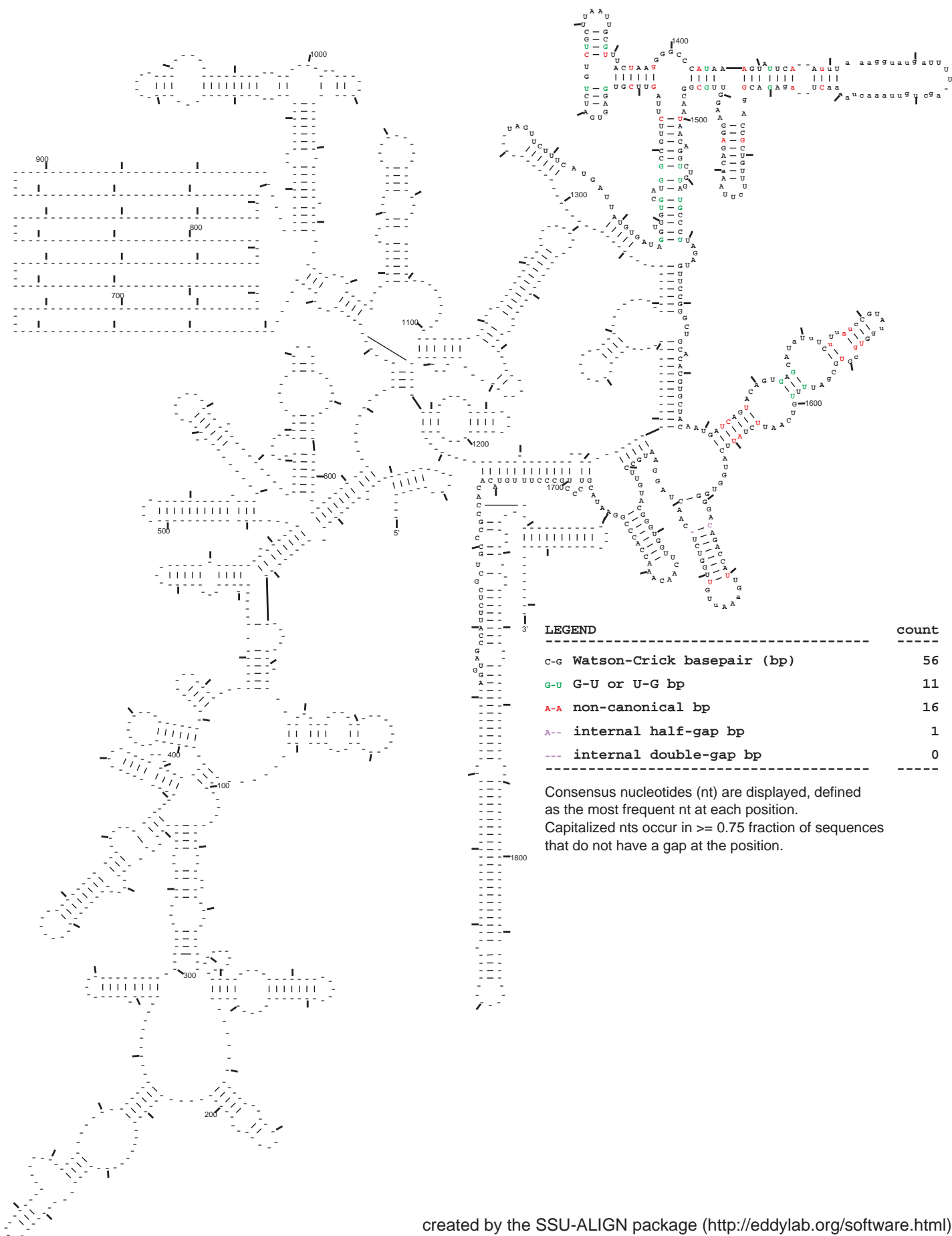
