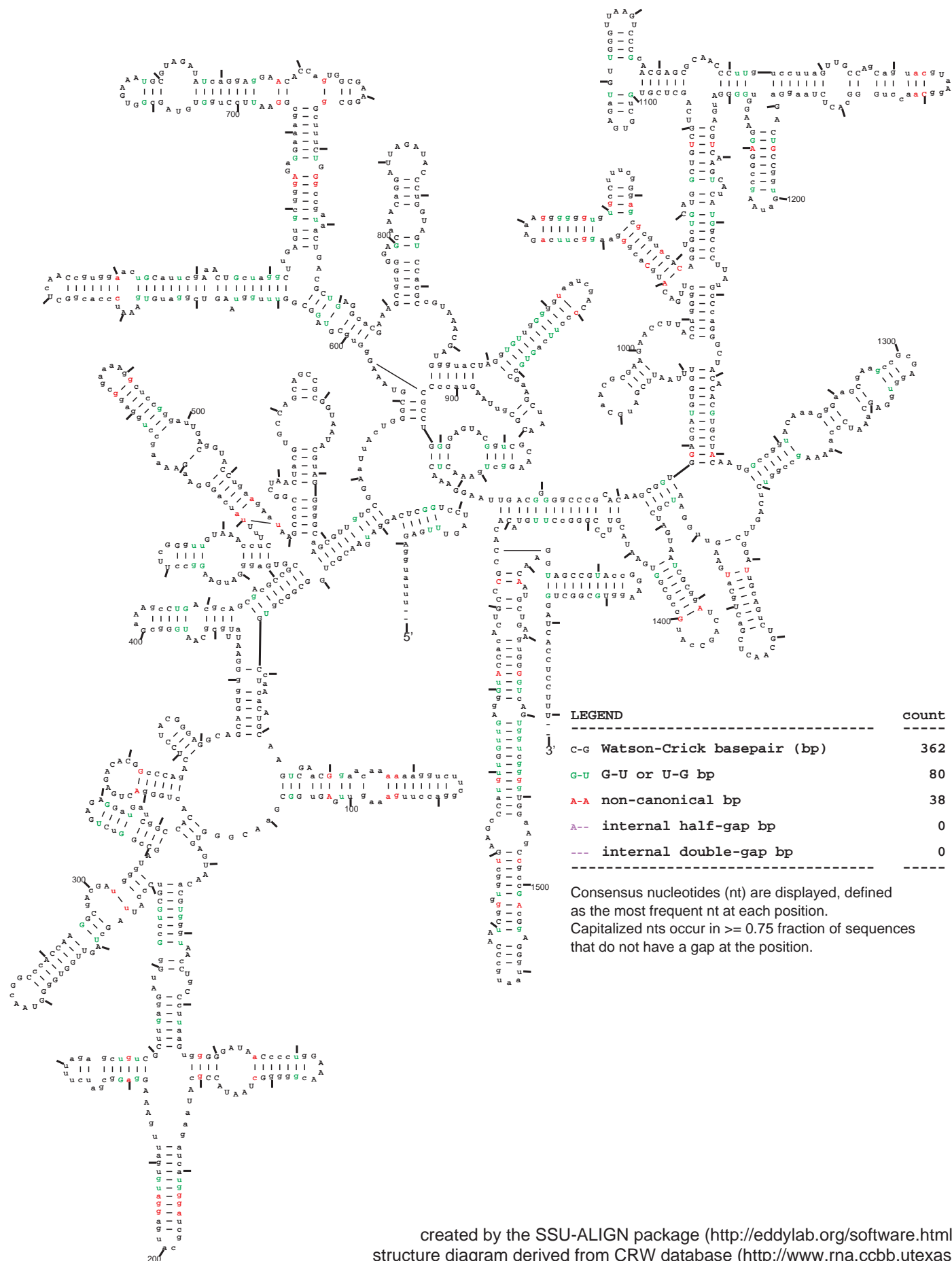
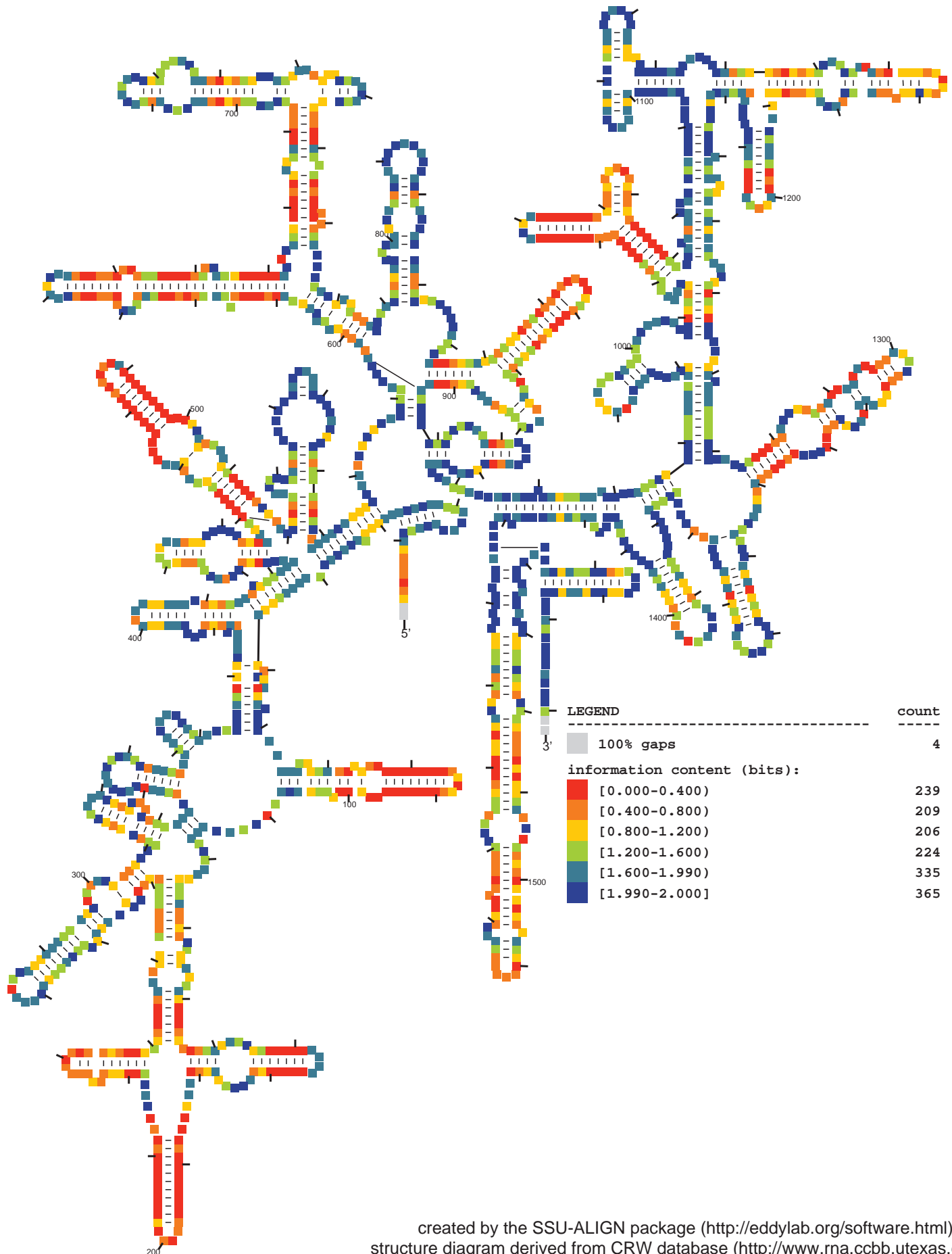


