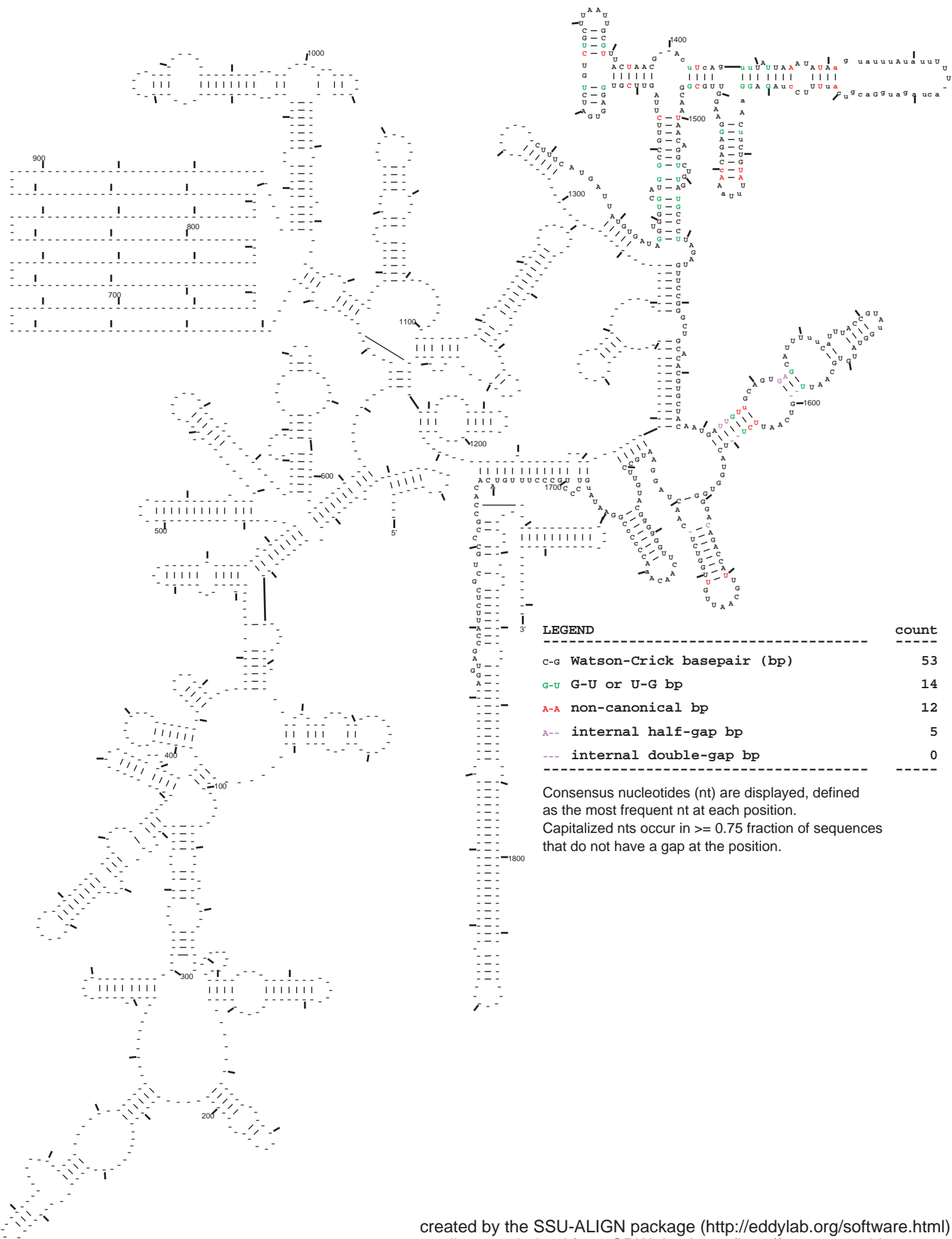
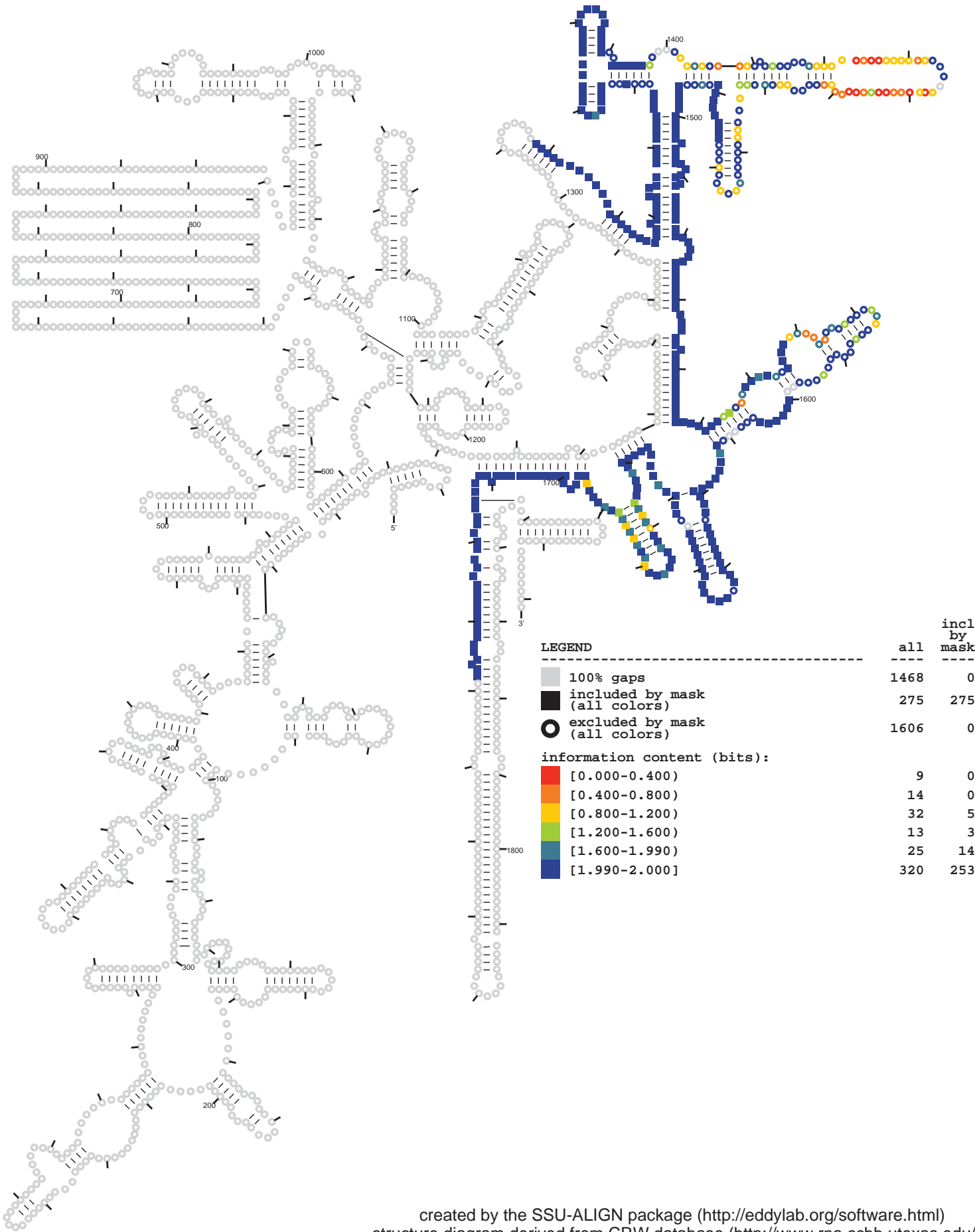


model #pos #bps
eukarya 1881 448

