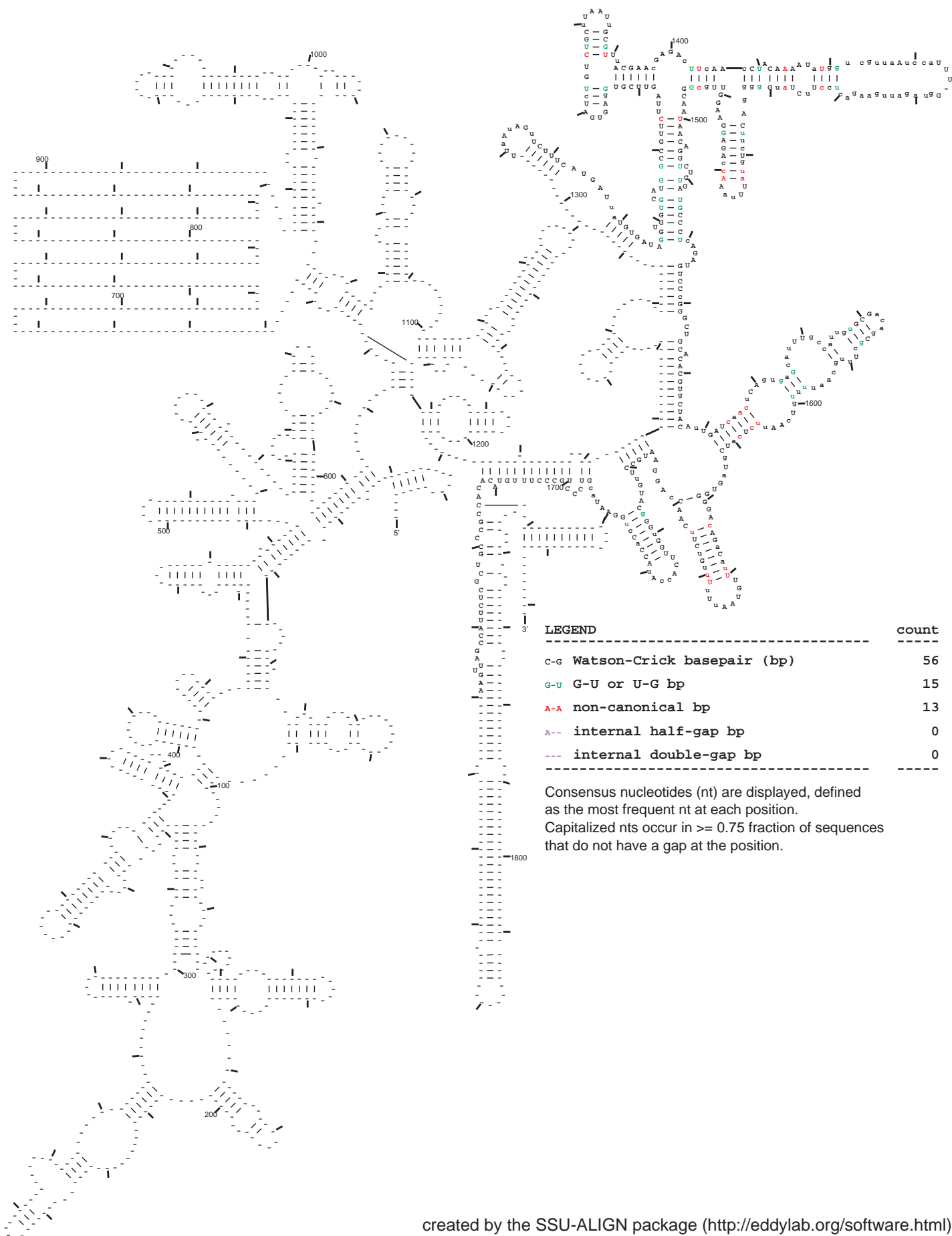
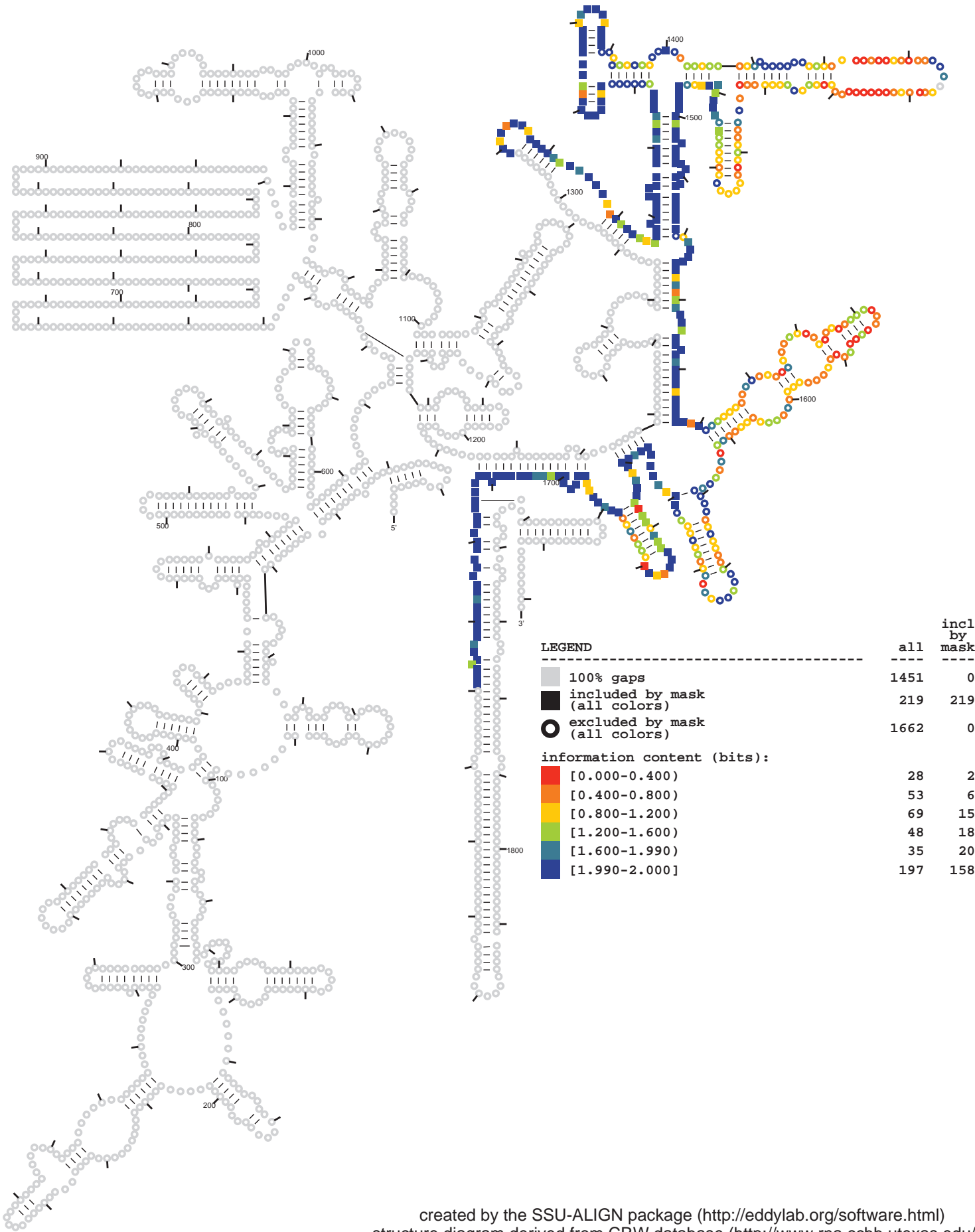


model	#pos	#bps
eukarya	1881	448

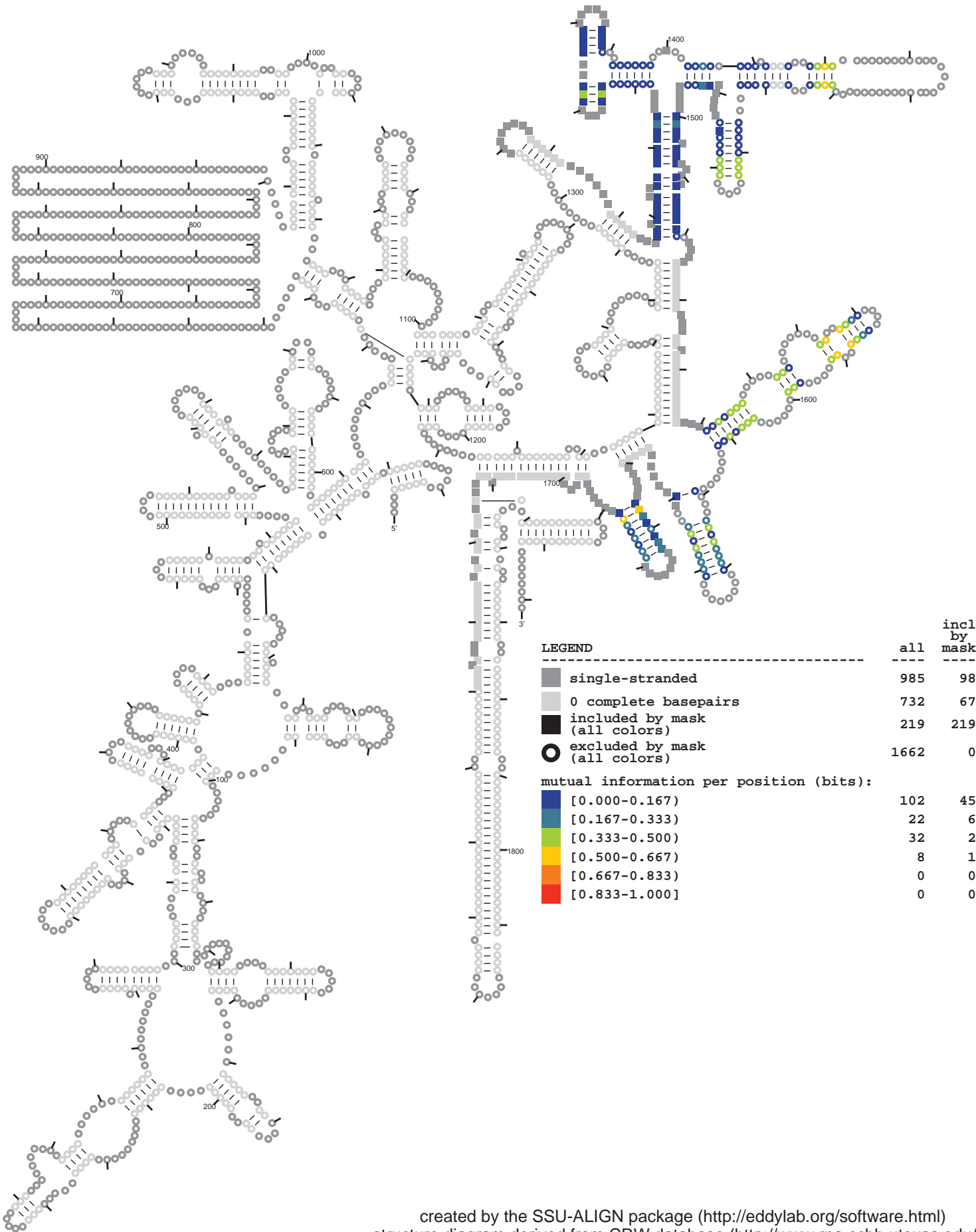
