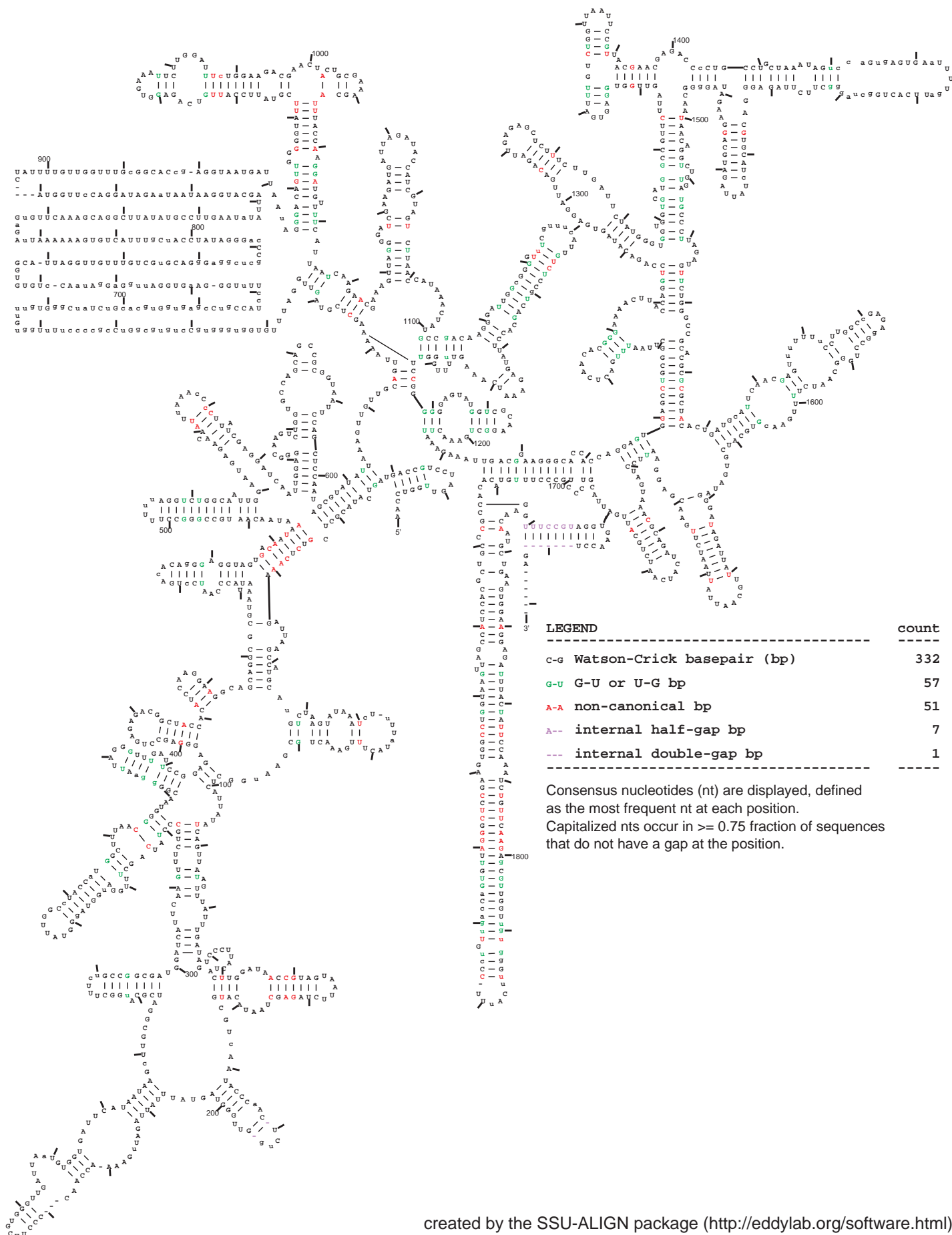


model #pos #bps

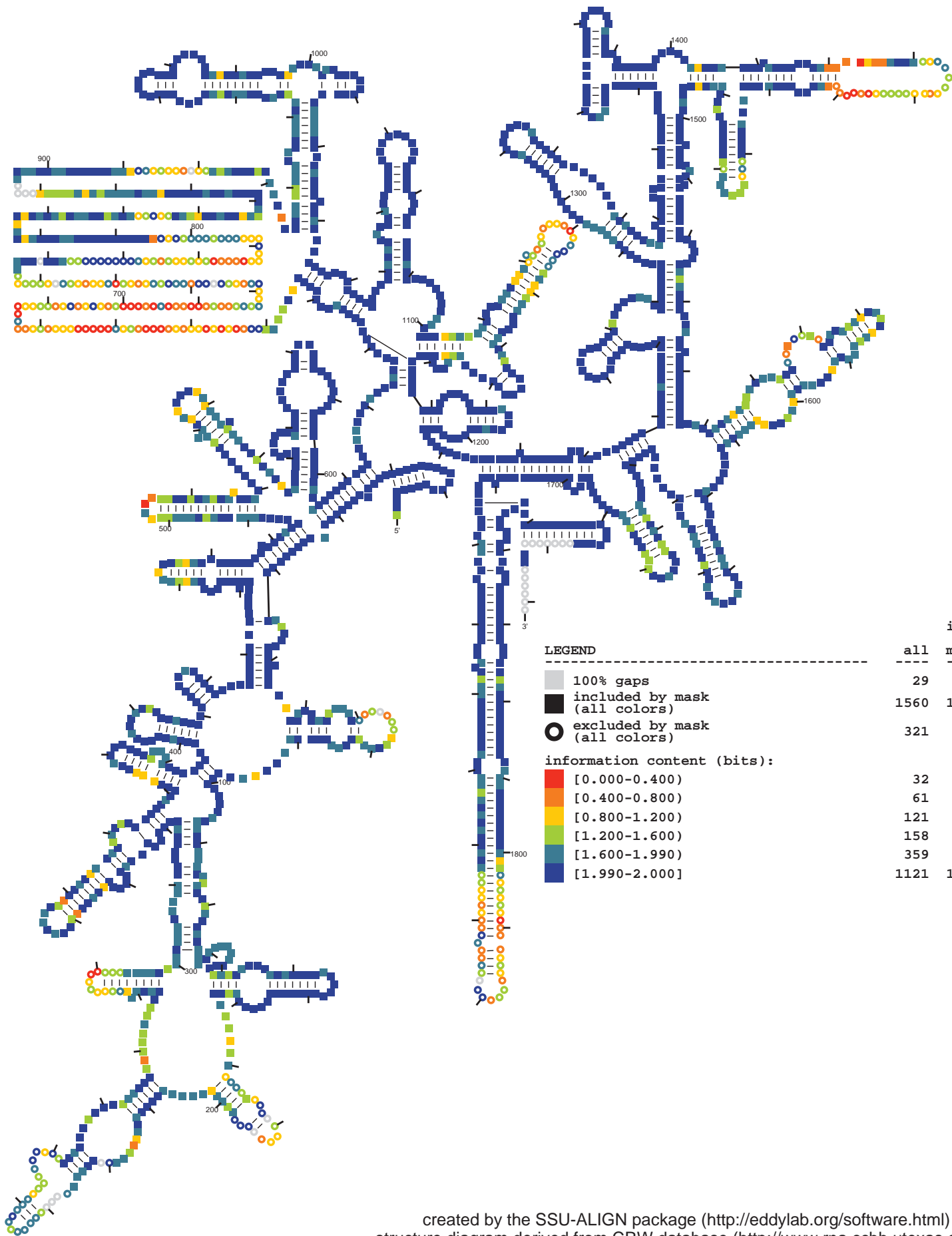
 eukarya 1881 448

sequence name