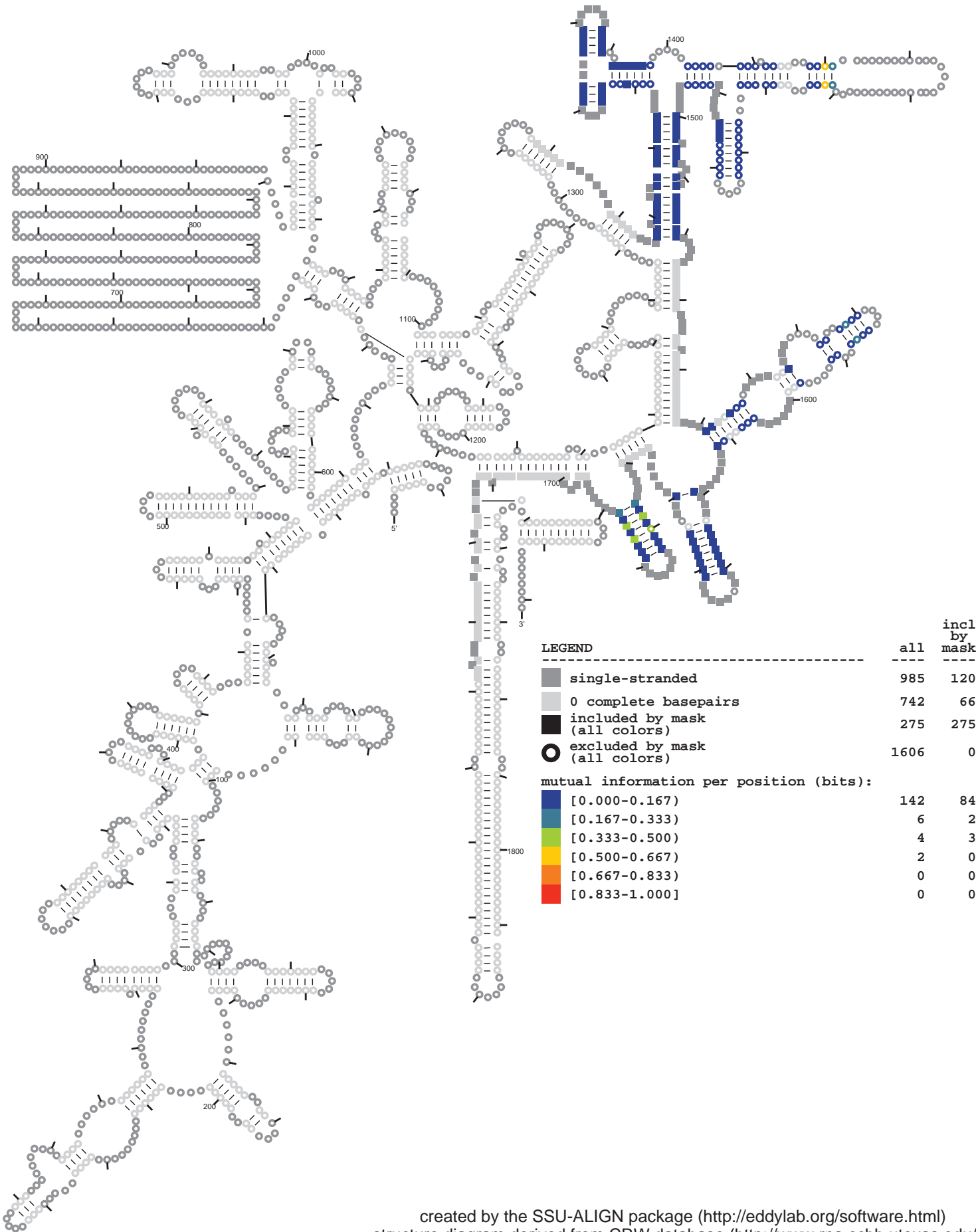
sequence name
alignment consensus sequence



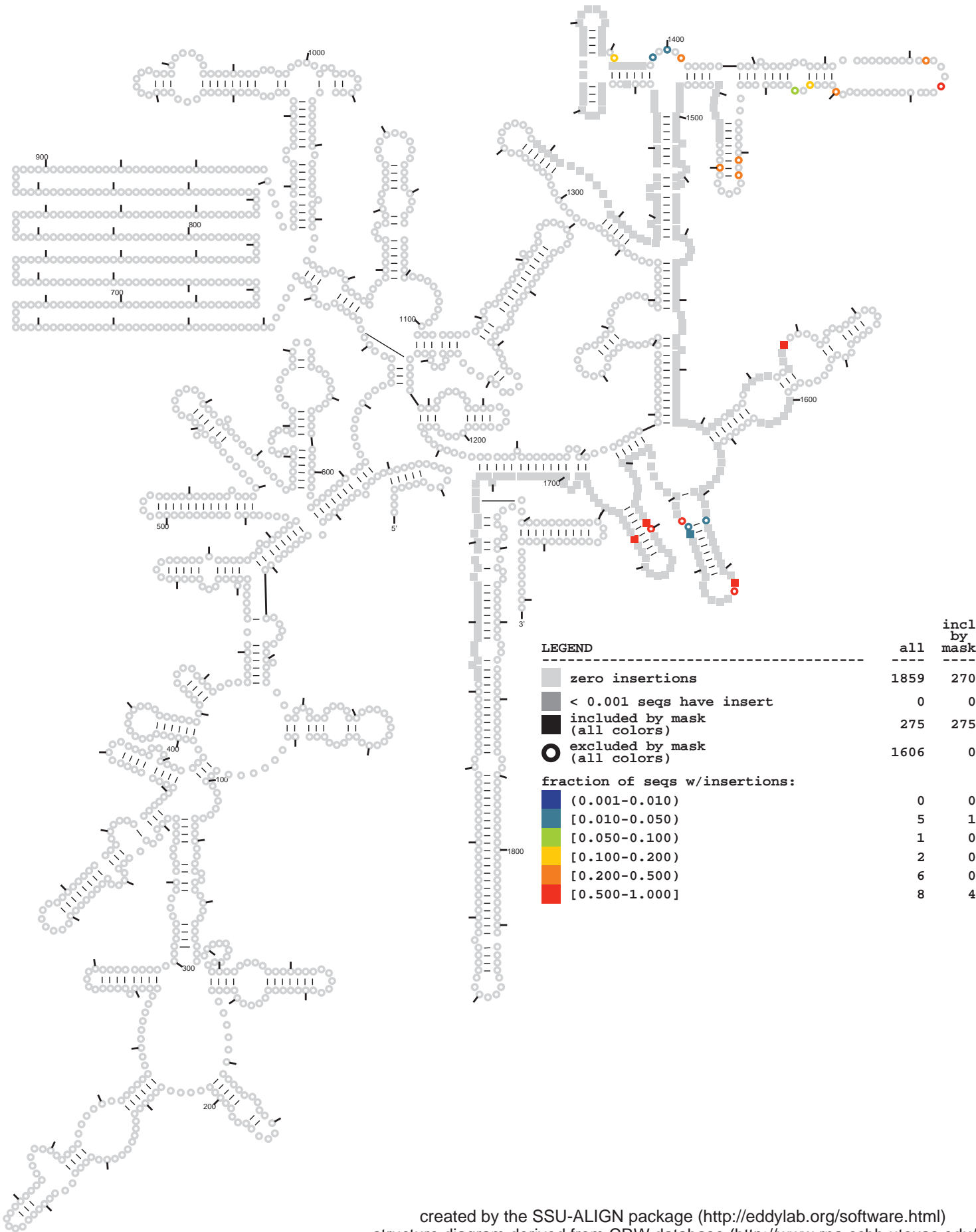
