

sequence	length	ref
SV11	115	[1]
MS2	122	3'UTR from the whole mRNA (3569 nt) NCBI acc. no. NC_001417
MS2 ₉₀₀	900	from the whole mRNA (3569 nt) NCBI acc. no. NC_001417
KU1	136	3'UTR from the whole mRNA (3486 nt) NCBI acc. no. NC_002250
KU1 ₉₅₀	950	from the whole mRNA (3486 nt) NCBI acc. no. NC_002250
SAM	184	[2]
7SK	319	Fugu rubripes 7SK small nuclear RNA, Genbank acc. no. AJ890104.1
Hok	443	NCBI acc. no. AP000342
C. elegans 16S	697	C. elegans 16S rRNA, CompRNA acc. no. X54252
D. virilis 16S	784	D. virilis 16S rRNA, CompRNA acc. no. X05914
RASSF1	1024	H. sapiens antisense intronic RASSF1 transcript 2 mRNA, Genbank acc. no. AY545528.1
S. acidocaldarius 16S	1492	S. acidocaldarius 16S rRNA, CompRNA acc. no. D14876

Table 1: List of sequences used for testing *Kinwalker*. Accession numbers refer to NCBI, Genbank or the comparative RNA web [3] site as stated.

References

- [1] Biebricher, C. K. & Luce, R. (1992). In vitro recombination and terminal elongation of RNA by Q β replicase. *EMBO J.*, **11**, 5129–5135.
- [2] Winkler, W. C., Nahvi, A., Sudarsan, N., Barrick, J. E. & Breaker, R. R. (2003). An mRNA structure that controls gene expression by binding S-adenosylmethionine. *Nat. Struct. Biol.*, **10**, 701–707.
- [3] Cannone, J. J. *et al.* (2002). The comparative rna web (crw) site: an online database of comparative sequence and structure information for ribosomal, intron, and other rnas. *BMC Bioinformatics*, **3**.