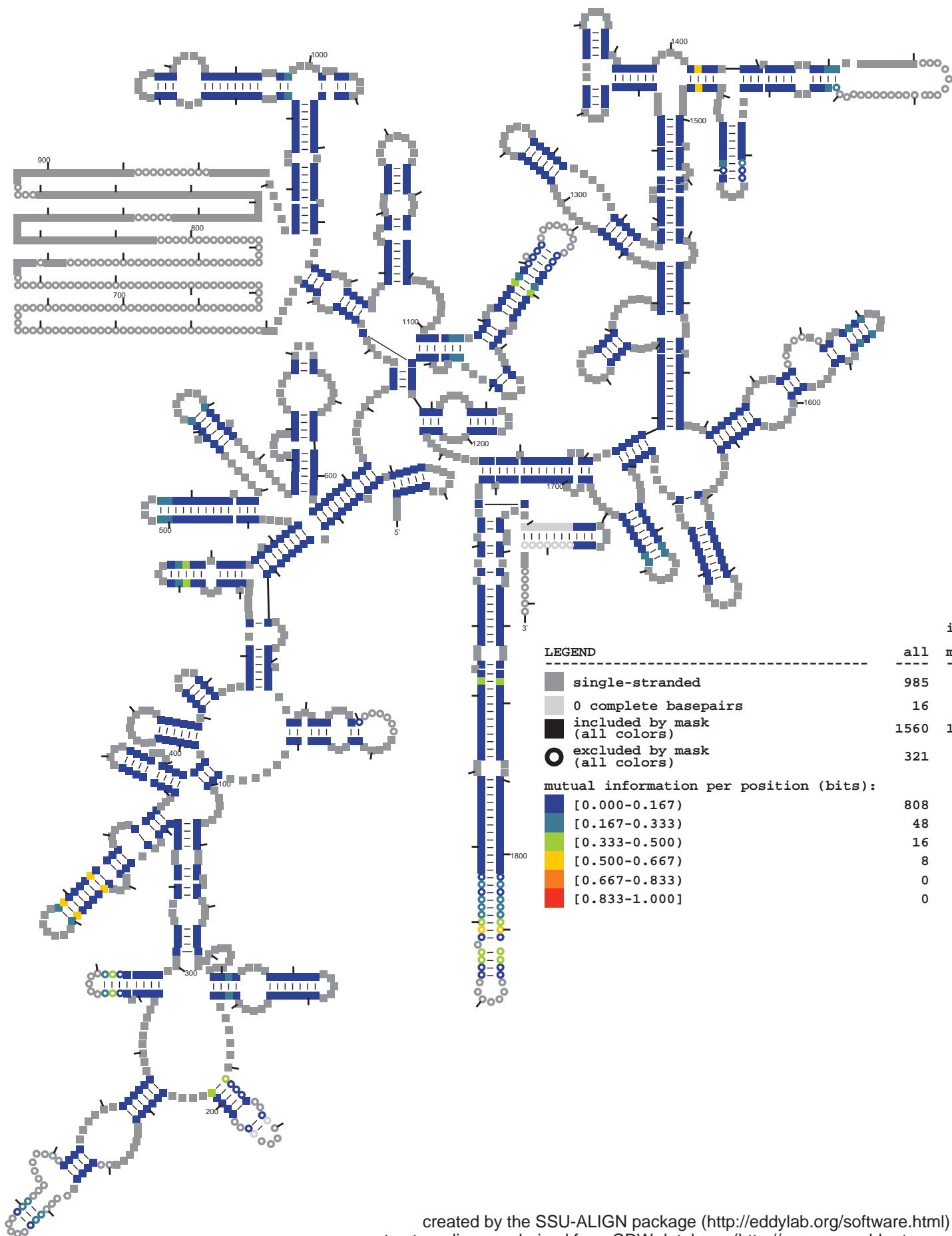
 alignment consensus sequence



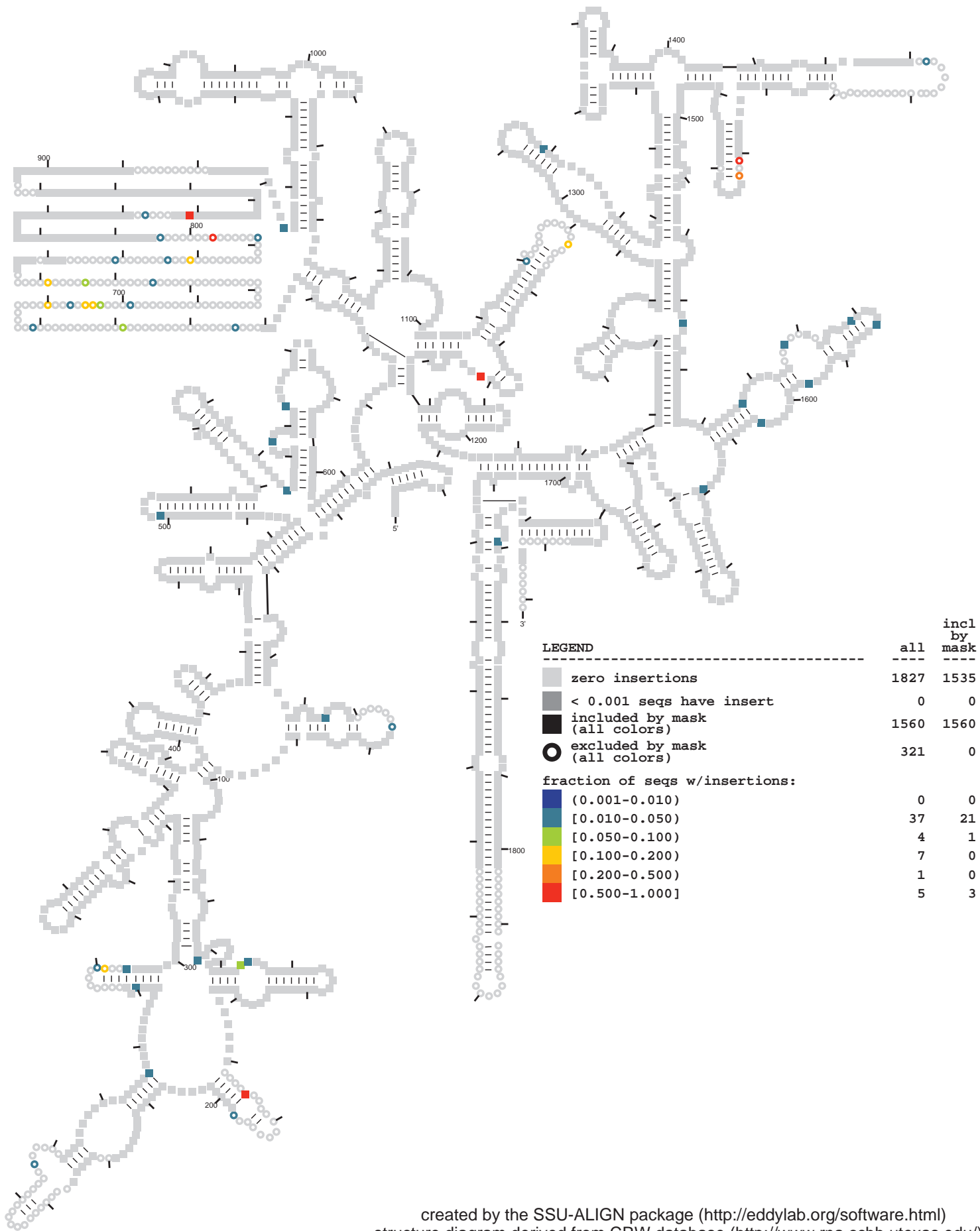
model	#pos	#bps	#seqs	description