model	#pos	#bps	#seqs	description
eukarya	1881	448	67	information content per position



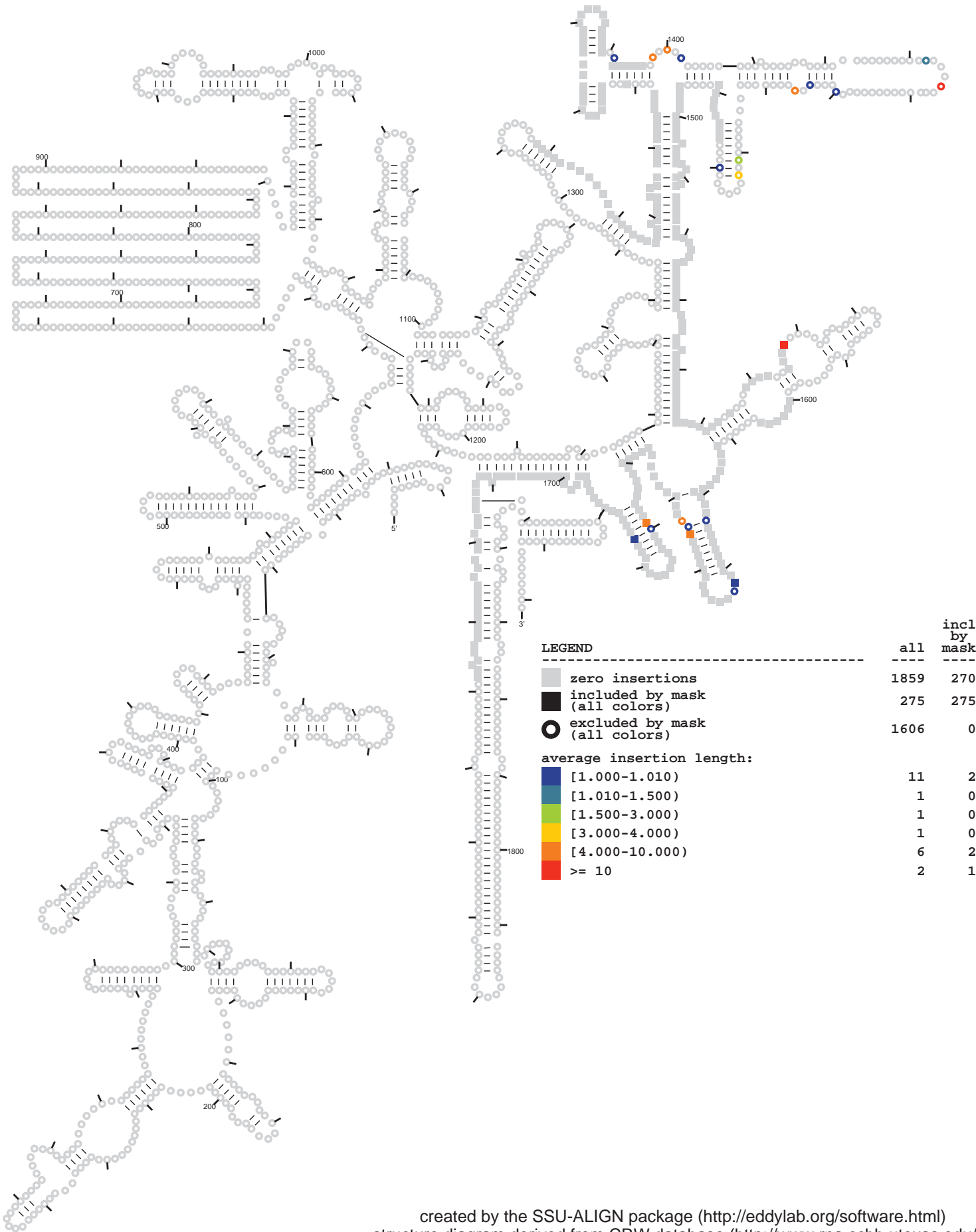