sequence name
alignment consensus sequence



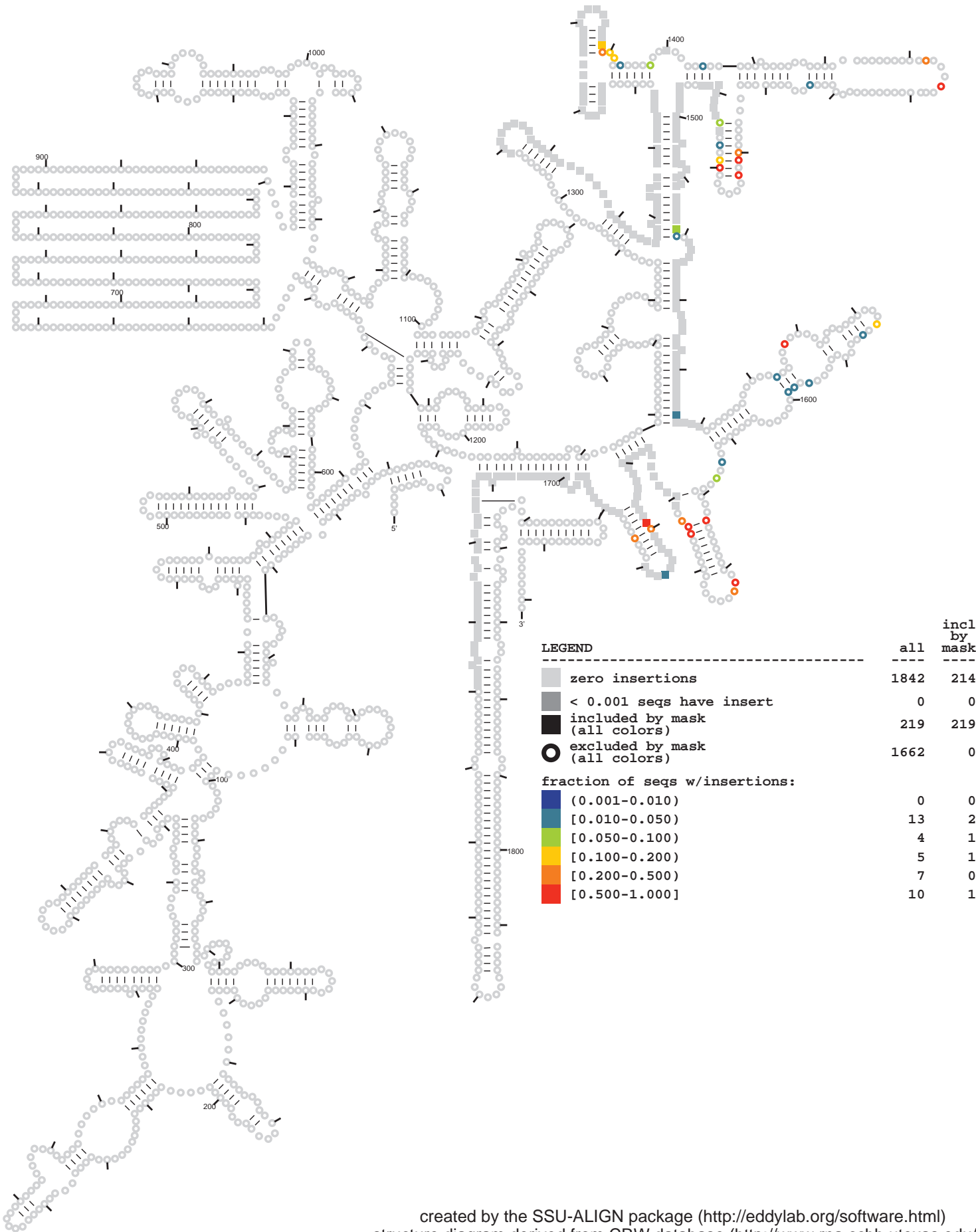
model	#pos	#bps	#seqs	description