eukarya	1881	448	94	information content per position



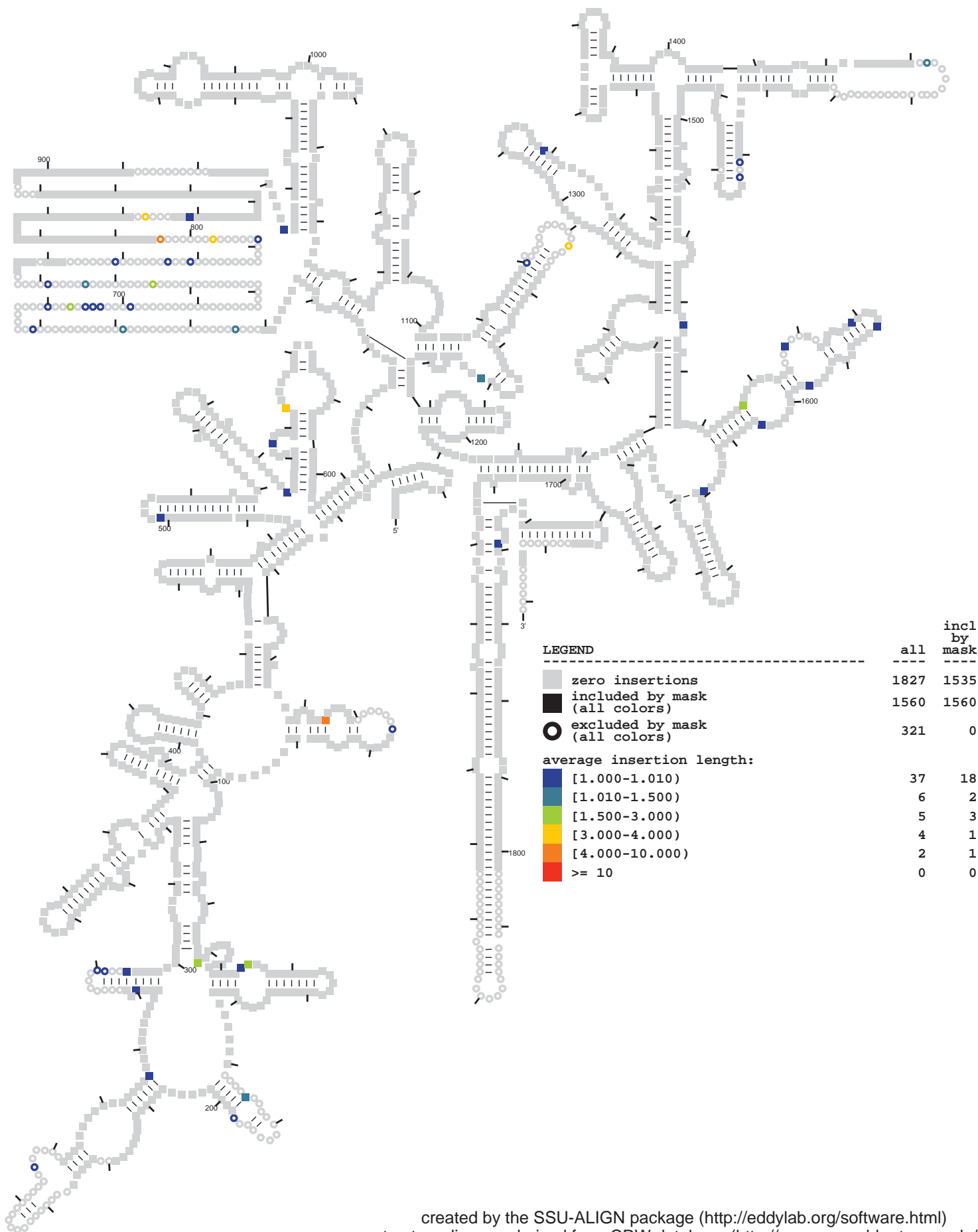
model	#pos	#bps	#seqs	description
eukarya	1881	448	94	mutual information