model	#pos	#bps	#seqs	description
eukarya	1881	448	67	mutual information per basepaired position



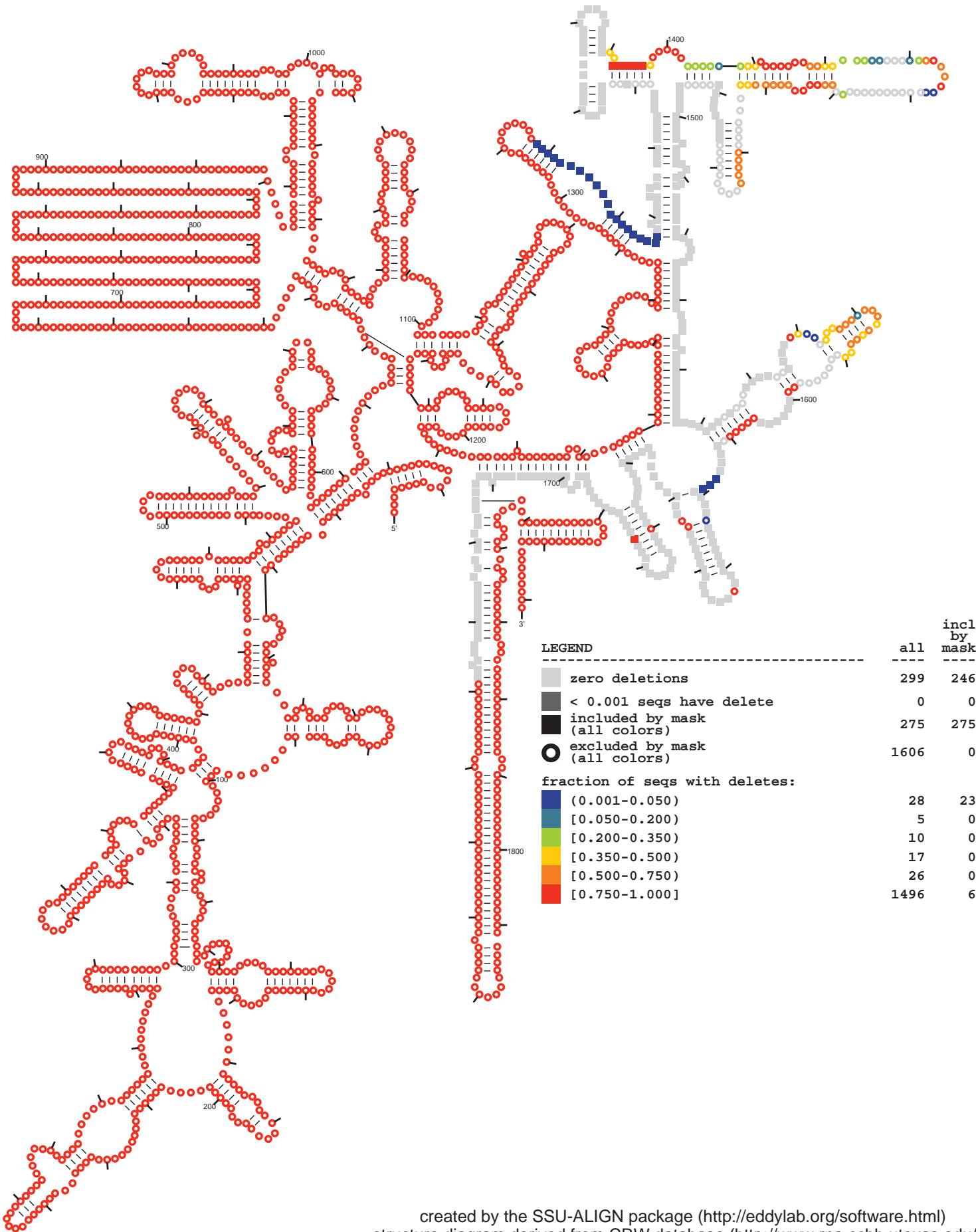