model	#pos	#bps
bacteria	1582	480

sequence name
alignment consensus sequence

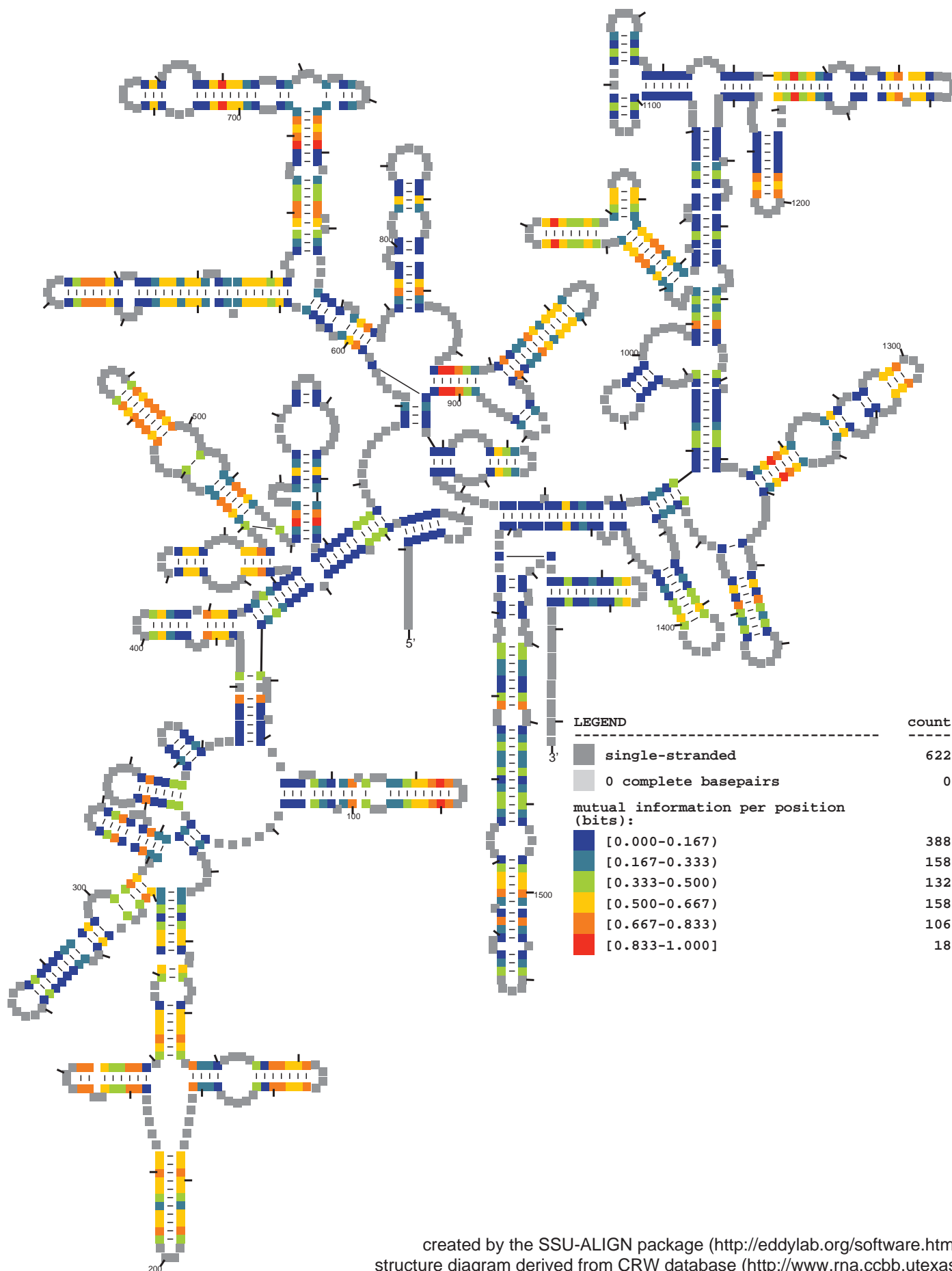


model	#pos	#bps	#seqs	description
bacteria	1582	480	99	information content per position



