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=====
miranda v3.3a      microRNA Target Scanning Algorithm
=====
(c) 2003 Memorial Sloan-Kettering Cancer Center, New York
```

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If you use this software please cite:  
Enright AJ, John B, Gaul U, Tuschl T, Sander C and Marks DS;  
(2003) Genome Biology; 5(1):R1.

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Current Settings:

```
=====
Query Filename:    ./seq/mirna/sof_mirna.fasta
Reference Filename: ./seq/gene/sof/HQ342888.fasta
Gap Open Penalty:-9.000000
Gap Extend Penalty: -4.000000
Score Threshold: 130.000000
Energy Threshold:-15.000000 kcal/mol
Scaling Parameter: 4.000000
=====
Read Sequence:sof-miR156 (20 nt)
Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,
complete genome
(5837 nt)
=====
Performing Scan: sof-miR156 vs HQ342888.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete
```

```
Read Sequence:sof-miR159a (21 nt)
Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,
complete genome
(5837 nt)
=====
Performing Scan: sof-miR159a vs HQ342888.1
=====
Score for this Scan:
No Hits Found above Threshold
Complete
```

```
Read Sequence:sof-miR159b (21 nt)
Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,
complete genome
(5837 nt)
```

=====

Performing Scan: sof-miR159b vs HQ342888.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:sof-miR159c (21 nt)  
Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: sof-miR159c vs HQ342888.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:sof-miR159d (21 nt)  
Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: sof-miR159d vs HQ342888.1

=====

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:sof-miR159e (21 nt)  
Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: sof-miR159e vs HQ342888.1

=====

Forward: Score: 130.000000 Q:2 to 20 R:4545 to 4569 Align Len (22)  
(63.64%) (77.27%)

Query: 3' uuCUCGAGGAAA---GUUAGGUUu 5'  
|:|:|:| | | | | | | | |  
Ref: 5' gcGGGTTTCTTTGTGACAATGCAAA 3'

Energy: -16.639999 kCal/Mol

Scores for this hit:

>sof-miR159e	HQ342888.1	130.00	-16.64	2	20	4545	4569	22
	63.64%	77.27%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>sof-miR159e	HQ342888.1	130.00	-16.64	130.00	-16.64
6	21	5837	4545		

Complete

Read Sequence:sof-miR167a (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: sof-miR167a vs HQ342888.1

Forward: Score: 149.000000 Q:2 to 20 R:1646 to 1665 Align Len (18)  
(72.22%) (72.22%)

Query: 3' guCUAGUACGACCGUCGAAGu 5'  
          || || || || || || ||  
Ref: 5' aaGAGCAGACT-CCAGCTTCg 3'

Energy: -16.510000 kCal/Mol

Scores for this hit:

>sof-miR167a	HQ342888.1	149.00	-16.51	2	20	1646	1665	18
	72.22%	72.22%						

Forward: Score: 133.000000 Q:2 to 20 R:2279 to 2298 Align Len (18)  
(77.78%) (77.78%)

Query: 3' guCUAGUACGACCGUCGAAGu 5'  
          | || | || || || || ||  
Ref: 5' caGCTCCT-CTGGCAGCCTCa 3'

Energy: -21.719999 kCal/Mol

Scores for this hit:

>sof-miR167a	HQ342888.1	133.00	-21.72	2	20	2279	2298	18
	77.78%	77.78%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>sof-miR167a	HQ342888.1	282.00	-38.23	149.00	-21.72
7	21	5837	1646	2279	

Complete

Read Sequence:sof-miR167b (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: sof-miR167b vs HQ342888.1

Forward: Score: 149.000000 Q:2 to 20 R:1646 to 1665 Align Len (18)  
(72.22%) (72.22%)

Query: 3' guCUAGUACGACCGUCGAAGu 5'  
          || || || || || || ||  
Ref: 5' aaGAGCAGACT-CCAGCTTCg 3'

Energy: -16.510000 kCal/Mol

Scores for this hit:

```
