

[illegible]

[illegible]

```
>32_6_67          hairpin:28:32
UGUGGAUCCGGUGAGGUAGUAGGUUGUAUAGUUUGGAAUAAUACCACCUUACCGGAGACAGA
4          0.237467094951    5          36
38         134.014470118    3          4
>35_6_68          hairpin:28:32
UGUGGAUCCGGUGAGGUAGUAGGUUGUAUAGUUUGGAAUAAUACCACCGUUACCGGAGACAGA
4          0.237467094951    5          36
38         440.257548663    3          4
>38_6_70          hairpin:29:36
UGUGGAUCCGGUGAGGUAGUAGGUUGUAUAGUUUGGAAUAAUACCACCGGCUUACCGGAGACAGA
5          2.88264718668    5          40
40         613.409228083    3          4
>39_6_69          hairpin:28:32
UGUGGAUCCGGUGAGGUAGUAGGUUGUAUAGUUUGGAAUAAUACCACCGGUUACCGGAGACAGA
4          0.237467094951    5          36
39         147.182907489    3          4
>43_6_70          hairpin:29:36
```

```
UGUGGAUCCGGUGAGGUAGUAGGUUGUAUAGUUUGGAAUAUUACCACCGGUUACCGGAGACAGA
5      2.88264718668    5      40
40     613.409228083    3      4
>44_6_69      hairpin:28:32
UGUGGAUCCGGUGAGGUAGUAGGUUGUAUAGUUUGGAAUAUUACCACCGGUUACCGGAGACAGA
4      0.237467094951    5      36
39     147.182907489    3      4
>46_5_62      hairpin:29:33
CUGUGGAUCCGGUGAGGUAGUAGGUUGUAUAGUUUGGAAUAUUACCACCGGUCCGGAG
3      0.138828816298    5      39
35     1.38043715688    3      2
```

=====
4) "Target.miRNAs"

=====
miranda v3.3a microRNA Target Scanning Algorithm
=====

(c) 2003 Memorial Sloan-Kettering Cancer Center, New York

Authors: Anton Enright, Bino John, Chris Sander and Debora Marks
(mirnatargets (at) cbio.mskcc.org - reaches all authors)

Software written by: Anton Enright
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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: Mature_miRNAs.txt
Reference Filename: vin.fasta
Gap Open Penalty: -9.000000
Gap Extend Penalty: -4.000000
Score Threshold: 140.000000
Energy Threshold: 1.000000 kcal/mol
Scaling Parameter: 4.000000
=====

Read Sequence:cel-let-7:1-99:12_22 (22 nt)
Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)
=====

Performing Scan: cel-let-7:1-99:12_22 vs NC_027779.1
=====

Score for this Scan:
No Hits Found above Threshold
Complete

Read Sequence:cel-let-7:1-99:14_24 (24 nt)
Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)
=====

Performing Scan: cel-let-7:1-99:14_24 vs NC_027779.1
=====

Forward: Score: 141.000000 Q:4 to 22 R:6770 to 6793 Align Len (18) (77.78%) (88.89
%)

Query: 3' ugaUAUGUUGGAUGAUGGAGUggc 5'
 | | : | | | | | | | | | |
 Ref: 5' agaACATATTCTACTACCTCAggt 3'

Energy: -22.620001 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:14_24	NC_027779.1	141.00	-22.62	4	22	6770	6793	18	77.
78%	88.89%								

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand,	Len1,Len2,Positions
>>cel-let-7:1-99:14_24	NC_027779.1	141.00	-22.62	141.00	-22.62 2 24 732
0	6770				

Complete

Read Sequence:cel-let-7:1-99:15_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:15_21 vs NC_027779.1

Forward: Score: 154.000000 Q:3 to 19 R:6772 to 6792 Align Len (16) (81.25%) (93.75 %)

Query: 3' auaUGUUGGAUGAUGGAGUgg 5'
 | : | : | | | | | | | | | |
 Ref: 5' aacATATTCTACTACCTCAggt 3'

Energy: -22.790001 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:15_21	NC_027779.1	154.00	-22.79	3	19	6772	6792	16	81.
25%	93.75%								

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand,	Len1,Len2,Positions
>>cel-let-7:1-99:15_21	NC_027779.1	154.00	-22.79	154.00	-22.79 3 21 732
0	6772				

Complete

Read Sequence:cel-let-7:1-99:15_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:15_22 vs NC_027779.1

Forward: Score: 156.000000 Q:3 to 21 R:6771 to 6792 Align Len (18) (77.78%) (88.89 %)

Query: 3' gaUAUGUUGGAUGAUGGAGUgg 5'
 | | : | | | | | | | | | |
 Ref: 5' gaACATATTCTACTACCTCAggt 3'

Energy: -22.790001 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:15_22	NC_027779.1	156.00	-22.79	3	21	6771	6792	18	77.
78%	88.89%								

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand,	Len1,Len2,Positions
>>cel-let-7:1-99:15_22	NC_027779.1	156.00	-22.79	156.00	-22.79 4 22 732
0	6771				

Complete

Read Sequence:cel-let-7:1-99:15_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

=====

Performing Scan: cel-let-7:1-99:15_23 vs NC_027779.1

=====

Forward: Score: 156.000000 Q:3 to 21 R:6770 to 6792 Align Len (18) (77.78%) (88.89%)

Query: 3' ugaUAUGUUGGAUGAUGGAGUgg 5'
| | : | : | | | | | | | | | |
Ref: 5' agaACATATTCTACTACCTCAgg 3'

Energy: -22.790001 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:15_23	NC_027779.1	156.00	-22.79	3	21	6770	6792	18	77.78%	88.89%
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Score for this Scan:

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

>>cel-let-7:1-99:15_23	NC_027779.1	156.00	-22.79	156.00	-22.79	5	23	732
0	6770							

Complete

Read Sequence:cel-let-7:1-99:15_24 (24 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

=====

Performing Scan: cel-let-7:1-99:15_24 vs NC_027779.1

=====

Forward: Score: 156.000000 Q:3 to 21 R:6769 to 6792 Align Len (18) (77.78%) (88.89%)

Query: 3' uugaUAUGUUGGAUGAUGGAGUgg 5'
| | : | : | | | | | | | | | |
Ref: 5' cagaACATATTCTACTACCTCAgg 3'

Energy: -22.790001 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:15_24	NC_027779.1	156.00	-22.79	3	21	6769	6792	18	77.78%	88.89%
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Score for this Scan:

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

>>cel-let-7:1-99:15_24	NC_027779.1	156.00	-22.79	156.00	-22.79	6	24	732
0	6769							

Complete

Read Sequence:cel-let-7:1-99:16_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

=====

Performing Scan: cel-let-7:1-99:16_20 vs NC_027779.1

=====

Forward: Score: 169.000000 Q:2 to 18 R:6772 to 6791 Align Len (16) (81.25%) (93.75%)

Query: 3' auaUGUUGGAUGAUGGAGUg 5'
| : | : | | | | | | | | | |
Ref: 5' aacATATTCTACTACCTCAg 3'

Energy: -22.990000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_20	NC_027779.1	169.00	-22.99	2	18	6772	6791	16	81.25%	93.75%
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miRPV_Output

Sun Jun 14 15:12:23 2020

7

Forward: Score: 153.000000 Q:2 to 18 R:6057 to 6076 Align Len (16) (68.75%) (81.25%)

Query: 3' auaUGUUGGAUGAUGGAGUg 5'
| :| |||||
Ref: 5' ctcAAGGCGCACTACCTCAg 3'

Energy: -15.510000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_20	NC_027779.1	153.00	-15.51	2 18	6057 6076	16	68.75%
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Forward: Score: 144.000000 Q:3 to 17 R:3070 to 3089 Align Len (14) (85.71%) (85.71%)

Query: 3' auauGUUGGAUGAUGGAGUg 5'
||||| |||||
Ref: 5' caccCAACCCTCTACCTCcg 3'

Energy: -20.629999 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_20	NC_027779.1	144.00	-20.63	3 17	3070 3089	14	85.71%
-----------------------	-------------	--------	--------	------	-----------	----	--------

Score for this Scan:

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

>>cel-let-7:1-99:16_20	NC_027779.1	466.00	-59.13	169.00	-22.99	7	20	732
------------------------	-------------	--------	--------	--------	--------	---	----	-----

Complete

Read Sequence:cel-let-7:1-99:16_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:16_21 vs NC_027779.1

Forward: Score: 171.000000 Q:2 to 20 R:6771 to 6791 Align Len (18) (77.78%) (88.89%)

Query: 3' gaUAUGUUGGAUGAUGGAGUg 5'
| |:| :|||||
Ref: 5' gaACATATTCTACTACCTCAg 3'

Energy: -22.990000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_21	NC_027779.1	171.00	-22.99	2 20	6771 6791	18	77.78%
-----------------------	-------------	--------	--------	------	-----------	----	--------