eukarya	1881	448	80	information content per position



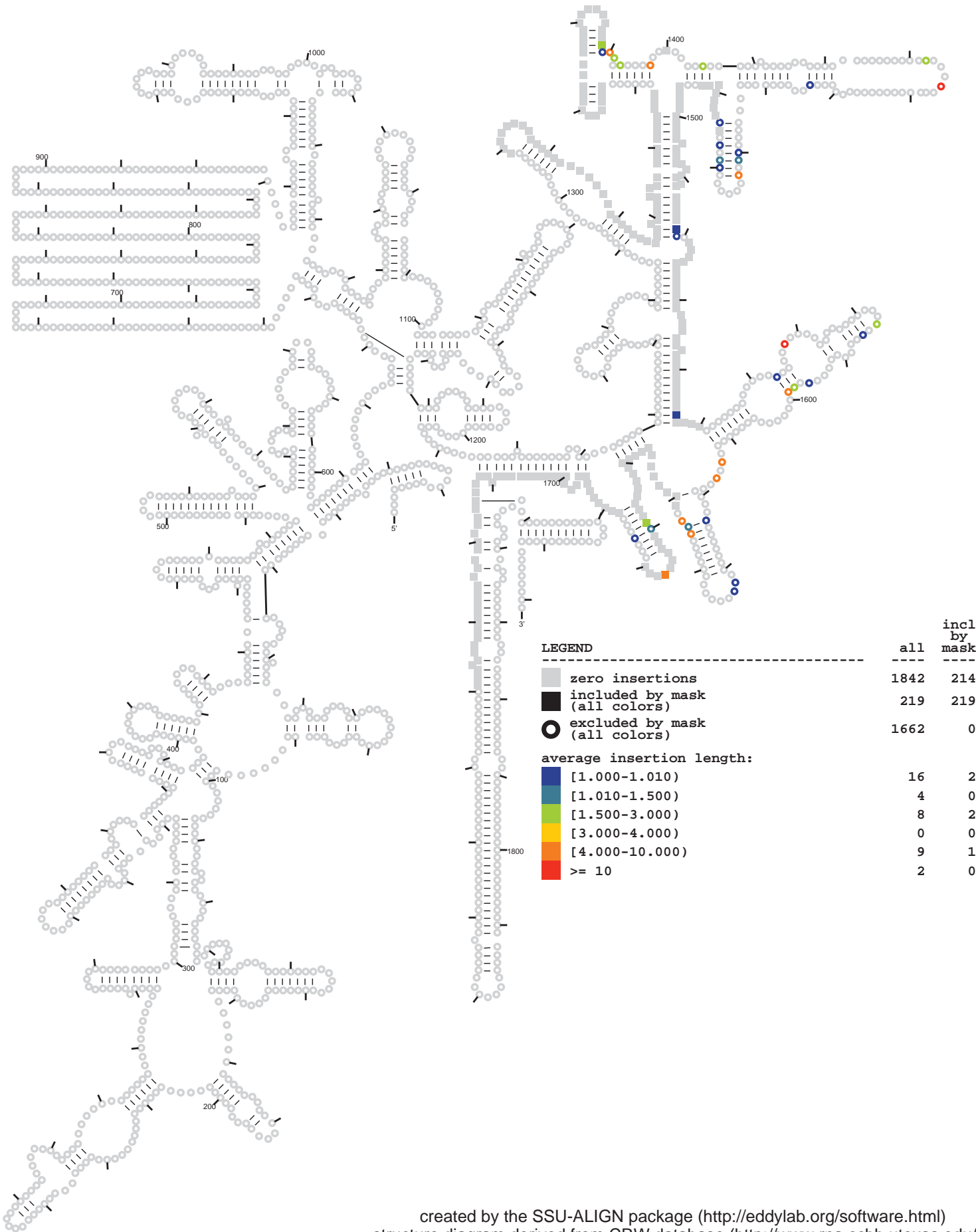
model	#pos	#bps	#seqs	description
eukarya	1881	448	80	mutual information per