>sof-miR167b      HQ342888.1  149.00      -16.51      2 20  1646 1665   18
      72.22%      72.22%
```

Forward: Score: 133.000000 Q:2 to 20 R:2279 to 2298 Align Len (18)  
(77.78%) (77.78%)

Query: 3' guCUAGUACGACCGUCGAAGu 5'

| || | ||||| ||

Ref: 5' caGCTCCT-CTGGCAGCCTCa 3'

Energy: -21.719999 kCal/Mol

Scores for this hit:

```
>sof-miR167b      HQ342888.1  133.00      -21.72      2 20  2279 2298   18
      77.78%      77.78%
```

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

```
>>sof-miR167b      HQ342888.1  282.00      -38.23      149.00      -21.72
      8      21      5837      1646 2279
```

Complete

Read Sequence:sof-miR168a (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: sof-miR168a vs HQ342888.1

Forward: Score: 151.000000 Q:2 to 17 R:374 to 395 Align Len (16)  
(75.00%) (81.25%)

Query: 3' cagggCUA-GACGUGGUUCGcu 5'

||| | |: |||||

Ref: 5' taaggGATGCCGTTCCAAGCGg 3'

Energy: -19.100000 kCal/Mol

Scores for this hit:

```
>sof-miR168a      HQ342888.1  151.00      -19.10      2 17  374 395   16
      75.00%      81.25%
```

Forward: Score: 146.000000 Q:2 to 16 R:2140 to 2163 Align Len (17)  
(70.59%) (76.47%)

Query: 3' cagggcUAGAC---GUGGUUCGcu 5'

:||| | |||||

Ref: 5' agacaaGTCTGAGACTCCAAGCGg 3'

Energy: -22.100000 kCal/Mol

Scores for this hit:

>sof-miR168a      HQ342888.1 146.00      -22.10      2 16 2140 2163 17  
70.59%      76.47%

Forward: Score: 134.000000 Q:3 to 20 R:2115 to 2136 Align Len (18)  
(66.67%) (77.78%)

Query:      3' caGGGCUAGACGU-GGUUCGcu 5'  
             |:|    ||    |:    |||||  
Ref:      5' ccCTCCTTCGGCGCCCAAGCcg 3'

Energy: -18.000000 kCal/Mol

Scores for this hit:

>sof-miR168a      HQ342888.1 134.00      -18.00      3 20 2115 2136 18  
66.67%      77.78%

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>sof-miR168a      HQ342888.1 431.00      -59.20      151.00      -22.10  
9      21      5837      374 2140 2115

Complete

Read Sequence:sof-miR168b (20 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: sof-miR168b vs HQ342888.1

=====

Forward: Score: 145.000000 Q:2 to 16 R:374 to 395 Align Len (16)  
(75.00%) (81.25%)

Query:      3' cagggCUA-GAC-GGGUUCGcu 5'  
             |||    |    :|||  
Ref:      5' taaggGATGCCGTTC AAGCGg 3'

Energy: -20.719999 kCal/Mol

Scores for this hit:

>sof-miR168b      HQ342888.1 145.00      -20.72      2 16 374 395 16  
75.00%      81.25%

Forward: Score: 142.000000 Q:2 to 19 R:2145 to 2163 Align Len (18)  
(66.67%) (77.78%)

Query:      3' caGGGCU-AGACGGGUUCGcu 5'  
             :|:|    ||    |||||  
Ref:      5' agTCTGAGACT--CCAAGCGg 3'

Energy: -22.129999 kCal/Mol

Scores for this hit:

>sof-miR168b      HQ342888.1 142.00      -22.13      2 19 2145 2163 18  
66.67%      77.78%

Forward: Score: 130.000000 Q:3 to 11 R:2117 to 2136 Align Len (8)  
(100.00%) (100.00%)

Query: 3' cagggcuagaCGGGUUCGcu 5'

Ref: 5' ctccttcggcGCCCAAGCcg 3'

Energy: -21.360001 kCal/Mol

Scores for this hit:

>sof-miR168b	HQ342888.1	130.00	-21.36	3	11	2117	2136	8
	100.00%	100.00%						

Forward: Score: 130.000000 Q:3 to 11 R:5791 to 5810 Align Len (8)  
(100.00%) (100.00%)

Query: 3' cagggcuagaCGGGUUCGcu 5'

Ref: 5' atcctttggaaGCCCAAGCta 3'

Energy: -16.330000 kCal/Mol

Scores for this hit:

>sof-miR168b	HQ342888.1	130.00	-16.33	3	11	5791	5810	8
	100.00%	100.00%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>sof-miR168b	HQ342888.1	547.00	-80.54	145.00	-22.13
10	20	5837	374	2145	2117 5791

Complete

Read Sequence:sof-miR396 (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: sof-miR396 vs HQ342888.1

