Figure S1A. Locations, structures and scores of predicted vertebrate miRNA target sites.

```
miRNA: mir-1

Human predicted target: ENSG00000108654

Mouse predicted target: ENSMUSG00000020719

Rat predicted target: ENSRNOG00000013899

Fugu predicted target: SINFRUG00000143955

Hs Gene description: PROBABLE RNA-DEPENDENT HELICASE P68 (DEAD-BOX PROTEIN
P68) (DEAD-BOX PROTEIN 5). [Source:SWISSPROT;Acc:P17844]    NM_004396

mir-1     ENSG00000108654     2307 nt UTR    1 hits 163

------1-------------------------------------------------------------------
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>ENSG00000108654 hs-mir-1    163    170

UGGAAUGUAAAGAAGUAUGUAU&UGCACUUUUUCGCUAUUUAAGUUGGAUAUUUCUCUACAUUCCU

.((((((((.((((((((.((.&......................)).)))))))).)))))))). -24.30

mir-1     ENSMUSG00000020719  2302 nt UTR    2 hits 164 2013

------1-------------------------------------------------------------------
------1------------

>ENSMUSG00000020719 hs-mir-1    164    171

UGGAAUGUAAAGAAGUAUGUAU&GCACUUUUUUCGCUAUUUAAGUUGGAUAUUUCUCUACAUUCCU

.((((((((.((((((((.((.&......................)).)))))))).)))))))). -24.30

>ENSMUSG00000020719 hs-mir-1   2013   2020

UGGAAUGUAAAGAAGUAUGUAU&UUUGCCAGCAUUAGUAUAAACUAAAAGUGCACAACACAUUCCC

.(((((((......((((....&..........................))))......))))))). -14.40

mir-1     ENSRNOG00000013899  2307 nt UTR    1 hits 167

------1-------------------------------------------------------------------
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```
>ENSRNOG00000013899 hs-mir-1    167    174

UGGAAUGUAAAGAAGUAUGUAU&GCACUUUUUCGCUAUUUAAGUUGGAUAUUUCUCUACAUUCCU

.((((((((.((((((((.((.&.....................)).)))))))).)))))))). -24.30

mir-1     SINFRUG00000143955  2000 nt UTR    1 hits 212

--------1-----------------------------------------------------------------
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>SINFRUG00000143955 hs-mir-1    212    219

UGGAAUGUAAAGAAGUAUGUAU&GAUGCACAUUUUUCAUCCUUUAUUGCAUAUUUGUUACAUUCCU

.(((((((((..(((((((((.&.......................))))))))).))))))))). -24.30



miRNA: mir-1

Human predicted target: ENSG00000145925

Mouse predicted target: ENSMUSG00000025867

Rat predicted target: ENSRNOG00000000105

Fugu predicted target: SINFRUG00000121517

Fugu predicted target: SINFRUG00000145582

Hs Gene description: COMPLEXIN 2 (SYNAPHIN 1) (921-L).
[Source:SWISSPROT;Acc:Q13329] NM_006651

mir-1     ENSG00000145925     2183 nt UTR    2 hits 295 357

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>ENSG00000145925 hs-mir-1    295    302

UGGAAUGUAAAGAAGUAUGUAU&GAAGCCUAAGGUCGUGCUAGUGUGGUGACCCCCAUACAUUCCU

.((((((((....((((((...&............))))))................)))))))). -15.95
```

```
>ENSG00000145925 hs-mir-1    357    364
UGGAAUGUAAAGAAGUAUGUAU&GAGGACCACUGUCCCCAGCCAGCCAAAGUAAUGACACAUUCCAG
((((((((..............&...................................)))))))). -14.90
mir-1     ENSMUSG00000025867  2000 nt UTR    2 hits 340 402
-------------1--1---------------------------------------------------------
------
>ENSMUSG00000025867 hs-mir-1    340    347
UGGAAUGUAAAGAAGUAUGUAU&AUGGUCUAUGUUAAUGUGGUGACACUCCCCCCCAUACAUUCCU
.((((((((.............&..................................)))))))). -15.10
>ENSMUSG00000025867 hs-mir-1    402    409
UGGAAUGUAAAGAAGUAUGUAU&GAGGACCACUGUCCCCAGCCAGCCAAAGUAAUGACACAUUCCAG
((((((((..............&...................................)))))))). -14.90
mir-1     ENSRNOG00000000105  2000 nt UTR    2 hits 329 391
-------------1-1----------------------------------------------------------
------
>ENSRNOG00000000105 hs-mir-1    329    336
UGGAAUGUAAAGAAGUAUGUAU&AUGGUCUACAUUAGUGUGGUAACACUCCCCCCCAUACAUUCCU
.((((((((.............&..................................)))))))). -15.10
>ENSRNOG00000000105 hs-mir-1    391    398
UGGAAUGUAAAGAAGUAUGUAU&GAGGACCACUGUCCCCAGCCAGCCAAAGUAAUGACACAUUCCAG
((((((((..............&...................................)))))))). -14.90
mir-1     SINFRUG00000121517  2000 nt UTR    1 hits 1874
--------------------------------------------------------------------------
1-----
>SINFRUG00000121517 hs-mir-1   1874   1881
UGGAAUGUAAAGAAGUAUGUAU&AAACCCUGAAAAAGAUAUUGUAUUAAUACUCAACACAUUCCU
```

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.(((((((...(.(((((((((&....................))))..))))))...))))))). -15.80

mir-1     SINFRUG00000145582  2000 nt UTR    3 hits 956 974 1187

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>SINFRUG00000145582 hs-mir-1    956    963

UGGAAUGUAAAGAAGUAUGUAU&GUCUUAGUUCGUCUGUGAUCUUCCGUCACGUCAAAACAUUCCAG

((((((((...((.(((((...&.......................))).)).))...)))))))). -16.40

>SINFRUG00000145582 hs-mir-1    974    981

UGGAAUGUAAAGAAGUAUGUAU&UCUUCCGUCACGUCAAAACAUUCCAGAGAUCUCAAACAUUCCAC

((((((((..(((.........&.............................)))...)))))))). -15.50

>SINFRUG00000145582 hs-mir-1   1187   1194

UGGAAUGUAAAGAAGUAUGUAU&GUAGGAGCCACUGGAACGGAACUGUGUCCGGCUCAACAUUCCAA

((((((((..((..(.(..((.&......................))..).)..))..)))))))). -16.90



miRNA: let-7a

Human predicted target: ENSG00000108821

Mouse predicted target: ENSMUSG00000001506

Rat predicted target: ENSRNOG00000003897

Fugu predicted target: SINFRUG00000130987

Hs Gene description: COLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
[Source:SWISSPROT;Acc:P02452]

let-7a    ENSG00000108821     2000 nt UTR    1 hits 789

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>ENSG00000108821 hs-let-7a    789    796

