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**miR-Synth - Artificial miRNA Designer v 2.0**  
=====

**Input parameters**

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Date: 2014-06-16 16:15:54 -0400

Target sequences:

BACE1\_(NM\_001207048\_-\_Entrez\_ID:\_23621)

BACE1\_(NM\_001207049\_-\_Entrez\_ID:\_23621)

BACE1\_(NM\_012104\_-\_Entrez\_ID:\_23621)

BACE1\_(NM\_138971\_-\_Entrez\_ID:\_23621)

BACE1\_(NM\_138972\_-\_Entrez\_ID:\_23621)

BACE1\_(NM\_138973\_-\_Entrez\_ID:\_23621)

Non-target sequences:

BACE2\_(NM\_012105\_-\_Entrez\_ID:\_25825)

BACE2\_(NM\_138991\_-\_Entrez\_ID:\_25825)

BACE2\_(NM\_138992\_-\_Entrez\_ID:\_25825)

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**

=====

*127 miRNA created.*

*Showing Top 10 miRNAs only.*

*miRNAs are ranked by C-tree and M5P scores.*

**miRNA ID:139**

Rank: 1

Sequence:

UGUAUUUCGGACUCCCUUGGCA

Total binding sites: 12

Sites on BACE1\_(NM\_001207048\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_001207049\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_012104\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138971\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138972\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138973\_-\_Entrez\_ID:\_23621)

2

Seed score: 1.0

3' Match score: 0.6071428571428572

AU Content score: 0.45

Nucleotide Composition score: 0.6794871794871796

Structural Accessibility score: 0.29273750764999995

ARE/CPE score: 0.5

-----  
C-tree score: -0.22488171570287555

M5P score: -0.2603702541918329

### *Binding sites details*

Position: 1296

Type: 8mer

Alignment:

```
      AC      CC      GG      U
3' -  GGUU  CUCA  CUUUAUG -5' miRNA
      ||||  ||||  |||||
5' -  CCAA  GAGU  GAAAUAC -3' mRNA
      UA      AUGA      A
```

Free energy: -15.5 Kcal/mol

Position: 1672

Type: 8mer

Alignment:

```
      A G      AGG      U
3' -  C GUUCCCUC  CUUUAUG -5' miRNA
      | |||||
5' -  G UAAGGGAG  GAAAUAC -3' mRNA
      U A      AGG      A
```

Free energy: -20.1 Kcal/mol

Position: 1296

Type: 8mer

Alignment:

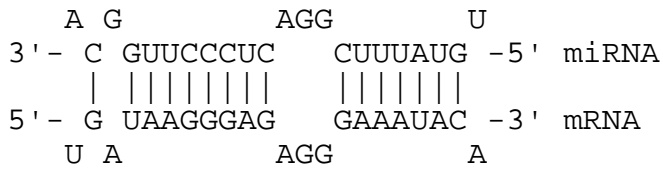
```
      AC      CC      GG      U
3' -  GGUU  CUCA  CUUUAUG -5' miRNA
      ||||  ||||  |||||
5' -  CCAA  GAGU  GAAAUAC -3' mRNA
      UA      AUGA      A
```

Free energy: -15.5 Kcal/mol

Position: 1672

Type: 8mer

Alignment:

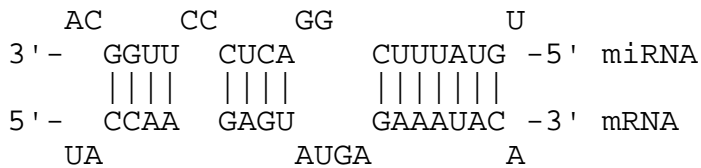


Free energy: -20.1 Kcal/mol

Position: 1296

Type: 8mer

Alignment:

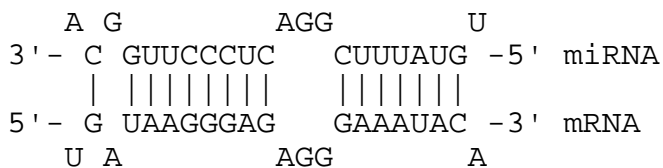


Free energy: -15.5 Kcal/mol

Position: 1672

Type: 8mer

Alignment:

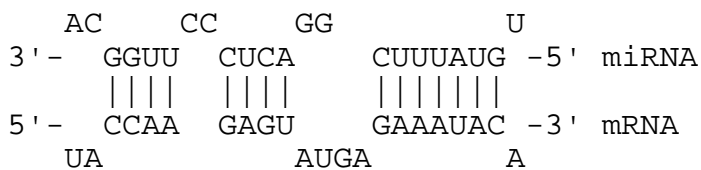


Free energy: -20.1 Kcal/mol

Position: 1296

Type: 8mer

Alignment:

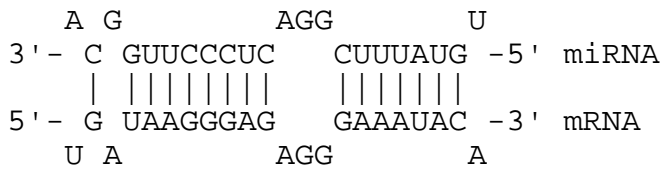


Free energy: -15.5 Kcal/mol

Position: 1672

Type: 8mer

Alignment:

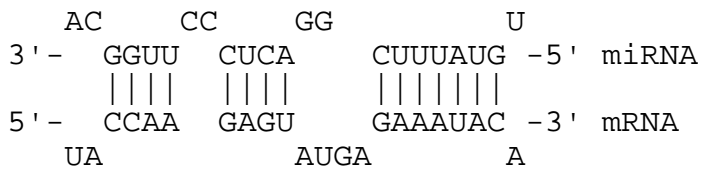


Free energy: -20.1 Kcal/mol

Position: 1296

Type: 8mer

Alignment:

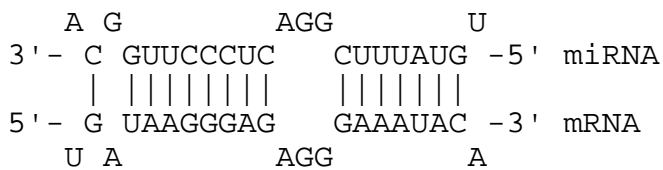


Free energy: -15.5 Kcal/mol

Position: 1672

Type: 8mer

Alignment:

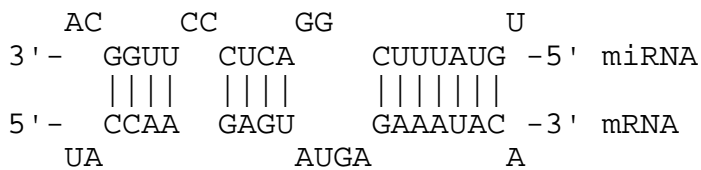


Free energy: -20.1 Kcal/mol

Position: 1296

Type: 8mer

Alignment:

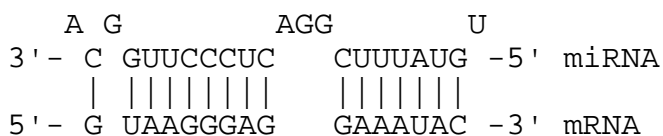


Free energy: -15.5 Kcal/mol

Position: 1672

Type: 8mer

Alignment:



U A AGG A

Free energy: -20.1 Kcal/mol

=====

**miRNA ID:204**

Rank: 2

Sequence:

UCUGUCCAGGCGCCUGCCUGGA

Total binding sites: 12

Sites on BACE1\_(NM\_001207048\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_001207049\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_012104\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138971\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138972\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138973\_-\_Entrez\_ID:\_23621)

