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miR-Synth - Artificial miRNA Designer v 2.0
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Input parameters
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Date: 2014-06-24 15:23:56 -0400
Target sequences:
PTGER2_(NM_000956_-_Entrez_ID:_5732)
Non-target sequences:
Not provided
Off-target computation: NO
Top 10 results only: YES
Source organism: Human
Seed type: 7mer-m8 / 8mer
miRNAs must target all input sequences: NO
Minimum number of binding sites on each sequence: 2
Minimum GC content allowed: 23%
Maximum GC content allowed: 78%
Homologous miRNA filter enabled: YES


Report
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44 miRNA created.
Showing Top 10 miRNAs only.
miRNAs are ranked by C-tree and M5P scores.


miRNA ID:23
Rank: 1
Sequence:
CCACUGAGCCGAGGCUUGGUAG
Total binding sites: 2

Sites on PTGER2_(NM_000956_-_Entrez_ID:_5732)
2

Seed score: 0.85
3' Match score: 0.5
AU Content score: 0.5
Nucleotide Composition score: 0.6758241758241759
Structural Accessibility score: 0.23335528457499993
ARE/CPE score: 0.30000000000000004
----------------------------------------------------------------------
C-tree score: -0.22488171570287555
M5P score: -0.22883668354058584
```

Binding sites details

Position: 204
Type: 8mer
Alignment:

```
       GUUC   GCC       C
3'-GAUG    GGA   GAGUCAC -5' miRNA
   ||||    |||   |||||||
5'-CUAC    CCU   CUCAGUG -3' mRNA
       AAAA   ACC       A
```

Free energy: -18.5 Kcal/mol

Position: 584
Type: 7mer-m8
Alignment:

```
   GAUG    GGA
3'-    GUUC   GCC GAGUCACC-5' miRNA
       ||||   ||| ||||||||
5'-    CAAG   UGG CUCAGUGG-3' mRNA
   CUUA    AG    A
```

Free energy: -22.6 Kcal/mol

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miRNA ID:62
Rank: 2
Sequence:
UGAGUUUAGUGUGUCACGCCGA
Total binding sites: 2

Sites on PTGER2_(NM_000956_-_Entrez_ID:_5732)
2

Seed score: 1.0
3' Match score: 0.5
AU Content score: 0.6499999999999999
Nucleotide Composition score: 0.836996336996337
Structural Accessibility score: 0.19211299974999999
ARE/CPE score: 1.0

C-tree score: -0.22488171570287555
M5P score: -0.228057446285573

Binding sites details

Position: 1043

Type: 8mer
Alignment:

```
        C  UG    G       U
3'-AGCCG AC   UGU AUUUGAG -5' miRNA
   ||||| ||   ||| |||||||
5'-UUGGC UG   AUG UAAACUC -3' mRNA
        A  UAA           A
```

Free energy: -14.8 Kcal/mol

Position: 1100
Type: 8mer
Alignment:

```
   AGCCG  C  UGUG       U
3'-     CA UG    AUUUGAG -5' miRNA
        || ||    |||||||
5'-     GU AC    UAAACUC -3' mRNA
   UCAUA  U  UGUG       A
```

Free energy: -9.7 Kcal/mol

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miRNA ID:31
Rank: 3
Sequence:
UGAUUAAAGACGGCAGUUCCGC
Total binding sites: 2

Sites on PTGER2_(NM_000956_-_Entrez_ID:_5732)
2

Seed score: 0.85
3' Match score: 0.5714285714285714
AU Content score: 0.7
Nucleotide Composition score: 0.7060439560439561
Structural Accessibility score: 0.41456072494999996
ARE/CPE score: 0.7

C-tree score: -0.22488171570287555
M5P score: -0.2222827195233692

Binding sites details

Position: 351
Type: 7mer-m8
Alignment:

```
   CGCCU     GC              U
```

```
3'-     UGACG    AGA   AAUUAG -5' miRNA
        |||||    |||   ||||||
5'-     ACUGU    UCU   UUAAUC -3' mRNA
             ACUU   AUU      U
```

Free energy: -9.2 Kcal/mol

Position: 1081
Type: 8mer
Alignment:

```
   CG          GC G       U
3'-  C CUU GACG  A AAAUUAG -5' miRNA
     | ||| ||||  | |||||||
5'-  G GAA UUGC  U UUUAAUC -3' mRNA
      U   U    AC G       A
```

Free energy: -12.0 Kcal/mol

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miRNA ID:3
Rank: 4
Sequence:
UCAUUUCUGGAAGGUCCUGUUG
Total binding sites: 2

Sites on PTGER2_(NM_000956_-_Entrez_ID:_5732)
2

Seed score: 0.85
3' Match score: 0.5714285714285714
AU Content score: 0.75
Nucleotide Composition score: 0.7152014652014653
Structural Accessibility score: 0.3451366285
ARE/CPE score: 0.3

C-tree score: -0.22488171570287555
M5P score: -0.2205202378402108

Binding sites details

Position: 65
Type: 8mer
Alignment:

```
   G   U CU    GG
3'- UUG C  GGAA  UCUUUACU-5' miRNA
    ||| |  ||||  ||||||||
5'- AAU G  CCUU  AGAAAUGA-3' mRNA
   A   U UU    GG
```

Free energy: -14.5 Kcal/mol

Position: 723
Type: 7mer-m8
Alignment:

```
        C  GGAAG        U
3'-GUUGU CU     GUCUUUAC -5' miRNA
   ||||| ||     ||||||||
5'-CAACA GA     UAGAAAUG -3' mRNA
        A  AAUAA        U
```

Free energy: -14.0 Kcal/mol

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miRNA ID:53
Rank: 5
Sequence:
UAAUAUUUCCGUGCUGAGUUGG
Total binding sites: 2

Sites on PTGER2_(NM_000956_-_Entrez_ID:_5732)
2

Seed score: 0.85
3' Match score: 0.6428571428571428
AU Content score: 0.55
Nucleotide Composition score: 0.7188644688644689
Structural Accessibility score: 0.4021779302499999
ARE/CPE score: 0.9

C-tree score: -0.22488171570287555
M5P score: -0.2197409153206505

Binding sites details

Position: 810
Type: 8mer
Alignment:

```
      UGAGU     C
3'-GGU     CGUGC     UUUAUAAU-5' miRNA
   |||     |||||     ||||||||
5'-CCA     GUAUG     AAAUAUUA-3' mRNA
      U         AAGCC
```

Free energy: -6.6 Kcal/mol

Position: 1057

Type: 7mer-m8
Alignment:

```
   GG          CC       U
3'-  UUGAGUCGUG  UUUAUAA -5' miRNA
     ||||||||||  |||||||
5'-  AACUCAGCAU  AAAUAUU -3' mRNA
   UA          CA       U
```

Free energy: -18.8 Kcal/mol

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```

miRNA ID:35
Rank: 6
Sequence:
UAAAGGGUAGCCGUAGUGCUGA
Total binding sites: 2

Sites on PTGER2_(NM_000956_-_Entrez_ID:_5732)
2

Seed score: 0.85
3' Match score: 0.5357142857142857
AU Content score: 0.6499999999999999
Nucleotide Composition score: 0.739010989010989
Structural Accessibility score: 0.23218293650000002
ARE/CPE score: 0.6000000000000001

C-tree score: -0.22488171570287555
M5P score: -0.21576999140110603

Binding sites details

Position: 477
Type: 8mer
Alignment:

```
   AGUC    UGC  A
3'-    GUGA   CG  UGGGAAAU-5' miRNA
       ||||   ||  ||||||||
5'-    CACU   GC  ACCCUUUA-3' mRNA
   UGAU    UA   GA
```

Free energy: -15.6 Kcal/mol

Position: 863
Type: 7mer-m8
Alignment:

```
       GUG      GA       U
```

```
3'-AGUC   AUG CC  UGGGAAA -5' miRNA
   ||||   ||| ||  |||||||
5'-UCAG   UAC GG  ACCCUUU -3' mRNA
       AUA   U  A        U
```

Free energy: -17.0 Kcal/mol

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miRNA ID:20
Rank: 7
Sequence:
CAUGAAGUCGGUUGUGGGCUGG
Total binding sites: 2

Sites on PTGER2_(NM_000956_-_Entrez_ID:_5732)
2

Seed score: 0.85
3' Match score: 0.5714285714285714
AU Content score: 0.75
Nucleotide Composition score: 0.5238095238095238
Structural Accessibility score: 0.3080164781275
ARE/CPE score: 0.30000000000000004

C-tree score: -0.22488171570287555
M5P score: -0.21377302326492334

Binding sites details

Position: 165
Type: 7mer-m8
Alignment:

```
   GGU   G    GGC
3'-   CGG UGUU   UGAAGUAC-5' miRNA
      ||| ||||   ||||||||
5'-   GCU ACAA   ACUUCAUG-3' mRNA
   UGU   G    GGC
```

Free energy: -17.7 Kcal/mol

Position: 405
Type: 8mer
Alignment:

```
       G   G U GC       C
3'-GGUC GGU U G  UGAAGUA -5' miRNA
   |||| ||| | |  |||||||
5'-CCAG CCA A U  ACUUCAU -3' mRNA
       A   G U AA       A
```

Free energy: -17.1 Kcal/mol

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miRNA ID:54
Rank: 8
Sequence:
UACACAGUGUGCUUGUUUAAUC
Total binding sites: 2

Sites on PTGER2_(NM_000956_-_Entrez_ID:_5732)
2

Seed score: 0.85
3' Match score: 0.6785714285714286
AU Content score: 0.7
Nucleotide Composition score: 0.5247252747252747
Structural Accessibility score: 0.24433496324999998
ARE/CPE score: 0.9

C-tree score: -0.22488171570287555
M5P score: -0.2134586150165915

Binding sites details

Position: 915
Type: 7mer-m8
Alignment:

```
       UU     GUG       U
3'-CUAA  UGUUC   UGACACA -5' miRNA
   ||||  |||||   |||||||
5'-GAUU  AUAAG   ACUGUGU -3' mRNA
       UU     AUG       U
```

Free energy: -15.7 Kcal/mol

Position: 1094
Type: 8mer
Alignment:

```
   CU    U      U
3'-  AAUU GU UCG GUGACACAU-5' miRNA
     |||| || ||| |||||||||
5'-  UUAA CA AGU UACUGUGUA-3' mRNA
   GU    U  U
```

Free energy: -13.5 Kcal/mol

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miRNA ID:44
Rank: 9
Sequence:
`UAAGAGUAAAUCUGUGGUGUUG`
Total binding sites: 2

Sites on PTGER2_(NM_000956_-_Entrez_ID:_5732)
2

Seed score: 0.85
3' Match score: 0.5357142857142857
AU Content score: 0.85
Nucleotide Composition score: 0.7664835164835164
Structural Accessibility score: 0.235534089
ARE/CPE score: 0.5

C-tree score: -0.22488171570287555
M5P score: -0.21003708525396594

Binding sites details

Position: 566
Type: 8mer
Alignment:

```
     U        UA
3'-GU GUGGUGUC  AAUGAGAAU-5' miRNA
   || ||||||||  |||||||||
5'-CA CACUACAG  UUACUCUUA-3' mRNA
     U        UA
```

Free energy: -21.4 Kcal/mol

Position: 755
Type: 7mer-m8
Alignment:

```
   GUUGU      UCUAA       U
3'-       GGUG     AUGAGAA -5' miRNA
          ||||     |||||||
5'-       UCAU     UACUCUU -3' mRNA
   UUAAUUC    UAA         U
```

Free energy: -7.9 Kcal/mol

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miRNA ID:29
Rank: 10

Sequence:
`CAAACAAAAGAGAUGUCCACCC`
Total binding sites: 2

Sites on PTGER2_(NM_000956_-_Entrez_ID:_5732)
2

Seed score: 0.85
3' Match score: 0.5714285714285714
AU Content score: 0.6499999999999999
Nucleotide Composition score: 0.5384615384615384
Structural Accessibility score: 0.222411600175
ARE/CPE score: 0.4

C-tree score: -0.22488171570287555
M5P score: -0.20931252186753485

Binding sites details

Position: 314
Type: 7mer-m8
Alignment:

```
   CC    UGU G GA
3'-  CACC   A A  AAACAAAC-5' miRNA
     ||||   | |  ||||||||
5'-  GUGG   U U  UUUGUUUG-3' mRNA
   AU    UUU G AA
```

Free energy: -11.7 Kcal/mol

Position: 604
Type: 8mer
Alignment:

```
       CC     AG       C
3'-CCCA  UGUAG  AAAACAAA -5' miRNA
   ||||  |||||  ||||||||
5'-GGGU  ACAUC  UUUUGUUU -3' mRNA
       UA     AG       A
```

Free energy: -18.2 Kcal/mol

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