UGAGGUAGUAGGUUGUAUAGUU&UGUUCUGUUCCUUGUGUAACUGUGUUGCUGAAAGACUACCUCGU

(((((((((.(((..(((((((&.................)))))))..))).....))))))))). -25.50

let-7a    ENSMUSG00000001506  2228 nt UTR    1 hits 786

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>ENSMUSG00000001506 hs-let-7a    786    793

UGAGGUAGUAGGUUGUAUAGUU&GUUCUAUUCCUCAGUGCAAUUGUGUUGCUGAAAGACUACCUCGU

(((((((((.(((..(((((((&.................)))))))..))).....))))))))). -23.30

let-7a    ENSRNOG00000003897  2000 nt UTR    1 hits 1992

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-----1

>ENSRNOG00000003897 hs-let-7a   1992   1999

UGAGGUAGUAGGUUGUAUAGUU&UGUUCUGUUCCUUGUGUAAUUGUGUUGCUGAAAGACUACCUCGU

(((((((((.(((..(((((((&.................)))))))..))).....))))))))). -23.20

let-7a    SINFRUG00000130987  2000 nt UTR    1 hits 508

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>SINFRUG00000130987 hs-let-7a    508    515

UGAGGUAGUAGGUUGUAUAGUU&AAAGAAGCUUCACCUUAAUGGCAAUAUGUAGAUGGCUACCUCAU

(((((((((...(((((((...&........................)))))))...))))))))). -21.20



miRNA: let-7a

Human predicted target: ENSG00000119906

Mouse predicted target: ENSMUSG00000036097
```

```
Rat predicted target: ENSRNOG00000014489

Fugu predicted target: SINFRUG00000140611

Hs Gene description: C10ORF6. [Source:RefSeq;Acc:NM_018121] NM_144592

let-7a    ENSG00000119906     2862 nt UTR    2 hits 1326 1560

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>ENSG00000119906 hs-let-7a   1326   1333

UGAGGUAGUAGGUUGUAUAGUU&UUGCGGUUUGAGAGGCAAGAAAAUAAAAUAACUUUCUACCUCU

.(((((((.(((((((......&...........................))))))).))))))). -22.20

>ENSG00000119906 hs-let-7a   1560   1567

UGAGGUAGUAGGUUGUAUAGUU&UGUUGUUUACUGGUAAGAAUAUUAUUAUCUUGAUACUACCUCU

.(((((((((....(.(((((.&.......................))))))....))))))))). -19.70

let-7a    ENSMUSG00000036097  4668 nt UTR    2 hits 1314 1542

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>ENSMUSG00000036097 hs-let-7a   1314   1321

UGAGGUAGUAGGUUGUAUAGUU&GAGAGGAGAAAAUAAGUUCUGAGAGCUAACUCUUUCUACCUCU

.(((((((.(((..((.(((((&.......................))))))).))).))))))). -20.70

>ENSMUSG00000036097 hs-let-7a   1542   1549

UGAGGUAGUAGGUUGUAUAGUU&GUGUUGAGUUUACUGGUAAGAAUAUUGUCUUGAUGCUACCUCU

.(((((((((....(.(((((.&.......................))))))....))))))))). -19.70

let-7a    ENSRNOG00000014489  4549 nt UTR    2 hits 1194 1424

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>ENSRNOG00000014489 hs-let-7a   1194   1201

UGAGGUAGUAGGUUGUAUAGUU&UUGAGAGGAGAAAAUAAGUUCUGAGAGCUAACUUUCUACCUCU

.(((((((.((((((.......&............................)))))).))))))). -20.50

>ENSRNOG00000014489 hs-let-7a   1424   1431

UGAGGUAGUAGGUUGUAUAGUU&GUGUUGAGUUUACUGGUAAGAAUAUUGUCUUGAUGCUACCUCU

.(((((((((....(.(((((.&.......................))))))....))))))))). -19.70

let-7a    SINFRUG00000140611  2000 nt UTR    1 hits 673

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>SINFRUG00000140611 hs-let-7a    673    680

UGAGGUAGUAGGUUGUAUAGUU&UAUGACUGAAUGGUUUAUCCACCAUCUUAGGCCUACUACCUCU

.(((((((((((((........&.............................))))))))))))). -27.00



miRNA: let-7a

Human predicted target: ENSG00000140807

Mouse predicted target: ENSMUSG00000031661

Rat predicted target: ENSRNOG00000014293

Fugu predicted target: SINFRUG00000134205

Hs Gene description: NAKED CUTICLE HOMOLOG 1; NAKED CUTICLE-1; DVL-BINDING
PROTEIN. [Source:RefSeq;Acc:NM_033119]  NM_033119

let-7a    ENSG00000140807     2436 nt UTR    1 hits 427

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>ENSG00000140807 hs-let-7a    427    434

UGAGGUAGUAGGUUGUAUAGUU&GAGACCCUCGAAAUCUCCGAGAAGAUAAACAGCUGCUACCUCU
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.((((((((((.((((......&............................))))))))))))))). -24.30

let-7a    ENSMUSG00000031661  2172 nt UTR    1 hits 376

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>ENSMUSG00000031661 hs-let-7a    376    383

UGAGGUAGUAGGUUGUAUAGUU&CGGAGACCCUCAAGAGCCCCAGAGGACAACAGCUGCUACCUCU

.(((((((((((((((......&.........................)))))..))))))))))). -25.40

let-7a    ENSRNOG00000014293  2000 nt UTR    1 hits 379

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>ENSRNOG00000014293 hs-let-7a    379    386

UGAGGUAGUAGGUUGUAUAGUU&CAGAGACCCUCAAGAGCUCCAGAGGACAACAGCUGCUACCUCU

.(((((((((((((((......&.........................)))))..))))))))))). -25.40

let-7a    SINFRUG00000134205  2000 nt UTR    1 hits 776

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>SINFRUG00000134205 hs-let-7a    776    783

UGAGGUAGUAGGUUGUAUAGUU&AAGUUUAGGAAAAGUAAGAGACCCAAAAUCAGCUGCUACCUCU

.((((((((((.(((.......&.............................)))))))))))))). -22.30



miRNA: let-7a

Human predicted target: ENSG00000156966

Mouse predicted target: ENSMUSG00000047290

Rat predicted target: ENSRNOG00000018267
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Fugu predicted target: SINFRUG00000151687

Hs Gene description: UDP-GLCNAC:BETAGAL BETA-1,3-N-
ACETYLGLUCOSAMINYLTRANSFERASE 7. [Source:RefSeq;Acc:NM_145236]  NM_145236

let-7a    ENSG00000156966     2048 nt UTR    2 hits 637 1105

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>ENSG00000156966 hs-let-7a    637    644