model	#pos	#bps	#seqs	description
eukarya	1881	448	67	frequency of insertions after each position



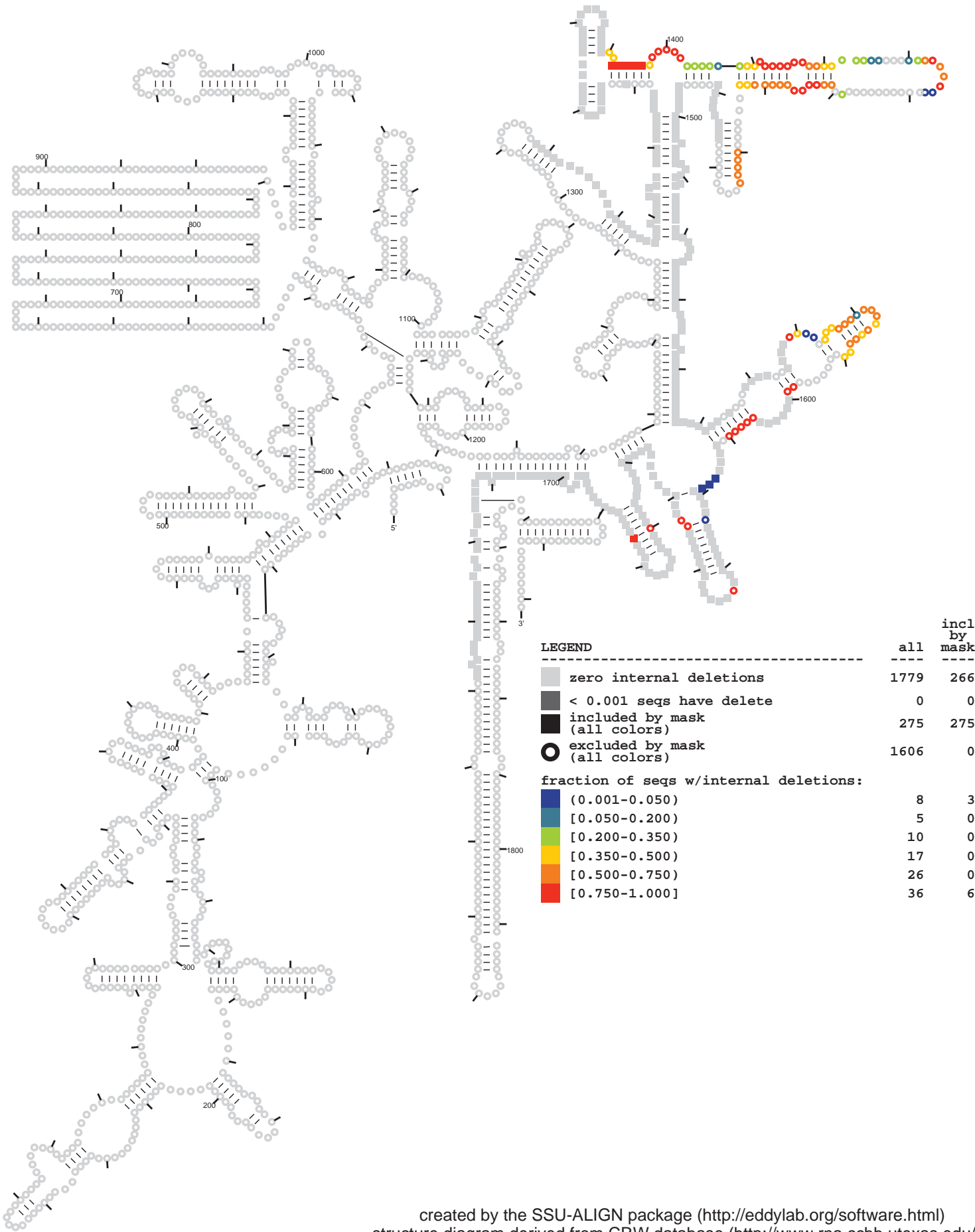
model	#pos	#bps	#seqs	description
eukarya	1881	448	67	average insertion length after each position