Forward: Score: 153.000000 Q:2 to 18 R:6056 to 6076 Align Len (16) (68.75%) (81.25%)

Query: 3' gaauUGUUGGAUGAUGGAGUg 5'
| :| |||||
Ref: 5' tctcAAGGCGCACTACCTCAg 3'

Energy: -16.180000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_21	NC_027779.1	153.00	-16.18	2 18	6056 6076	16	68.75%
-----------------------	-------------	--------	--------	------	-----------	----	--------

Forward: Score: 144.000000 Q:3 to 17 R:3069 to 3089 Align Len (14) (85.71%) (85.71%)

%)

Query: 3' gauauGUUGGAUGAUGGAGug 5'

Ref: 5' tcaccCAACCCTCTACCTCcg 3'

Energy: -20.629999 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_21	NC_027779.1	144.00	-20.63	3 17	3069 3089	14	85.
71%	85.71%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions							
>>cel-let-7:1-99:16_21	NC_027779.1	468.00	-59.80	171.00	-22.99	8	21 732
0	6771 6056 3069						

Complete

Read Sequence:cel-let-7:1-99:16_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:16_22 vs NC_027779.1

Forward: Score: 171.000000 Q:2 to 20 R:6770 to 6791 Align Len (18) (77.78%) (88.89 %)

Query: 3' ugaUAUGUUGGAUGAUGGAGUg 5'

Ref: 5' agaACATATTCTACTACCTCAg 3'

Energy: -22.990000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_22	NC_027779.1	171.00	-22.99	2 20	6770 6791	18	77.
78%	88.89%						

Forward: Score: 153.000000 Q:2 to 18 R:6055 to 6076 Align Len (16) (68.75%) (81.25 %)

Query: 3' ugauaUGUUGGAUGAUGGAGUg 5'

Ref: 5' ttctcAAGGCGCACTACCTCAg 3'

Energy: -16.180000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_22	NC_027779.1	153.00	-16.18	2 18	6055 6076	16	68.
75%	81.25%						

Forward: Score: 144.000000 Q:3 to 17 R:3068 to 3089 Align Len (14) (85.71%) (85.71 %)

Query: 3' ugauauGUUGGAUGAUGGAGug 5'

Ref: 5' ttcaccCAACCCTCTACCTCcg 3'

Energy: -20.629999 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_22	NC_027779.1	144.00	-20.63	3 17	3068 3089	14	85.
71%	85.71%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions							
>>cel-let-7:1-99:16_22	NC_027779.1	468.00	-59.80	171.00	-22.99	9	22 732

0 6770 6055 3068
Complete

Read Sequence:cel-let-7:1-99:16_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:16_23 vs NC_027779.1

Forward: Score: 171.000000 Q:2 to 20 R:6769 to 6791 Align Len (18) (77.78%) (88.89%)

Query: 3' uugaUAUGUUGGAUGAUGGAGUg 5'
| |:| :|||||||
Ref: 5' cagaACATATTCTACTACCTCAg 3'

Energy: -22.990000 kCal/Mol

Scores for this hit:

Seq1	Seq2	Tot Score	Tot Energy	Max Score	Max Energy	Strand	Len1	Len2	Positions
>cel-let-7:1-99:16_23	NC_027779.1	171.00	-22.99	2 20	6769 6791	18	77.78%	88.89%	

Forward: Score: 153.000000 Q:2 to 18 R:6054 to 6076 Align Len (16) (68.75%) (81.25%)

Query: 3' uugauaUGUUGGAUGAUGGAGUg 5'
| ::| |||||
Ref: 5' gttctcAAGGCGCACTACCTCAg 3'

Energy: -16.180000 kCal/Mol

Scores for this hit:

Seq1	Seq2	Tot Score	Tot Energy	Max Score	Max Energy	Strand	Len1	Len2	Positions
>cel-let-7:1-99:16_23	NC_027779.1	153.00	-16.18	2 18	6054 6076	16	68.75%	81.25%	

Forward: Score: 144.000000 Q:3 to 17 R:3067 to 3089 Align Len (14) (85.71%) (85.71%)

Query: 3' uugauauGUUGGAUGAUGGAGUg 5'
||||| |||||
Ref: 5' cttcaccCAACCCTCTACCTCcg 3'

Energy: -20.629999 kCal/Mol

Scores for this hit:

Seq1	Seq2	Tot Score	Tot Energy	Max Score	Max Energy	Strand	Len1	Len2	Positions
>cel-let-7:1-99:16_23	NC_027779.1	144.00	-20.63	3 17	3067 3089	14	85.71%	85.71%	

Score for this Scan:

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

Seq1	Seq2	Tot Score	Tot Energy	Max Score	Max Energy	Strand	Len1	Len2	Positions
>>cel-let-7:1-99:16_23	NC_027779.1	468.00	-59.80	171.00	-22.99	10	23	732	

0 6769 6054 3067
Complete

Read Sequence:cel-let-7:1-99:16_24 (24 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:16_24 vs NC_027779.1

Forward: Score: 171.000000 Q:2 to 20 R:6768 to 6791 Align Len (18) (77.78%) (88.89%)

Query: 3' uuugaUAUGUUGGAUGAUGGAGUg 5'
| |:| :|||||||
Ref: 5' tcagaACATATTCTACTACCTCAg 3'

Energy: -23.290001 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_24	NC_027779.1	171.00	-23.29	2 20	6768 6791	18	77.
78%	88.89%						

Forward: Score: 153.000000 Q:2 to 18 R:6053 to 6076 Align Len (16) (68.75%) (81.25%)

Query: 3' uuugauaUGUUGGAUGAUGGAGUg 5'

Ref: 5' cgttctcAAGGCGCACTACCTCAg 3'

Energy: -16.180000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_24	NC_027779.1	153.00	-16.18	2 18	6053 6076	16	68.
75%	81.25%						

Forward: Score: 144.000000 Q:3 to 17 R:3066 to 3089 Align Len (14) (85.71%) (85.71%)

Query: 3' uuugauauGUUGGAUGAUGGAGug 5'

Ref: 5' ccttcaccCAACCCTCTACCTCcg 3'

Energy: -20.629999 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_24	NC_027779.1	144.00	-20.63	3 17	3066 3089	14	85.
71%	85.71%						

Forward: Score: 141.000000 Q:2 to 23 R:588 to 612 Align Len (22) (50.00%) (86.36%)

Query: 3' uuUGAUAUGU-UGGAUGAUGGAGUg 5'

Ref: 5' agAGTGTGTGTTTTGCTACTTCAa 3'

Energy: -19.160000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:16_24	NC_027779.1	141.00	-19.16	2 23	588 612 22	50.00%	86.
36%							

Score for this Scan:

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

>>cel-let-7:1-99:16_24	NC_027779.1	609.00	-79.26	171.00	-23.29	11	24	732
0	6768 6053 3066 588							

Complete

Read Sequence:cel-let-7:1-99:17_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:17_20 vs NC_027779.1

Forward: Score: 166.000000 Q:2 to 19 R:6771 to 6790 Align Len (17) (76.47%) (88.24%)

Query: 3' gaUAUGUUGGAUGAUGGAGu 5'

Ref: 5' gaACATATTCTACTACCTCa 3'

Energy: -23.480000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_20 NC_027779.1 166.00 -23.48 2 19 6771 6790 17 76.
47% 88.24%

Forward: Score: 159.000000 Q:2 to 16 R:3069 to 3088 Align Len (14) (85.71%) (85.71%)

Query: 3' gauauGUUGGAUGAUGGAGu 5'

Ref: 5' tcaccCAACCCTCTACCTCc 3'

Energy: -19.629999 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_20 NC_027779.1 159.00 -19.63 2 16 3069 3088 14 85.
71% 85.71%

Forward: Score: 148.000000 Q:2 to 17 R:6056 to 6075 Align Len (15) (66.67%) (80.00%)

Query: 3' gaauUGUUGGAUGAUGGAGu 5'

Ref: 5' tctcAAGGCGCACTACCTCa 3'

Energy: -16.670000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_20 NC_027779.1 148.00 -16.67 2 17 6056 6075 15 66.
67% 80.00%

Score for this Scan:

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

>>cel-let-7:1-99:17_20 NC_027779.1 473.00 -59.78 166.00 -23.48 12 20 732
0 6771 3069 6056

Complete

Read Sequence:cel-let-7:1-99:17_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:17_21 vs NC_027779.1

Forward: Score: 166.000000 Q:2 to 19 R:6770 to 6790 Align Len (17) (76.47%) (88.24%)

Query: 3' ugaUAUGUUGGAUGAUGGAGu 5'

Ref: 5' agaACATATTCTACTACCTCa 3'

Energy: -23.480000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_21 NC_027779.1 166.00 -23.48 2 19 6770 6790 17 76.
47% 88.24%

Forward: Score: 159.000000 Q:2 to 16 R:3068 to 3088 Align Len (14) (85.71%) (85.71%)

