

pri-mir-3619

chr22: 46091026-46091150 (+)

	Features	Optimality
Stem length (bp)	34	Suboptimal
Lower stem length (bp)	12	Suboptimal
Mismatched pairs in the stem	5	
Bulged bases in the stem	4	Optimal
Apical loop size (nt)	5	Suboptimal
3' basal segment length (nt)	1	Suboptimal
Mismatch at -6	Not possessed	
bGWG at -10/-11	Not possessed	

	w/o SRSF3	w/ SRSF3
Cleavage efficiency	0.0 (476 / 476)	0.0 (476 / 476)
Cleavage homogeneity	0.0 (476 / 476)	0.13 (449 / 476)

Rank among tested pri-miRs

Top

Bottom

The diagram illustrates the secondary structure of pri-mir-3619, a 100-nucleotide RNA molecule. The structure is composed of several stem-loops and bulges, with specific regions highlighted and labeled:

- Loop: 5 nt**: A small loop at the 5' end of the structure.
- US: 22 bp**: The Upper Stem, a 22-base-pair stem region.
- LS: 12 bp**: The Lower Stem, a 12-base-pair stem region.
- 5' BS: 13 nt**: The 5' Basal Segment, a 13-nucleotide segment.
- 3' BS: 1 nt**: The 3' Basal Segment, a single-nucleotide segment.

The RNA sequence is shown with nucleotides color-coded by their rank among tested pri-miRs, ranging from red (Top) to blue (Bottom). The structure includes several stem-loops and bulges, with specific regions highlighted in green, orange, and purple. Red arrows indicate specific cleavage sites within the stem regions.