UGAGGUAGUAGGUUGUAUAGUU&GUGUCCUGUAAGGUCUGGAAGGGCGACCGCUCUGACUACCUCAG

(((((((((.((((((.(((..&..............))).....))))))......))))))))). -26.10

>ENSG00000156966 hs-let-7a   1105   1112

UGAGGUAGUAGGUUGUAUAGUU&CAGCUGUGGGGGUGGGUGCAGAAGGUUGCCACCUCCUACCUCAG

((((((((.((((.(((.....&..........................))).)))).)))))))). -25.00

let-7a    ENSMUSG00000047290  3076 nt UTR    1 hits 576

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>ENSMUSG00000047290 hs-let-7a    576    583

UGAGGUAGUAGGUUGUAUAGUU&CUUCUCUUGUCCAGAAGCCUGACUGGCCGCUCUGACUACCUCAG

(((((((((((..((..(((((&....................)))))..))..)).))))))))). -24.50

let-7a    ENSRNOG00000018267  2000 nt UTR    1 hits 566

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>ENSRNOG00000018267 hs-let-7a    566    573

UGAGGUAGUAGGUUGUAUAGUU&CUUCUCUCGUCCAGAAGCCUGACUGGCCACUCUGACUACCUCAG

(((((((((((..((..(((((&....................)))))..))..)).))))))))). -25.20

let-7a    SINFRUG00000151687  2000 nt UTR    1 hits 749

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>SINFRUG00000151687 hs-let-7a    749    756

UGAGGUAGUAGGUUGUAUAGUU&AUAGGUUAAAGCCGAGAAGGAAAAUGAAUAACACUCUACCUCAG

((((((((.(((((((......&...........................))))).)))))))))). -22.00
```

```
miRNA: let-7a

Human predicted target: ENSG00000168758

Mouse predicted target: ENSMUSG00000026121

Rat predicted target: ENSRNOG00000016254

Fugu predicted target: SINFRUG00000125424

Hs Gene description: SEMA DOMAIN, IMMUNOGLOBULIN DOMAIN (IG),
TRANSMEMBRANE DOMAIN TM. [Source:RefSeq;Acc:NM_017789] NM_017789

let-7a    ENSG00000168758     2884 nt UTR    1 hits 67

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>ENSG00000168758 hs-let-7a     67     74

UGAGGUAGUAGGUUGUAUAGUU&GGGAGGUGUAGCUCCUACUUUUGCACAGGCACCAGCUACCUCAG

(((((((((.(((((((.(((.&................)))..)))).....))).))))))))). -24.70

let-7a    ENSMUSG00000026121  2000 nt UTR    1 hits 74

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>ENSMUSG00000026121 hs-let-7a     74     81

UGAGGUAGUAGGUUGUAUAGUU&GGGAGGUGCACUCUUAACUUUUGCACAGGCACCAGCUACCUCAG

(((((((((.(((((((.((((&...............))))..)))).....))).))))))))). -25.50

let-7a    ENSRNOG00000016254  2862 nt UTR    1 hits 75
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>ENSRNOG00000016254 hs-let-7a     75     82

UGAGGUAGUAGGUUGUAUAGUU&GGGAGGUGCACUCUUAACUUUUGCACAGGCACCAGCUACCUCAG

(((((((((.(((((((.((((&...............))))..)))).....))).))))))))). -25.50

let-7a    SINFRUG00000125424  2000 nt UTR    1 hits 57

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>SINFRUG00000125424 hs-let-7a     57     64

UGAGGUAGUAGGUUGUAUAGUU&UCAUGUCUGCAAGUCAGAAAAACAAAACAACCAAUCUACCUCC

.(((((((..((((((...(((&....................)))...))))))...))))))). -23.50



miRNA: let-7a

Human predicted target: ENSG00000169635

Mouse predicted target: ENSMUSG00000050240

Rat predicted target: ENSRNOG00000001863

Fugu predicted target: SINFRUG00000140659

Hs Gene description: HYPERMETHYLATED IN CANCER 2 PROTEIN (HIC-2) (HIC-3)
(HIC1-RELATED GENE ON CHROMOSOME 22). [Source:SWISSPROT;Acc:Q96JB3]

let-7a    ENSG00000169635     2050 nt UTR    3 hits 211 543 1158

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>ENSG00000169635 hs-let-7a    211    218

UGAGGUAGUAGGUUGUAUAGUU&AGCCGAGAGGAGGGAAGCCAGGGGUCCCAGCCCGUCUACCUCC

.(((((((..(((((.......&...........................)))))...))))))). -22.00
```

```
>ENSG00000169635 hs-let-7a    543    550

UGAGGUAGUAGGUUGUAUAGUU&CACUGGCGCUGGGACAGUCAGGGUGACCCCACCGCCUACCUCU

.(((((((..((((((.((((.&.......))))..)))..............)))..))))))). -21.53

>ENSG00000169635 hs-let-7a   1158   1165

UGAGGUAGUAGGUUGUAUAGUU&CCUCGCUGAACAAGGUGGAGACUUCUGACCUUUUGCUACCUCU

.(((((((((((..((..((((&...................))))....))..))))))))))). -23.20

let-7a    ENSMUSG00000050240  2000 nt UTR    3 hits 307 635 1286

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>ENSMUSG00000050240 hs-let-7a    307    314

UGAGGUAGUAGGUUGUAUAGUU&AGUCUAGCCCUAUGCAUGUGGUGCUGGUGACUAUUCUACCUCC

.(((((((..(((..(.((((.&......................)))))..)))...))))))). -20.80

>ENSMUSG00000050240 hs-let-7a    635    642

UGAGGUAGUAGGUUGUAUAGUU&UAGCUGGCACUGGAACAGUCAGGGUGACCCAUUGCCUACCUCU

.((((((((((((..(.(((((&.)))))).................)..)))...)).))))))). -19.17

>ENSMUSG00000050240 hs-let-7a   1286   1293

UGAGGUAGUAGGUUGUAUAGUU&CUCACUGAACAUGGUGGGGAGCCUUCUGACCUUUGCUACCUCU

.(((((((((((.(((.((((.&...)))).)))....................))))))))))). -20.00

let-7a    ENSRNOG00000001863  2000 nt UTR    3 hits 197 511 1139

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>ENSRNOG00000001863 hs-let-7a    197    204