Query: 3' ugauauGUUGGAUGAUGGAGu 5'

Ref: 5' ttccaccCAACCCTCTACCTCc 3'

Energy: -19.629999 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_21 NC_027779.1 159.00 -19.63 2 16 3068 3088 14 85.71% 85.71%

Forward: Score: 148.000000 Q:2 to 17 R:6055 to 6075 Align Len (15) (66.67%) (80.00%)

Query: 3' ugauaUGUUGGAUGAUGGAGu 5'

Ref: 5' ttctcAAGGCGCACTACCTCa 3'

Energy: -16.670000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_21 NC_027779.1 148.00 -16.67 2 17 6055 6075 15 66.67% 80.00%

Score for this Scan:

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

>>cel-let-7:1-99:17_21 NC_027779.1 473.00 -59.78 166.00 -23.48 13 21 7320 6770 3068 6055

Complete

Read Sequence:cel-let-7:1-99:17_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:17_22 vs NC_027779.1

Forward: Score: 166.000000 Q:2 to 19 R:6769 to 6790 Align Len (17) (76.47%) (88.24%)

Query: 3' uugaUAUGUUGGAUGAUGGAGu 5'

Ref: 5' cagaACATATTCTACTACCTCa 3'

Energy: -23.480000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_22 NC_027779.1 166.00 -23.48 2 19 6769 6790 17 76.47% 88.24%

Forward: Score: 159.000000 Q:2 to 16 R:3067 to 3088 Align Len (14) (85.71%) (85.71%)

Query: 3' uugauauGUUGGAUGAUGGAGu 5'

Ref: 5' cttcaccCAACCCTCTACCTCc 3'

Energy: -19.629999 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_22 NC_027779.1 159.00 -19.63 2 16 3067 3088 14 85.71% 85.71%

Forward: Score: 148.000000 Q:2 to 17 R:6054 to 6075 Align Len (15) (66.67%) (80.00%)

Query: 3' uugauaUGUUGGAUGAUGGAGu 5'

Ref: 5' gttctcAAGGCGCACTACCTCa 3'

Energy: -16.670000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_22 NC_027779.1 148.00 -16.67 2 17 6054 6075 15 66.
67% 80.00%

Score for this Scan:

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

>>cel-let-7:1-99:17_22 NC_027779.1 473.00 -59.78 166.00 -23.48 14 22 732
0 6769 3067 6054

Complete

Read Sequence:cel-let-7:1-99:17_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:17_23 vs NC_027779.1

Forward: Score: 166.000000 Q:2 to 19 R:6768 to 6790 Align Len (17) (76.47%) (88.24
%)

Query: 3' uuugaUAUGUUGGAUGAUGGAGu 5'

| |:| :|||||

Ref: 5' tcagaACATATTCTACTACCTCa 3'

Energy: -23.780001 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_23 NC_027779.1 166.00 -23.78 2 19 6768 6790 17 76.
47% 88.24%

Forward: Score: 159.000000 Q:2 to 16 R:3066 to 3088 Align Len (14) (85.71%) (85.71
%)

Query: 3' uuugauauGUUGGAUGAUGGAGu 5'

||||| |||||

Ref: 5' ccttcaccCAACCCTCTACCTCc 3'

Energy: -19.629999 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_23 NC_027779.1 159.00 -19.63 2 16 3066 3088 14 85.
71% 85.71%

Forward: Score: 148.000000 Q:2 to 17 R:6053 to 6075 Align Len (15) (66.67%) (80.00
%)

Query: 3' uuugauaUGUUGGAUGAUGGAGu 5'

| ::| |||||

Ref: 5' cgttctcAAGGCGCACTACCTCa 3'

Energy: -16.670000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_23 NC_027779.1 148.00 -16.67 2 17 6053 6075 15 66.
67% 80.00%

Score for this Scan:

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

>>cel-let-7:1-99:17_23 NC_027779.1 473.00 -60.08 166.00 -23.78 15 23 732
0 6768 3066 6053

Complete

Read Sequence:cel-let-7:1-99:17_24 (24 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:17_24 vs NC_027779.1

Forward: Score: 166.000000 Q:2 to 19 R:6767 to 6790 Align Len (17) (76.47%) (88.24%)

Query: 3' guuugaUAUGUUGGAUGAUGGAGu 5'
 | | : | : |||||
Ref: 5' ttcagaACATATTCTACTACCTCa 3'

Energy: -25.360001 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_24	NC_027779.1	166.00	-25.36	2 19	6767 6790	17	76.47%
							88.24%

Forward: Score: 159.000000 Q:2 to 16 R:3065 to 3088 Align Len (14) (85.71%) (85.71%)

Query: 3' guuugauauGUUGGAUGAUGGAGu 5'
 ||| | ||| |
Ref: 5' gccttcaccCAACCCTCTACCTCc 3'

Energy: -19.629999 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_24	NC_027779.1	159.00	-19.63	2 16	3065 3088	14	85.71%
							85.71%

Forward: Score: 148.000000 Q:2 to 17 R:6052 to 6075 Align Len (15) (66.67%) (80.00%)

Query: 3' guuugauaUGUUGGAUGAUGGAGu 5'
 | : | | | | |
Ref: 5' tcgttctcAAGGCGCACTACCTCa 3'

Energy: -19.379999 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:17_24	NC_027779.1	148.00	-19.38	2 17	6052 6075	15	66.67%
							80.00%

Score for this Scan:

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

>>cel-let-7:1-99:17_24	NC_027779.1	473.00	-64.37	166.00	-25.36	16	24	732
0		6767	3065	6052				

Complete

Read Sequence:cel-let-7:1-99:18_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:18_20 vs NC_027779.1

Forward: Score: 161.000000 Q:2 to 18 R:6770 to 6789 Align Len (16) (75.00%) (87.50%)

Query: 3' ugaUAUGUUGGAUGAUGGAg 5'
 | | : | : |||||
Ref: 5' agaACATATTCTACTACCTc 3'

Energy: -21.700001 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_20	NC_027779.1	161.00	-21.70	2 18	6770 6789	16	75.00%
							87.50%

Forward: Score: 143.000000 Q:2 to 16 R:6055 to 6074 Align Len (14) (64.29%) (78.57%)

%)

Query: 3' ugaauUGUUGGAUGAUGGAg 5'

Ref: 5' ttctcAAGGCGCACTACCTc 3'

Energy: -14.890000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_20	NC_027779.1	143.00	-14.89	2 16	6055 6074	14	64.
29%	78.57%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions							
>>cel-let-7:1-99:18_20	NC_027779.1	304.00	-36.59	161.00	-21.70	17	20 732
0	6770 6055						

Complete

Read Sequence:cel-let-7:1-99:18_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:18_21 vs NC_027779.1

Forward: Score: 161.000000 Q:2 to 18 R:6769 to 6789 Align Len (16) (75.00%) (87.50 %)

Query: 3' uugaUAUGUUGGAUGAUGGAg 5'

Ref: 5' cagaACATATTCTACTACCTc 3'

Energy: -21.700001 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_21	NC_027779.1	161.00	-21.70	2 18	6769 6789	16	75.
00%	87.50%						

Forward: Score: 143.000000 Q:2 to 16 R:6054 to 6074 Align Len (14) (64.29%) (78.57 %)

Query: 3' ugaauUGUUGGAUGAUGGAg 5'

Ref: 5' gttctcAAGGCGCACTACCTc 3'

Energy: -14.890000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_21	NC_027779.1	143.00	-14.89	2 16	6054 6074	14	64.
29%	78.57%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions							
>>cel-let-7:1-99:18_21	NC_027779.1	304.00	-36.59	161.00	-21.70	18	21 732
0	6769 6054						

Complete

Read Sequence:cel-let-7:1-99:18_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:18_22 vs NC_027779.1

Forward: Score: 161.000000 Q:2 to 18 R:6768 to 6789 Align Len (16) (75.00%) (87.50 %)

Query: 3' uuugaUAUGUUGGAUGAUGGAg 5'

| |:| :|||||

Ref: 5' tcagaACATATTCTACTACCTc 3'

Energy: -22.000000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_22	NC_027779.1	161.00	-22.00	2 18	6768 6789	16	75.00%	87.50%
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Forward: Score: 143.000000 Q:2 to 16 R:6053 to 6074 Align Len (14) (64.29%) (78.57%)

Query: 3' uuugauaUGUUGGAUGAUGGAg 5'

Ref: 5' cgttctcAAGGCGCACTACCTc 3'

Energy: -14.890000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_22	NC_027779.1	143.00	-14.89	2 16	6053 6074	14	64.29%	78.57%
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Score for this Scan:

Seq1	Seq2	Tot Score	Tot Energy	Max Score	Max Energy	Strand	Len1	Len2	Positions
>>cel-let-7:1-99:18_22	NC_027779.1	304.00	-36.89	161.00	-22.00	19	22	732	
0	6768 6053								