basepaired position



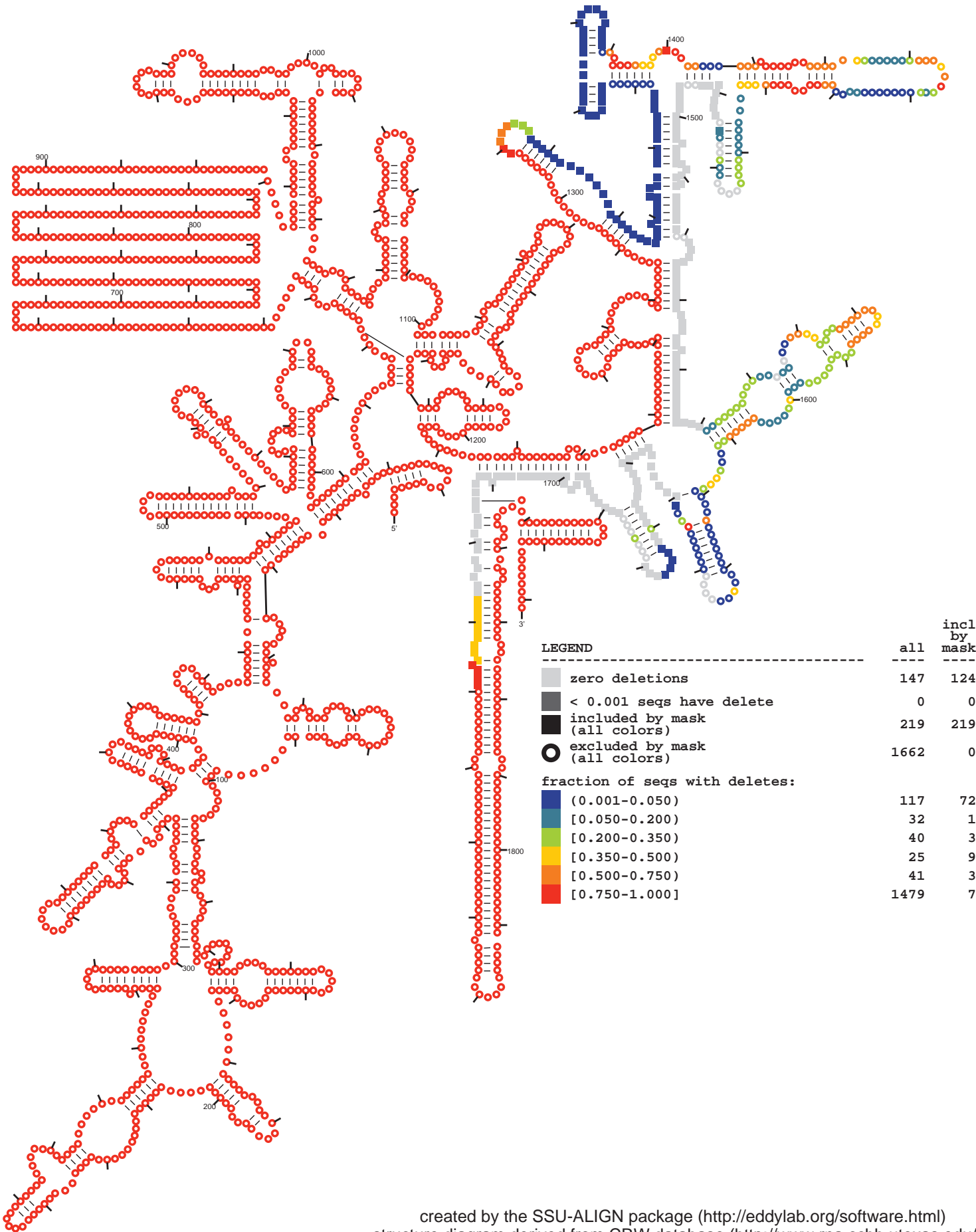
model	#pos	#bps	#seqs	description
eukarya	1881	448	80	frequency of insertions after each position