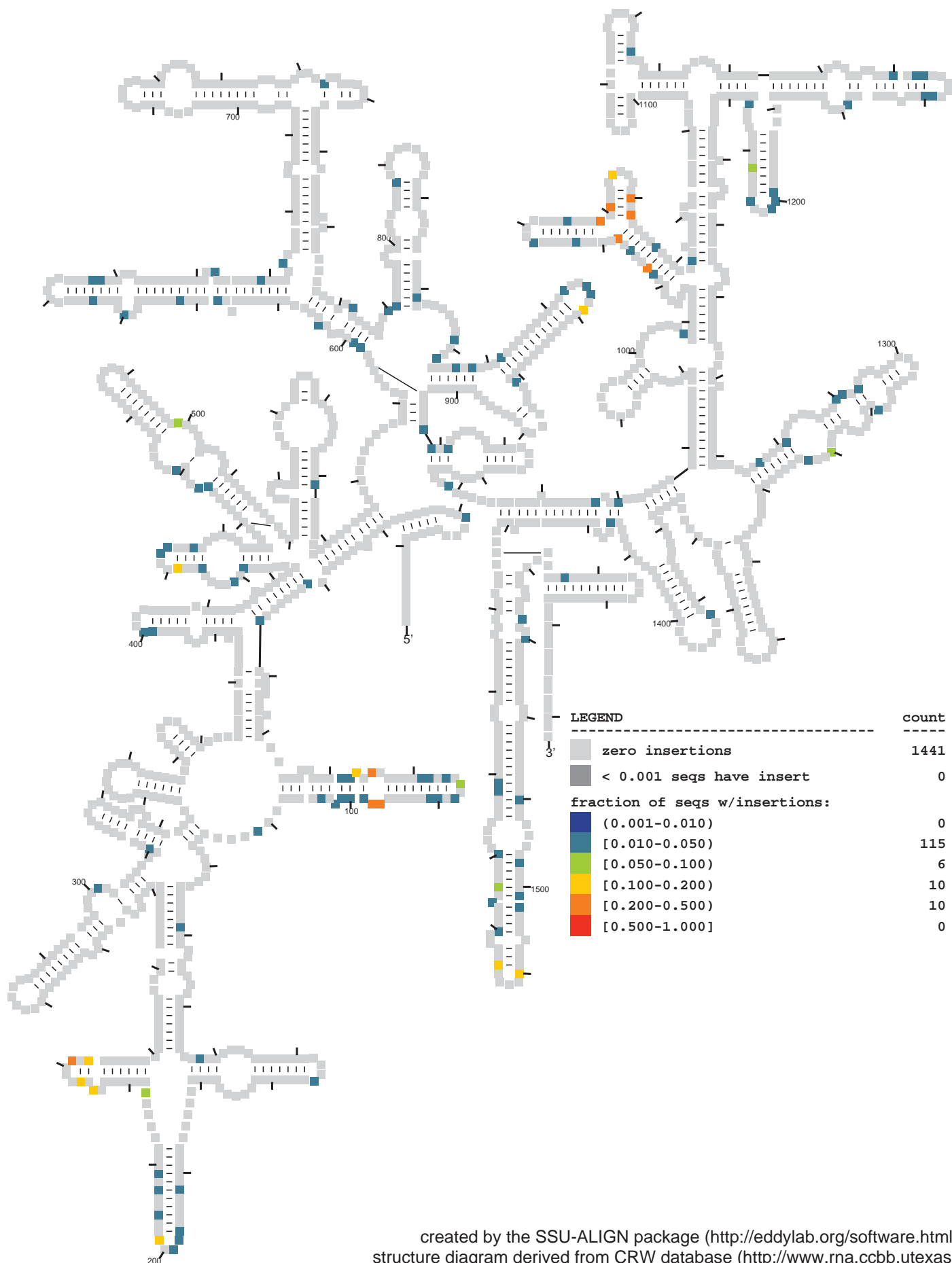
created by the SSU-ALIGN package (<http://eddylib.org/software.html>)
 structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

model	#pos	#bps	#seqs	description