UGAGGUAGUAGGUUGUAUAGUU&AGUCUGGCCCUCUGCAUGUGGUGCUGGUGACUACUCUACCUCC

.(((((((..(((..(.((((.&......................)))))..)))...))))))). -20.80

>ENSRNOG00000001863 hs-let-7a    511    518
```

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UGAGGUAGUAGGUUGUAUAGUU&UAGCUGGCACUGGAACAGUCAGGGUGACCCAUUGCCUACCUCU

.((((((((((((..(.(((((&.))))).................)..)))...)).))))))). -19.17

>ENSRNOG00000001863 hs-let-7a   1139   1146

UGAGGUAGUAGGUUGUAUAGUU&UUCACUGAACAUGAUGGAGAGCCUUCUGACCUUUGCUACCUCU

.(((((((((((.(((.((((.&...)))).)))....................))))))))))). -20.00

let-7a    SINFRUG00000140659  2000 nt UTR    1 hits 1077

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>SINFRUG00000140659 hs-let-7a   1077   1084

UGAGGUAGUAGGUUGUAUAGUU&AACUAGAAGUCUAUUUAUAUAGGCUCCUAACCUUGCUACCUCU

.(((((((((((((((((((..&..............))))))))).........))))))))))). -23.10



miRNA: let-7a

Human predicted target: ENSG00000174437

Mouse predicted target: ENSMUSG00000029467

Rat predicted target: ENSRNOG00000001285

Fugu predicted target: SINFRUG00000134916

Hs Gene description: SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE 2
(EC 3.6.3.8) (CALCIUM PUMP 2) (SERCA2) (SR CA(2+)-ATPASE 2) (CALCIUM-
TRANSPORTING ATPASE SARCOPLASMIC RETICULUM TYPE, SLOW TWITCH SKELETAL
MUSCLE ISOFORM) (ENDOPLASMIC RETICULUM CLASS 1/2 CA(2+) ATPASE).
[Source:SWISSPROT;Acc:P16615] NM_001681

let-7a    ENSG00000174437     2856 nt UTR    1 hits 490

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>ENSG00000174437 hs-let-7a    490    497
```

```
UGAGGUAGUAGGUUGUAUAGUU&CAUAAGCCAAUUUUUCUGCACUGAGCAGAGUCUUGCUACCUCAG

((((((((((((((((.((((.&...................)))).)))))...))))))))))). -27.00

let-7a    ENSMUSG00000029467  2000 nt UTR    1 hits 642

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>ENSMUSG00000029467 hs-let-7a    642    649

UGAGGUAGUAGGUUGUAUAGUU&CAUAAGCCAAUUUUUCUGCACUGAGCAGAGUCCUGCUACCUCAG

((((((((((((((((.((((.&...................)))).)))))...))))))))))). -29.70

let-7a    ENSRNOG00000001285  4048 nt UTR    1 hits 494

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>ENSRNOG00000001285 hs-let-7a    494    501

UGAGGUAGUAGGUUGUAUAGUU&CAUAAGCCAAUUUUUCUGCACUGAGCAGAGUCCUGCUACCUCAG

((((((((((((((((.((((.&...................)))).)))))...))))))))))). -29.70

let-7a    SINFRUG00000134916  2000 nt UTR    1 hits 658

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>SINFRUG00000134916 hs-let-7a    658    665

UGAGGUAGUAGGUUGUAUAGUU&CAUUCUGUUUGUUUUCUGCAGUCGGCAGAGCACAGCUACCUCAA

(((((((((.(..((((.....&................))))..)...........))))))))). -20.90



miRNA: let-7a

Human predicted target: ENSG00000174498

Mouse predicted target: ENSMUSG00000032394
```

```
Rat predicted target: ENSRNOG00000013322

Fugu predicted target: SINFRUG00000135911

Hs Gene description: SIMILAR TO PUTATIVE NEURONAL CELL ADHESION MOLECULE.
[Source:SPTREMBL;Acc:Q8IVU1]

let-7a    ENSG00000174498     2458 nt UTR    4 hits 452 534 685 762

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>ENSG00000174498 hs-let-7a    452    459

UGAGGUAGUAGGUUGUAUAGUU&UCAGGAUGGAUUUUUGCUGUUUUGGCUCUCAGCACCUACCUCAG

((((((((...((((...((((&.......................))))..))))..)))))))). -22.30

>ENSG00000174498 hs-let-7a    534    541

UGAGGUAGUAGGUUGUAUAGUU&UCAGCCCCCUUACCCCACAGAGCCCGAAUGCACUCCUACCUCAA

((((((((.((..(((((....&...........................))))))).)))))))). -20.70

>ENSG00000174498 hs-let-7a    685    692

UGAGGUAGUAGGUUGUAUAGUU&AGCACUUCCCCAUUUCCAGAUGUGAAAGAAAAUGUCUACCUCAA

((((((((.(.(((........&..............................))).))))))))). -17.60

>ENSG00000174498 hs-let-7a    762    769

UGAGGUAGUAGGUUGUAUAGUU&GACCUGCCUCCCCGCCCCUCCUGCCCACAGCCCACCUACCUCU

.(((((((..((((((......&..........................))))))...))))))). -23.50

let-7a    ENSMUSG00000032394  2523 nt UTR    4 hits 388 468 633 714

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>ENSMUSG00000032394 hs-let-7a    388    395

UGAGGUAGUAGGUUGUAUAGUU&CAGGAUGGAUUUUGAGCUGUUGUGACUCUCAGCACCUACCUCAG

((((((((...((((...((((&.......................))))..))))..)))))))). -22.80

>ENSMUSG00000032394 hs-let-7a    468    475
```

```
UGAGGUAGUAGGUUGUAUAGUU&CCUCCGCCUCUACCCCACAGAGCCCGAAAGCACUCCUACCUCAA

((((((((.(((((.....(((&....................))).....))).)).)))))))). -20.30

>ENSMUSG00000032394 hs-let-7a    633    640

UGAGGUAGUAGGUUGUAUAGUU&ACCACUGUCCCAACUCCAAGUGUGAAAGAAACUGUCUACCUCAG

(((((((((((((((.(((((.&...)))))..)))).................))).)))))))). -20.92

>ENSMUSG00000032394 hs-let-7a    714    721

UGAGGUAGUAGGUUGUAUAGUU&GACCCUCCCCCAGCCUCCUUCAUCCCUGGCCUAGCCUACCUCU

.(((((((((((((........&...........................))))))..))))))). -21.40

let-7a    ENSRNOG00000013322  2000 nt UTR    4 hits 470 550 703 788

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>ENSRNOG00000013322 hs-let-7a    470    477

UGAGGUAGUAGGUUGUAUAGUU&CUCAGGAUGGAUUUUUAGCUGUUGUGACUCAGCACCUACCUCAG

((((((((...((((.((((((&................)))))).......))))..)))))))). -22.50

>ENSRNOG00000013322 hs-let-7a    550    557

UGAGGUAGUAGGUUGUAUAGUU&CCUCAGCCUCUACCCCACAGAGCCCGAAAGCACUCCUACCUCAA