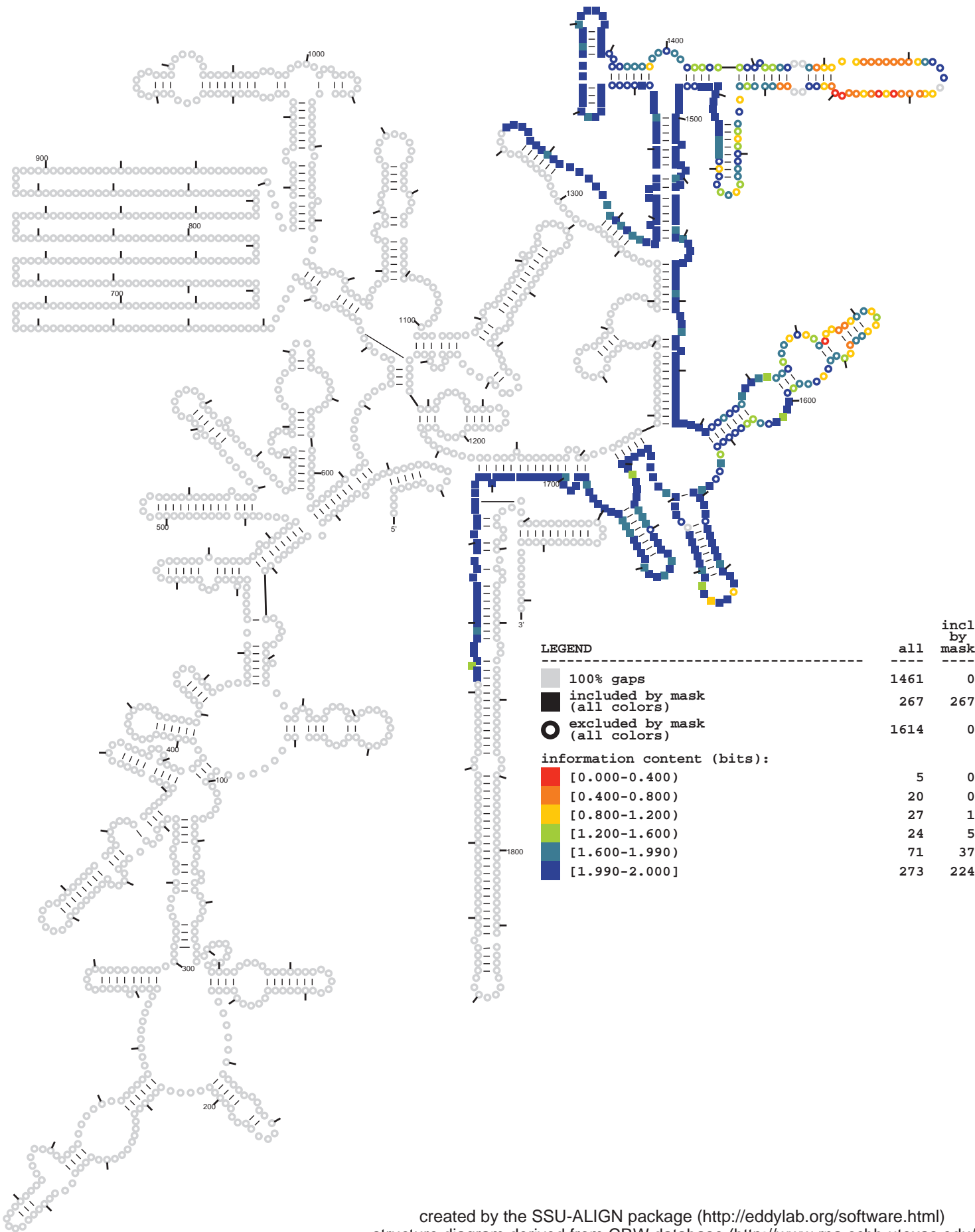