Complete

Read Sequence:cel-let-7:1-99:18_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:18_23 vs NC_027779.1

Forward: Score: 161.000000 Q:2 to 18 R:6767 to 6789 Align Len (16) (75.00%) (87.50%)

Query: 3' guuugaUAUGUUGGAUGAUGGAg 5'

Ref: 5' ttcagaACATATTCTACTACCTc 3'

Energy: -23.580000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_23	NC_027779.1	161.00	-23.58	2 18	6767 6789	16	75.00%	87.50%
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Forward: Score: 143.000000 Q:2 to 22 R:3308 to 3329 Align Len (20) (65.00%) (80.00%)

Query: 3' guUUGAUAUGUUGGAUGAUGGAg 5'

Ref: 5' ggAACAGGAC-ATCGACTACTTg 3'

Energy: -12.280000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_23	NC_027779.1	143.00	-12.28	2 22	3308 3329	20	65.00%	80.00%
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Forward: Score: 143.000000 Q:2 to 16 R:6052 to 6074 Align Len (14) (64.29%) (78.57%)

Query: 3' guuugauaUGUUGGAUGAUGGAg 5'

Ref: 5' tcggttctcAAGGCGCACTACCTc 3'

Energy: -17.600000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_23	NC_027779.1	143.00	-17.60	2	16	6052	6074	14	64.
29%	78.57%								

Forward: Score: 142.000000 Q:3 to 22 R:2731 to 2753 Align Len (20) (75.00%) (80.00%)

Query: 3' guUUG-AUAUGUUGGAUGAUGGag 5'

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

Ref: 5' tgAACTTATA-AATACACTACCaa 3'

Energy: -13.780000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_23	NC_027779.1	142.00	-13.78	3	22	2731	2753	20	75.
00%	80.00%								

Score for this Scan:

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

>>cel-let-7:1-99:18_23	NC_027779.1	589.00	-67.24	161.00	-23.58	20	23	732
0	6767	3308	6052	2731				

Complete

Read Sequence:cel-let-7:1-99:18_24 (24 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:18_24 vs NC_027779.1

Forward: Score: 161.000000 Q:2 to 18 R:6766 to 6789 Align Len (16) (75.00%) (87.50%)

Query: 3' gguuugaUAUGUUGGAUGAUGGag 5'

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

Ref: 5' attcagaACATATTCTACTACCTc 3'

Energy: -24.260000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_24	NC_027779.1	161.00	-24.26	2	18	6766	6789	16	75.
00%	87.50%								

Forward: Score: 144.000000 Q:3 to 23 R:2731 to 2753 Align Len (20) (70.00%) (80.00%)

Query: 3' ggUUUGAUAUGUUGGAUGAUGGag 5'

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

Ref: 5' tgAACTTATA-AATACACTACCaa 3'

Energy: -13.780000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_24	NC_027779.1	144.00	-13.78	3	23	2731	2753	20	70.
00%	80.00%								

Forward: Score: 144.000000 Q:2 to 23 R:3307 to 3329 Align Len (21) (61.90%) (80.95%)

Query: 3' ggUUUGAUAUGUUGGAUGAUGGag 5'

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

Ref: 5' ggGAACAGGAC-ATCGACTACTTg 3'

Energy: -12.280000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_24	NC_027779.1	144.00	-12.28	2 23	3307 3329	21	61.
90%	80.95%						

Forward: Score: 143.000000 Q:2 to 16 R:6051 to 6074 Align Len (14) (64.29%) (78.57 %)

Query: 3' gguuugauaUGUUGGAUGAUGGAg 5'

Ref: 5' atcgttctcAAGGCGCACTACCTc 3'

Energy: -18.930000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:18_24	NC_027779.1	143.00	-18.93	2 16	6051 6074	14	64.
29%	78.57%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions	
>>cel-let-7:1-99:18_24 NC_027779.1	592.00 -69.25 161.00 -24.26 21 24 732
0 6766 2731 3307 6051	
Complete	

Read Sequence:cel-let-7:1-99:19_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:19_20 vs NC_027779.1

Forward: Score: 156.000000 Q:2 to 17 R:6769 to 6788 Align Len (15) (73.33%) (86.67 %)

Query: 3' uugaUAUGUUGGAUGAUGGa 5'

Ref: 5' cagaACATATTCTACTACCT 3'

Energy: -18.270000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:19_20	NC_027779.1	156.00	-18.27	2 17	6769 6788	15	73.
33%	86.67%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions	
>>cel-let-7:1-99:19_20 NC_027779.1	156.00 -18.27 156.00 -18.27 22 20 732
0 6769	
Complete	

Read Sequence:cel-let-7:1-99:19_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:19_21 vs NC_027779.1

Forward: Score: 156.000000 Q:2 to 17 R:6768 to 6788 Align Len (15) (73.33%) (86.67 %)

Query: 3' uuugaUAUGUUGGAUGAUGGa 5'

Ref: 5' tcagaACATATTCTACTACCT 3'

Energy: -18.570000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:19_21	NC_027779.1	156.00	-18.57	2 17	6768 6788	15	73.
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33% 86.67%

Forward: Score: 141.000000 Q:2 to 20 R:2998 to 3017 Align Len (18) (66.67%) (83.33%)

Query: 3' uuUGAUAUGUUGGAUGAUGGa 5'
|:|||| |:| |||||:
Ref: 5' gcATTATA-GAGATACTACTa 3'

Energy: -12.640000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:19_21	NC_027779.1	141.00	-12.64	2 20	2998 3017	18	66.67%	83.33%
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Score for this Scan:

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

>>cel-let-7:1-99:19_21	NC_027779.1	297.00	-31.21	156.00	-18.57	23	21	732
0	6768 2998							

Complete

Read Sequence:cel-let-7:1-99:19_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:19_22 vs NC_027779.1

Forward: Score: 156.000000 Q:2 to 17 R:6767 to 6788 Align Len (15) (73.33%) (86.67%)

Query: 3' guuugaUAUGUUGGAUGAUGGa 5'
| |:| :|||||||
Ref: 5' ttcagaACATATTCTACTACct 3'

Energy: -20.150000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:19_22	NC_027779.1	156.00	-20.15	2 17	6767 6788	15	73.33%	86.67%
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Forward: Score: 141.000000 Q:2 to 20 R:2997 to 3017 Align Len (18) (66.67%) (83.33%)

Query: 3' guuUGAUAUGUUGGAUGAUGGa 5'
|:|||| |:| |||||:
Ref: 5' tgcATTATA-GAGATACTACTa 3'

Energy: -12.640000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:19_22	NC_027779.1	141.00	-12.64	2 20	2997 3017	18	66.67%	83.33%
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Score for this Scan:

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

>>cel-let-7:1-99:19_22	NC_027779.1	297.00	-32.79	156.00	-20.15	24	22	732
0	6767 2997							

Complete

Read Sequence:cel-let-7:1-99:19_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:19_23 vs NC_027779.1

Forward: Score: 156.000000 Q:2 to 17 R:6766 to 6788 Align Len (15) (73.33%) (86.67%)

%)

Query: 3' gguuugaUAUGUUGGAUGAUGGa 5'

Ref: 5' attcagaACATATTCTACTACct 3'

Energy: -20.830000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:19_23	NC_027779.1	156.00	-20.83	2 17	6766 6788	15	73.
33%	86.67%						

Forward: Score: 141.000000 Q:2 to 20 R:2996 to 3017 Align Len (18) (66.67%) (83.33%)

Query: 3' gguuUGAUAUGUUGGAUGAUGGa 5'

Ref: 5' gtgcATTATA-GAGATACTACTa 3'

Energy: -12.640000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:19_23	NC_027779.1	141.00	-12.64	2 20	2996 3017	18	66.
67%	83.33%						

Forward: Score: 140.000000 Q:2 to 22 R:5408 to 5431 Align Len (21) (57.14%) (80.95%)

Query: 3' ggUUUGAUAUGU-UGGAUGAUGGa 5'

Ref: 5' agAGTTTTTAGATGCTTATTACCa 3'

Energy: -11.900000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:19_23	NC_027779.1	140.00	-11.90	2 22	5408 5431	21	57.
14%	80.95%						

Score for this Scan:

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

>>cel-let-7:1-99:19_23	NC_027779.1	437.00	-45.37	156.00	-20.83	25	23	732
0	6766	2996	5408					

Complete

Read Sequence:cel-let-7:1-99:20_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

=====

Performing Scan: cel-let-7:1-99:20_20 vs NC_027779.1

=====

Forward: Score: 151.000000 Q:2 to 16 R:6768 to 6787 Align Len (14) (71.43%) (85.71%)

Query: 3' uuugaUAUGUUGGAUGGg 5'

Ref: 5' tcagaACATATTCTACTACc 3'

Energy: -17.100000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:20_20	NC_027779.1	151.00	-17.10	2 16	6768 6787	14	71.
43%	85.71%						