((((((((.(((((.....(((&....................))).....))).)).)))))))). -20.30

>ENSRNOG00000013322 hs-let-7a    703    710

UGAGGUAGUAGGUUGUAUAGUU&ACCACUGUCCCAACUCCAAGUGUGAAAGAAACUGUCUACCUCAA

(((((((((((((((.(((((.&...)))))..)))).................))).)))))))). -20.92

>ENSRNOG00000013322 hs-let-7a    788    795

UGAGGUAGUAGGUUGUAUAGUU&CUCCUUGGCCUCCUCCUUCCCUGGCCUGGCCUGGCCUACCUCU

.((((((((((((((..(((..&....................)))...)))))))..))))))). -21.80

let-7a    SINFRUG00000135911  2000 nt UTR    3 hits 1368 1451 1562
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>SINFRUG00000135911 hs-let-7a   1368   1375

UGAGGUAGUAGGUUGUAUAGUU&CUUGGCUGUGUGAAACUUAGCGAUUCAACUAAAACCUACCUCAG

((((((((((((((.(((((((&...)))))))...))))))................)))))))). -22.19

>SINFRUG00000135911 hs-let-7a   1451   1458

UGAGGUAGUAGGUUGUAUAGUU&ACUUCUCACCUUAAAUGACCAGAUCAGGCGCCGCGCUACCUCAG

(((((((((.((.(((...(((&.....................)))...)))))..))))))))). -23.00

>SINFRUG00000135911 hs-let-7a   1562   1569

UGAGGUAGUAGGUUGUAUAGUU&AACAUAAAGCACUUCCAAAUGCUGAAGUUAAUGUUCUACCUCAC

((((((((.(.((((..((((.&....................))))....)))).).)))))))). -19.80



miRNA: mir-7

Human predicted target: ENSG00000139219

Mouse predicted target: ENSMUSG00000022483

Rat predicted target: ENSRNOG00000008809

Fugu predicted target: SINFRUG00000135764

Hs Gene description: COLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS:
CHONDROCALCIN]. [Source:SWISSPROT;Acc:P02458]

mir-7     ENSG00000139219     2439 nt UTR    2 hits 217 2416

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>ENSG00000139219 hs-mir-7    217    224

UGGAAGACUAGUGAUUUUGUU&UGCAAAAUAAAAUCUCGGUGUUCUAUUUAUUUAUUGUCUUCCU

.(((((((..(.(((((((((&.....))))))))).)...................))))))). -19.60
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>ENSG00000139219 hs-mir-7   2416   2423

UGGAAGACUAGUGAUUUUGUU&GGCUGGCAGGUCUGUGCUCCCUGUGCCGCUUCCUUGUCUUCCU

.(((((((.((((........&..........................)))).....))))))). -18.60

mir-7     ENSMUSG00000022483  2205 nt UTR    2 hits 217 1514

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>ENSMUSG00000022483 hs-mir-7    217    224

UGGAAGACUAGUGAUUUUGUU&UGCAAAAUAAAAUCUCGGUGUUCUAUUUAUUUAUUGUCUUCCU

.(((((((..(.(((((((((&.....))))))))).)...................))))))). -19.60

>ENSMUSG00000022483 hs-mir-7   1514   1521

UGGAAGACUAGUGAUUUUGUU&CCUUCUCUGUAUUCCAUCCAGAUGAGGAAUGGAAAGUCUUCCC

.((((((((..(.(((((...&.........................))))).)..)))))))). -19.40

mir-7     ENSRNOG00000008809  3494 nt UTR    2 hits 1271 1592

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>ENSRNOG00000008809 hs-mir-7   1271   1278

UGGAAGACUAGUGAUUUUGUU&UGCAAAAUAAAAUCUCGAAGUUCUAUUUAUUUAUUGUCUUCCU

.(((((((..(.(((((((((&.....))))))))).)...................))))))). -19.60

>ENSRNOG00000008809 hs-mir-7   1592   1599

UGGAAGACUAGUGAUUUUGUU&ACCCUGAGCAUCUCCUGCUACCCAAAAGGCUUGGGGUCUUCCU

.(((((((((((..(((((..&......................))))).)))...)))))))). -20.40

mir-7     SINFRUG00000135764  2000 nt UTR    1 hits 398

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>SINFRUG00000135764 hs-mir-7    398    405
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UGGAAGACUAGUGAUUUUGUU&CAGGAAAUGAACUCAACUAAGAAACAUAAUACACAGUCUUCCAU

(((((((((.((((((.((((&......................)))).))).)))))))))))). -24.30



miRNA: mir-9

Human predicted target: ENSG00000119547

Mouse predicted target: ENSMUSG00000045991

Rat predicted target: ENSRNOG00000018299

Fugu predicted target: SINFRUG00000154314

Hs Gene description: ONE CUT DOMAIN FAMILY MEMBER 2 (ONECUT-2
TRANSCRIPTION FACTOR) (OC-2). [Source:SWISSPROT;Acc:O95948] NM_004852

mir-9     ENSG00000119547     2109 nt UTR    4 hits 1273 1296 1671 2033

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>ENSG00000119547 hs-mir-9   1273   1280

UCUUUGGUUAUCUAGCUGUAUGA&AAAACAGCUGAAUACAUCUGGAGAAAACACAGCACACCAAAGAA

((((((((..(((((.(((((..&...........))))).)))))............)))))))). -
21.66

>ENSG00000119547 hs-mir-9   1296   1303

UCUUUGGUUAUCUAGCUGUAUGA&AAAACACAGCACACCAAAGAAGCAGAAUACUGCAAACCAAAGAC

(((((((((.....((.((((..&..........................)))).)).))))))))). -
18.20

>ENSG00000119547 hs-mir-9   1671   1678

UCUUUGGUUAUCUAGCUGUAUGA&UUGAGACUGACUUUUUUAUGAAUUACUUAGUCGAAACCAAAGAA

(((((((((.((..((((..(((&......................)))..)))).))))))))))). -
17.60

>ENSG00000119547 hs-mir-9   2033   2040
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UCUUUGGUUAUCUAGCUGUAUGA&CGGAACAGAGCAACAGAAACCUCAACAGCUACAAUACCAAAGAU

((((((((....(((((((.(((&.....................))))))))))....)))))))). -
25.40

mir-9     ENSMUSG00000045991  2000 nt UTR    3 hits 1316 1339 1717

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>ENSMUSG00000045991 hs-mir-9   1316   1323

UCUUUGGUUAUCUAGCUGUAUGA&AAUACAGCUGACAGAACCUGGAGAGAACACAGCACACCAAAGAA

((((((((....(((((((((..&.))))))))).........................)))))))). -
21.95

>ENSMUSG00000045991 hs-mir-9   1339   1346

UCUUUGGUUAUCUAGCUGUAUGA&AGAACACAGCACACCAAAGAAGCAGAAUACUGCAAACCAAAGAC

