

Identification and molecular structure analysis of a new noncoding RNA, a sbRNA homologous, in the silkworm *Bombyx mori* genome

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SUPPLEMENTARY DATA

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> gi|185050365|dbj|AP009009.1| Bombyx mori genomic DNA,
chromosome 4, partial sequence
GAAACGATCTCACGGTTTTATGTGATGATTTTCTATTAATATCGTCTTTGTCACAATATA
ACTCATTATTTTCTAGAGGTAACATTCTGTCAGTACAGTTACTACTGT TATAAAA CCGTT
TTAATTTCTTCAATACA GCTTGAACGTCTCGTGGCTTATCCATATCGATGTCTTCAAAG
ATTCTTCTAGTTTT ATATTTCTTTATAGAAATAATCGTGAGGTACAGGAAACCTTTAA
CTATAAAATCAGCAGCTCCGCCGTAGTTAGGTGTGGTTATTGTCTGTCGGTATGCACATT
CGAAATTGCCGGTCGAAGCATTTTTGTCAGCAGCATAATCTATCACAAC
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Fig 1S. The *Bombyx mori* sbRNA gene and regulatory sequences. The promoter region, presenting a TATA-box, is shown in light blue, the *Bmsb*RNA gene sequence in yellow, and the termination signal, made up of T residues, in green. The promoter and stopping motifs for RNA pol III was according to described elsewhere.³¹