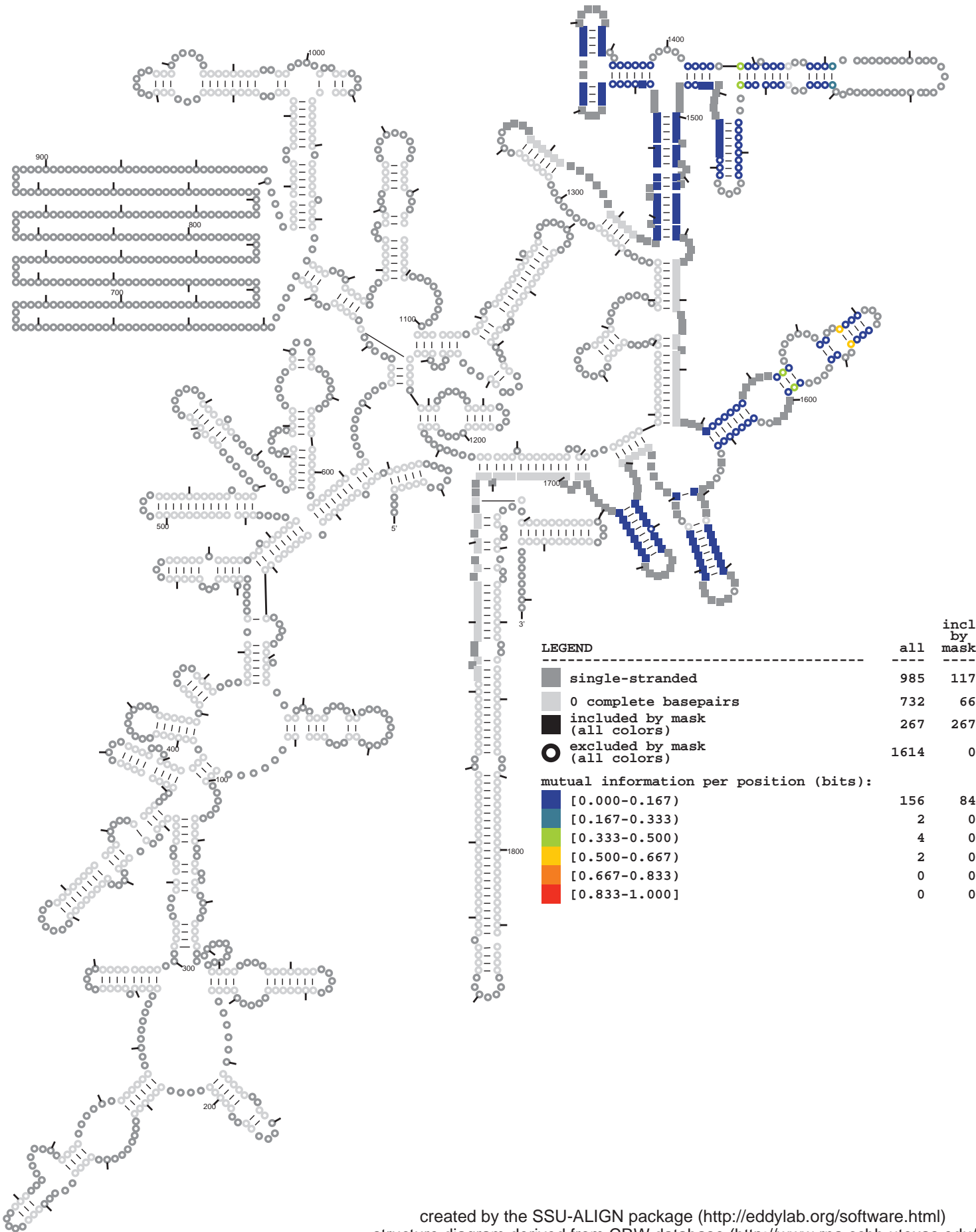
model	#pos	#bps
eukarya	1881	448

sequence name