bacteria	1582	480	99	mutual information per basepaired position



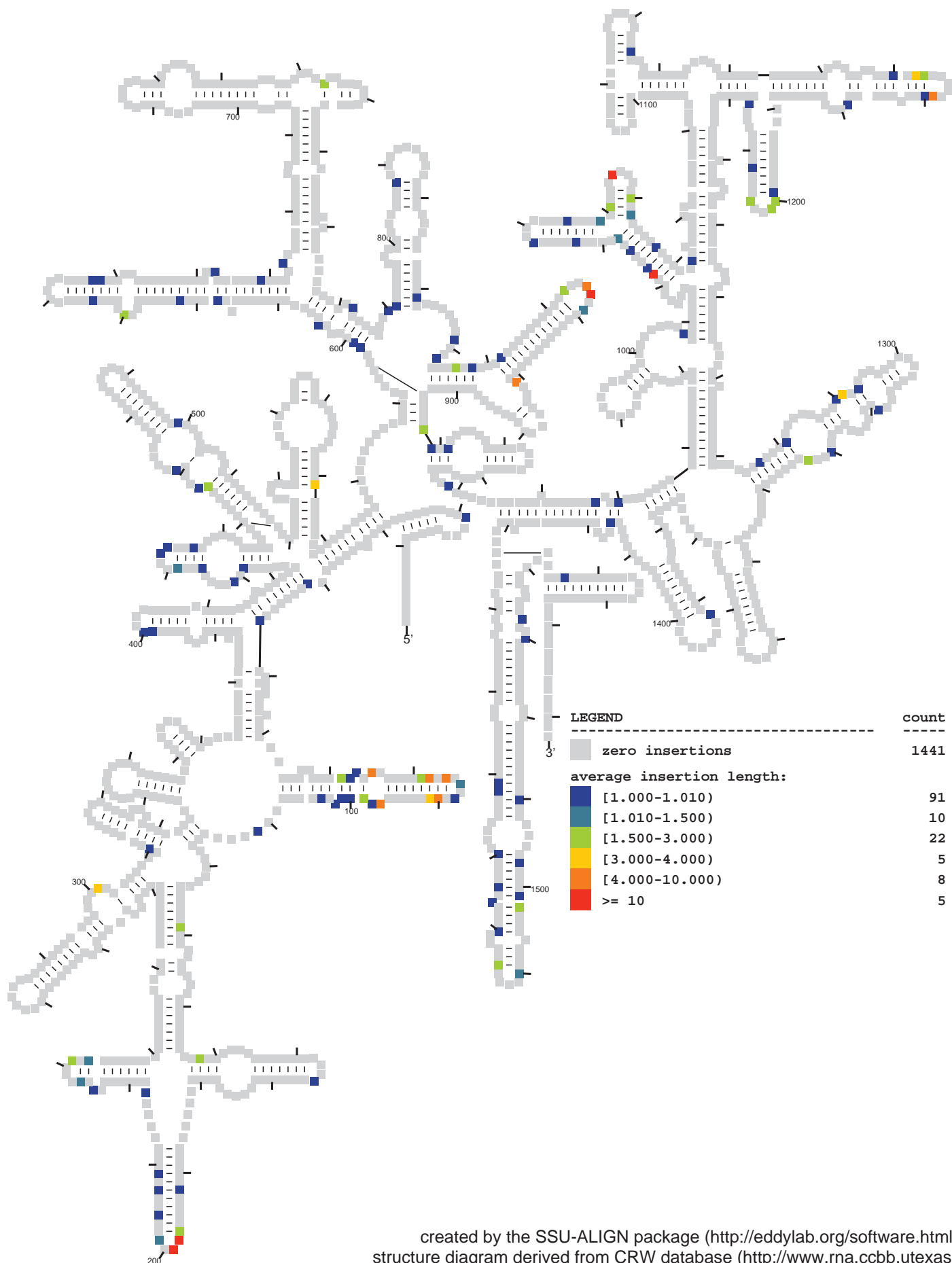
created by the SSU-ALIGN package (<http://eddylab.org/software.html>)
structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