Forward: Score: 140.000000 Q:2 to 19 R:2998 to 3019 Align Len (19) (68.42%) (84.21%)

Query: 3' uuUGAUAUGU-UG-GAUGAUGg 5'
|:||||| |:|||||:
Ref: 5' gcATTATAGAGATACTACTATt 3'

Energy: -14.710000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:20_20	NC_027779.1	140.00	-14.71	2	19	2998	3019	19	68.
42%	84.21%								

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand	Len1,Len2	Positions			
>>cel-let-7:1-99:20_20	NC_027779.1	291.00	-31.81	151.00	-17.10	26	20	732	
0	6768	2998							

Complete

Read Sequence:cel-let-7:1-99:20_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

=====

Performing Scan: cel-let-7:1-99:20_21 vs NC_027779.1

=====

Forward: Score: 151.000000 Q:2 to 16 R:6767 to 6787 Align Len (14) (71.43%) (85.71 %)

Query: 3' guuugaUAUGUUGGAUGAUGg 5'
| |:| :|||||
Ref: 5' ttcagaACATATTCTACTACc 3'

Energy: -18.680000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:20_21	NC_027779.1	151.00	-18.68	2	16	6767	6787	14	71.
43%	85.71%								

Forward: Score: 140.000000 Q:2 to 19 R:2997 to 3019 Align Len (19) (68.42%) (84.21 %)

Query: 3' guuUGAUAUGU-UG-GAUGAUGg 5'
|:||||| |:|||||:
Ref: 5' tgcATTATAGAGATACTACTATt 3'

Energy: -14.710000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:20_21	NC_027779.1	140.00	-14.71	2	19	2997	3019	19	68.
42%	84.21%								

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand	Len1,Len2	Positions			
>>cel-let-7:1-99:20_21	NC_027779.1	291.00	-33.39	151.00	-18.68	27	21	732	
0	6767	2997							

Complete

Read Sequence:cel-let-7:1-99:20_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

=====

Performing Scan: cel-let-7:1-99:20_22 vs NC_027779.1

=====

Forward: Score: 151.000000 Q:2 to 16 R:6766 to 6787 Align Len (14) (71.43%) (85.71 %)

Query: 3' gguuugaUAUGUUGGAUGAUGg 5'
| |:| :|||||
Ref: 5' attcagaACATATTCTACTACc 3'

Energy: -19.360001 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:20_22	NC_027779.1	151.00	-19.36	2	16	6766	6787	14	71.
43%	85.71%								

Forward: Score: 140.000000 Q:2 to 19 R:2996 to 3019 Align Len (19) (68.42%) (84.21 %)

Query: 3' gguuUGAUAUGU-UG-GAUGAUGg 5'

Ref: 5' gtgcATTATAGAGATACTACTATt 3'

Energy: -14.710000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:20_22	NC_027779.1	140.00	-14.71	2	19	2996	3019	19	68.
42%	84.21%								

Score for this Scan:

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

>>cel-let-7:1-99:20_22	NC_027779.1	291.00	-34.07	151.00	-19.36	28	22	732
0	6766	2996						

Complete

Read Sequence:cel-let-7:1-99:21_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

=====

Performing Scan: cel-let-7:1-99:21_20 vs NC_027779.1

=====

Forward: Score: 144.000000 Q:2 to 18 R:3941 to 3961 Align Len (17) (76.47%) (82.35 %)

Query: 3' guuUG-AUAUGUUGGAUGAUg 5'

Ref: 5' tacACGTATAGATCCTATTAg 3'

Energy: -10.920000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:21_20	NC_027779.1	144.00	-10.92	2	18	3941	3961	17	76.
47%	82.35%								

Score for this Scan:

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

>>cel-let-7:1-99:21_20	NC_027779.1	144.00	-10.92	144.00	-10.92	29	20	732
0	3941							

Complete

Read Sequence:cel-let-7:1-99:21_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

=====

Performing Scan: cel-let-7:1-99:21_21 vs NC_027779.1

=====

Forward: Score: 146.000000 Q:2 to 20 R:3940 to 3961 Align Len (19) (73.68%) (78.95 %)

Query: 3' ggUUUG-AUAUGUUGGAUGAUg 5'

Ref: 5' gtACACGTATAGATCCTATTAg 3'

Energy: -11.330000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:21_21 NC_027779.1 146.00 -11.33 2 20 3940 3961 19 73.
68% 78.95%

Score for this Scan:

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

>>cel-let-7:1-99:21_21 NC_027779.1 146.00 -11.33 146.00 -11.33 30 21 732
0 3940

Complete

Read Sequence:cel-let-7:1-99:21_24 (24 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:21_24 vs NC_027779.1

Forward: Score: 147.000000 Q:2 to 21 R:3937 to 3961 Align Len (20) (70.00%) (80.00%)

Query: 3' uaagGUUUG-AUAUGUUGGAUGAUg 5'

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

Ref: 5' ttggTACACGTATAGATCCTATTAg 3'

Energy: -11.330000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:21_24 NC_027779.1 147.00 -11.33 2 21 3937 3961 20 70.
00% 80.00%

Forward: Score: 145.000000 Q:3 to 22 R:4955 to 4978 Align Len (19) (68.42%) (78.95%)

Query: 3' uaaGGUUUGAUAUGUUGGAUGAug 5'

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

Ref: 5' ggaTCAAATCATTGTACCTACTtt 3'

Energy: -15.770000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:21_24 NC_027779.1 145.00 -15.77 3 22 4955 4978 19 68.
42% 78.95%

Forward: Score: 143.000000 Q:2 to 23 R:6765 to 6786 Align Len (21) (61.90%) (80.95%)

Query: 3' uaAGGUUUGAUAUGUUGGAUGAUg 5'

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

Ref: 5' taTTCAGA--ACATATTCTACTAc 3'

Energy: -17.350000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:21_24 NC_027779.1 143.00 -17.35 2 23 6765 6786 21 61.
90% 80.95%

Score for this Scan:

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

>>cel-let-7:1-99:21_24 NC_027779.1 435.00 -44.45 147.00 -17.35 31 24 732
0 3937 4955 6765

Complete

Read Sequence:cel-let-7:1-99:54_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:54_23 vs NC_027779.1

Forward: Score: 147.000000 Q:2 to 21 R:3544 to 3568 Align Len (21) (66.67%) (80.95 %)

Query: 3' ccaUCUUUUU--AACGUAUCAAGUGg 5'
|||| : |||:| ||||:|

Ref: 5' aagAGAACGCTTTGTACAGTTTACT 3'

Energy: -15.880000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:54_23	NC_027779.1	147.00	-15.88	2	21	3544	3568	21	66.67%	80.95%
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Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand	Len1,Len2	Positions
>>cel-let-7:1-99:54_23	NC_027779.1	147.00	-15.88	147.00	-15.88	32 23 732
0	3544					

Complete

Read Sequence:cel-let-7:1-99:54_24 (24 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:54_24 vs NC_027779.1

Forward: Score: 147.000000 Q:2 to 21 R:3543 to 3568 Align Len (21) (66.67%) (80.95 %)

Query: 3' uccaUCUUUUU--AACGUAUCAAGUGg 5'
|||| : |||:| ||||:|

Ref: 5' aaagAGAACGCTTTGTACAGTTTACT 3'

Energy: -15.880000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:54_24	NC_027779.1	147.00	-15.88	2	21	3543	3568	21	66.67%	80.95%
-----------------------	-------------	--------	--------	---	----	------	------	----	--------	--------

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand	Len1,Len2	Positions
>>cel-let-7:1-99:54_24	NC_027779.1	147.00	-15.88	147.00	-15.88	33 24 732
0	3543					

Complete

Read Sequence:cel-let-7:1-99:55_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:55_21 vs NC_027779.1

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:cel-let-7:1-99:55_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:55_22 vs NC_027779.1

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:cel-let-7:1-99:55_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:55_23 vs NC_027779.1

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:cel-let-7:1-99:55_24 (24 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:55_24 vs NC_027779.1

Score for this Scan:

No Hits Found above Threshold

Complete

Read Sequence:cel-let-7:1-99:56_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:56_20 vs NC_027779.1

Forward: Score: 142.000000 Q:3 to 19 R:1948 to 1967 Align Len (16) (81.25%) (93.75 %)

Query: 3' caUCUUUUUACGUAUCAAGu 5'

| |||||:|:|

Ref: 5' aaAAAAATTGTATGGTTat 3'

Energy: -14.060000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:56_20	NC_027779.1	142.00	-14.06	3 19	1948 1967	16	81.25%
93.75%							

Score for this Scan:

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

>>cel-let-7:1-99:56_20	NC_027779.1	142.00	-14.06	142.00	-14.06	38	20	732
0	1948							

Complete

Read Sequence:cel-let-7:1-99:56_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:56_21 vs NC_027779.1