Forward: Score: 134.000000 Q:2 to 16 R:2661 to 2683 Align Len (16)  
(68.75%) (81.25%)

Query: 3' gucaagUUCUUUC--GACACCUu 5'

Ref: 5' aaaagaGAGATAGCTTTGTGGAg 3'

Energy: -17.260000 kCal/Mol

Scores for this hit:

>sof-miR396	HQ342888.1	134.00	-17.26	2	16	2661	2683	16
	68.75%	81.25%						

Forward: Score: 130.000000 Q:2 to 20 R:3732 to 3755 Align Len (21)  
(71.43%) (80.95%)

Query: 3' guCAAGUUCUUU--CGACAC-CUu 5'  
||| :||:| | ||||| |  
Ref: 5' gtGTTGGAGGAAACGCTGTGCGAg 3'

Energy: -19.180000 kCal/Mol

Scores for this hit:

>sof-miR396 HQ342888.1	130.00	-19.18	2	20	3732	3755	21
	71.43%	80.95%					

Forward: Score: 130.000000 Q:3 to 17 R:5115 to 5137 Align Len (16)  
(75.00%) (81.25%)

Query: 3' gucaaGUUCU-U-UCGACACCuu 5'  
|:| | | | | | | | | |  
Ref: 5' accagCGAGATATACCTGTGGtg 3'

Energy: -17.270000 kCal/Mol

Scores for this hit:

>sof-miR396 HQ342888.1	130.00	-17.27	3	17	5115	5137	16
	75.00%	81.25%					

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>sof-miR396	HQ342888.1	394.00	-53.71	134.00	-19.18
11	21	5837	2661	3732	5115

Complete

Read Sequence:sof-miR408a (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: sof-miR408a vs HQ342888.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:sof-miR408b (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: sof-miR408b vs HQ342888.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:sof-miR408c (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: sof-miR408c vs HQ342888.1

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:sof-miR408d (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: sof-miR408d vs HQ342888.1

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:sof-miR408e (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: sof-miR408e vs HQ342888.1

Forward: Score: 136.000000 Q:3 to 20 R:888 to 906 Align Len (17)  
(76.47%) (76.47%)

Query: 3' cgGUCCCUUCUCAGUCACGuc 5'

|||| | | |||||

Ref: 5' acCAGG--ACACTCAGTGctt 3'

Energy: -20.040001 kCal/Mol

Scores for this hit:

>sof-miR408e	HQ342888.1	136.00	-20.04	3	20	888	906	17
	76.47%	76.47%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>sof-miR408e	HQ342888.1	136.00	-20.04	136.00	-20.04
	16	21	5837	888	

Complete

Read Sequence:ssp-miR166 (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: ssp-miR166 vs HQ342888.1



Forward: Score: 147.000000 Q:2 to 18 R:3672 to 3691 Align Len (16)  
(68.75%) (81.25%)

Query: 3' ccccUUACUUCGGACCAGGCu 5'

|:| | : | | | | |

Ref: 5' ggccAGTG-GTCGTGGTCCGg 3'

Energy: -22.709999 kCal/Mol

Scores for this hit:

>ssp-miR166 HQ342888.1	147.00	-22.71	2	18	3672	3691	16
	68.75%	81.25%					

Forward: Score: 146.000000 Q:2 to 11 R:2288 to 2308 Align Len (9)  
(88.89%) (100.00%)

Query: 3' ccccuuacuucGGACCAGGCu 5'

:| | | | | | |

Ref: 5' tggcagcctcaTCTGGTCCGa 3'

Energy: -21.420000 kCal/Mol

Scores for this hit:

>ssp-miR166 HQ342888.1	146.00	-21.42	2	11	2288	2308	9
	88.89%	100.00%					

Forward: Score: 130.000000 Q:3 to 20 R:834 to 855 Align Len (18)  
(66.67%) (72.22%)

Query: 3' ccCCUUACU-UCGGACCAGGcu 5'

||:| | | | | | |

Ref: 5' agGGGACGAGAAAATGGTCCaa 3'

Energy: -21.190001 kCal/Mol

Scores for this hit:

>ssp-miR166 HQ342888.1	130.00	-21.19	3	20	834	855	18
	66.67%	72.22%					

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>ssp-miR166	HQ342888.1	423.00	-65.32	147.00	-22.71
17	21	5837	3672	2288	834

Complete

Read Sequence:ssp-miR169 (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: ssp-miR169 vs HQ342888.1