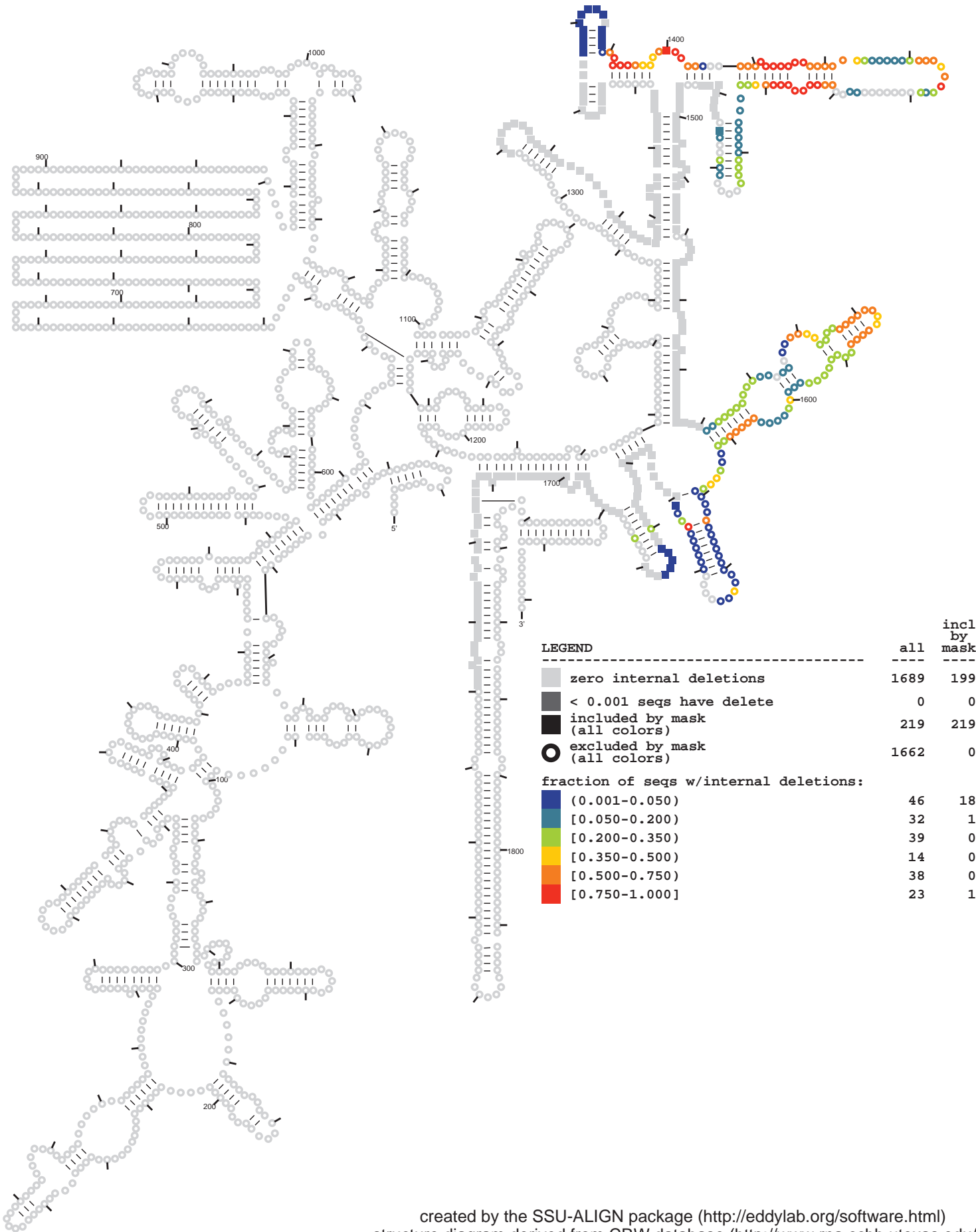
model	#pos	#bps	#seqs	description
eukarya	1881	448	80	average insertion length after each position