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

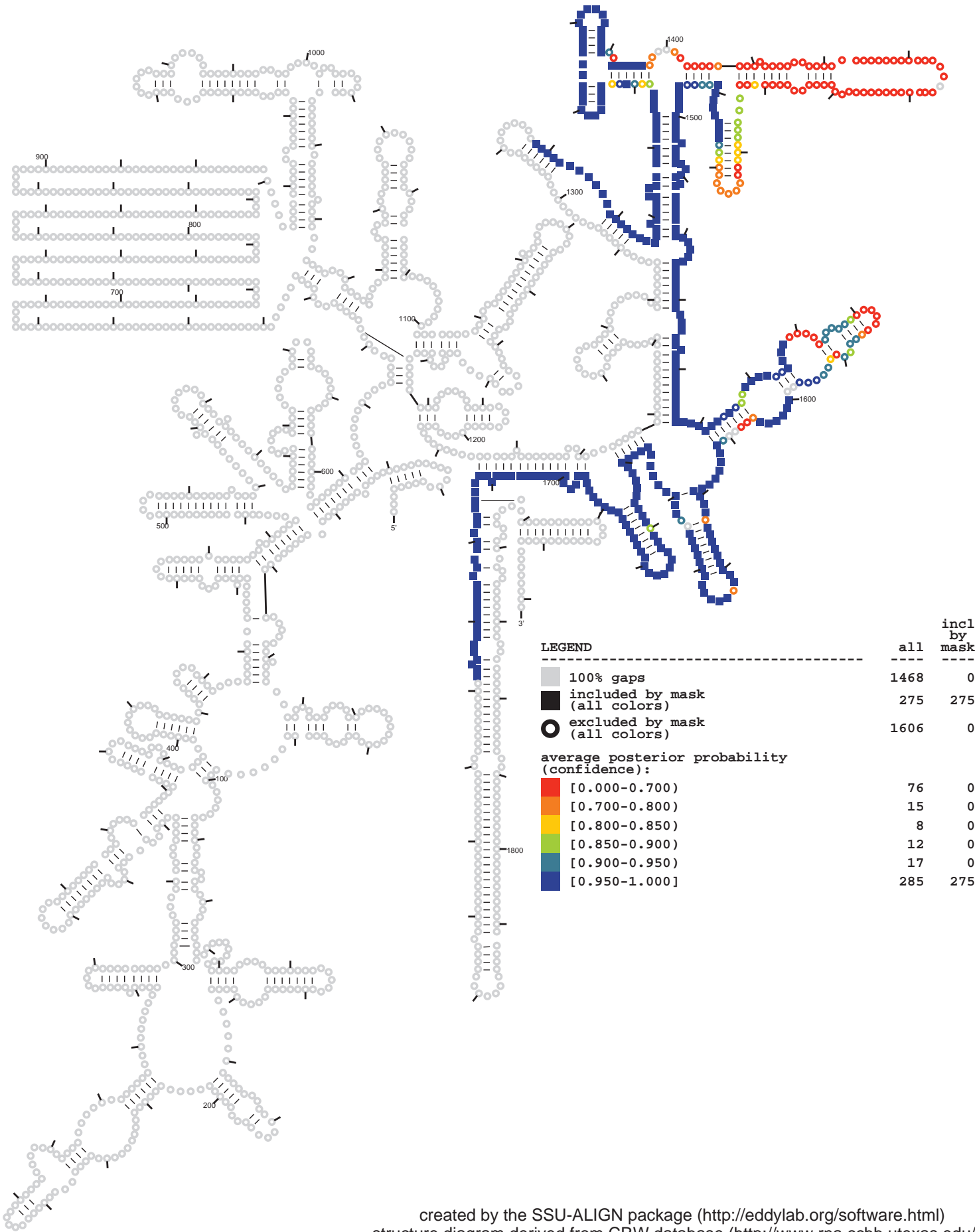


model	#pos	#bps	#seqs	description
eukarya	1881	448	67	frequency of internal deletions in each position



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

