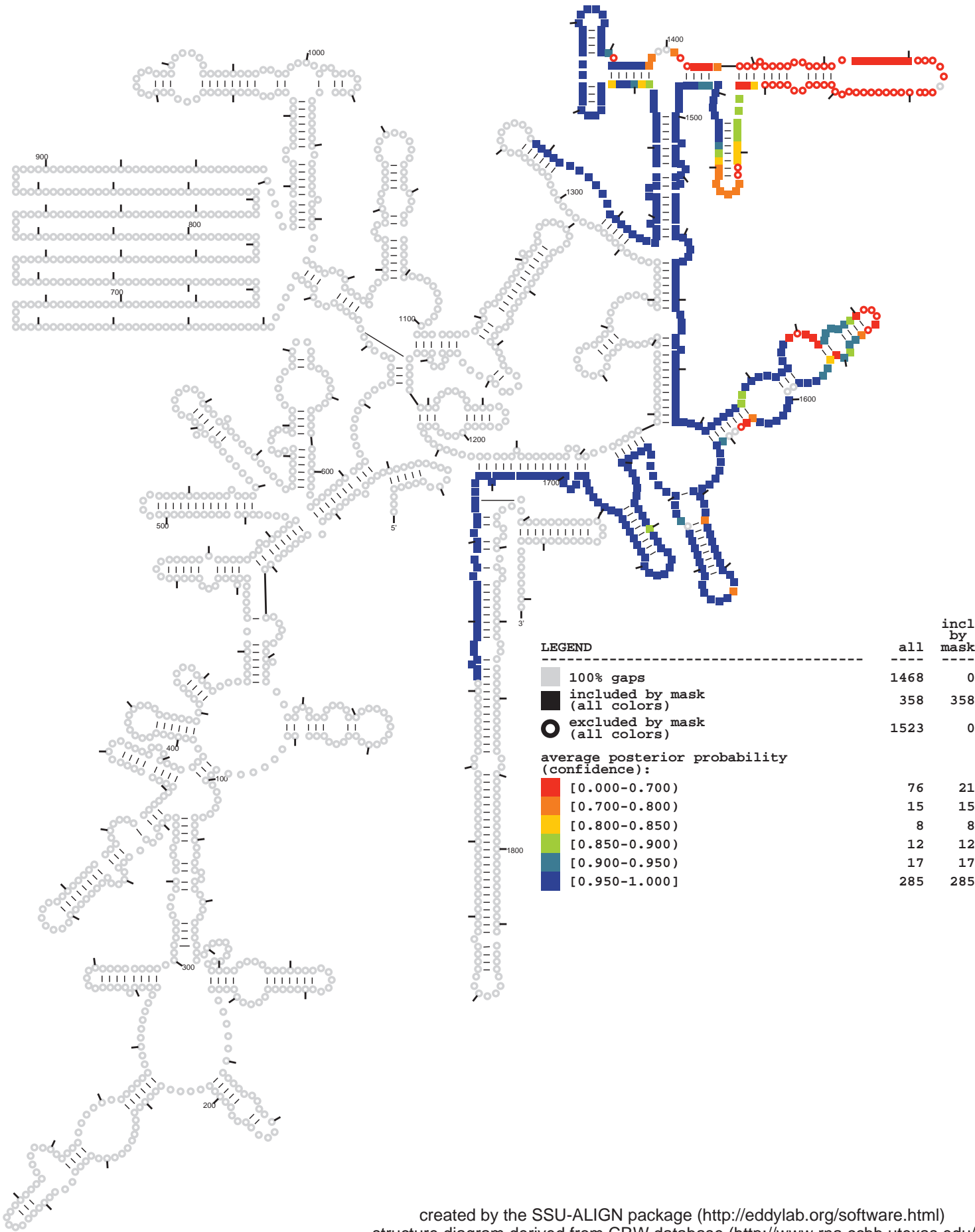
model	#pos	#bps	#seqs	description
eukarya	1881	448	67	frequency of internal deletions in each position





model	#pos	#bps	#seqs	description
eukarya	1881	448	67	

average posterior probability per position





model	#pos	#bps	#seqs	description
eukarya	1881	448	67	fraction of sequences that span each position