Forward: Score: 142.000000 Q:3 to 19 R:1947 to 1967 Align Len (16) (81.25%) (93.75 %)

Query: 3' ccaUCUUUUUACGUAUCAAGu 5'

| |||||:|:|

Ref: 5' caaAAAAATTGTATGGTTat 3'

Energy: -14.060000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:56_21	NC_027779.1	142.00	-14.06	3 19	1947 1967	16	81.25%
93.75%							

Score for this Scan:

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

>>cel-let-7:1-99:56_21	NC_027779.1	142.00	-14.06	142.00	-14.06	39	21	732
0	1947							

Complete

Read Sequence:cel-let-7:1-99:56_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:56_22 vs NC_027779.1

Forward: Score: 142.000000 Q:3 to 19 R:1946 to 1967 Align Len (16) (81.25%) (93.75%)

Query: 3' uccaUCUUUUUAACGUAUCAAGu 5'
| | | | | | | | : | | : | | |

Ref: 5' ccaaAAAAAATTGTATGGTTat 3'

Energy: -14.060000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:56_22	NC_027779.1	142.00	-14.06	3 19	1946 1967	16	81.25%
25%	93.75%						

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand	Len1,Len2	Positions	
>>cel-let-7:1-99:56_22	NC_027779.1	142.00	-14.06	142.00	-14.06	40	22
0	1946						732

Complete

Read Sequence:cel-let-7:1-99:56_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:56_23 vs NC_027779.1

Forward: Score: 142.000000 Q:3 to 19 R:1945 to 1967 Align Len (16) (81.25%) (93.75%)

Query: 3' uuccaUCUUUUUAACGUAUCAAGu 5'
| | | | | | | | : | | : | | |

Ref: 5' cccaaAAAAAATTGTATGGTTat 3'

Energy: -14.060000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:56_23	NC_027779.1	142.00	-14.06	3 19	1945 1967	16	81.25%
25%	93.75%						

Forward: Score: 141.000000 Q:3 to 22 R:4437 to 4459 Align Len (19) (68.42%) (73.68%)

Query: 3' uuCCAUCUUUUUAACGUAUCAAGu 5'
| | : | | | | | | | |

Ref: 5' caGTTGTATAATCGAATAGTTga 3'

Energy: -8.010000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:56_23	NC_027779.1	141.00	-8.01	3 22	4437 4459	19	68.42%
42%	73.68%						

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand	Len1,Len2	Positions	
>>cel-let-7:1-99:56_23	NC_027779.1	283.00	-22.07	142.00	-14.06	41	23
0	1945 4437						732

Complete

Read Sequence:cel-let-7:1-99:56_24 (24 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:56_24 vs NC_027779.1

Forward: Score: 146.000000 Q:3 to 23 R:4436 to 4459 Align Len (20) (70.00%) (75.00%)

Query: 3' auUCCAUCUUUUUAACGUAUCAAGu 5'

Ref: 5' acAGTTGTATAATCGAATAGTTga 3'

Energy: -8.010000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:56_24	NC_027779.1	146.00	-8.01	3 23	4436 4459	20	70.
00%	75.00%						

Forward: Score: 142.000000 Q:3 to 19 R:1944 to 1967 Align Len (16) (81.25%) (93.75 %)

Query: 3' auuccaUCUUUUUAACGUAUCAAg 5'

Ref: 5' acccaaAAAAAATTGTATGGTTat 3'

Energy: -14.060000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:56_24	NC_027779.1	142.00	-14.06	3 19	1944 1967	16	81.
25%	93.75%						

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand	Len1,Len2	Positions
>>cel-let-7:1-99:56_24	NC_027779.1	288.00	-22.07	146.00	-14.06	42 24 732
0	4436 1944					

Complete

Read Sequence:cel-let-7:1-99:57_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:57_20 vs NC_027779.1

Forward: Score: 145.000000 Q:2 to 18 R:1947 to 1966 Align Len (16) (81.25%) (93.75 %)

Query: 3' ccaUCUUUUUAACGUAUCAAg 5'

Ref: 5' caaAAAAAATTGTATGGTTa 3'

Energy: -14.260000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:57_20	NC_027779.1	145.00	-14.26	2 18	1947 1966	16	81.
25%	93.75%						

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand	Len1,Len2	Positions
>>cel-let-7:1-99:57_20	NC_027779.1	145.00	-14.26	145.00	-14.26	43 20 732
0	1947					

Complete

Read Sequence:cel-let-7:1-99:57_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:57_21 vs NC_027779.1

Forward: Score: 145.000000 Q:2 to 18 R:1946 to 1966 Align Len (16) (81.25%) (93.75 %)

Query: 3' uccaUCUUUUUAACGUAUCAAg 5'

Ref: 5' ccaaAAAAAATTGTATGGTTa 3'

Energy: -14.260000 kCal/Mol

Scores for this hit:

```
>cel-let-7:1-99:57_21  NC_027779.1      145.00  -14.26  2 18      1946 1966      16      81.
25%      93.75%
```

Score for this Scan:

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

```
>>cel-let-7:1-99:57_21  NC_027779.1      145.00  -14.26  145.00  -14.26  44      21      732
0      1946
```

Complete

Read Sequence:cel-let-7:1-99:57_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:57_22 vs NC_027779.1

```
Forward:      Score: 145.000000  Q:2 to 18  R:1945 to 1966 Align Len (16) (81.25%) (93.75
%)
```

Query: 3' uuccaUCUUUUUACGUAUCAAg 5'

| |||||:|:|

Ref: 5' cccaaAAAAAATTGTATGGTTa 3'

Energy: -14.260000 kCal/Mol

Scores for this hit:

```
>cel-let-7:1-99:57_22  NC_027779.1      145.00  -14.26  2 18      1945 1966      16      81.
25%      93.75%
```

Score for this Scan:

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

```
>>cel-let-7:1-99:57_22  NC_027779.1      145.00  -14.26  145.00  -14.26  45      22      732
0      1945
```

Complete

Read Sequence:cel-let-7:1-99:57_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:57_23 vs NC_027779.1

```
Forward:      Score: 145.000000  Q:2 to 18  R:1944 to 1966 Align Len (16) (81.25%) (93.75
%)
```

Query: 3' auuccaUCUUUUUACGUAUCAAg 5'

| |||||:|:|

Ref: 5' acccaaAAAAAATTGTATGGTTa 3'

Energy: -14.260000 kCal/Mol

Scores for this hit:

```
>cel-let-7:1-99:57_23  NC_027779.1      145.00  -14.26  2 18      1944 1966      16      81.
25%      93.75%
```

Score for this Scan:

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

```
>>cel-let-7:1-99:57_23  NC_027779.1      145.00  -14.26  145.00  -14.26  46      23      732
0      1944
```

Complete

Read Sequence:cel-let-7:1-99:57_24 (24 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:57_24 vs NC_027779.1

```
Forward:      Score: 145.000000  Q:2 to 18  R:1943 to 1966 Align Len (16) (81.25%) (93.75
```

%)

Query: 3' cauuccaUCUUUUUAACGUAUCAAg 5'

Ref: 5' cacccaaAAAAAATTGTATGGTTa 3'

Energy: -14.260000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:57_24	NC_027779.1	145.00	-14.26	2	18	1943	1966	16	81.
25%	93.75%								

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand	Len1,Len2	Positions			
>>cel-let-7:1-99:57_24	NC_027779.1	145.00	-14.26	145.00	-14.26	47	24	732	
0	1943								

Complete

Read Sequence:cel-let-7:1-99:58_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:58_20 vs NC_027779.1

Forward: Score: 140.000000 Q:2 to 17 R:1946 to 1965 Align Len (15) (80.00%) (93.33 %)

Query: 3' uccaUCUUUUUAACGUAUCAa 5'

Ref: 5' ccaaAAAAAATTGTATGGTt 3'

Energy: -13.950000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:58_20	NC_027779.1	140.00	-13.95	2	17	1946	1965	15	80.
00%	93.33%								

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand	Len1,Len2	Positions			
>>cel-let-7:1-99:58_20	NC_027779.1	140.00	-13.95	140.00	-13.95	48	20	732	
0	1946								

Complete

Read Sequence:cel-let-7:1-99:58_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:58_21 vs NC_027779.1

Forward: Score: 140.000000 Q:2 to 17 R:1945 to 1965 Align Len (15) (80.00%) (93.33 %)

Query: 3' uuccaUCUUUUUAACGUAUCAa 5'

Ref: 5' cccaaAAAAAATTGTATGGTt 3'

Energy: -13.950000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:58_21	NC_027779.1	140.00	-13.95	2	17	1945	1965	15	80.
00%	93.33%								

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand	Len1,Len2	Positions			
>>cel-let-7:1-99:58_21	NC_027779.1	140.00	-13.95	140.00	-13.95	49	21	732	
0	1945								

Complete

Read Sequence:cel-let-7:1-99:58_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:58_22 vs NC_027779.1