(((((((((.....((.((((..&..........................)))).)).))))))))). -
18.20

>ENSMUSG00000045991 hs-mir-9   1717   1724

UCUUUGGUUAUCUAGCUGUAUGA&UUGAGACUGACUUUUGUAUGAAUUGCUUAAUUGAAACCAAAGAA

(((((((((.((.(((..((((.&................))))....))).....))))))))))). -
18.50

mir-9     ENSRNOG00000018299  2000 nt UTR    3 hits 1294 1318 1702

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>ENSRNOG00000018299 hs-mir-9   1294   1301

UCUUUGGUUAUCUAGCUGUAUGA&AAAACAGCCGACGGAAUCUGGAGAGAACACAGCACACCAAAGAA

((((((((......(((((....&............................)))))..)))))))). -
19.50

>ENSRNOG00000018299 hs-mir-9   1318   1325

UCUUUGGUUAUCUAGCUGUAUGA&GAACACAGCACACCAAAGAAGCAGAAAUUCUGCAAACCAAAGAU
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(((((((((.....(((((....&....))))).........................))))))))). -
17.81

>ENSRNOG00000018299 hs-mir-9   1702   1709

UCUUUGGUUAUCUAGCUGUAUGA&UUGAGACUGACUUUUGUAUGAAUUACUUAAUUGAAACCAAAGAA

(((((((((.((.....(((...&.......................)))......))))))))))). -
16.70

mir-9     SINFRUG00000154314  2000 nt UTR    5 hits 527 549 1155 1622 1770

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>SINFRUG00000154314 hs-mir-9    527    534

UCUUUGGUUAUCUAGCUGUAUGA&UCAAGUUUGGCGGAUGCACAGUCAGGAAUCACCAAACCAAAGC

.((((((((.(((..((((....&.................))))..))).........)))))))). -17.60

>SINFRUG00000154314 hs-mir-9    549    556

UCUUUGGUUAUCUAGCUGUAUGA&CAGGAAUCACCAAACCAAAGCUUAGCUAAAGAUUAACCAAAGC

.(((((((((((((((((.....&......................)))))..))).))))))))). -21.10

>SINFRUG00000154314 hs-mir-9   1155   1162

UCUUUGGUUAUCUAGCUGUAUGA&UCCCCCAAGAUUCCUAUUUUAAUCACAGCAACAGCACCAAAGAA

((((((((......(((((....&........................)))))......)))))))). -
21.10

>SINFRUG00000154314 hs-mir-9   1622   1629

UCUUUGGUUAUCUAGCUGUAUGA&CAUCCCUCACUCGAGCUAUAAACCAAAAGAAUCAAACCAAAGGA

(((((((((.((((((((..(((&......)))..).))))..........)))....))))))))). -
17.20

>SINFRUG00000154314 hs-mir-9   1770   1777

UCUUUGGUUAUCUAGCUGUAUGA&CACUUGAGACUUUUUCUAUUUAUUGACAAAUCGAAACCAAAGAA

(((((((((.((.(..(((....&.........................)))..).))))))))))). -
17.00
```

```
miRNA: mir-9

Human predicted target: ENSG00000119946

Mouse predicted target: ENSMUSG00000025189

Rat predicted target: ENSRNOG00000016302

Fugu predicted target: SINFRUG00000123133

Hs Gene description: CYCLIN M1; ANCIENT CONSERVED DOMAIN PROTEIN 1.
[Source:RefSeq;Acc:NM_020348]

mir-9     ENSG00000119946     4814 nt UTR    2 hits 901 3281

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>ENSG00000119946 hs-mir-9    901    908

UCUUUGGUUAUCUAGCUGUAUGA&ACUGUAAGUGCUGAAAGCAAGUUUAGCCAUGACAAACCAAAGAG

(((((((((.((..((((.....&.......................))))...))..))))))))). -
19.10

>ENSG00000119946 hs-mir-9   3281   3288

UCUUUGGUUAUCUAGCUGUAUGA&AAGGAGUCCAAGUGGCAUGACUCUGGCAGUUUGCAACCAAAGGC

(((((((((....((((((..((&.....................))..))))))...))))))))). -
20.40

mir-9     ENSMUSG00000025189  2710 nt UTR    1 hits 776

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>ENSMUSG00000025189 hs-mir-9    776    783

UCUUUGGUUAUCUAGCUGUAUGA&AUUGUAAGUUGUUAAAAUUUGUGUAGCCAUGAUAAACCAAAGAG

((((((((((((..((((((..(&..................)..))))))...))).))))))))). -
22.90
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mir-9     ENSRNOG00000016302  2000 nt UTR    1 hits 768

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>ENSRNOG00000016302 hs-mir-9    768    775

UCUUUGGUUAUCUAGCUGUAUGA&GAUUGUAAGUUGUUCAGUUUGUGUAGCCAUGAUAAACCAAAGAG

((((((((((((..((((((..(&..................)..))))))...))).))))))))). -
22.90

mir-9     SINFRUG00000123133  2000 nt UTR    1 hits 1622

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>SINFRUG00000123133 hs-mir-9   1622   1629

UCUUUGGUUAUCUAGCUGUAUGA&AUGUUCACAGGUGGAGCCCUGAUGAAGUUAGAUGGACCAAAGU

.((((((((((((((((.(((.(&...................).))).)))))))).)))))))). -23.20



miRNA: mir-9

Human predicted target: ENSG00000157978

Mouse predicted target: ENSMUSG00000037295

Rat predicted target: ENSRNOG00000000151

Fugu predicted target: SINFRUG00000138412

Hs Gene description: LDL RECEPTOR ADAPTOR PROTEIN.
[Source:RefSeq;Acc:NM_015627] NM_015627

mir-9     ENSG00000157978     3898 nt UTR    4 hits 45 355 588 2637

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>ENSG00000157978 hs-mir-9     45     52
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UCUUUGGUUAUCUAGCUGUAUGA&GCCAGCCGGACACAAGCGGCCCUGACACGUGAUGGACCAAAGC

.(((((((((((..(((((.((.&............)).)))))..........))).)))))))). -20.40

>ENSG00000157978 hs-mir-9    355    362

UCUUUGGUUAUCUAGCUGUAUGA&CAAGCUCUGCCCUGGCUGUGGGUAUCAGGACUGUGACCAAAGC

.((((((((((....((((((..&.....................))).)))....)))))))))). -18.60

>ENSG00000157978 hs-mir-9    588    595

UCUUUGGUUAUCUAGCUGUAUGA&ACCCCAGGCUCUUAGAGACUAAGGGGCAGCUCCUGACCAAAGAC

((((((((((...((((((....&.........................))))))..)))))))))). -
25.30

>ENSG00000157978 hs-mir-9   2637   2644

UCUUUGGUUAUCUAGCUGUAUGA&UUGGUAGAACACUUGUGCAUUCAGGUUAUCUCAGAACCAAAGGC

(((((((((...(((((..(((.&.................)))...)))))......))))))))). -
18.80