per basepaired position



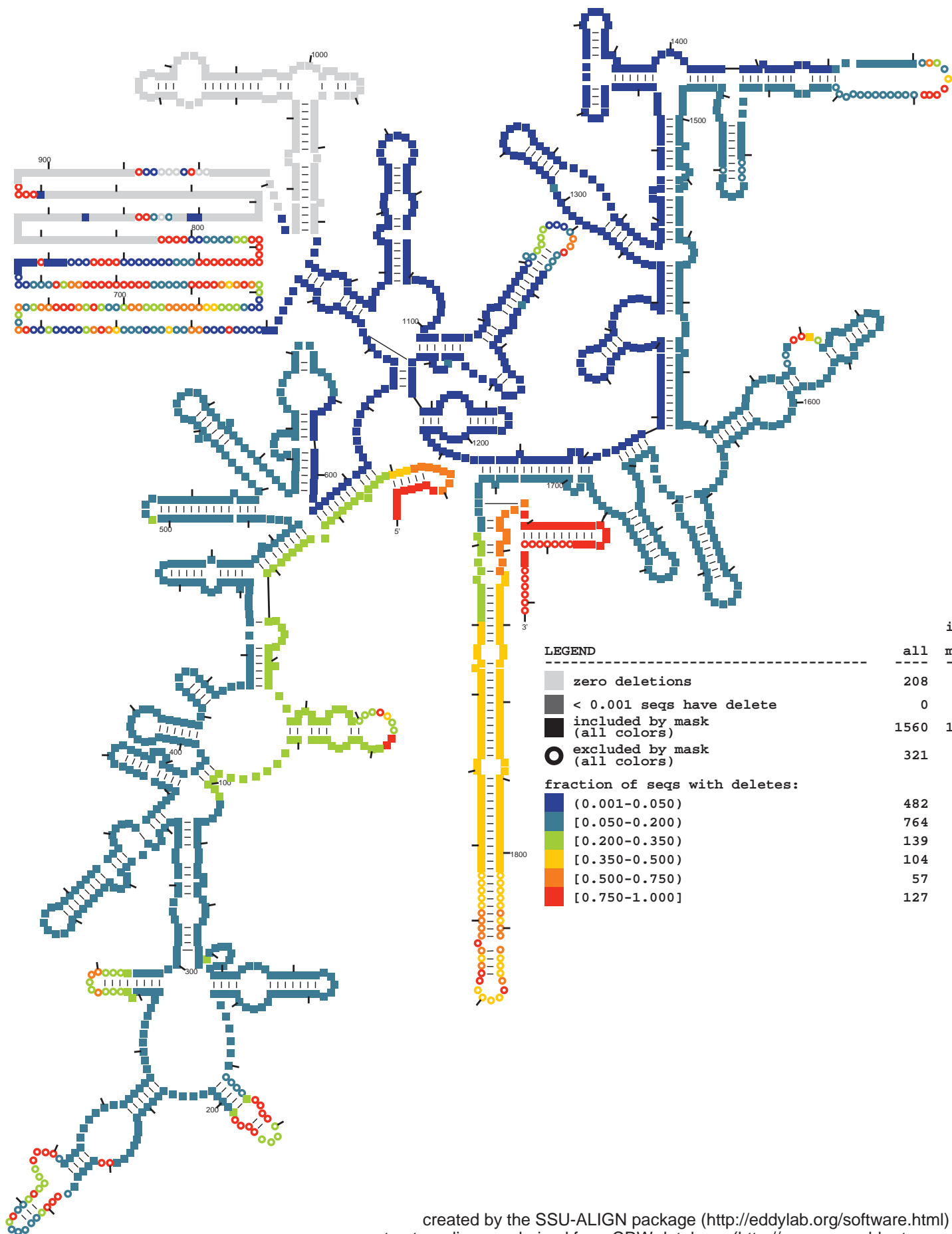
model	#pos	#bps	#seqs	description
eukarya	1881	448	94	frequency of insertions after each position