Forward: Score: 144.000000 Q:2 to 17 R:2777 to 2797 Align Len (15)  
(86.67%) (93.33%)

Query: 3' ggccgUUCAGUAGGAACCGAu 5'

|||||||:| |||||  
Ref: 5' agcagAAGTCATTCATGGCTg 3'

Energy: -23.040001 kCal/Mol

Scores for this hit:

>ssp-miR169 HQ342888.1	144.00	-23.04	2 17	2777 2797	15
	86.67%	93.33%			

Forward: Score: 134.000000 Q:2 to 20 R:682 to 703 Align Len (19)  
(57.89%) (78.95%)

Query: 3' ggCCGUUCAGUAG-GAACCGAu 5'

| :|| ::|| |||||:|  
Ref: 5' ttGATAATCTGTCTCTTGGTTg 3'

Energy: -15.870000 kCal/Mol

Scores for this hit:

>ssp-miR169 HQ342888.1	134.00	-15.87	2 20	682 703	19
	57.89%	78.95%			

Forward: Score: 133.000000 Q:4 to 19 R:1118 to 1139 Align Len (16)  
(87.50%) (87.50%)

Query: 3' ggcCGUUCA-GUAGGAACCGau 5'

| |||| |||||  
Ref: 5' agtGGAAGTCCATCCTTGGagc 3'

Energy: -24.969999 kCal/Mol

Scores for this hit:

>ssp-miR169 HQ342888.1	133.00	-24.97	4 19	1118 1139	16
	87.50%	87.50%			

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>ssp-miR169	HQ342888.1	411.00	-63.88	144.00	-24.97
18	21	5837	2777 682 1118		

Complete

Read Sequence:ssp-miR437a (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: ssp-miR437a vs HQ342888.1

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:ssp-miR437b (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: ssp-miR437b vs HQ342888.1

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:ssp-miR437c (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: ssp-miR437c vs HQ342888.1

Score for this Scan:  
No Hits Found above Threshold  
Complete

Read Sequence:ssp-miR528 (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

Performing Scan: ssp-miR528 vs HQ342888.1

Forward: Score: 141.000000 Q:2 to 18 R:4162 to 4182 Align Len (16)  
(75.00%) (93.75%)

Query: 3' gaggAGACGUACGGGGAAGGu 5'

|:||| |||||:|||||

Ref: 5' ccgaTTTGAATGCCTTTTCCa 3'

Energy: -22.930000 kCal/Mol

Scores for this hit:

>ssp-miR528 HQ342888.1	141.00	-22.93	2 18	4162 4182	16
	75.00%	93.75%			

Forward: Score: 133.000000 Q:2 to 19 R:5368 to 5389 Align Len (18)  
(61.11%) (77.78%)

Query: 3' gagGAGA-CGUACGGGGAAGGu 5'

:||| || :|:|||||

Ref: 5' gggTTCTCGCCCCTCTCTTCCg 3'

Energy: -21.860001 kCal/Mol

Scores for this hit:

>ssp-miR528 HQ342888.1	133.00	-21.86	2 19	5368 5389	18
	61.11%	77.78%			

Forward: Score: 131.000000 Q:3 to 20 R:4048 to 4068 Align Len (17)  
(58.82%) (76.47%)

Query: 3' gaGGAGACGUACGGGGAAGgu 5'  
          :| |: | : |||||

Ref: 5' agTCTTCCCGGCCCTTCat 3'

Energy: -20.020000 kCal/Mol

Scores for this hit:

>ssp-miR528 HQ342888.1	131.00	-20.02	3	20	4048	4068	17
	58.82%	76.47%					

Forward: Score: 130.000000 Q:2 to 19 R:4436 to 4456 Align Len (17)  
(64.71%) (82.35%)

Query: 3' gagGAGACGUACGGGGAAGGu 5'  
          | || |:| |:|:||||

Ref: 5' ataCCCTTCGTCCTCTTTCCa 3'

Energy: -21.270000 kCal/Mol

Scores for this hit:

>ssp-miR528 HQ342888.1	130.00	-21.27	2	19	4436	4456	17
	64.71%	82.35%					

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>ssp-miR528	HQ342888.1	535.00	-86.08	141.00	-22.93
22	21	5837	4162	5368	4048 4436

Complete

Read Sequence:ssp-miR827 (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: ssp-miR827 vs HQ342888.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:ssp-miR444a (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: ssp-miR444a vs HQ342888.1

=====

Forward: Score: 130.000000 Q:2 to 11 R:4381 to 4401 Align Len (9)  
(77.78%) (100.00%)

Query: 3' uucgaacuccgUUGUUGACGu 5'  
          |:|||||:

Ref: 5' gtggagcattgAGCAACTGTc 3'

Energy: -16.370001 kCal/Mol

Scores for this hit:

>ssp-miR444a	HQ342888.1	130.00	-16.37	2	11	4381	4401	9
77.78%	100.00%							

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>ssp-miR444a	HQ342888.1	130.00	-16.37	130.00	-16.37
24	21	5837	4381		

Complete

Read Sequence:ssp-miR444b (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: ssp-miR444b vs HQ342888.1

=====

Forward: Score: 130.000000 Q:2 to 11 R:4381 to 4401 Align Len (9)  
(77.78%) (100.00%)

Query: 3' uucgaacuccgUUGUUGACGu 5'

|:|||||:

Ref: 5' gtggagcattgAGCAACTGTc 3'

Energy: -16.370001 kCal/Mol

Scores for this hit:

>ssp-miR444b	HQ342888.1	130.00	-16.37	2	11	4381	4401	9
77.78%	100.00%							

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max

Energy,Strand,Len1,Len2,Positions

>>ssp-miR444b	HQ342888.1	130.00	-16.37	130.00	-16.37
25	21	5837	4381		

Complete

Read Sequence:ssp-miR444c-3p (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: ssp-miR444c-3p vs HQ342888.1

=====

Forward: Score: 131.000000 Q:2 to 18 R:4378 to 4401 Align Len (19)  
(63.16%) (78.95%)

Query: 3' uucgAACUC-UG--UUGUUGACGu 5'

| ||| |: |:|||||:

Ref: 5' atcgTGGAGCATTGAGCAACTGTc 3'

Energy: -16.370001 kCal/Mol

Scores for this hit:

>ssp-miR444c-3p	HQ342888.1	131.00	-16.37	2	18	4378	4401	19
	63.16%	78.95%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>ssp-miR444c-3p	HQ342888.1	131.00	-16.37	131.00	-16.37
	26	21	5837	4378	

Complete

Read Sequence:ssp-miR1128 (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: ssp-miR1128 vs HQ342888.1

=====

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:ssp-miR1432 (21 nt)

Read Sequence:HQ342888.1 Sugarcane yellow leaf virus isolate CHN-HN1,  
complete genome  
(5837 nt)

=====

Performing Scan: ssp-miR1432 vs HQ342888.1

=====

Forward: Score: 134.000000 Q:2 to 20 R:4627 to 4648 Align Len (19)  
(63.16%) (73.68%)

Query: 3' caGCCACAG-UAGAAAGGACUc 5'

||| || | : |||||:

Ref: 5' atCGGACTCTAATGTTTCCTGGt 3'

Energy: -16.570000 kCal/Mol

Scores for this hit:

>ssp-miR1432	HQ342888.1	134.00	-16.57	2	20	4627	4648	19
	63.16%	73.68%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max  
Energy,Strand,Len1,Len2,Positions

>>ssp-miR1432	HQ342888.1	134.00	-16.57	134.00	-16.57
	28	21	5837	4627	

Complete

Scan Complete

## RNA22. Algorithm results

ssp\_miR528 HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[252,272]  
-13.00 GTCACATGGTGCCTATTCTG TGGAAGGGGCATGCAGAGGAG .(((.(((((((.(((  
.)))))))))).)). 16 21 0.045600

ssp\_miR528 HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[262,281]  
-16.90 TGCCTATTCTGCTCCTGCCA TGGAAGGGGCATGCAGAGGAG ..(((....(((((((  
)))..))))))....)). 13 20 0.045600

sof\_miR168a HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1045,1069]  
-12.90 ATCCCTCTAACGGAATTCCAAGTGC TCGCTTGGTGCAGATCGGGAC  
..(((.....(....(((((((. .))))))..).....))). 12 25 0.231000

sof\_miR159a HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1142,1163]  
-14.90 AAGCAGCCCATTTCACTCCAGT TTTGGATTGAAGGGAGCTCTG .(((.(((.(((.(((  
.))))..)))))). 17 22 0.040800

sof\_miR159b HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1142,1163]  
-14.90 AAGCAGCCCATTTCACTCCAGT TTTGGATTGAAGGGAGCTCTG .(((.(((.(((.(((  
.))))..)))))). 17 22 0.040800

sof\_miR159c HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1120,1143]  
-12.50 TGGAAGTCCATCCTTGAGCCAAA CTTGGATTGAAGGGAGCTCCT  
..(((.(((.(((.(((.(((. .))))..).....))). 16 24 0.040800

sof\_miR159c HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1143,1163]  
-15.20 AGCAGCCCATTTCACTCCAGT CTTGGATTGAAGGGAGCTCCT ((.(((.(((.(((.(((  
.))))..)))))). 17 21 0.040800