mir-9     ENSMUSG00000037295  3630 nt UTR    4 hits 294 462 791 906

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>ENSMUSG00000037295 hs-mir-9    294    301

UCUUUGGUUAUCUAGCUGUAUGA&CAGUGCCCCCUCCUGCUGUGGGCGUCAGGACAAUGACCAAAGC

.((((((((((....(((.(((.&......................))))))....)))))))))). -19.30

>ENSMUSG00000037295 hs-mir-9    462    469

UCUUUGGUUAUCUAGCUGUAUGA&CCGAGUAACUGAGGCUCUCAGAGAGGCAGCCCCUGACCAAAGAC

((((((((((....(((((.(((&.................))).....)))))...)))))))))). -
23.80

>ENSMUSG00000037295 hs-mir-9    791    798

UCUUUGGUUAUCUAGCUGUAUGA&UCCAUUUUCUGCUUCCCCACAAUUCCUGGGAUGAUACCAAAGC

.(((((((((((((((.(.(((.&..)))...).)))...............)))))..))))))). -16.16
```

```
>ENSMUSG00000037295 hs-mir-9    906    913

UCUUUGGUUAUCUAGCUGUAUGA&GAGGGGUGGAGUUGAGAACAGAACCCAGAUCUGAUACCAAAGC

.(((((((.(((...(((.....&.........................)))....)))))))))). -17.20

mir-9     ENSRNOG00000000151  2000 nt UTR    3 hits 310 478 917

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>ENSRNOG00000000151 hs-mir-9    310    317

UCUUUGGUUAUCUAGCUGUAUGA&GAGCCAGUAUCCCCGCUGUGGGUGUCCAGACAAUGACCAAAGU

.((((((((((....(((.....&..........................)))...)))))))))). -18.40

>ENSRNOG00000000151 hs-mir-9    478    485

UCUUUGGUUAUCUAGCUGUAUGA&CUGAGAAGCUGAGGCUUUCAAAGAGGCAGCCCCUGACCAAAGAC

((((((((((....(((((.(((&.................))).....)))))...)))))))))). -
22.80

>ENSRNOG00000000151 hs-mir-9    917    924

UCUUUGGUUAUCUAGCUGUAUGA&GGGCGGUGGAGUUGAGAAUAGAACCCAGAUCUGAUACCAAAGC

.(((((((.(((...(((.....&.........................)))....)))))))))). -17.20

mir-9     SINFRUG00000138412  2000 nt UTR    1 hits 1856

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1-----

>SINFRUG00000138412 hs-mir-9   1856   1863

UCUUUGGUUAUCUAGCUGUAUGA&CAGCGCUCCCGCUAGCAGGGCCAAACAGCCGACGAACCAAAGAC

(((((((((.....(((((.((.&.....................)).))))).....))))))))). -
24.30




miRNA: mir-18
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Human predicted target: ENSG00000137104

Mouse predicted target: ENSMUSG00000036073

Rat predicted target: ENSRNOG00000014766

Fugu predicted target: SINFRUG00000126591

Hs Gene description: GALACTOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC
2.7.7.10). [Source:SWISSPROT;Acc:P07902]     NM_147132

mir-18    ENSG00000137104     2000 nt UTR    1 hits 1437

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>ENSG00000137104 hs-mir-18   1437   1444

UAAGGUGCAUCUAGUGCAGAUA&GCCCUCCUUCUUCUUUAUCUUAUCUGGAGUCAGGGGCACCUUC

.(((((((..(((.(.((((((&....................)))))).).).))..))))))). -24.10

mir-18    ENSMUSG00000036073  2000 nt UTR    1 hits 1534

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>ENSMUSG00000036073 hs-mir-18   1534   1541

UAAGGUGCAUCUAGUGCAGAUA&AACCCCCUGGCUCCCUAUCUUAUCUGGAGUCAGGGGCACCUUC

.(((((((..(((.(.((((((&....................)))))).).).))..))))))). -24.10

mir-18    ENSRNOG00000014766  2000 nt UTR    1 hits 1591

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>ENSRNOG00000014766 hs-mir-18   1591   1598

UAAGGUGCAUCUAGUGCAGAUA&CCAACCACUGCCCCCUAUCUUAUCUGGAGUCAGGGGCACCUUC

.(((((((..(((.(.((((((&....................)))))).).).))..))))))). -24.10

mir-18    SINFRUG00000126591  2000 nt UTR    1 hits 975
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>SINFRUG00000126591 hs-mir-18    975    982

UAAGGUGCAUCUAGUGCAGAUA&GACGUCCCCCAGGAAGGCCAACUCUCAGCACUGCAGCACCUUC

.(((((((...((((((.((..&........................)).))))))..))))))). -23.10




miRNA: mir-18

Human predicted target: ENSG00000146830

Mouse predicted target: ENSMUSG00000029714

Rat predicted target: ENSRNOG00000001410

Fugu predicted target: SINFRUG00000150734

Hs Gene description: PERQ AMINO ACID RICH WITH GYF DOMAIN PROTEIN 1.
[Source:SWISSPROT;Acc:O75420] NM_022574

mir-18    ENSG00000146830     3237 nt UTR    1 hits 143

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>ENSG00000146830 hs-mir-18    143    150

UAAGGUGCAUCUAGUGCAGAUA&GGCGGGGUCCCCAGCACUUGUUACAAACACACGAUGCACCUUAA

(((((((((((.(((((.....&.............)))))..............))))))))))). -26.96

mir-18    ENSMUSG00000029714  2368 nt UTR    1 hits 161

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>ENSMUSG00000029714 hs-mir-18    161    168

UAAGGUGCAUCUAGUGCAGAUA&GCAGGGUCCCCAGCACUUGUUACAAACCACACGAUGCACCUUAA

(((((((((((.(((((.....&............)))))...............))))))))))). -26.89
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mir-18    ENSRNOG00000001410  2000 nt UTR    1 hits 150

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>ENSRNOG00000001410 hs-mir-18    150    157

UAAGGUGCAUCUAGUGCAGAUA&GCAGGGUCCCCAGCACUUGUUACAAACCACACGAUGCACCUUAA

(((((((((((.(((((.....&............)))))...............))))))))))). -26.89

mir-18    SINFRUG00000150734  2000 nt UTR    1 hits 1570

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>SINFRUG00000150734 hs-mir-18   1570   1577

UAAGGUGCAUCUAGUGCAGAUA&GGAAGAUGGGUAUCCUCUGGCACUCAAAAGAUUAAGCACCUUAC

((((((((((((((((((((..&...............)))).))))....))))...)))))))). -25.40




miRNA: mir-19a

Human predicted target: ENSG00000069345