model	#pos	#bps	#seqs	description
bacteria	1582	480	99	frequency of insertions after each position



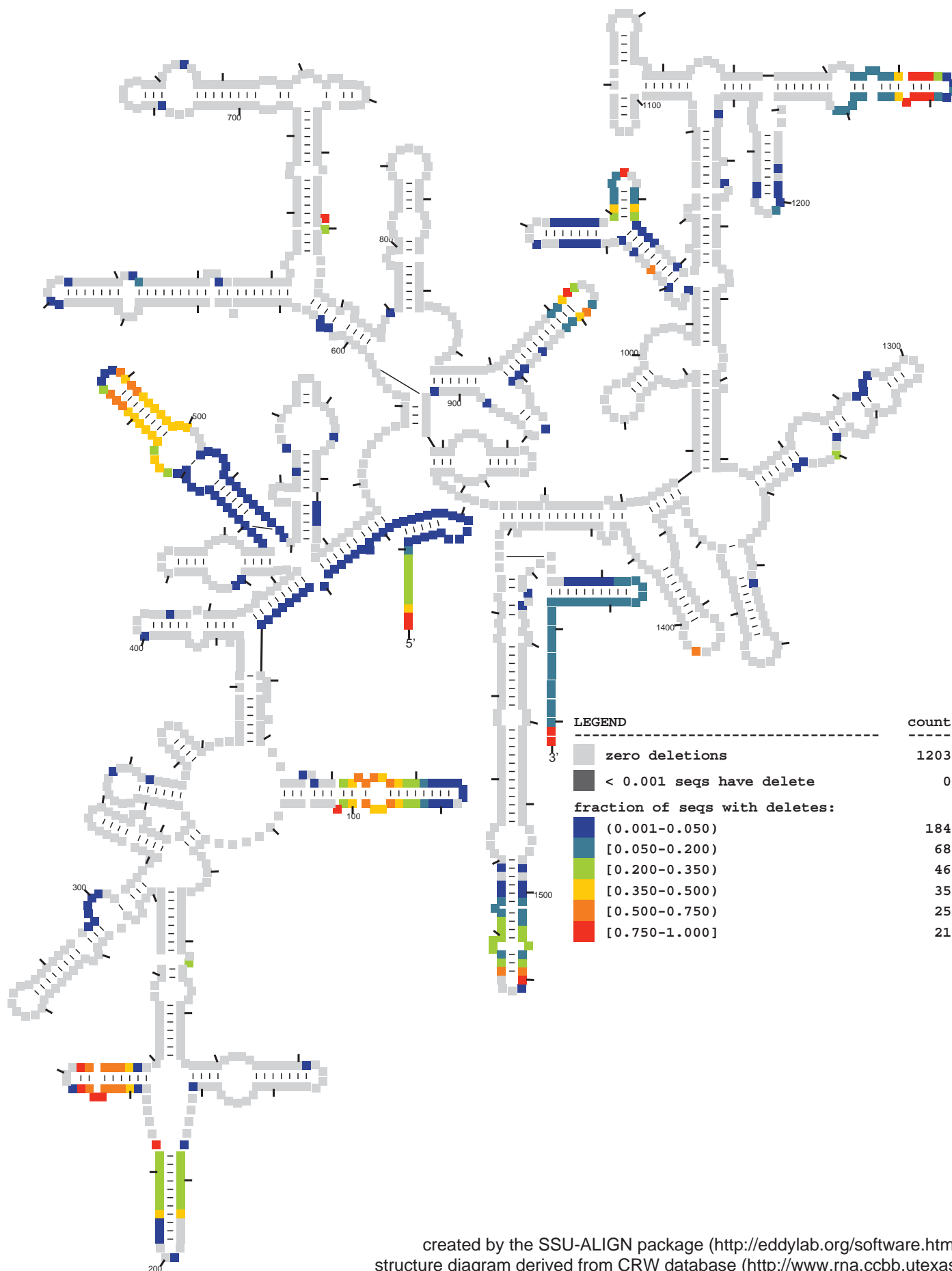
created by the SSU-ALIGN package (<http://eddylib.org/software.html>)
 structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