Forward: Score: 140.000000 Q:2 to 17 R:1944 to 1965 Align Len (15) (80.00%) (93.33 %)

Query: 3' auuccaUCUUUUUACGUAUCAa 5'

Ref: 5' acccaaAAAAAATTGTATGGTt 3'

Energy: -13.950000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:58_22	NC_027779.1	140.00	-13.95	2 17	1944 1965	15	80.00%	93.33%
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Score for this Scan:

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

>>cel-let-7:1-99:58_22	NC_027779.1	140.00	-13.95	140.00	-13.95	50	22	732
0	1944							

Complete

Read Sequence:cel-let-7:1-99:58_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:58_23 vs NC_027779.1

Forward: Score: 140.000000 Q:2 to 17 R:1943 to 1965 Align Len (15) (80.00%) (93.33 %)

Query: 3' cauuccaUCUUUUUACGUAUCAa 5'

Ref: 5' cacccaaAAAAAATTGTATGGTt 3'

Energy: -13.950000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:58_23	NC_027779.1	140.00	-13.95	2 17	1943 1965	15	80.00%	93.33%
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Score for this Scan:

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

>>cel-let-7:1-99:58_23	NC_027779.1	140.00	-13.95	140.00	-13.95	51	23	732
0	1943							

Complete

Read Sequence:cel-let-7:1-99:58_24 (24 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:58_24 vs NC_027779.1

Forward: Score: 140.000000 Q:2 to 17 R:1942 to 1965 Align Len (15) (80.00%) (93.33 %)

Query: 3' ccauuccaUCUUUUUACGUAUCAa 5'

Ref: 5' acacccaaAAAAAATTGTATGGTt 3'

Energy: -13.950000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:58_24	NC_027779.1	140.00	-13.95	2 17	1942 1965	15	80.00%	93.33%
-----------------------	-------------	--------	--------	------	-----------	----	--------	--------

Score for this Scan:

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

>>cel-let-7:1-99:58_24 NC_027779.1 140.00 -13.95 140.00 -13.95 52 24 732
0 1942

Complete

Read Sequence:cel-let-7:1-99:59_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:59_20 vs NC_027779.1

Forward: Score: 140.000000 Q:2 to 17 R:3610 to 3629 Align Len (15) (73.33%) (80.00 %)

Query: 3' uuccAUCUUUUAACGUAUCa 5'

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

Ref: 5' atcaTTGTAAAATGTATAGa 3'

Energy: -7.180000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:59_20 NC_027779.1 140.00 -7.18 2 17 3610 3629 15 73.
33% 80.00%

Score for this Scan:

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

>>cel-let-7:1-99:59_20 NC_027779.1 140.00 -7.18 140.00 -7.18 53 20 732
0 3610

Complete

Read Sequence:cel-let-7:1-99:59_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:59_21 vs NC_027779.1

Forward: Score: 140.000000 Q:2 to 17 R:3609 to 3629 Align Len (15) (73.33%) (80.00 %)

Query: 3' auuccAUCUUUUAACGUAUCa 5'

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

Ref: 5' aatcaTTGTAAAATGTATAGa 3'

Energy: -7.180000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:59_21 NC_027779.1 140.00 -7.18 2 17 3609 3629 15 73.
33% 80.00%

Score for this Scan:

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

>>cel-let-7:1-99:59_21 NC_027779.1 140.00 -7.18 140.00 -7.18 54 21 732
0 3609

Complete

Read Sequence:cel-let-7:1-99:59_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:59_22 vs NC_027779.1

Forward: Score: 140.000000 Q:2 to 17 R:3608 to 3629 Align Len (15) (73.33%) (80.00 %)

Query: 3' cauuccAUCUUUUAACGUAUCa 5'

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

Ref: 5' gaatcaTTGTAAAATGTATAGa 3'

Energy: -7.180000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:59_22	NC_027779.1	140.00	-7.18	2 17	3608 3629	15	73.
33%	80.00%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions	
>>cel-let-7:1-99:59_22 NC_027779.1	140.00 -7.18 140.00 -7.18 55 22 732
0 3608	
Complete	

Read Sequence:cel-let-7:1-99:59_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:59_23 vs NC_027779.1

Forward: Score: 140.000000 Q:2 to 17 R:3607 to 3629 Align Len (15) (73.33%) (80.00 %)

Query: 3' ccauuccAUCUUUUAACGUAUCa 5'

Ref: 5' agaatcaTTGTAAAATGTATAGa 3'

Energy: -7.180000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:59_23	NC_027779.1	140.00	-7.18	2 17	3607 3629	15	73.
33%	80.00%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions	
>>cel-let-7:1-99:59_23 NC_027779.1	140.00 -7.18 140.00 -7.18 56 23 732
0 3607	
Complete	

Read Sequence:cel-let-7:1-99:59_24 (24 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:59_24 vs NC_027779.1

Forward: Score: 140.000000 Q:2 to 17 R:3606 to 3629 Align Len (15) (73.33%) (80.00 %)

Query: 3' gccauuccAUCUUUUAACGUAUCa 5'

Ref: 5' tagaatcaTTGTAAAATGTATAGa 3'

Energy: -7.180000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:59_24	NC_027779.1	140.00	-7.18	2 17	3606 3629	15	73.
33%	80.00%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions	
>>cel-let-7:1-99:59_24 NC_027779.1	140.00 -7.18 140.00 -7.18 57 24 732
0 3606	
Complete	

Read Sequence:cel-let-7:1-99:60_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:60_20 vs NC_027779.1

=====

Forward: Score: 147.000000 Q:2 to 12 R:55 to 74 Align Len (10) (90.00%) (90.00%)

Query: 3' auuccaucuUUUAACGUAUc 5'

Ref: 5' acttttttttAATTGTCATAt 3'

Energy: -4.680000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_20 NC_027779.1 147.00 -4.68 2 12 55 74 10 90.00% 90.00%

Forward: Score: 145.000000 Q:2 to 10 R:7069 to 7088 Align Len (8) (100.00%) (100.00%)

Query: 3' auuccaucuuuUAACGUAUc 5'

Ref: 5' cgccaacggctATTGCATAc 3'

Energy: -7.940000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_20 NC_027779.1 145.00 -7.94 2 10 7069 7088 8 100.00% 100.00%

Forward: Score: 142.000000 Q:2 to 15 R:4428 to 4447 Align Len (13) (76.92%) (92.31%)

Query: 3' auuccaUCUUUUUAACGUAUc 5'

Ref: 5' cgcgccAGACAGTTGTATAa 3'

Energy: -9.460000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_20 NC_027779.1 142.00 -9.46 2 15 4428 4447 13 76.92% 92.31%

Score for this Scan:

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

>>cel-let-7:1-99:60_20 NC_027779.1 434.00 -22.08 147.00 -9.46 58 20 732 0 55 7069 4428

Complete

Read Sequence:cel-let-7:1-99:60_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:60_21 vs NC_027779.1

=====

Forward: Score: 147.000000 Q:2 to 12 R:54 to 74 Align Len (10) (90.00%) (90.00%)

Query: 3' cauuccaucuUUUAACGUAUc 5'

Ref: 5' tacttttttttAATTGTCATAt 3'

Energy: -4.680000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_21 NC_027779.1 147.00 -4.68 2 12 54 74 10 90.00% 90.00%

Forward: Score: 145.000000 Q:2 to 10 R:7068 to 7088 Align Len (8) (100.00%) (100.00%)

0%)

Query: 3' cauuccaucuuuUAACGUAUc 5'

Ref: 5' gcgccaacggctATTGCATAc 3'

Energy: -8.670000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_21	NC_027779.1	145.00	-8.67	2 10	7068 7088	8	100
.00%	100.00%						

Forward: Score: 142.000000 Q:2 to 15 R:4427 to 4447 Align Len (13) (76.92%) (92.31 %)

Query: 3' cauuccaUCUUUUAACGUAUc 5'

Ref: 5' gcgcgccAGACAGTTGTATAa 3'

Energy: -9.460000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_21	NC_027779.1	142.00	-9.46	2 15	4427 4447	13	76.
92%	92.31%						

Score for this Scan:

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

>>cel-let-7:1-99:60_21	NC_027779.1	434.00	-22.81	147.00	-9.46	59	21	732
0	54	7068	4427					

Complete

Read Sequence:cel-let-7:1-99:60_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:60_22 vs NC_027779.1

Forward: Score: 147.000000 Q:2 to 12 R:53 to 74 Align Len (10) (90.00%) (90.00%)

Query: 3' ccauuccaucuUUUAACGUAUc 5'

Ref: 5' ctactttttttAATTTGCATAt 3'

Energy: -4.680000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_22	NC_027779.1	147.00	-4.68	2 12	53 74	10	90.00%	90.
00%								

Forward: Score: 145.000000 Q:2 to 10 R:7067 to 7088 Align Len (8) (100.00%) (100.00 %)