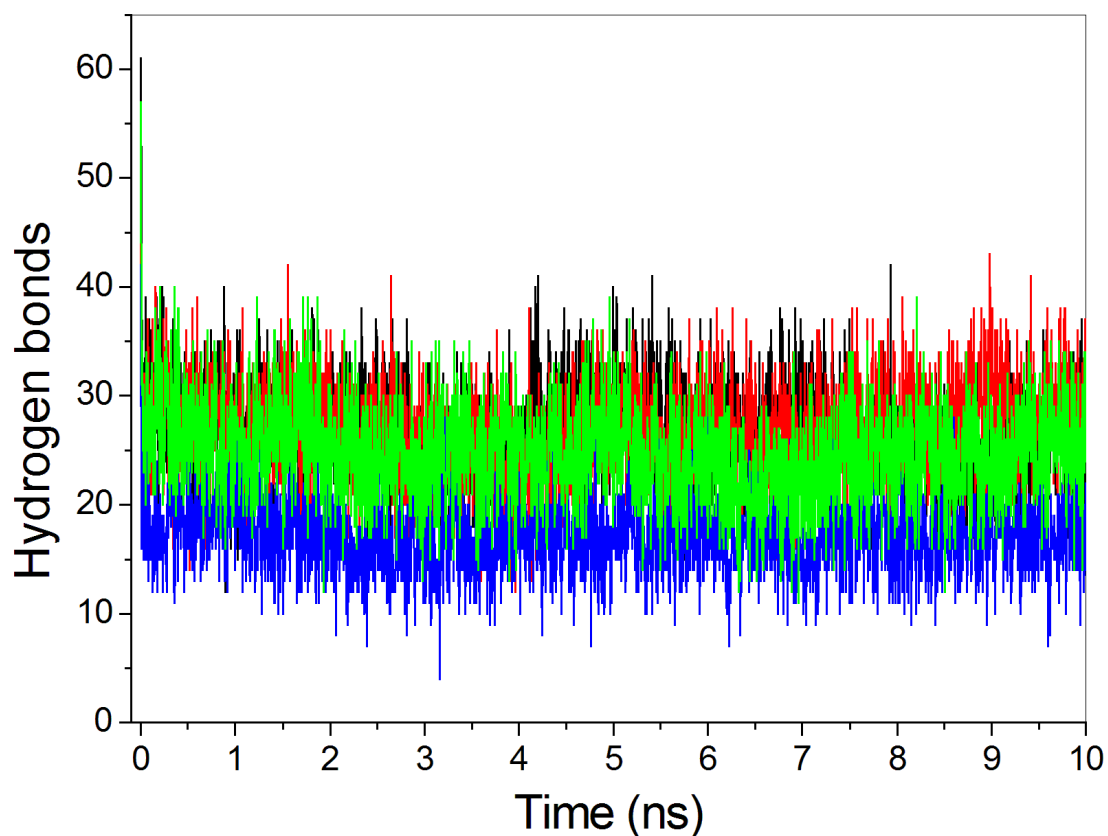


Fig 2S. Number of hydrogen bonds along 10ns simulation. The colours indicate the RNA segments for human Y5 RNA, Chinese hamster Y5 RNA, *B. mori* sbRNA and *C. elegans* sbRNA in black, red, blue and green, respectively. The continuing trend of the number of hydrogen bonds along simulation also indicates the stability of the segments.

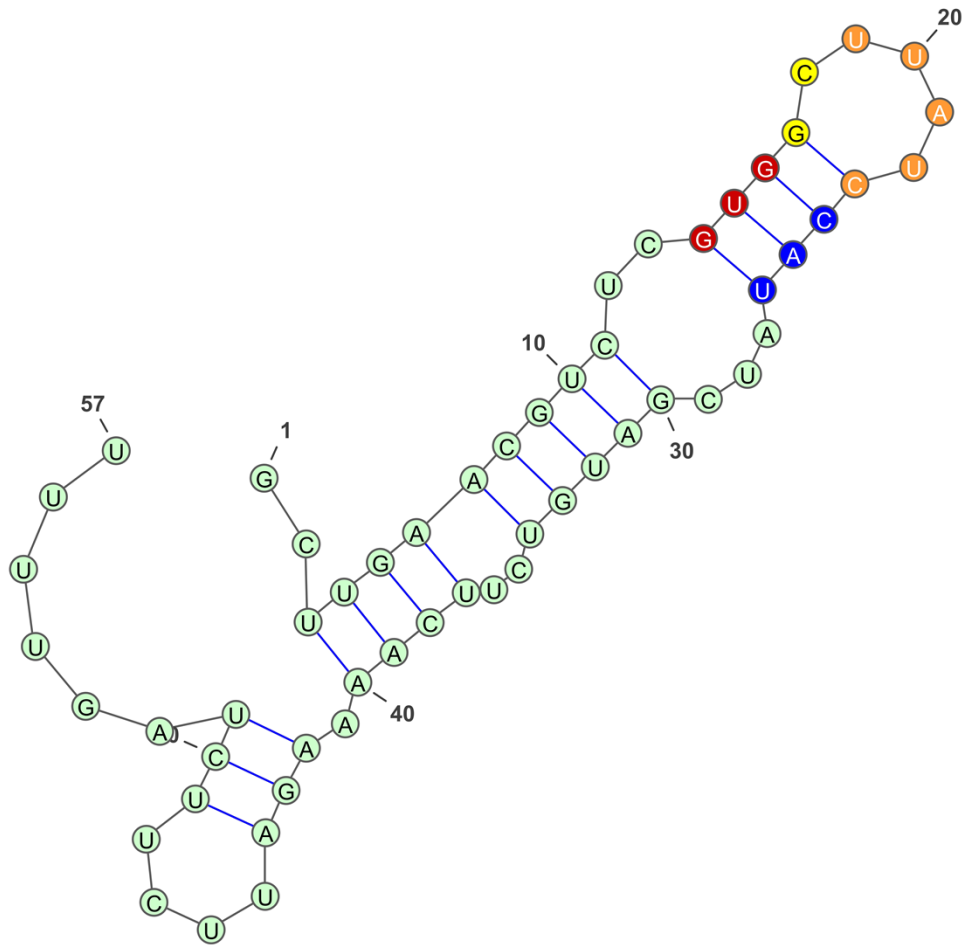


Fig 3S. Alternative model of *Bombyx mori* sbRNA, generated by MFold Server and drawn by Varna.³³ See that UUAUC segment (19 to 23) is unstructured as a single hairpin loop as also observed in vertebrates Y RNAs. Conserved motif for Y RNAs in red and blue, variable region in yellow, conserved sequence for sbRNAs in orange.