model	#pos	#bps	#seqs	description
bacteria	1582	480	99	average insertion length after each position



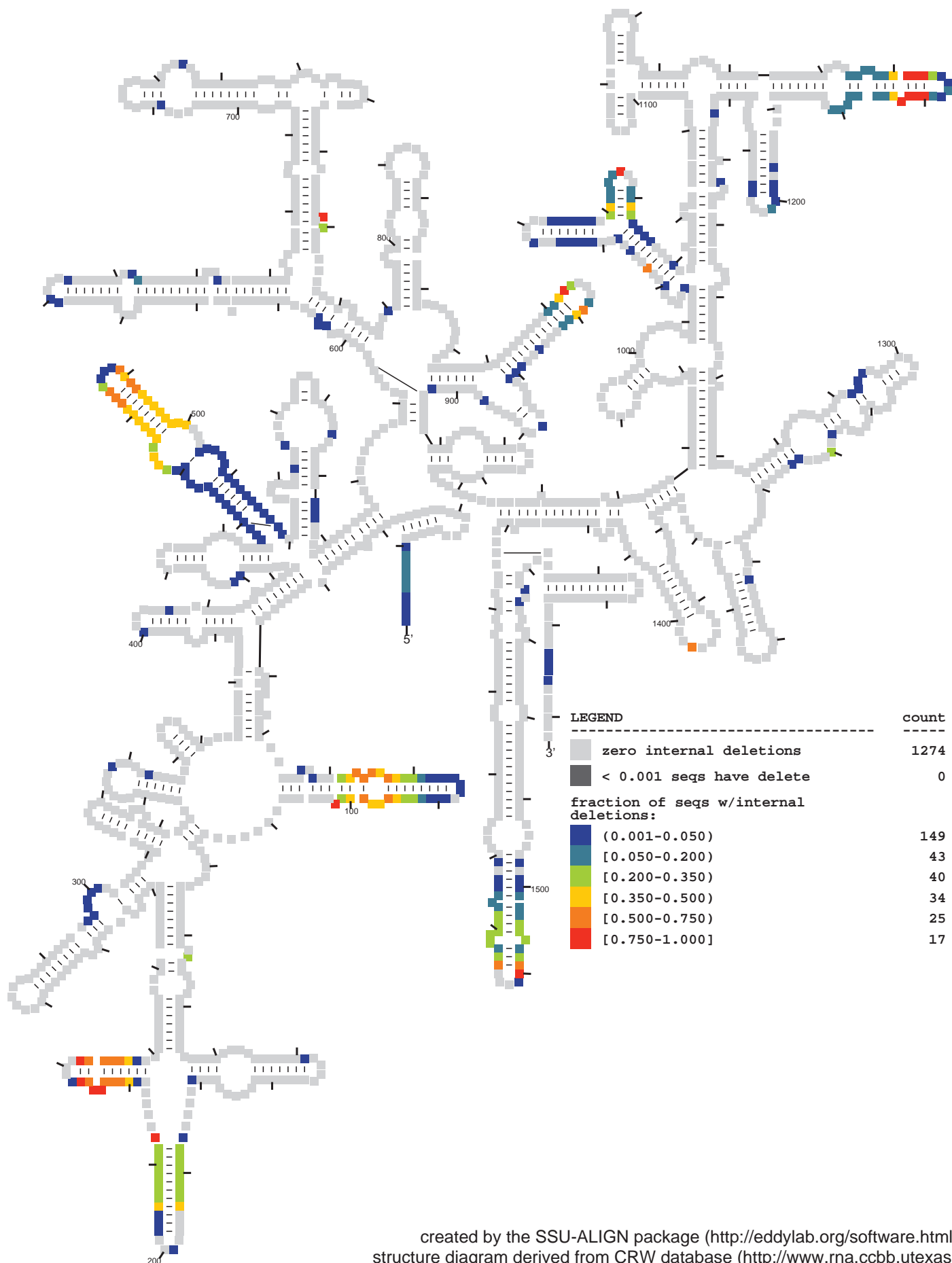
created by the SSU-ALIGN package (<http://eddylib.org/software.html>)
 structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

model	#pos	#bps	#seqs	description
bacteria	1582	480	99	frequency of deletions at each position