2

Seed score: 1.0

3' Match score: 0.6785714285714287

AU Content score: 0.45

Nucleotide Composition score: 0.6978021978021979

Structural Accessibility score: 0.24471294065000004

ARE/CPE score: 0.8333333333333334

C-tree score: -0.22488171570287555

M5P score: -0.25660688289553957

*Binding sites details*

Position: 2271

Type: 8mer

Alignment:

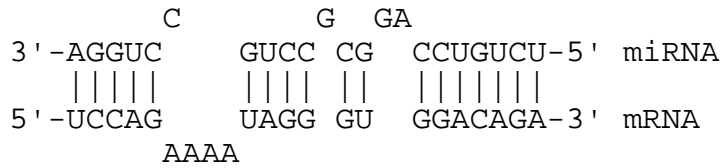
|        |         |   |             |       |
|--------|---------|---|-------------|-------|
|        | GUC     |   | C G         |       |
| 3' -AG | CGUCCG  | G | ACCUGUCU-5' | miRNA |
|        |         |   |             |       |
| 5' -UC | G CAGGC | C | UGGACAGA-3' | mRNA  |
|        | AUU     |   | AG          |       |

Free energy: -25.2 Kcal/mol

Position: 3709

Type: 8mer

Alignment:

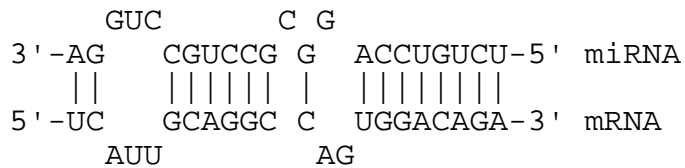


Free energy: -20.4 Kcal/mol

Position: 2271

Type: 8mer

Alignment:

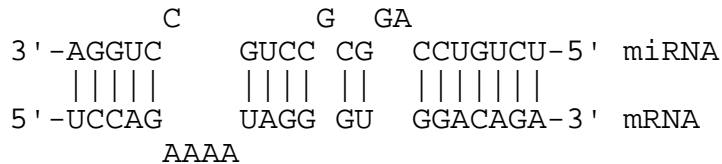


Free energy: -25.2 Kcal/mol

Position: 3709

Type: 8mer

Alignment:

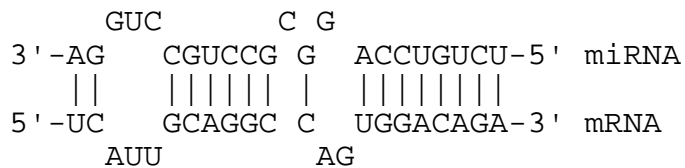


Free energy: -20.4 Kcal/mol

Position: 2271

Type: 8mer

Alignment:

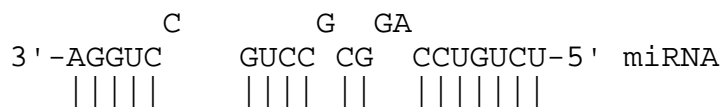


Free energy: -25.2 Kcal/mol

Position: 3709

Type: 8mer

Alignment:



5' -UCCAG UAGG GU GGACAGA-3' mRNA  
AAAA

Free energy: -20.4 Kcal/mol

Position: 2271

Type: 8mer

Alignment:

```
      GUC      C G
3' -AG  CGUCCG G  ACCUGUCU-5' miRNA
      ||  |||||  |  |||||
5' -UC  GCAGGC C  UGGACAGA-3' mRNA
      AUU      AG
```

Free energy: -25.2 Kcal/mol

Position: 3709

Type: 8mer

Alignment:

```
      C      G GA
3' -AGGUC  GUCC CG  CCUGUCU-5' miRNA
      |||||  |||  ||  |||||
5' -UCCAG  UAGG GU  GGACAGA-3' mRNA
      AAAAA
```

Free energy: -20.4 Kcal/mol

Position: 2271

Type: 8mer

Alignment:

```
      GUC      C G
3' -AG  CGUCCG G  ACCUGUCU-5' miRNA
      ||  |||||  |  |||||
5' -UC  GCAGGC C  UGGACAGA-3' mRNA
      AUU      AG
```

Free energy: -25.2 Kcal/mol

Position: 3709

Type: 8mer

Alignment:

```
      C      G GA
3' -AGGUC  GUCC CG  CCUGUCU-5' miRNA
      |||||  |||  ||  |||||
5' -UCCAG  UAGG GU  GGACAGA-3' mRNA
      AAAAA
```

Free energy: -20.4 Kcal/mol

Position: 2271

Type: 8mer

Alignment:

```

      GUC      C G
3' -AG  CGUCCG G  ACCUGUCU-5' miRNA
  ||    ||| ||| |  ||| ||| |||
5' -UC  GCAGGC C  UGGACAGA-3' mRNA
      AUU      AG

```

Free energy: -25.2 Kcal/mol

Position: 3709

Type: 8mer

Alignment:

```

      C      G  GA
3' -AGGUC  GUCC CG  CCUGUCU-5' miRNA
  ||| |||  ||  ||| ||| |||
5' -UCCAG  UAGG GU  GGACAGA-3' mRNA
      AAAA

```

Free energy: -20.4 Kcal/mol

=====

**miRNA ID:33**

Rank: 3

Sequence:

UCCUACAGCCUCUGGCCCGGC

Total binding sites: 12

Sites on BACE1\_(NM\_001207048\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_001207049\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_012104\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138971\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138972\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138973\_-\_Entrez\_ID:\_23621)

2

Seed score: 1.0

3' Match score: 0.5357142857142858

AU Content score: 0.5999999999999999

Nucleotide Composition score: 0.7124542124542125

Structural Accessibility score: 0.14365648132500003

ARE/CPE score: 0.4166666666666667

-----  
C-tree score: -0.22488171570287555



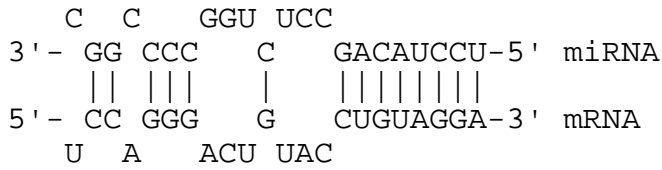
M5P score: -0.253684225650324

*Binding sites details*

Position: 183

Type: 8mer

Alignment:

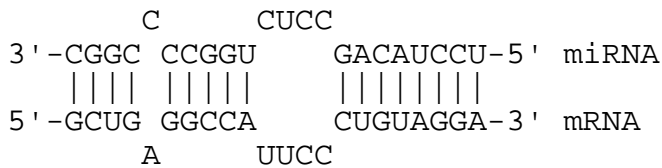


Free energy: -19.4 Kcal/mol

Position: 3161

Type: 8mer

Alignment:

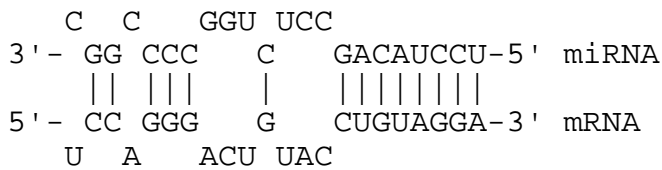


Free energy: -26.6 Kcal/mol

Position: 183

Type: 8mer

Alignment:

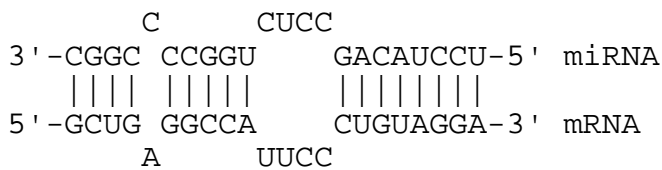


Free energy: -19.4 Kcal/mol

Position: 3161

Type: 8mer

Alignment:



Free energy: -26.6 Kcal/mol

Position: 183

Type: 8mer

Alignment:

```
      C C   GGU UCC
3'- GG CCC   C   GACAUCCU-5' miRNA
      || |||   |   |||||
5'- CC GGG   G   CUGUAGGA-3' mRNA
      U A   ACU UAC
```

Free energy: -19.4 Kcal/mol

Position: 3161

Type: 8mer

Alignment:

```
      C       CUCC
3'-CGGC CCGGU   GACAUCCU-5' miRNA
      |||| | ||||   |||||
5'-GCUG GGCCA   CUGUAGGA-3' mRNA
      A       UUCC
```

Free energy: -26.6 Kcal/mol

Position: 183

Type: 8mer

Alignment:

```
      C C   GGU UCC
3'- GG CCC   C   GACAUCCU-5' miRNA
      || |||   |   |||||
5'- CC GGG   G   CUGUAGGA-3' mRNA
      U A   ACU UAC
```

Free energy: -19.4 Kcal/mol

Position: 3161

Type: 8mer

Alignment:

```
      C       CUCC
3'-CGGC CCGGU   GACAUCCU-5' miRNA
      |||| | ||||   |||||
5'-GCUG GGCCA   CUGUAGGA-3' mRNA
      A       UUCC
```

Free energy: -26.6 Kcal/mol

Position: 183

Type: 8mer

Alignment:

```
      C C   GGU UCC
3'- GG CCC   C   GACAUCCU-5' miRNA
```

```

      ||| ||| | |||||
5' - CC GGG G CUGUAGGA - 3' mRNA
      U A ACU UAC

```

Free energy: -19.4 Kcal/mol

Position: 3161

Type: 8mer

Alignment:

```

          C      CUCC
3' -CGGC CCGGU      GACAUCCU-5' miRNA
      ||||| ||||| |||||
5' -GCUG GGCCA      CUGUAGGA-3' mRNA
          A      UUCC

```

Free energy: -26.6 Kcal/mol

Position: 183

Type: 8mer

Alignment:

```

          C C      GGU UCC
3' - GG CCC      C GACAUCCU-5' miRNA
      ||| ||| | |||||
5' - CC GGG      G CUGUAGGA-3' mRNA
          U A ACU UAC

```

Free energy: -19.4 Kcal/mol

Position: 3161

Type: 8mer

Alignment:

```

          C      CUCC
3' -CGGC CCGGU      GACAUCCU-5' miRNA
      ||||| ||||| |||||
5' -GCUG GGCCA      CUGUAGGA-3' mRNA
          A      UUCC

```

Free energy: -26.6 Kcal/mol

=====

**miRNA ID:144**

Rank: 4

Sequence:

UCCUUUCUCGGGGCGGCCUGU

Total binding sites: 12

Sites on BACE1\_(NM\_001207048\_-\_Entrez\_ID:\_23621)

Sites on BACE1\_(NM\_001207049\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_012104\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138971\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138972\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138973\_-\_Entrez\_ID:\_23621)

2

Seed score: 1.0

3' Match score: 0.5

AU Content score: 0.45

Nucleotide Composition score: 0.7197802197802198

Structural Accessibility score: 0.43911225225

ARE/CPE score: 0.5833333333333334

-----  
C-tree score: -0.22488171570287555

M5P score: -0.25199401142718747

*Binding sites details*

Position: 1352

Type: 8mer

Alignment:

```

      U   C           G
3' - GU CCGGCGGG CUCUUUCCU-5' miRNA
      || ||||| ||||| ||||| |||||
5' - CA GGCUGCCU GAGAAAGGA-3' mRNA
      U   A           G

```

Free energy: -33.6 Kcal/mol

Position: 2946

Type: 8mer

Alignment:

```

      UGUC           GCGGGGC
3' -           CCG           UCUUCCU-5' miRNA
      |||           ||||| |||||
5' -           GGC           AGAAAGGA-3' mRNA
      AGAGUAUCAA

```

Free energy: -12.11 Kcal/mol

Position: 1352

Type: 8mer

Alignment:

```

      U   C           G

```

```

3'- GU CCGGCGGG CUCUUUCCU-5' miRNA
   || ||||| |||||
5'- CA GGCUGCCU GAGAAAGGA-3' mRNA
   U  A      G

```

Free energy: -33.6 Kcal/mol

Position: 2946

Type: 8mer

Alignment:

```

      UGUC          GCGGGGC
3'-          CCG          UCUUUCCU-5' miRNA
   |||          |||||
5'-          GGC          AGAAAGGA-3' mRNA
AGAGUAUCAAA

```

Free energy: -12.11 Kcal/mol

Position: 1352

Type: 8mer

Alignment:

```

      U  C      G
3'- GU CCGGCGGG CUCUUUCCU-5' miRNA
   || ||||| |||||
5'- CA GGCUGCCU GAGAAAGGA-3' mRNA
   U  A      G

```

Free energy: -33.6 Kcal/mol

Position: 2946

Type: 8mer

Alignment:

```

      UGUC          GCGGGGC
3'-          CCG          UCUUUCCU-5' miRNA
   |||          |||||
5'-          GGC          AGAAAGGA-3' mRNA
AGAGUAUCAAA

```

Free energy: -12.11 Kcal/mol

Position: 1352

Type: 8mer

Alignment:

```

      U  C      G
3'- GU CCGGCGGG CUCUUUCCU-5' miRNA
   || ||||| |||||
5'- CA GGCUGCCU GAGAAAGGA-3' mRNA
   U  A      G

```

Free energy: -33.6 Kcal/mol

Position: 2946

Type: 8mer

Alignment:

```
      UGUC          GCGGGGC
3' -          CCG          UCUUUCCU-5' miRNA
      |||          |||||
5' -          GGC          AGAAAGGA-3' mRNA
      AGAGUAUCAAA
```

Free energy: -12.11 Kcal/mol

Position: 1352

Type: 8mer

Alignment:

```
      U  C          G
3' - GU CCGGCGGG CUCUUUCCU-5' miRNA
      || ||||| |||||
5' - CA GGCUGCCU GAGAAAGGA-3' mRNA
      U  A          G
```

Free energy: -33.6 Kcal/mol

Position: 2946

Type: 8mer

Alignment:

```
      UGUC          GCGGGGC
3' -          CCG          UCUUUCCU-5' miRNA
      |||          |||||
5' -          GGC          AGAAAGGA-3' mRNA
      AGAGUAUCAAA
```

Free energy: -12.11 Kcal/mol

Position: 1352

Type: 8mer

Alignment:

```
      U  C          G
3' - GU CCGGCGGG CUCUUUCCU-5' miRNA
      || ||||| |||||
5' - CA GGCUGCCU GAGAAAGGA-3' mRNA
      U  A          G
```

Free energy: -33.6 Kcal/mol

Position: 2946

Type: 8mer

Alignment:

```

      UGUC           GCGGGGC
3' -           CCG           UCUUCCU-5' miRNA
      |||           |||||
5' -           GGC           AGAAAGGA-3' mRNA
      AGAGUAUCAA