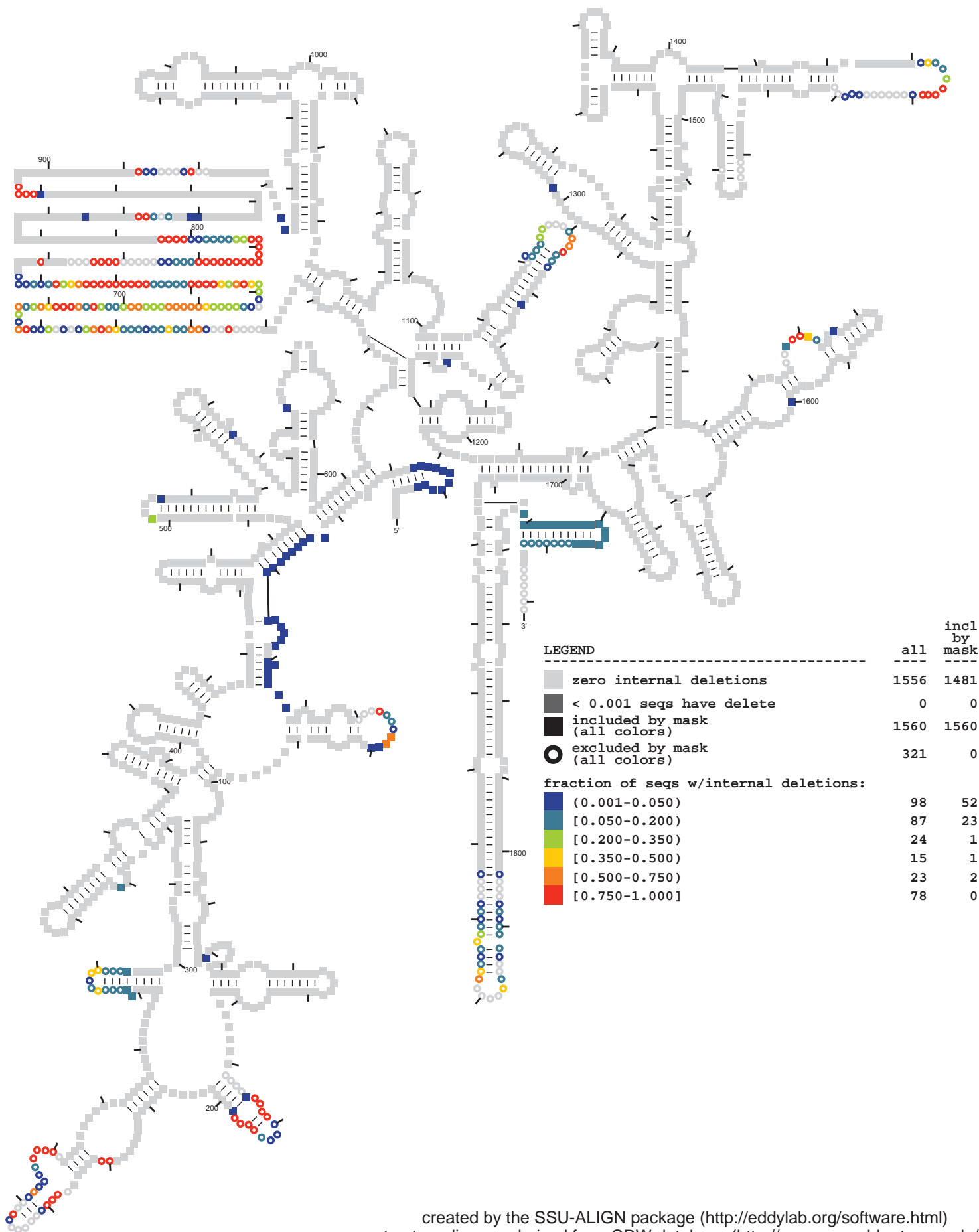
model	#pos	#bps	#seqs	description
eukarya	1881	448	94	average insertion length after each position