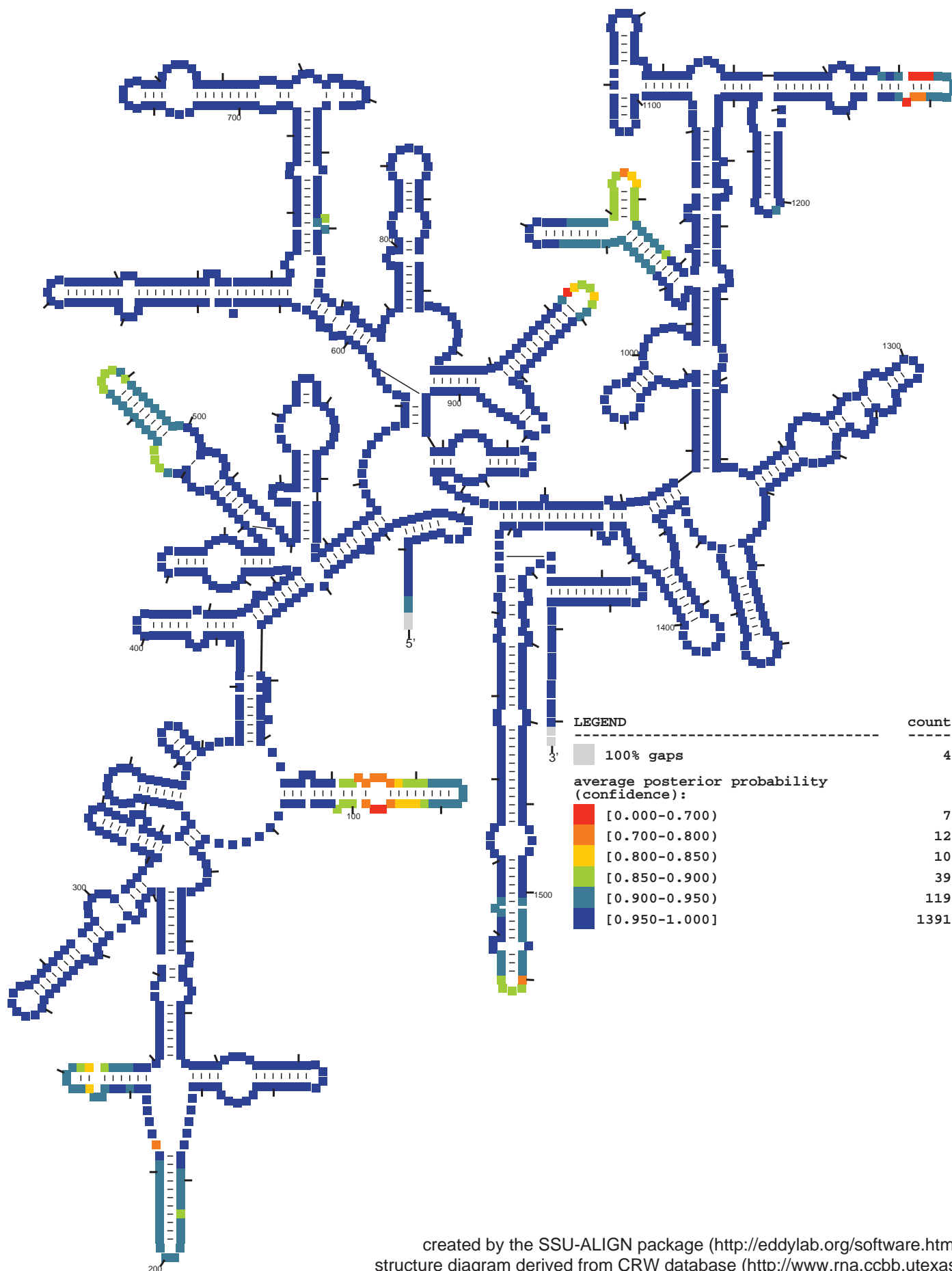
created by the SSU-ALIGN package (<http://eddylab.org/software.html>)
 structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

model	#pos	#bps	#seqs	description
bacteria	1582	480	99	frequency of internal deletions in each position