model	#pos	#bps	#seqs	description
eukarya	1881	448	80	frequency of deletions at each position

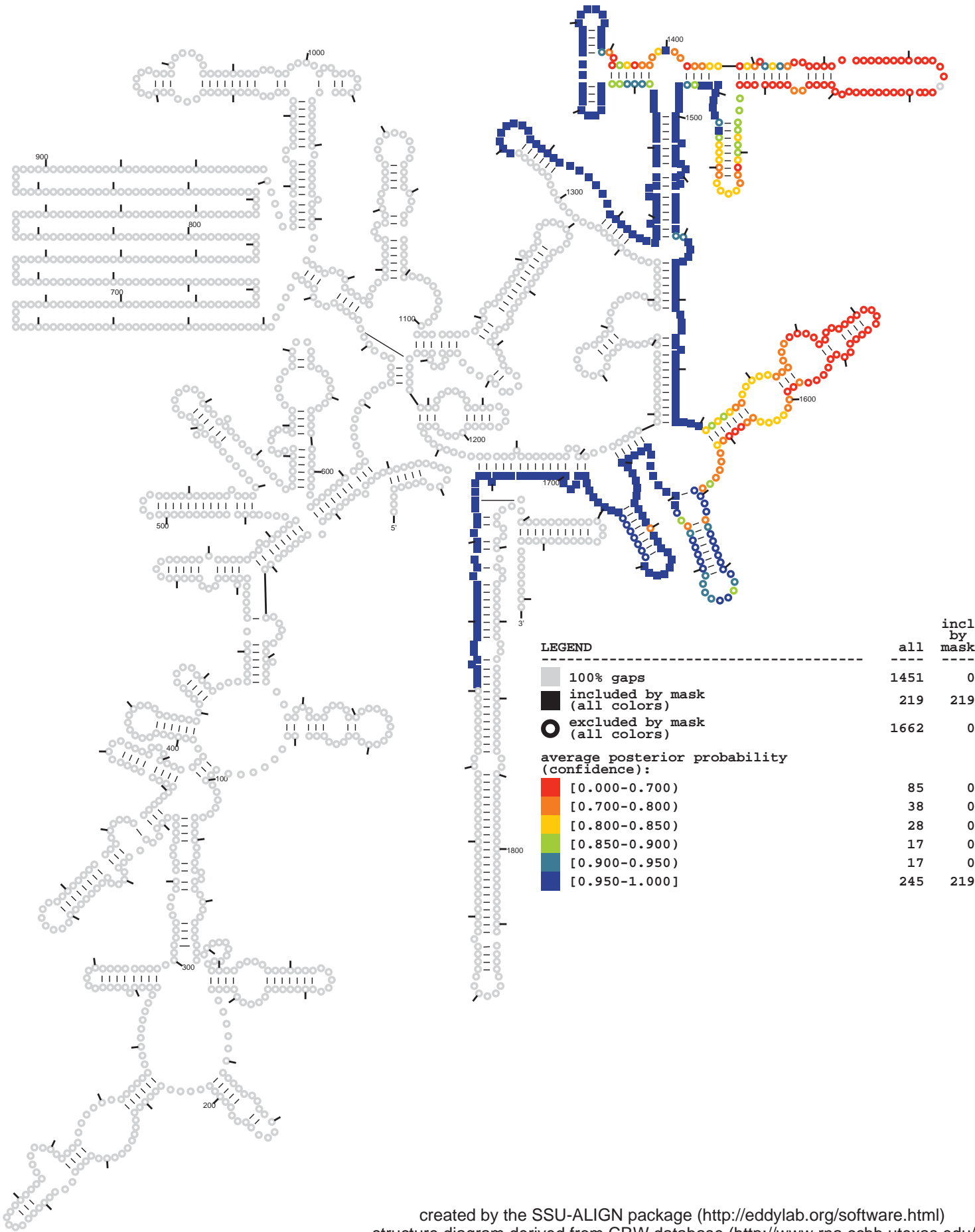


model	#pos	#bps	#seqs	description
eukarya	1881	448	80	frequency of internal deletions in each position



model	#pos	#bps	#seqs	description
eukarya	1881	448	80	

average posterior probability per position



model	#pos	#bps	#seqs	description
eukarya	1881	448	80	fraction of sequences that span each position