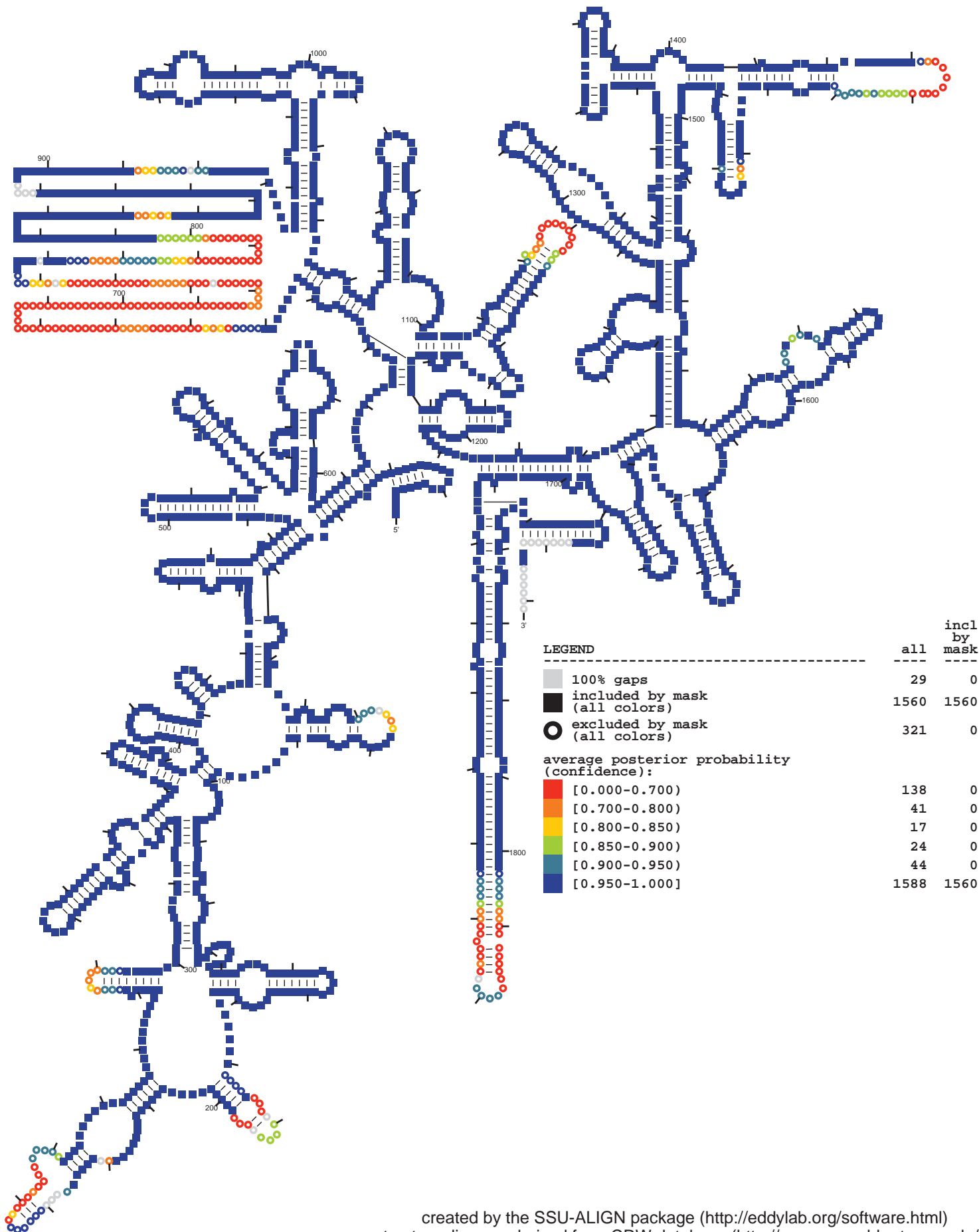
model	#pos	#bps	#seqs	description
eukarya	1881	448	94	frequency of deletions at each position



model	#pos	#bps	#seqs	description
eukarya	1881	448	94	frequency of internal deletions in each position



model	#pos	#bps	#seqs	description
eukarya	1881	448	94	average posterior probability per position



model	#pos	#bps	#seqs	description
eukarya	1881	448	94	fraction of sequences that span each position