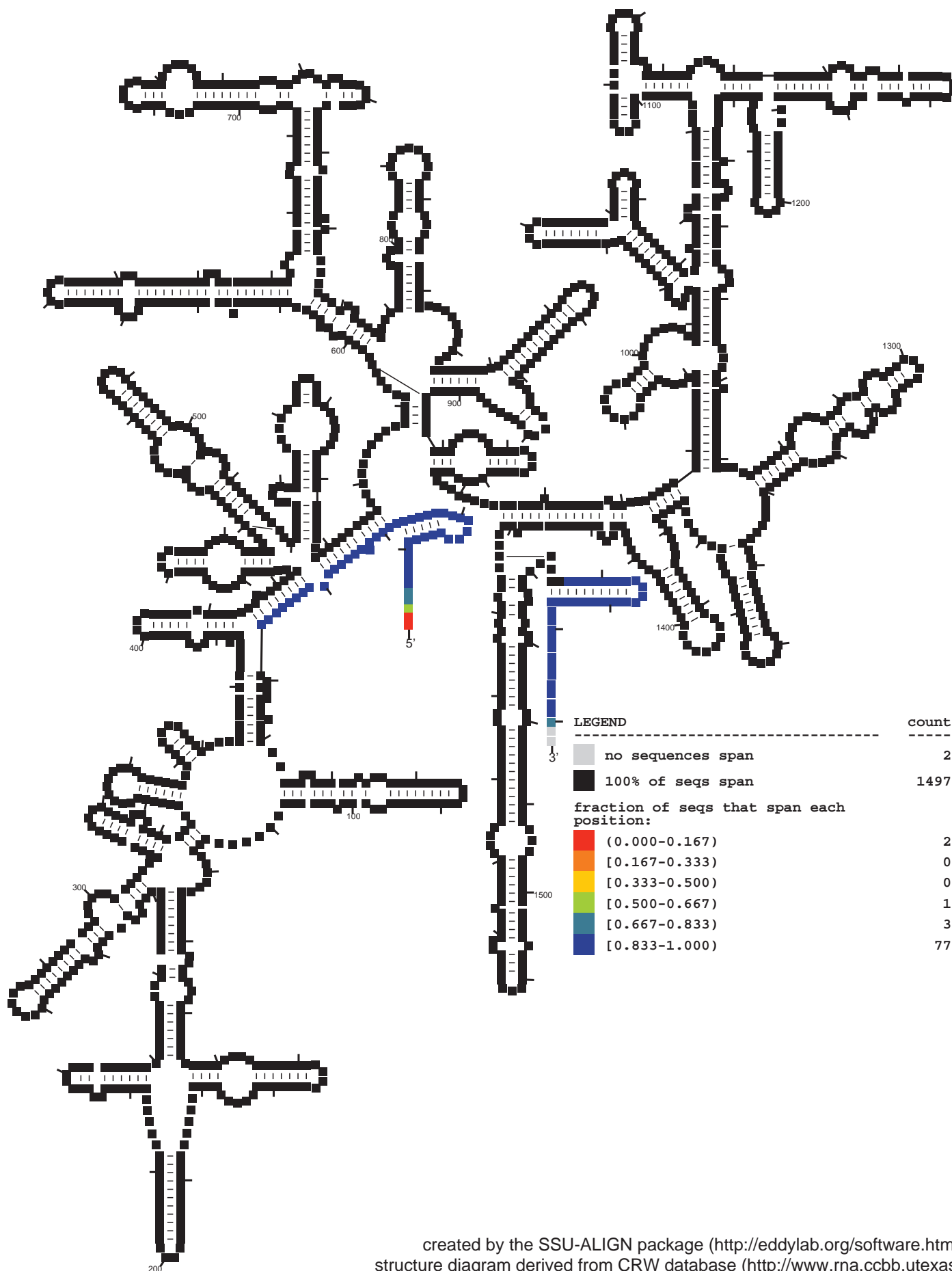
created by the SSU-ALIGN package (<http://eddylib.org/software.html>)
 structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

model	#pos	#bps	#seqs	description
bacteria	1582	480	99	average posterior probability per position



created by the SSU-ALIGN package (<http://eddylib.org/software.html>)
 structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)

model	#pos	#bps	#seqs	description
bacteria	1582	480	99	fraction of sequences that span each position



created by the SSU-ALIGN package (<http://eddylib.org/software.html>)
 structure diagram derived from CRW database (<http://www.rna.ccbb.utexas.edu/>)