sof\_miR159d HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1142,1163]  
-14.90 AAGCAGCCCATTTCACTCCAGT TTTGGATTGAAGGGAGCTCTG .(((.(((.(((.(((  
.))))..)))))). 17 22 0.040800

sof\_miR159e HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1142,1163]  
-16.10 AAGCAGCCCATTTCACTCCAGT TTTGGATTGAAGGGAGCTCTT (((.(((.(((.(((  
.))))..)))))). 18 22 0.040800

ssp\_miR528 HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1137,1156]  
-15.20 AGCCAAAGCAGCCCATTTCA TGGAAGGGGCATGCAGAGGAG ..(((.(((.(((.(((  
))))..).....))). 14 20 0.040800

sof\_miR167a HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1646,1665]  
-13.00 AAGAGCAGACTCCAGCTTCG TGAAGCTGCCAGCATGATCTG .(((.(((.(((.(((  
))))..).....))). 15 20 0.066600

sof\_miR167b HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1646,1665]  
 -13.00 AAGAGCAGACTCCAGCTTCG TGAAGCTGCCAGCATGATCTG .(((.(.(.(((((((  
 )))))))).)).)).)). 15 20 0.066600

ssp\_miR444a HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1850,1871]  
 -17.60 GGGTGGAGGAGAACTGCTGCG TGCAGTTGTTGCCTCAAGCTT (((.(((...(((.(((((  
 )))))))).)).)).)). 17 22 0.011500

ssp\_miR444b HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[1850,1871]  
 -17.60 GGGTGGAGGAGAACTGCTGCG TGCAGTTGTTGCCTCAAGCTT (((.(((...(((.(((((  
 )))))))).)).)).)). 17 22 0.011500

ssp\_miR444c\_3p HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target  
 from/to=[1850,1871] -16.00 GGGTGGAGGAGAACTGCTGCG TGCAGTTGTTGTCTCAAGCTT  
 (((...(((((((.(((((((.)))))).)).)).)).)) 17 22 0.011500

ssp\_miR444c\_3p HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target  
 from/to=[1874,1895] -13.30 AGGCCAGAACAAACAGCAGCA TGCAGTTGTTGTCTCAAGCTT  
 (((...(((.(((((((.(((((((.)))))).)).)).)).))...)) 16 22 0.011500

sof\_miR168b HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2145,2163]  
 -16.50 AGTCTGAGACTCCAAGCGG TCGCTTGGGCAGATCGGGAC ..((((...(((((((  
 ))))))))....)))).. 14 19 0.347000

sof\_miR159a HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2288,2309]  
 -13.40 TGGCAGCCTCATCTGGTCCGAC TTTGGATTGAAGGGAGCTCTG .(((.(((((((.(((((((  
 .)))))))))).)).)).)). 17 22 0.005020

sof\_miR159b HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2288,2309]  
 -13.40 TGGCAGCCTCATCTGGTCCGAC TTTGGATTGAAGGGAGCTCTG .(((.(((((((.(((((((  
 .)))))))))).)).)).)). 17 22 0.005020

sof\_miR159c HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2288,2309]  
 -15.10 TGGCAGCCTCATCTGGTCCGAC CTTGGATTGAAGGGAGCTCCT .(((.(((((((.(((((((  
 .)))))))))).)).)).)). 17 22 0.005020

sof\_miR159d HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2288,2309]  
 -13.40 TGGCAGCCTCATCTGGTCCGAC TTTGGATTGAAGGGAGCTCTG .(((.(((((((.(((((((  
 .)))))))))).)).)).)). 17 22 0.005020

sof\_miR167a HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2279,2298]  
 -20.50 CAGCTCCTCTGGCAGCCTCA TGAAGCTGCCAGCATGATCTG (((.(((.(((((((.(((  
 ))).))))))....)).)) 16 20 0.005020

sof\_miR167b HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2279,2298]



-20.50 CAGCTCCTCTGGCAGCCTCA TGAAGCTGCCAGCATGATCTG (((.(((.(((((((.(((  
)))..))))))..))) 16 20 0.005020

ssp\_miR528 HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2282,2302]  
-25.60 CTCCTCTGGCAGCCTCATCTG TGAAGGGGCATGCAGAGGAG ((((((.(((((((.(((  
.)))..))))))..)))) 18 21 0.005020

sof\_miR159e HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2513,2536]  
-13.30 GAGAGAAGGATTGTGCGATCCGAT TTTGGATTGAAAGGAGCTCTT  
((((.....((...(((((((. .))))))..))....)))) 15 24 0.140000

ssp\_miR444a HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2507,2527]  