Query: 3' ccauuccaucuuuUAACGUAUc 5'

Ref: 5' ggcgccaacggctATTGCATAc 3'

Energy: -8.850000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_22	NC_027779.1	145.00	-8.85	2 10	7067 7088	8	100
.00%	100.00%						

Forward: Score: 142.000000 Q:2 to 15 R:4426 to 4447 Align Len (13) (76.92%) (92.31 %)

Query: 3' ccauuccaUCUUUUUACGUAUc 5'
 ||| |:|:|:|
 Ref: 5' ggcgcgccAGACAGTTGTATAa 3'
 Energy: -9.640000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_22	NC_027779.1	142.00	-9.64	2 15	4426 4447	13	76.
92%	92.31%						

Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions
>>cel-let-7:1-99:60_22 NC_027779.1 434.00 -23.17 147.00 -9.64 60 22 732
0 53 7067 4426

Complete

Read Sequence:cel-let-7:1-99:60_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:60_23 vs NC_027779.1

Forward: Score: 147.000000 Q:2 to 12 R:52 to 74 Align Len (10) (90.00%) (90.00%)

Query: 3' gccauuccaucuUUUAACGUAUc 5'
 || |||||
 Ref: 5' actactttttttAATTGCATAt 3'
 Energy: -4.680000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_23	NC_027779.1	147.00	-4.68	2 12	52 74	10	90.00% 90.00%
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Forward: Score: 145.000000 Q:2 to 10 R:7066 to 7088 Align Len (8) (100.00%) (100.00%)

Query: 3' gccauuccaucuuuUAACGUAUc 5'
 |||||
 Ref: 5' tggcgccaacggctATTGCATAc 3'
 Energy: -10.950000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_23	NC_027779.1	145.00	-10.95	2 10	7066 7088	8	100.00% 100.00%
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Forward: Score: 142.000000 Q:2 to 15 R:4425 to 4447 Align Len (13) (76.92%) (92.31%)

Query: 3' gccauuccaUCUUUUUACGUAUc 5'
 ||| |:|:|:|
 Ref: 5' ggcgcgccAGACAGTTGTATAa 3'
 Energy: -11.220000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:60_23	NC_027779.1	142.00	-11.22	2 15	4425 4447	13	76.92% 92.31%
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Score for this Scan:

Seq1,Seq2,Tot Score,Tot Energy,Max Score,Max Energy,Strand,Len1,Len2,Positions
>>cel-let-7:1-99:60_23 NC_027779.1 434.00 -26.85 147.00 -11.22 61 23 732
0 52 7066 4425

Complete

Read Sequence:cel-let-7:1-99:61_20 (20 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:61_20 vs NC_027779.1

Forward: Score: 145.000000 Q:2 to 10 R:1903 to 1922 Align Len (8) (100.00%) (100.00%)

Query: 3' cauuccaucuuUUAACGUAu 5'

Ref: 5' cttgaattcctAATTGCATt 3'

Energy: -7.540000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_20	NC_027779.1	145.00	-7.54	2 10	1903 1922	8	100
.00%	100.00%						

Forward: Score: 141.000000 Q:2 to 14 R:1943 to 1962 Align Len (12) (83.33%) (91.67%)

Query: 3' cauuccaUCUUUUAACGUAu 5'

Ref: 5' cacccaaAAAAAATTGTATg 3'

Energy: -9.140000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_20	NC_027779.1	141.00	-9.14	2 14	1943 1962	12	83.
33%	91.67%						

Forward: Score: 140.000000 Q:2 to 9 R:7068 to 7087 Align Len (7) (100.00%) (100.00%)

Query: 3' cauuccaucuuuUAACGUAu 5'

Ref: 5' gcgccaacggctATTGCATa 3'

Energy: -9.830000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_20	NC_027779.1	140.00	-9.83	2 9	7068 7087	7	100
.00%	100.00%						

Score for this Scan:

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

>>cel-let-7:1-99:61_20	NC_027779.1	426.00	-26.51	145.00	-9.83	62	20	732
0	1903 1943 7068							

Complete

Read Sequence:cel-let-7:1-99:61_21 (21 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:61_21 vs NC_027779.1

Forward: Score: 145.000000 Q:2 to 10 R:1902 to 1922 Align Len (8) (100.00%) (100.00%)

Query: 3' ccauuccaucuuUUAACGUAu 5'

Ref: 5' tcttgaattcctAATTGCATt 3'

Energy: -7.540000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_21 NC_027779.1 145.00 -7.54 2 10 1902 1922 8 100
.00% 100.00%

Forward: Score: 141.000000 Q:2 to 14 R:1942 to 1962 Align Len (12) (83.33%) (91.67%)

Query: 3' ccauuccaUCUUUUUAACGUAu 5'

Ref: 5' acacccaaAAAAAATTGTATg 3'

Energy: -9.140000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_21 NC_027779.1 141.00 -9.14 2 14 1942 1962 12 83.33% 91.67%

Forward: Score: 140.000000 Q:2 to 9 R:7067 to 7087 Align Len (7) (100.00%) (100.00%)

Query: 3' ccauuccaucuuuUAACGUAu 5'

Ref: 5' ggcgccaacggctATTGCATa 3'

Energy: -10.010000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_21 NC_027779.1 140.00 -10.01 2 9 7067 7087 7 100.00% 100.00%

Score for this Scan:

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

>>cel-let-7:1-99:61_21 NC_027779.1 426.00 -26.69 145.00 -10.01 63 21 732
0 1902 1942 7067

Complete

Read Sequence:cel-let-7:1-99:61_22 (22 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

=====

Performing Scan: cel-let-7:1-99:61_22 vs NC_027779.1

=====

Forward: Score: 145.000000 Q:2 to 10 R:1901 to 1922 Align Len (8) (100.00%) (100.00%)

Query: 3' gccauuccaucuuUUAACGUAu 5'

Ref: 5' ttcttgaattcctAATTGCATt 3'

Energy: -7.540000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_22 NC_027779.1 145.00 -7.54 2 10 1901 1922 8 100.00% 100.00%

Forward: Score: 141.000000 Q:2 to 14 R:1941 to 1962 Align Len (12) (83.33%) (91.67%)

Query: 3' gccauuccaUCUUUUUAACGUAu 5'

Ref: 5' tacacccaaAAAAAATTGTATg 3'

Energy: -9.140000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_22 NC_027779.1 141.00 -9.14 2 14 1941 1962 12 83.
33% 91.67%

Forward: Score: 140.000000 Q:2 to 9 R:7066 to 7087 Align Len (7) (100.00%) (100.00%)

Query: 3' gccauuccaucuuUAACGUAu 5'

|||||

Ref: 5' tggcgccaacggctATTGCATa 3'

Energy: -12.110000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_22 NC_027779.1 140.00 -12.11 2 9 7066 7087 7 100
.00% 100.00%

Score for this Scan:

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

>>cel-let-7:1-99:61_22 NC_027779.1 426.00 -28.79 145.00 -12.11 64 22 732
0 1901 1941 7066

Complete

Read Sequence:cel-let-7:1-99:61_23 (23 nt)

Read Sequence:NC_027779.1 Human papillomavirus isolate SE379, complete genome(7320 nt)

Performing Scan: cel-let-7:1-99:61_23 vs NC_027779.1

Forward: Score: 145.000000 Q:2 to 10 R:1900 to 1922 Align Len (8) (100.00%) (100.00%)

Query: 3' ggccauuccaucuuUUAACGUAu 5'

|||||

Ref: 5' tttcttgaattcctAATTGCATt 3'

Energy: -8.020000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_23 NC_027779.1 145.00 -8.02 2 10 1900 1922 8 100
.00% 100.00%

Forward: Score: 141.000000 Q:2 to 14 R:1940 to 1962 Align Len (12) (83.33%) (91.67%)

Query: 3' ggccauuccaUCUUUUAACGUAu 5'

| |||||: ||

Ref: 5' gtacacccaaAAAAATTGTATg 3'

Energy: -9.620000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_23 NC_027779.1 141.00 -9.62 2 14 1940 1962 12 83.
33% 91.67%

Forward: Score: 140.000000 Q:2 to 9 R:7065 to 7087 Align Len (7) (100.00%) (100.00%)

Query: 3' ggccauuccaucuuUAACGUAu 5'

|||||

Ref: 5' ttggcgccaacggctATTGCATa 3'

Energy: -12.900000 kCal/Mol

Scores for this hit:

>cel-let-7:1-99:61_23 NC_027779.1 140.00 -12.90 2 9 7065 7087 7 100

.00% 100.00%

Score for this Scan:

Seq1,Seq2,Tot	Score,Tot	Energy,Max	Score,Max	Energy,Strand,	Len1,Len2,	Positions		
>>cel-let-7:1-99:61_23	NC_027779.1	426.00	-30.54	145.00	-12.90	65	23	732
0	1900	1940	7065					

Complete

Scan Complete