alignment consensus sequence

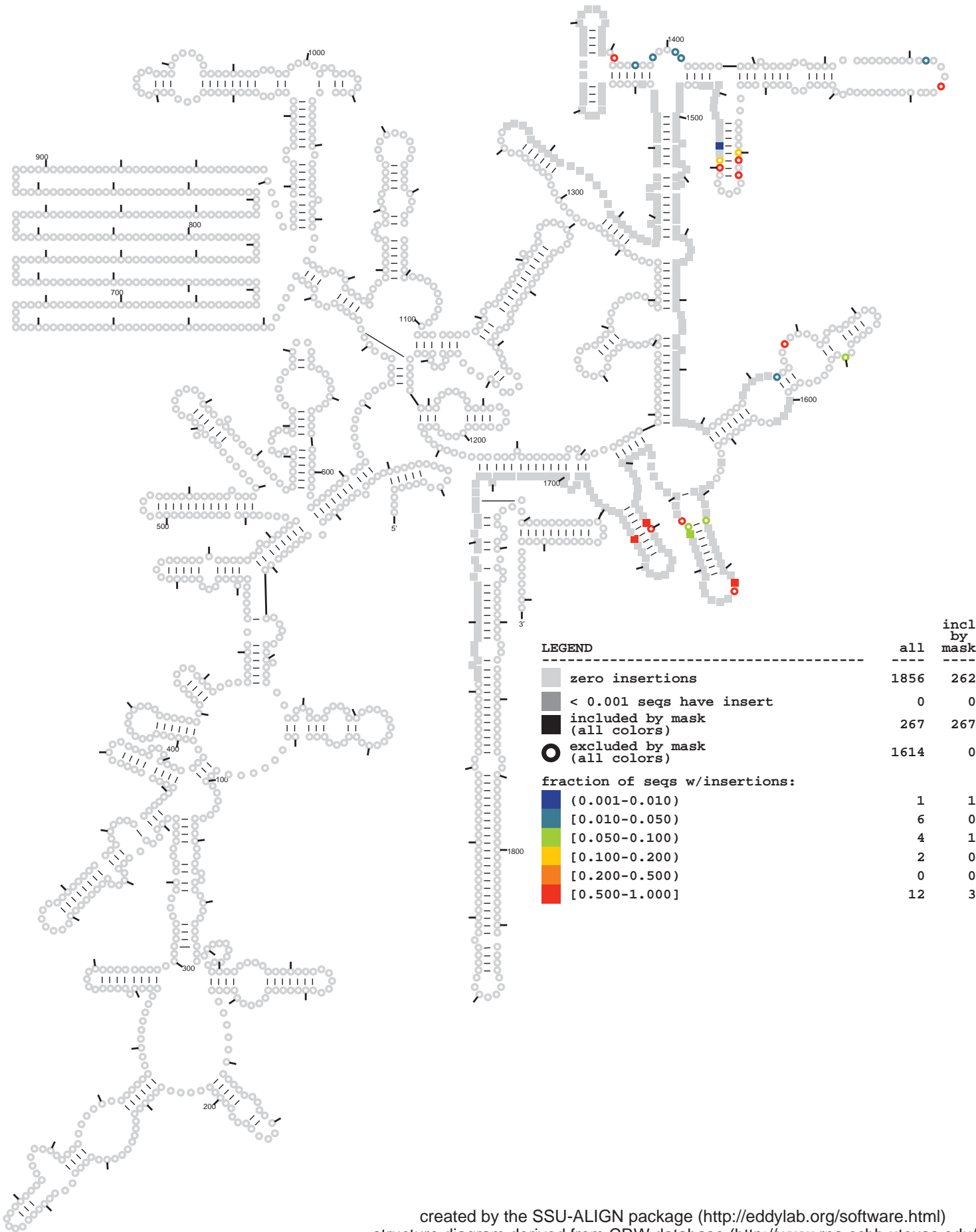




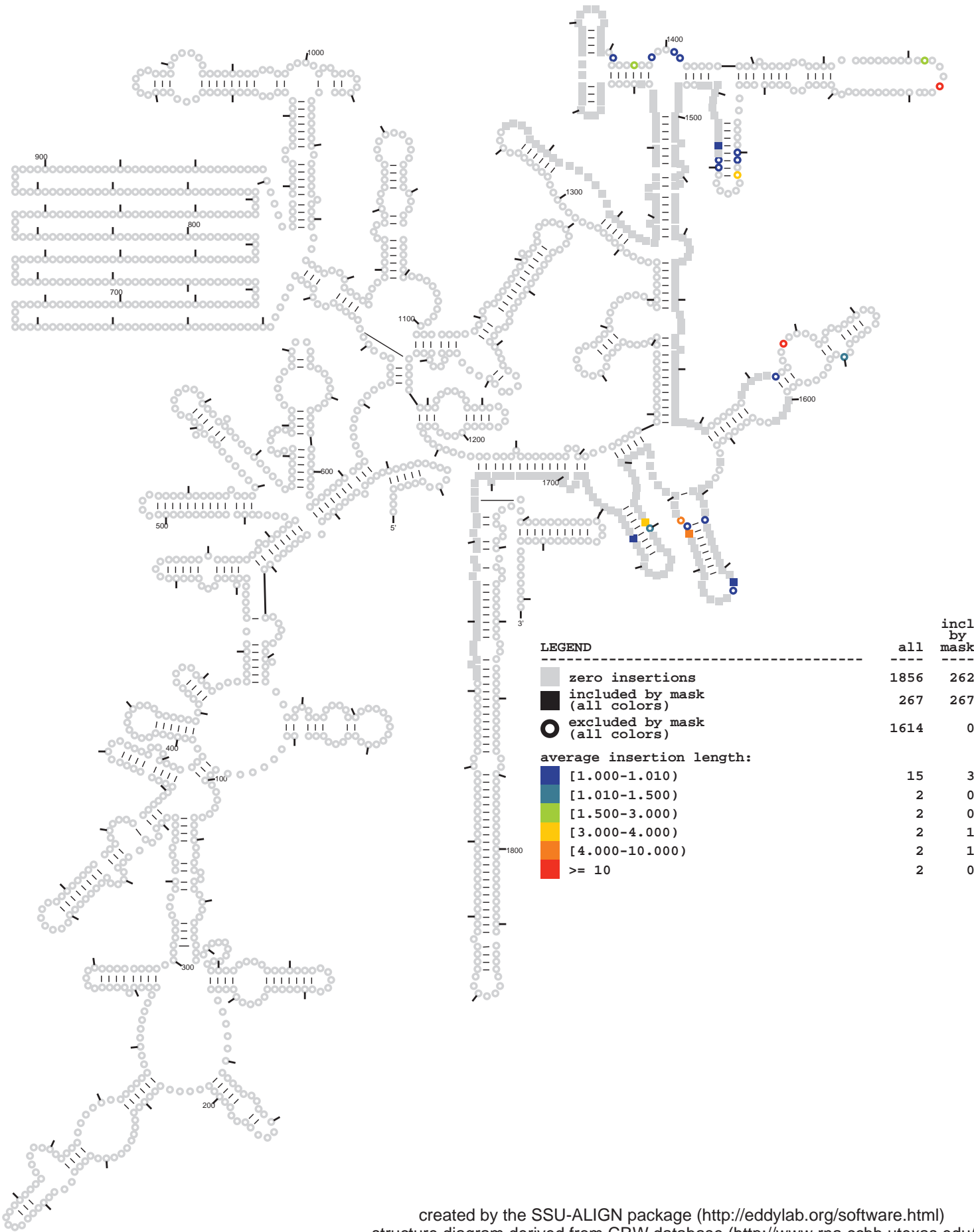
model	#pos	#bps	#seqs	description
eukarya	1881	448	206	mutual information per basepaired position