```

Free energy: -12.11 Kcal/mol

=====

**miRNA ID:142**

Rank: 5

Sequence:

UUGAUACUCAAGGCCGUCUUGG

Total binding sites: 12

Sites on BACE1\_(NM\_001207048\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_001207049\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_012104\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138971\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138972\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138973\_-\_Entrez\_ID:\_23621)

2

Seed score: 1.0

3' Match score: 0.5714285714285715

AU Content score: 0.5499999999999999

Nucleotide Composition score: 0.7454212454212453

Structural Accessibility score: 0.4607087415

ARE/CPE score: 0.5833333333333334

C-tree score: -0.22488171570287555

M5P score: -0.24666867715096505

*Binding sites details*

Position: 1334

Type: 8mer

Alignment:

```

      G  UC  C      C      U
3' - GU  UG CGGAA UCAUAGU -5' miRNA
      ||  ||  |||||  |||||
5' - CA  AC GCCUU AGUAUCA -3' mRNA
      A  UU  U      C      A

```

Free energy: -19.9 Kcal/mol

Position: 2934

Type: 8mer

Alignment:

```
      GG      G  GGAA          U
3'-  UUCU CC      CUCAUAGU -5' miRNA
      ||||| ||      |||||
5'-  AAGA GG      GAGUAUCA -3' mRNA
      CA      A  AAAA          A
```

Free energy: -16.9 Kcal/mol

Position: 1334

Type: 8mer

Alignment:

```
      G  UC  C      C      U
3'-  GU  UG CGGAA UCAUAGU -5' miRNA
      ||  ||  |||||  |||||
5'-  CA  AC GCCUU AGUAUCA -3' mRNA
      A  UU  U      C      A
```

Free energy: -19.9 Kcal/mol

Position: 2934

Type: 8mer

Alignment:

```
      GG      G  GGAA          U
3'-  UUCU CC      CUCAUAGU -5' miRNA
      ||||| ||      |||||
5'-  AAGA GG      GAGUAUCA -3' mRNA
      CA      A  AAAA          A
```

Free energy: -16.9 Kcal/mol

Position: 1334

Type: 8mer

Alignment:

```
      G  UC  C      C      U
3'-  GU  UG CGGAA UCAUAGU -5' miRNA
      ||  ||  |||||  |||||
5'-  CA  AC GCCUU AGUAUCA -3' mRNA
      A  UU  U      C      A
```

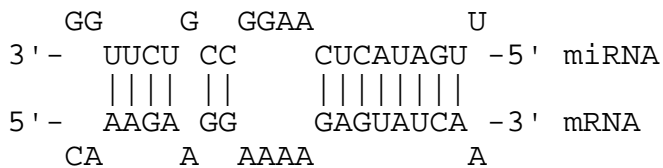
Free energy: -19.9 Kcal/mol

Position: 2934

Type: 8mer

Alignment:



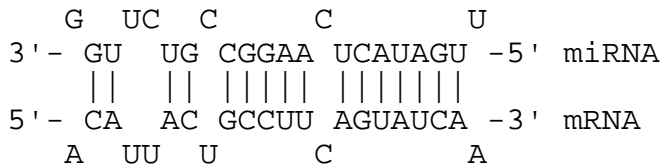


Free energy: -16.9 Kcal/mol

Position: 1334

Type: 8mer

Alignment:

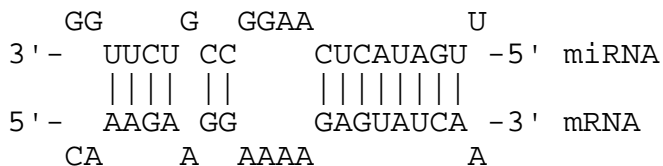


Free energy: -19.9 Kcal/mol

Position: 2934

Type: 8mer

Alignment:

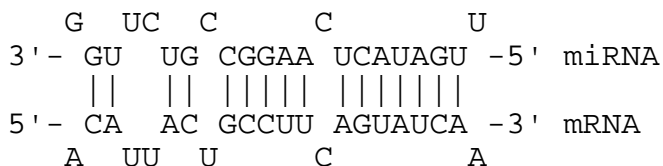


Free energy: -16.9 Kcal/mol

Position: 1334

Type: 8mer

Alignment:

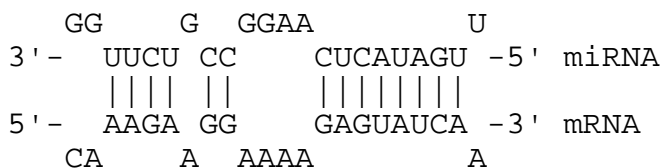


Free energy: -19.9 Kcal/mol

Position: 2934

Type: 8mer

Alignment:



Free energy: -16.9 Kcal/mol

Position: 1334

Type: 8mer

Alignment:

```
      G  UC  C      C      U
3' - GU  UG  CGGAA  UCAUAGU -5' miRNA
      ||  ||  |||||  |||||
5' - CA  AC  GCCUU  AGUAUCA -3' mRNA
      A  UU  U      C      A
```

Free energy: -19.9 Kcal/mol

Position: 2934

Type: 8mer

Alignment:

```
      GG      G  GGAA      U
3' -  UUCU  CC      CUCAUAGU -5' miRNA
      ||||  ||      |||||
5' -  AAGA  GG      GAGUAUCA -3' mRNA
      CA      A  AAAA      A
```

Free energy: -16.9 Kcal/mol

=====

**miRNA ID:52**

Rank: 6

Sequence:

UGUGAUGCGACUGCCUCUGAAA

Total binding sites: 12

Sites on BACE1\_(NM\_001207048\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_001207049\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_012104\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138971\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138972\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138973\_-\_Entrez\_ID:\_23621)

2

Seed score: 1.0

3' Match score: 0.35714285714285715

AU Content score: 0.55

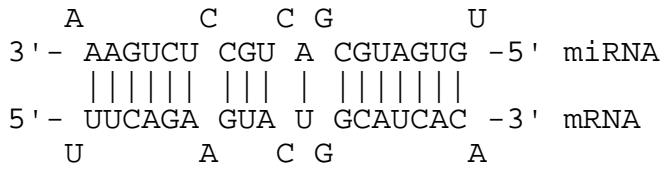
Nucleotide Composition score: 0.7564102564102564

Structural Accessibility score: 0.30407663325  
ARE/CPE score: 0.3333333333333333

-----  
C-tree score: -0.22488171570287555  
M5P score: -0.244615690004434

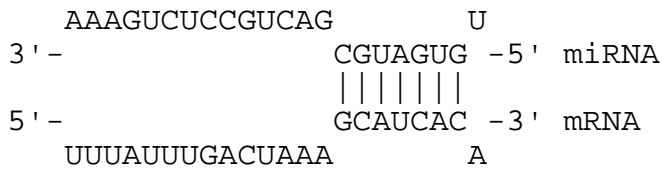
*Binding sites details*

Position: 360  
Type: 8mer  
Alignment:



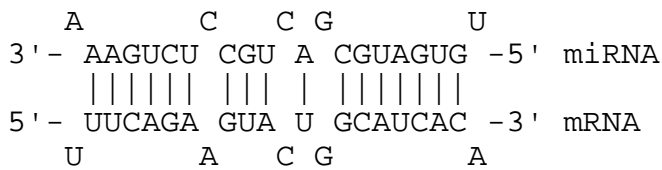
Free energy: -23.0 Kcal/mol

Position: 1257  
Type: 8mer  
Alignment:



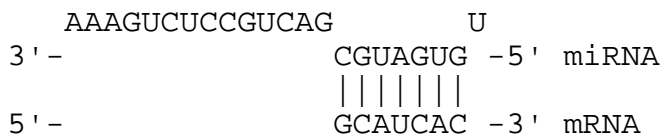
Free energy: -12.8 Kcal/mol

Position: 360  
Type: 8mer  
Alignment:



Free energy: -23.0 Kcal/mol

Position: 1257  
Type: 8mer  
Alignment:



UUUAUUUGACUAAA A

Free energy: -12.8 Kcal/mol

Position: 360

Type: 8mer

Alignment:

```
      A      C      C G      U
3' - AAGUCU CGU A CGUAGUG -5' miRNA
      |||||  ||| |  |||||
5' - UUCAGA GUA U GCAUCAC -3' mRNA
      U      A      C G      A
```

Free energy: -23.0 Kcal/mol

Position: 1257

Type: 8mer

Alignment:

```
      AAAGUCUCCGUCAG      U
3' -                CGUAGUG -5' miRNA
                |||||
5' -                GCAUCAC -3' mRNA
      UUUAUUUGACUAAA      A
```

Free energy: -12.8 Kcal/mol

Position: 360

Type: 8mer

Alignment:

```
      A      C      C G      U
3' - AAGUCU CGU A CGUAGUG -5' miRNA
      |||||  ||| |  |||||
5' - UUCAGA GUA U GCAUCAC -3' mRNA
      U      A      C G      A
```

Free energy: -23.0 Kcal/mol

Position: 1257

Type: 8mer

Alignment:

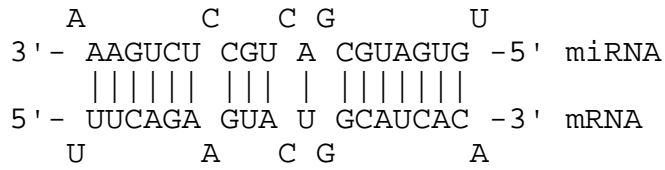
```
      AAAGUCUCCGUCAG      U
3' -                CGUAGUG -5' miRNA
                |||||
5' -                GCAUCAC -3' mRNA
      UUUAUUUGACUAAA      A
```

Free energy: -12.8 Kcal/mol

Position: 360

Type: 8mer

Alignment:

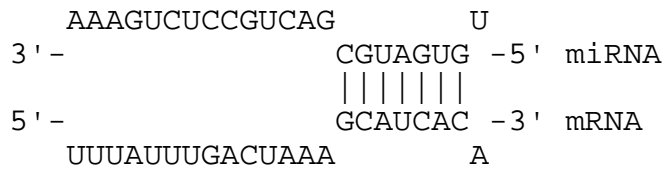


Free energy: -23.0 Kcal/mol

Position: 1257

Type: 8mer

Alignment:

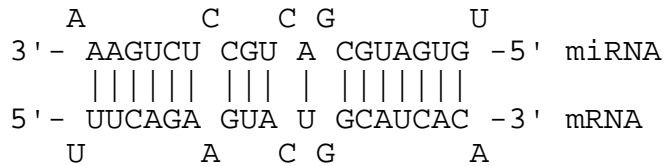


Free energy: -12.8 Kcal/mol

Position: 360

Type: 8mer

Alignment:

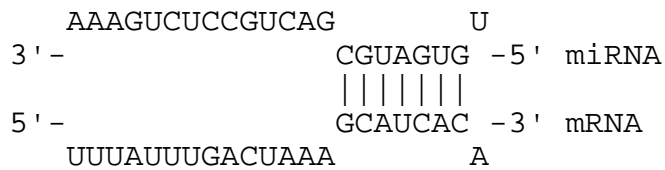


Free energy: -23.0 Kcal/mol

Position: 1257

Type: 8mer

Alignment:



Free energy: -12.8 Kcal/mol

=====

miRNA ID:28

Rank: 7

Sequence:

UACAGUCCGACGAUCCCAACCU

Total binding sites: 18

Sites on BACE1\_(NM\_001207048\_-\_Entrez\_ID:\_23621)

3

Sites on BACE1\_(NM\_001207049\_-\_Entrez\_ID:\_23621)

3

Sites on BACE1\_(NM\_012104\_-\_Entrez\_ID:\_23621)

3

Sites on BACE1\_(NM\_138971\_-\_Entrez\_ID:\_23621)

3

Sites on BACE1\_(NM\_138972\_-\_Entrez\_ID:\_23621)

3

Sites on BACE1\_(NM\_138973\_-\_Entrez\_ID:\_23621)

3

Seed score: 0.8999999999999999

3' Match score: 0.42857142857142866

AU Content score: 0.5333333333333332

Nucleotide Composition score: 0.6654456654456653

Structural Accessibility score: 0.16792356678333334

ARE/CPE score: 0.38888888888888889

-----  
C-tree score: -0.22488171570287555

M5P score: -0.24175375279477904

### *Binding sites details*

Position: 174

Type: 8mer

Alignment:

```
      A   U   CAG
3'- UCC ACCC AG   CCUGACAU-5' miRNA
   ||| ||||| ||   |||||
5'- AGG UGGG UC   GGACUGUA-3' mRNA
   A       U   CAG
```

Free energy: -22.7 Kcal/mol

Position: 488

Type: 8mer

Alignment:

```
      UCCAACCCUAGCAG
3'-                               CCUGACAU-5' miRNA
   |||||
5'-                               GGACUGUA-3' mRNA
      UGCUUUAGAGACAG
```

Free energy: -12.7 Kcal/mol

Position: 3767  
Type: 7mer-m8  
Alignment:

```
      UC      CC      C
3'-  CAAC  UAG  AGCCUGACAU-5' miRNA
      ||||  |||  |||||
5'-  GUUG  AUU  UCGGACUGUG-3' mRNA
      AU      UU      C
```

Free energy: -21.6 Kcal/mol

Position: 174  
Type: 8mer  
Alignment:

```
      A      U  CAG
3'-  UCC  ACCC  AG  CCUGACAU-5' miRNA
      |||  ||||  ||  |||||
5'-  AGG  UGGG  UC  GGACUGUA-3' mRNA
      A      U  CAG
```

Free energy: -22.7 Kcal/mol

Position: 488  
Type: 8mer  
Alignment:

```
      UCCAACCCUAGCAG
3'-  CCUGACAU-5' miRNA
      |||||
5'-  GGACUGUA-3' mRNA
      UGCUUUAGAGACAG
```

Free energy: -12.7 Kcal/mol

Position: 3767  
Type: 7mer-m8  
Alignment:

```
      UC      CC      C
3'-  CAAC  UAG  AGCCUGACAU-5' miRNA
      ||||  |||  |||||
5'-  GUUG  AUU  UCGGACUGUG-3' mRNA
      AU      UU      C
```

Free energy: -21.6 Kcal/mol

Position: 174  
Type: 8mer  
Alignment:

```
      A      U  CAG
3'-  UCC  ACCC  AG  CCUGACAU-5' miRNA
```

```

      |||  ||||  ||   |||||
5'- AGG UGGG UC   GGACUGUA-3' mRNA
      A       U   CAG

```

Free energy: -22.7 Kcal/mol

Position: 488

Type: 8mer

Alignment:

```

      UCCAACCCUAGCAG
3'-                CCUGACAU-5' miRNA
                |||||
5'-                GGACUGUA-3' mRNA
      UGCUUUAGAGACAG