-12.00 ACTAGTGAGAGAAGGATTGTG TGCAGTTGTTGCCTCAAGCTT .....(((.(((.(((((((  
.)))))..))..)).... 12 21 0.140000

ssp\_miR444b HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2507,2527]  
-12.00 ACTAGTGAGAGAAGGATTGTG TGCAGTTGTTGCCTCAAGCTT .....(((.(((.(((((((  
.)))))..))..)).... 12 21 0.140000

ssp\_miR444c\_3p HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target  
from/to=[2507,2527] -16.00 ACTAGTGAGAGAAGGATTGTG TGCAGTTGTTGTCTCAAGCTT  
.....(((.(((.(((((((. .))))))..)).... 13 21 0.140000

ssp\_miR528 HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2738,2757]  
-12.70 ATTCATTGAATCCCTGTCCA TGAAGGGGCATGCAGAGGAG .(((.(((.(((((((.((((  
)))..))))..))..)).. 16 20 0.177000

ssp\_miR169 HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[2775,2797]  
-23.50 CCAGCAGAAGTCATTCATGGCTG TAGCCAAGGATGACTTGCCGG ((.(((.(((((((.(((((((  
))))..))))..))))..)) 19 23 0.114000

ssp\_miR444c\_3p HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target  
from/to=[2792,2813] -13.30 TGGCTGGAGGGACAAGATCGTA TGCAGTTGTTGTCTCAAGCTT  
.(((.....(((((((.(((((((.))))..))))..)))).. 17 22 0.114000

sof\_miR168b HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[3581,3598]  
-13.10 GTGCACACATCCGAGCGA TCGCTTGGGCAGATCGGGAC ((.(((.(((((((.(((((((  
))))..))))..))))..)) 12 18 0.064700

ssp\_miR528 HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[4162,4182]  
-19.60 CCGATTTGAATGCCTTTTCCA TGAAGGGGCATGCAGAGGAG .....(((.(((((((.(((((((  
))))..))))..)))).. 16 21 0.020000

ssp\_miR528 HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[4437,4456]  
-15.90 TACCCTTCGTCTCTTTCCA TGAAGGGGCATGCAGAGGAG ..(((.(((.(((((((.(((((((

)))))))))).))).. 16 20 0.238000  
 ssp\_miR444c\_3p HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target  
 from/to=[4890,4912] -14.90 CAAAATGGGATAAGACTACTGCATGCAGTTGTTGTCTCAAGCTT  
 ....((((((..(((.(((( ( )))))))))))..... 15 23 0.192000  
 sof\_miR168a HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[5087,5107]  
 -13.50 GACCCGAAGGTGCTCAACTGG TCGCTTGGTGCAGATCGGGAC ..((((((..(((.((((  
 )))..)))..))..))).. 13 21 0.343000  
 sof\_miR168b HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[5087,5107]  
 -16.40 GACCCGAAGGTGCTCAACTGG TCGCTTGGGCAGATCGGGAC ..((((((..(((((((  
 )))..))))))..))).. 15 21 0.343000  
 ssp\_miR528 HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[5169,5189]  
 -18.30 CTCCTCCACCCCCCGTCTC TGAAGGGGCATGCAGAGGAG ((((((.....(((((((  
 .)))..))).....)))) 13 21 0.142000  
 ssp\_miR528 HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[5691,5709]  
 -16.40 TTAAACTGAGCTCTTTCCA TGAAGGGGCATGCAGAGGAG .....(((((((((((  
 ))))))))..))).. 13 19 0.242000  
 sof\_miR396 HQ342888.1 Sugarcane yellow leaf virus, CHN\_HN1 target from/to=[5799,5821]  
 -12.00 AAGCCCAAGCTAAAGGGGTGGAA TTCCACAGCTTTCTTGAAGT .....(((((((((  
 ))))))..))))))..... 14 23 0.107000

psRNATarget Results of SCYLV-CHN-HN1 (HQ342888)

miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end	Target_start	Target_end	miRNA_aligned_fragment	Target_aligned_fragment	Inhibition
Target_Desc.	Multiplicity									
sof-miR159e HQ342888.1	6.5	-1.0	1	21	1143	1163	UUUGGAUUUGAAAGGAGCUCUU	AGCAGCCCAUUUCACUCCAGU	Cleavage	Sugarcane yellow leaf virus 1
sof-miR167a HQ342888.1	6.5	-1.0	1	21	2279	2298	UGAAGCUGCCAGCAUGAUCUG	CAGCUCCU-CUGGCAGCCUCA	Cleavage	Sugarcane yellow leaf virus 1
sof-miR167b HQ342888.1	6.5	-1.0	1	21	2279	2298	UGAAGCUGCCAGCAUGAUCUG	CAGCUCCU-CUGGCAGCCUCA	Cleavage	Sugarcane yellow leaf virus 1
