model	#pos	#bps	#seqs	description
bacteria	1582	480	93	information content per position

LEGEND	count
100% gaps	0

information content (bits):

	count
[0.000-0.400)	146
[0.400-0.800)	190
[0.800-1.200)	213
[1.200-1.600)	197
[1.600-1.990)	292
[1.990-2.000]	544

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