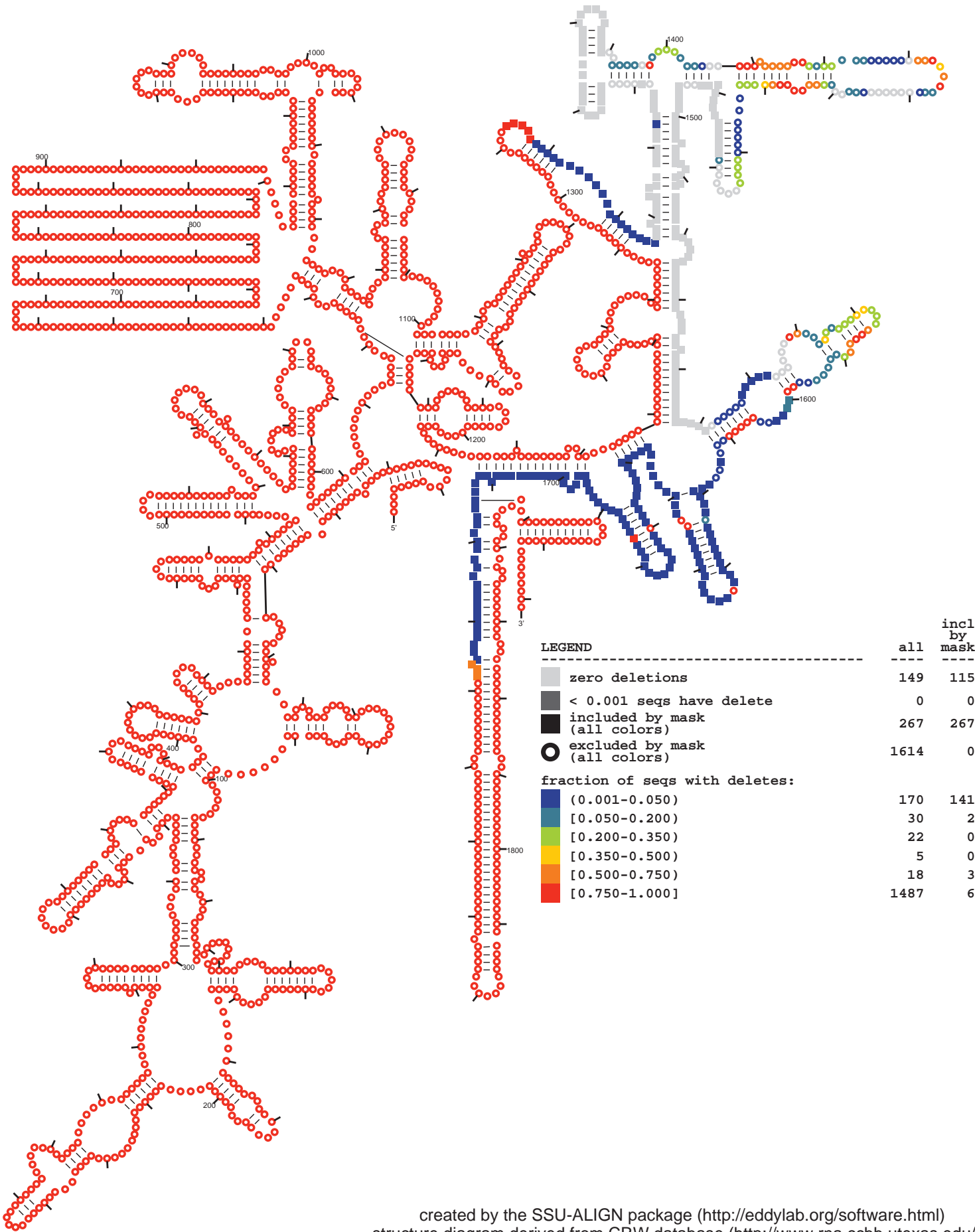
model	#pos	#bps	#seqs	description
eukarya	1881	448	206	frequency of insertions after each position