sof-miR396 HQ342888.1	6.5	-1.0	1	21	1666	1686	UUCCACAGCUUUUCUUGAACUG	ACUGUCGAGAAAGCUAUGGUU	Cleavage	Sugarcane yellow leaf virus 1
sof-miR159a HQ342888.1	7.0	-1.0	1	21	1143	1163	UUUGGAUUUGAAGGGAGCUCUG	AGCAGCCCAUUUCACUCCAGU	Cleavage	Sugarcane yellow leaf virus 2
sof-miR159a HQ342888.1	7.0	-1.0	1	21	1123	1143	UUUGGAUUUGAAGGGAGCUCUG	AAGUCCAUCCUUGGAGCCAAA	Cleavage	Sugarcane yellow leaf virus 2
sof-miR159b HQ342888.1	7.0	-1.0	1	21	1143	1163	UUUGGAUUUGAAGGGAGCUCUG	AGCAGCCCAUUUCACUCCAGU	Cleavage	Sugarcane yellow leaf virus 2
sof-miR159b HQ342888.1	7.0	-1.0	1	21	1123	1143	UUUGGAUUUGAAGGGAGCUCUG	AAGUCCAUCCUUGGAGCCAAA	Cleavage	Sugarcane yellow leaf virus 2
sof-miR159c HQ342888.1	7.0	-1.0	1	21	1143	1163	CUUGGAUUUGAAGGGAGCUCCU	AGCAGCCCAUUUCACUCCAGU	Cleavage	Sugarcane yellow leaf virus 1
sof-miR159d HQ342888.1	7.0	-1.0	1	21	1143	1163	UUUGGAUUUGAAGGGAGCUCUG	AGCAGCCCAUUUCACUCCAGU	Cleavage	Sugarcane yellow leaf virus 2
sof-miR159d HQ342888.1	7.0	-1.0	1	21	1123	1143	UUUGGAUUUGAAGGGAGCUCUG	AAGUCCAUCCUUGGAGCCAAA	Cleavage	Sugarcane yellow leaf virus 2
sof-miR168b HQ342888.1	7.0	-1.0	1	20	5620	5639	UCGCUUGGGCAGAUCCGGAC	CUCCUUGUUUGGUUGAGUGU	Cleavage	Sugarcane yellow leaf virus 1
sof-miR156 HQ342888.1	7.5	-1.0	1	20	1188	1207	UGACAGAAGAGAGUGAGCAC	GUCUUUCUUAUUUUUGACA	Translation	Sugarcane yellow leaf virus 1
ssp-miR444b.1 HQ342888.1	4.5	-1.0	1	21	1664	1684	CGACUGUCGAGAAAGCUAUGG	UUGUGGCUUUCUUGCAAGUUG	Cleavage	Sugarcane yellow leaf virus 4
ssp-miR528 HQ342888.1	5.0	-1.0	1	21	4162	4182	UGGAAGGGGCAUGCAGAGGAG	CCGAUUUGAAUGCCUUUCCA	Cleavage	Sugarcane yellow leaf virus 4
ssp-miR169 HQ342888.1	5.5	-1.0	1	21	2777	2797	UAGCCAAGGAUGACUUGCCGG	AGCAGAAGUCAUUAUGGCUG	Cleavage	Sugarcane yellow leaf virus 1
ssp-miR528 HQ342888.1	6.0	-1.0	1	21	4436	4456	UGGAAGGGGCAUGCAGAGGAG	AUACCCUUCGUCCUCUUCCA	Translation	Sugarcane yellow leaf virus 4
ssp-miR167b HQ342888.1	6.5	-1.0	1	21	2279	2298	UGAAGCUGCCAGCAUGAUCUG	CAGCUCCU-CUGGCAGCCUCA	Cleavage	Sugarcane yellow leaf virus 1
ssp-miR396 HQ342888.1	6.5	-1.0	1	21	1666	1686	UUCCACAGCUUUUCUUGAACUG	ACUGUCGAGAAAGCUAUGGUU	Cleavage	Sugarcane yellow leaf virus 1
ssp-miR444b.1 HQ342888.1	6.5	-1.0	1	21	2317	2337	AAGAUUUAAGGAGGCUGUCA	UUGUGGCUUUCUUGCAAGUUG	Cleavage	Sugarcane yellow leaf virus 4
ssp-miR159a HQ342888.1	7.0	-1.0	1	21	1143	1163	UUUGGAUUUGAAGGGAGCUCUG	AGCAGCCCAUUUCACUCCAGU	Cleavage	Sugarcane yellow leaf virus 2
ssp-miR159a HQ342888.1	7.0	-1.0	1	21	1123	1143	UUUGGAUUUGAAGGGAGCUCUG	AAGUCCAUCCUUGGAGCCAAA	Cleavage	Sugarcane yellow leaf virus 2
ssp-miR528 HQ342888.1	7.0	-1.0	1	21	262	281	UGGAAGGGGCAUGCAGAGGAG	UGCCUAUUC-UGCUCUGCCA	Cleavage	Sugarcane yellow leaf virus 4
ssp-miR156 HQ342888.1	7.5	-1.0	1	21	1187	1207	UGACAGAAGAGAGUGAGCACA	UGUCUUUCUUAUUUUUGACA	Translation	Sugarcane yellow leaf virus 1
ssp-miR437a HQ342888.1	7.5	-1.0	1	21	9	30	AAAGU-UAGAGAAGUUUGACUU	CUUGUAAACUGCUCUAUGCUUU	Translation	Sugarcane yellow leaf virus 1
ssp-miR444a HQ342888.1	7.5	-1.0	1	21	3732	3751	UGCAGUUGGUUGCCUCAAGCUU	GUGUUGGAGGAAACG-CUGUG	Translation	Sugarcane yellow leaf virus 1
ssp-miR444b.1 HQ342888.1	7.5	-1.0	1	21	1621	1642	UUGUGGCUUUCUU-			

GCAAGUUG	AAACCUGUUGAGAACGCUACAG	Cleavage	Sugarcane yellow leaf virus	4
ssp-miR444b.1	HQ342888.1	7.5 -1.0 1	21 3082 3102	
UUGUGGCUUUCUUGCAAGUUG	CAGAUUGGGCGAUAGCCAUGG	Cleavage	Sugarcane yellow	
leaf virus 4				
ssp-miR444b.2	HQ342888.1	7.5 -1.0 1	21 3732 3751	
UGCAGUUGUUGCCUCAAGCUU	GUGUUGGAGGAAACG-CUGUG	Translation	Sugarcane yellow	
leaf virus 1				
ssp-miR528	HQ342888.1	7.5 -1.0 1	21 4702 4722	UGGAAGGGGCAUGCAGAGGAG
AGAUUUUUCUUGUUCAUUUCA	Cleavage	Sugarcane yellow leaf virus	4	