```

Free energy: -12.7 Kcal/mol

Position: 3767

Type: 7mer-m8

Alignment:

```

      UC   CC   C
3'- CAAC UAG AGCCUGACAU-5' miRNA
      |||  |||  |||||
5'- GUUG AUU UCGGACUGUG-3' mRNA
      AU   UU   C

```

Free energy: -21.6 Kcal/mol

Position: 174

Type: 8mer

Alignment:

```

      A   U   CAG
3'- UCC ACCC AG   CCUGACAU-5' miRNA
      |||  ||||  ||   |||||
5'- AGG UGGG UC   GGACUGUA-3' mRNA
      A       U   CAG

```

Free energy: -22.7 Kcal/mol

Position: 488

Type: 8mer

Alignment:

```

      UCCAACCCUAGCAG
3'-                CCUGACAU-5' miRNA
                |||||
5'-                GGACUGUA-3' mRNA
      UGCUUUAGAGACAG

```

Free energy: -12.7 Kcal/mol



Position: 3767  
Type: 7mer-m8  
Alignment:

```
      UC      CC      C
3'-  CAAC  UAG  AGCCUGACAU-5' miRNA
      ||||  |||  |||||
5'-  GUUG  AUU  UCGGACUGUG-3' mRNA
      AU      UU      C
```

Free energy: -21.6 Kcal/mol

Position: 174  
Type: 8mer  
Alignment:

```
      A      U  CAG
3'-  UCC  ACCC  AG  CCUGACAU-5' miRNA
      |||  ||||  ||  |||||
5'-  AGG  UGGG  UC  GGACUGUA-3' mRNA
      A      U  CAG
```

Free energy: -22.7 Kcal/mol

Position: 488  
Type: 8mer  
Alignment:

```
      UCCAACCCUAGCAG
3'-  CCUGACAU-5' miRNA
      |||||
5'-  GGACUGUA-3' mRNA
      UGCUUUAGAGACAG
```

Free energy: -12.7 Kcal/mol

Position: 3767  
Type: 7mer-m8  
Alignment:

```
      UC      CC      C
3'-  CAAC  UAG  AGCCUGACAU-5' miRNA
      ||||  |||  |||||
5'-  GUUG  AUU  UCGGACUGUG-3' mRNA
      AU      UU      C
```

Free energy: -21.6 Kcal/mol

Position: 174  
Type: 8mer  
Alignment:

```
      A      U  CAG
3'-  UCC  ACCC  AG  CCUGACAU-5' miRNA
```

```

      |||  |||  ||  |||  |||  |||
5' - AGG UGGG UC  GGACUGUA-3' mRNA
      A      U  CAG

```

Free energy: -22.7 Kcal/mol

Position: 488

Type: 8mer

Alignment:

```

      UCCAACCCUAGCAG
3' -                      CCUGACAU-5' miRNA
      |||  |||  |||  |||
5' -                      GGACUGUA-3' mRNA
      UGCUUUAGAGACAG

```

Free energy: -12.7 Kcal/mol

Position: 3767

Type: 7mer-m8

Alignment:

```

      UC      CC      C
3' -  CAAC  UAG  AGCCUGACAU-5' miRNA
      |||  |||  |||  |||  |||  |||
5' -  GUUG  AUU  UCGGACUGUG-3' mRNA
      AU      UU      C

```

Free energy: -21.6 Kcal/mol

=====

**miRNA ID:231**

Rank: 8

Sequence:

UUAGGUUUAGAGCCUGGGCUGG

Total binding sites: 12

Sites on BACE1\_(NM\_001207048\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_001207049\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_012104\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138971\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138972\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138973\_-\_Entrez\_ID:\_23621)

2

Seed score: 1.0

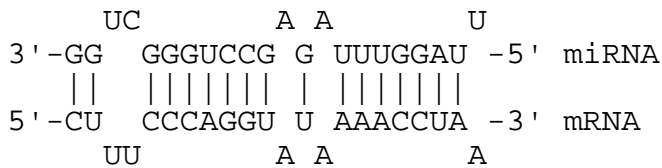
3' Match score: 0.6428571428571428  
AU Content score: 0.7999999999999999  
Nucleotide Composition score: 0.7802197802197802  
Structural Accessibility score: 0.20491608449999998  
ARE/CPE score: 0.9166666666666666

---

C-tree score: -0.22488171570287555  
M5P score: -0.23955136306973757

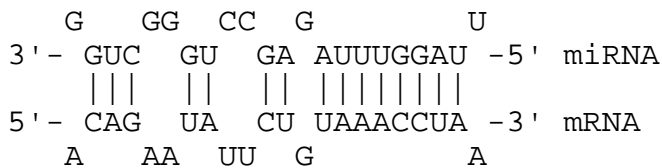
*Binding sites details*

Position: 3232  
Type: 8mer  
Alignment:



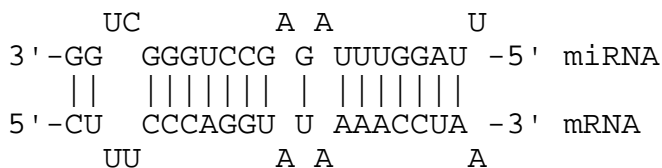
Free energy: -21.3 Kcal/mol

Position: 3806  
Type: 8mer  
Alignment:



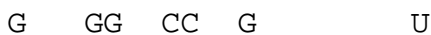
Free energy: -16.8 Kcal/mol

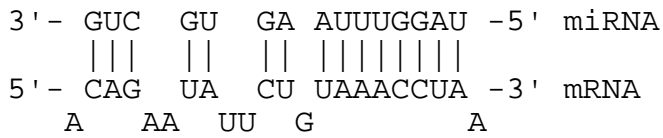
Position: 3232  
Type: 8mer  
Alignment:



Free energy: -21.3 Kcal/mol

Position: 3806  
Type: 8mer  
Alignment:



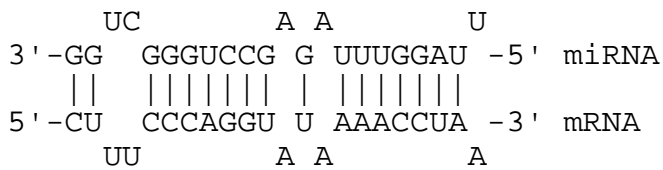


Free energy: -16.8 Kcal/mol

Position: 3232

Type: 8mer

Alignment:

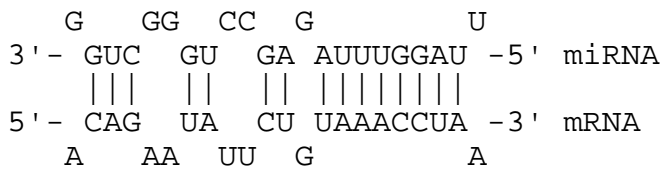


Free energy: -21.3 Kcal/mol

Position: 3806

Type: 8mer

Alignment:

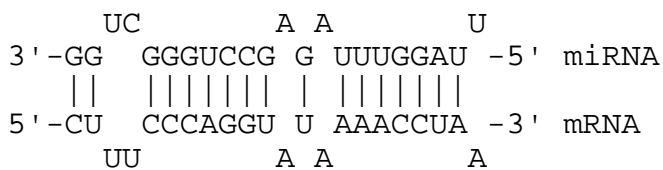


Free energy: -16.8 Kcal/mol

Position: 3232

Type: 8mer

Alignment:

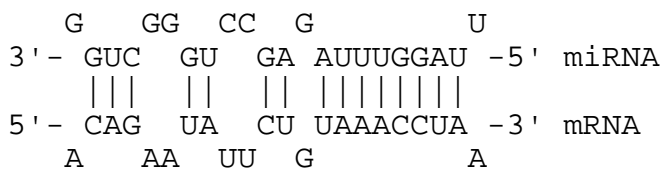


Free energy: -21.3 Kcal/mol

Position: 3806

Type: 8mer

Alignment:

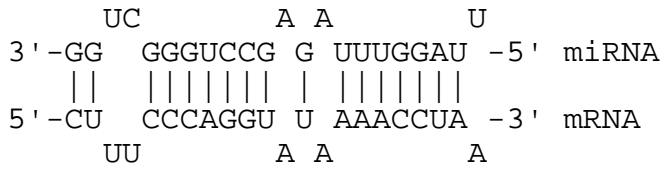


Free energy: -16.8 Kcal/mol

Position: 3232

Type: 8mer

Alignment:

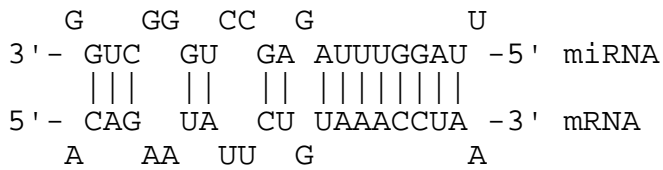


Free energy: -21.3 Kcal/mol

Position: 3806

Type: 8mer

Alignment:

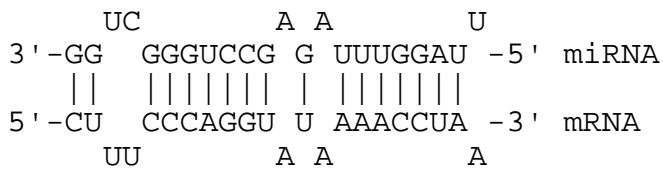


Free energy: -16.8 Kcal/mol

Position: 3232

Type: 8mer

Alignment:

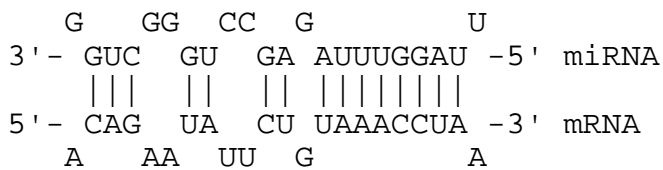


Free energy: -21.3 Kcal/mol

Position: 3806

Type: 8mer

Alignment:



Free energy: -16.8 Kcal/mol

=====

miRNA ID:206

Rank: 9

Sequence:

UCCCUUCUGGGUCUGUCCUCUG

Total binding sites: 12

Sites on BACE1\_(NM\_001207048\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_001207049\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_012104\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138971\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138972\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138973\_-\_Entrez\_ID:\_23621)

2

Seed score: 1.0

3' Match score: 0.35714285714285715

AU Content score: 0.5499999999999999

Nucleotide Composition score: 0.7893772893772893

Structural Accessibility score: 0.27669375787499995

ARE/CPE score: 0.75

-----  
C-tree score: -0.22488171570287555

M5P score: -0.23782513312707004

### *Binding sites details*

Position: 2282

Type: 8mer

Alignment:

```
      U      GGG
3' -GUC CCUGUCU   UCUUCCCU-5' miRNA
    ||| ||||| |||
5' -CAG GGACAGA   AGAAGGGA-3' mRNA
      U      GGG
```

Free energy: -27.5 Kcal/mol

Position: 3139

Type: 8mer

Alignment:

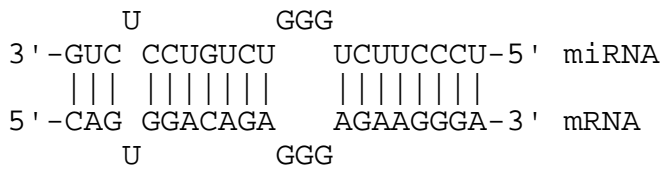
```
      GUCUCCUGUCUGGG
3' -                UCUUCCCU-5' miRNA
    |||||
5' -                AGAAGGGA-3' mRNA
UUUAAUUCUAAAAG
```

Free energy: -12.5 Kcal/mol

Position: 2282

Type: 8mer

Alignment:

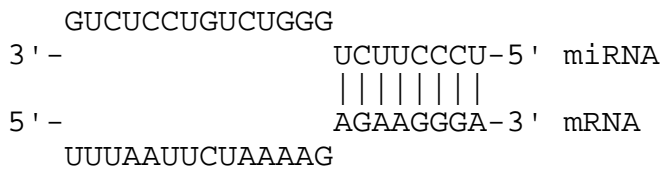


Free energy: -27.5 Kcal/mol

Position: 3139

Type: 8mer

Alignment:

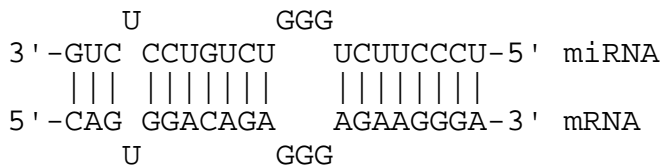


Free energy: -12.5 Kcal/mol

Position: 2282

Type: 8mer

Alignment:

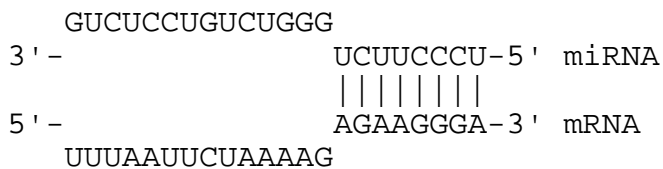


Free energy: -27.5 Kcal/mol

Position: 3139

Type: 8mer

Alignment:

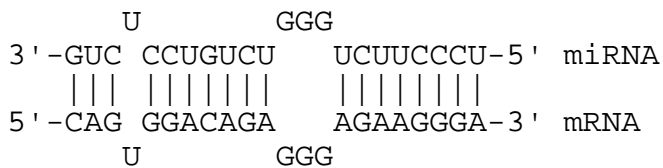


Free energy: -12.5 Kcal/mol

Position: 2282

Type: 8mer

Alignment:

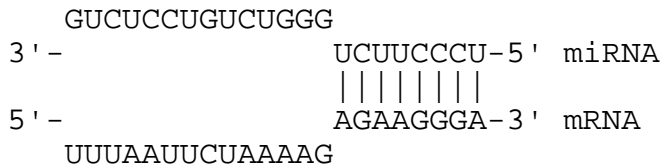


Free energy: -27.5 Kcal/mol

Position: 3139

Type: 8mer

Alignment:

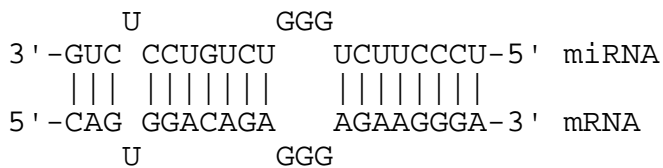


Free energy: -12.5 Kcal/mol

Position: 2282

Type: 8mer

Alignment:

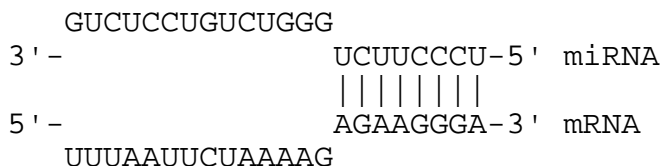


Free energy: -27.5 Kcal/mol

Position: 3139

Type: 8mer

Alignment:

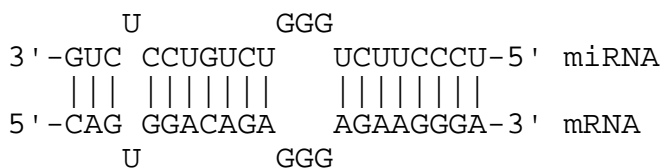


Free energy: -12.5 Kcal/mol

Position: 2282

Type: 8mer

Alignment:





Free energy: -27.5 Kcal/mol

Position: 3139

Type: 8mer

Alignment:

```
      GUCUCCUGUCUGGG
3' -                UCUUCCCU-5'  miRNA
      |||||
5' -                AGAAGGGA-3'  mRNA
      UUUA AUUCUAAAAG
```

Free energy: -12.5 Kcal/mol

=====

### miRNA ID:95

Rank: 10

Sequence:

GCACUUCAACCUAGCGGGCCUG

Total binding sites: 12

Sites on BACE1\_(NM\_001207048\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_001207049\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_012104\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138971\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138972\_-\_Entrez\_ID:\_23621)

2

Sites on BACE1\_(NM\_138973\_-\_Entrez\_ID:\_23621)

2

Seed score: 0.85

3' Match score: 0.5357142857142858

AU Content score: 0.6999999999999998

Nucleotide Composition score: 0.6602564102564104

Structural Accessibility score: 0.31975427374999993

ARE/CPE score: 0.5

-----  
C-tree score: -0.22488171570287555

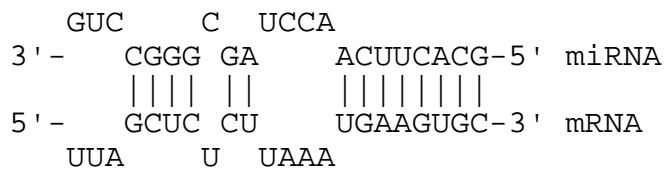
M5P score: -0.23175786217926603

### *Binding sites details*

Position: 815

Type: 7mer-m8

Alignment:

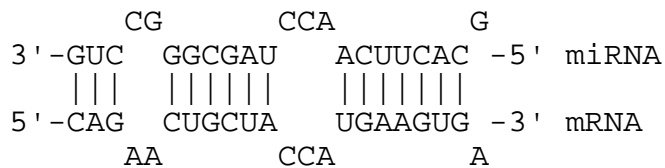


Free energy: -18.2 Kcal/mol

Position: 1911

Type: 8mer

Alignment:

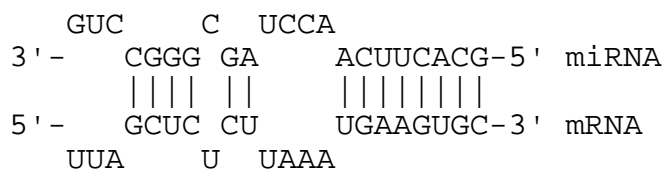


Free energy: -20.9 Kcal/mol

Position: 815

Type: 7mer-m8

Alignment:

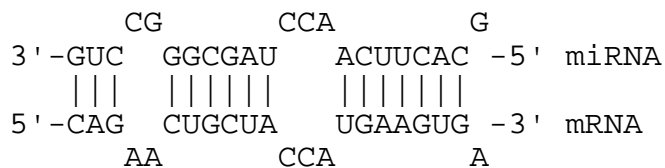


Free energy: -18.2 Kcal/mol

Position: 1911

Type: 8mer

Alignment:

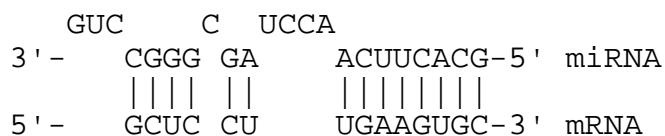


Free energy: -20.9 Kcal/mol

Position: 815

Type: 7mer-m8

Alignment:



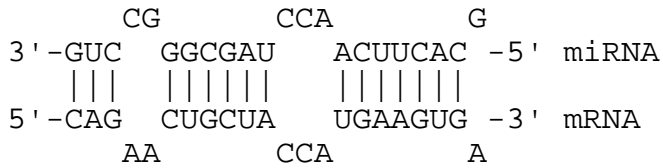
UUA U UAAA

Free energy: -18.2 Kcal/mol

Position: 1911

Type: 8mer

Alignment:

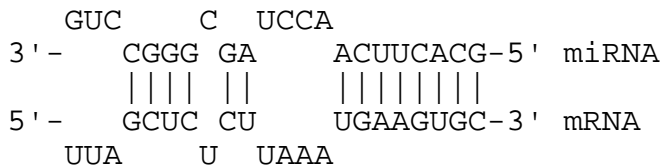


Free energy: -20.9 Kcal/mol

Position: 815

Type: 7mer-m8

Alignment:

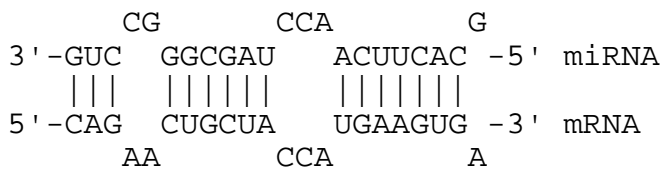


Free energy: -18.2 Kcal/mol

Position: 1911

Type: 8mer

Alignment:

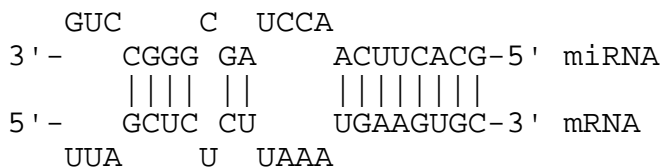


Free energy: -20.9 Kcal/mol

Position: 815

Type: 7mer-m8

Alignment:

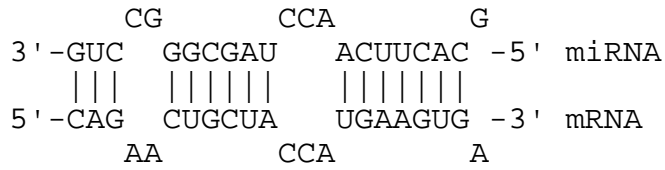


Free energy: -18.2 Kcal/mol

Position: 1911

Type: 8mer

Alignment:

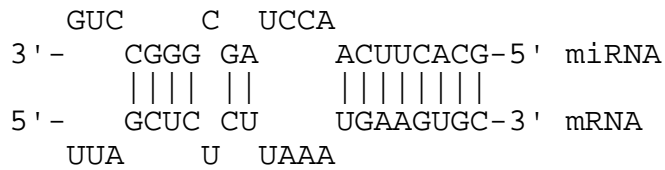


Free energy: -20.9 Kcal/mol

Position: 815

Type: 7mer-m8

Alignment:

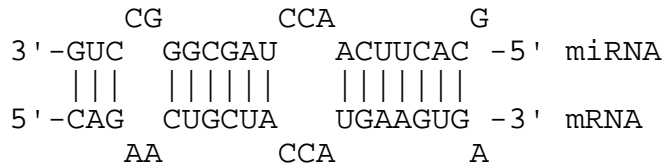


Free energy: -18.2 Kcal/mol

Position: 1911

Type: 8mer

Alignment:



Free energy: -20.9 Kcal/mol

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