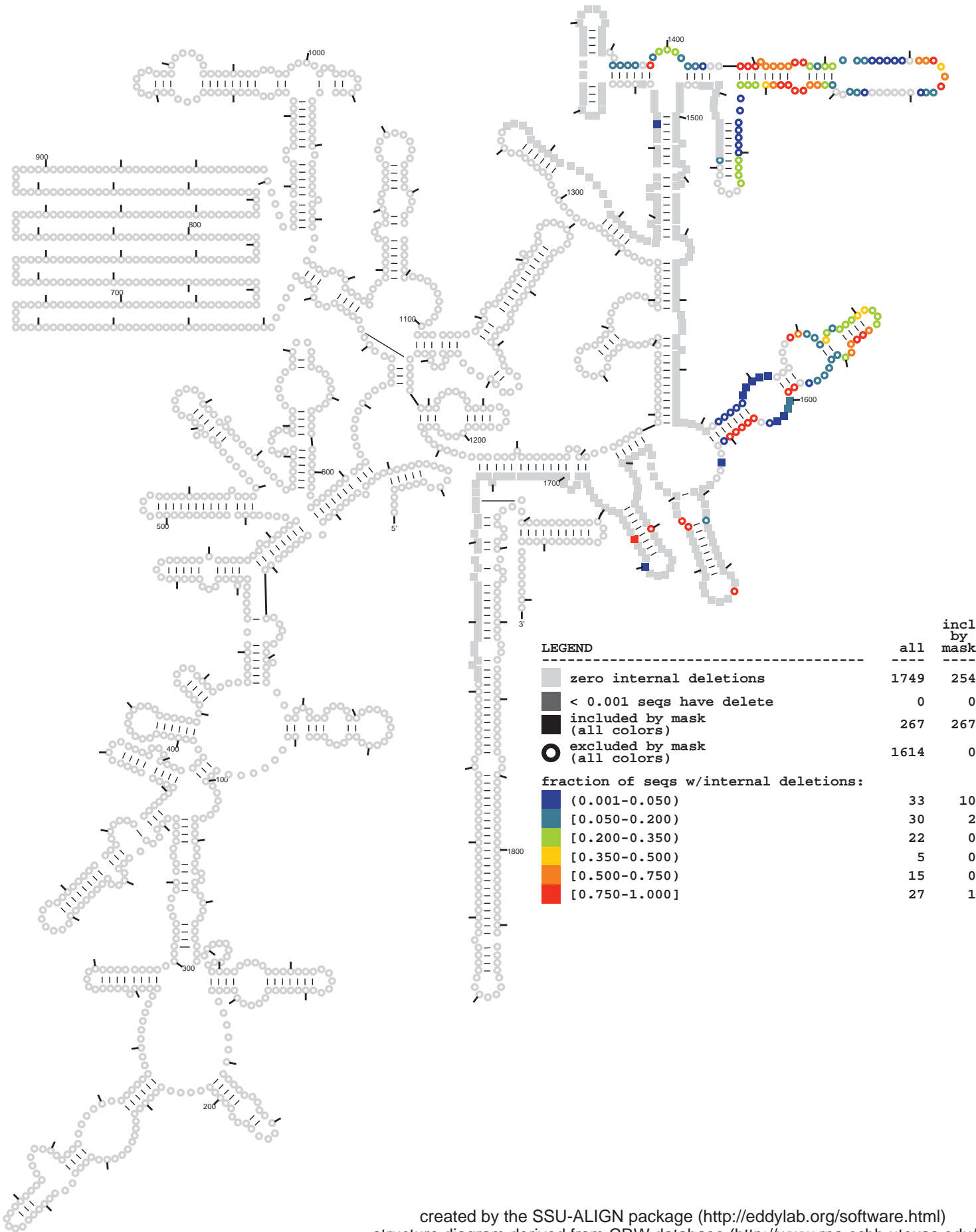
model	#pos	#bps	#seqs	description
eukarya	1881	448	206	average insertion length after each position



model	#pos	#bps	#seqs	description
eukarya	1881	448	206	frequency of deletions at each position



model	#pos	#bps	#seqs	description
eukarya	1881	448	206	frequency of internal deletions in each position



model

#pos

#bps

#seqs

description

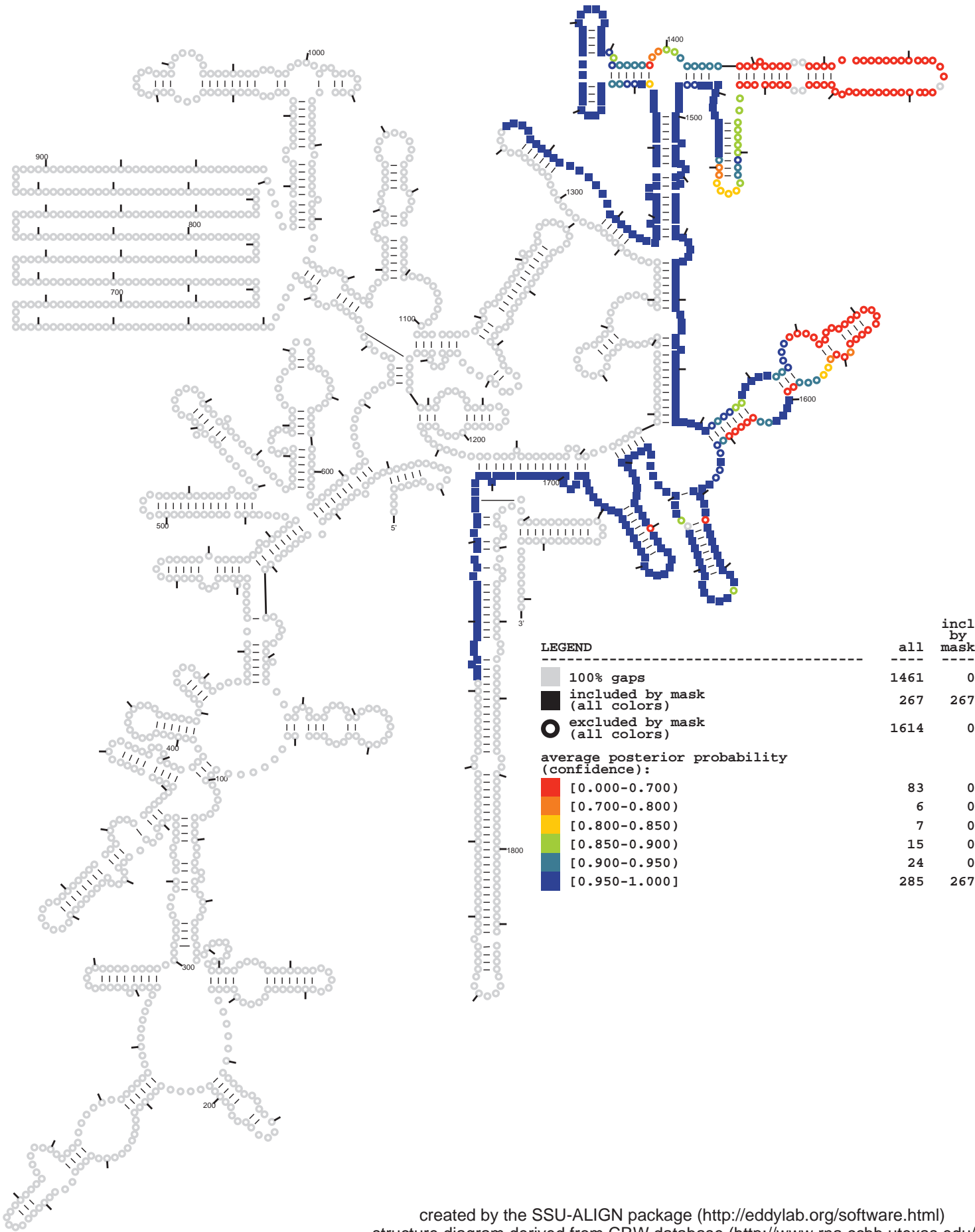
eukarya

1881

448

206

average posterior probability per position



model	#pos	#bps	#seqs	description
eukarya	1881	448	206	fraction of sequences that span each position