Mouse predicted target: ENSMUSG00000031701

Rat predicted target: ENSRNOG00000016251

Fugu predicted target: SINFRUG00000132559

Hs Gene description: DNAJ HOMOLOG SUBFAMILY A MEMBER 2 (HIRA INTERACTING
PROTEIN 4) (CELL CYCLE PROGRESSION RESTORATION GENE 3 PROTEIN) (DNJ3).
[Source:SWISSPROT;Acc:O60884] NM_005880

mir-19a   ENSG00000069345     2646 nt UTR    1 hits 471

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>ENSG00000069345 hs-mir-19a    471    478

UGUGCAAAUCUAUGCAAAACUGA&GUAUCUAUCAUUUAGAUGCAUGGAAAAAAAUGGGCUUUGCACAC
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((((((((((((((((...((((&...........)))).))))))))...........)))))))). -
22.60

mir-19a   ENSMUSG00000031701  3576 nt UTR    1 hits 446

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>ENSMUSG00000031701 hs-mir-19a    446    453

UGUGCAAAUCUAUGCAAAACUGA&CUGUAUCUAUCAUUUAGAUGCAUGGAAAAAUGGGCUUUGCACAC

((((((((((((((((...((((&.............)))).)))))))).........)))))))). -
22.80

mir-19a   ENSRNOG00000016251  3498 nt UTR    1 hits 445

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>ENSRNOG00000016251 hs-mir-19a    445    452

UGUGCAAAUCUAUGCAAAACUGA&CCUGUAUCUAUCAUUAGAUGCAUGGAAAACUGGGCUUUGCACAC

((((((((((((((((...((((&.............)))).)))))))).........)))))))). -
22.90

mir-19a   SINFRUG00000132559  2000 nt UTR    1 hits 209

--------1-----------------------------------------------------------------
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>SINFRUG00000132559 hs-mir-19a    209    216

UGUGCAAAUCUAUGCAAAACUGA&UGAGAAACUCGCACGGGGACAGCCAGAUGCAAGGUUUUGCACU

.(((((((.((.((((...(((.&.......................))).)))).)).))))))). -22.00



miRNA: mir-19a

Human predicted target: ENSG00000081479

Mouse predicted target: ENSMUSG00000027069
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Rat predicted target: ENSRNOG00000006837

Fugu predicted target: SINFRUG00000140256

Hs Gene description: LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2
PRECURSOR (MEGALIN) (GLYCOPROTEIN 330) (GP330).
[Source:SWISSPROT;Acc:P98164]

mir-19a   ENSG00000081479     2000 nt UTR    2 hits 38 209

-1------1-----------------------------------------------------------------
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>ENSG00000081479 hs-mir-19a     38     45

UGUGCAAAUCUAUGCAAAACUGA&AUACCAGCUAUUUAGGGAAUAAUUAGAAACACACUUUUGCACAU

((((((((((((.......((((&...........))))........))))........)))))))). -
15.66

>ENSG00000081479 hs-mir-19a    209    216

UGUGCAAAUCUAUGCAAAACUGA&UACAAAUAAUUAUCACAAUGUACUAUAUGUAUAUCUUUGCACU

.(((((((..((((((.......&...........................))))))..))))))). -19.20

mir-19a   ENSMUSG00000027069  2094 nt UTR    2 hits 38 1972

-1------------------------------------------------------------------------
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>ENSMUSG00000027069 hs-mir-19a     38     45

UGUGCAAAUCUAUGCAAAACUGA&UUGCCAACUCUCUAGGGAACAUUUAGACACUCACUUUUGCACAU

((((((((((((.......(((.&............)))........))))........)))))))). -
15.06

>ENSMUSG00000027069 hs-mir-19a   1972   1979

UGUGCAAAUCUAUGCAAAACUGA&GAACAUUCUUGUUUCAGAAAAAGGUGAAGAGCUCCUUUGCACAG

(((((((((((.(((....((((&.............))))......))).))).....)))))))). -
17.90

mir-19a   ENSRNOG00000006837  2097 nt UTR    3 hits 41 673 1690
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-1------------------------1----------------------------------------1------
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>ENSRNOG00000006837 hs-mir-19a     41     48

UGUGCAAAUCUAUGCAAAACUGA&UCGCCAGCUCUCUAGGGAACAUUUAGACACUCACUUUUGCACAU

((((((((((((.......(((.&............)))........))))........)))))))). -
15.06

>ENSRNOG00000006837 hs-mir-19a    673    680

UGUGCAAAUCUAUGCAAAACUGA&UUGAUUGUGCUUCGUCCCUAGUUGCCAAGUCAACAUUUGCACC

.((((((((((..(((..((((.&..................)))))))..)).....)))))))). -15.80

>ENSRNOG00000006837 hs-mir-19a   1690   1697

UGUGCAAAUCUAUGCAAAACUGA&GAACAUUCUUGUUUCAGAAAAAGGUGGAGAGUCCCUUUGCACAA

(((((((((((((......((((&.............))))......))))).......)))))))). -
18.21

mir-19a   SINFRUG00000140256  2000 nt UTR    2 hits 46 223

-1------1-----------------------------------------------------------------
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>SINFRUG00000140256 hs-mir-19a     46     53

UGUGCAAAUCUAUGCAAAACUGA&GCCAGAGACGGGAAUCGAAAGCAGAAGAGACACACUUUGCACAG

(((((((((((.(((........&....................)))....))).....)))))))). -
18.40

>SINFRUG00000140256 hs-mir-19a    223    230

UGUGCAAAUCUAUGCAAAACUGA&UGUUUUCUAUUACUCUGAUGUACUAUGUGUAUAUCUUUGCACU

.(((((((..((((((.......&...........................))))))..))))))). -19.10
```

miRNA: mir-19a

Human predicted target: ENSG00000113300

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Mouse predicted target: ENSMUSG00000020362

Rat predicted target: ENSRNOG00000002803

Fugu predicted target: SINFRUG00000136719

Hs Gene description: KIAA1194. [Source:RefSeq;Acc:NM_015455]     NM_015455

mir-19a   ENSG0000113300      2000 nt UTR    2 hits 219 615

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>ENSG0000113300 hs-mir-19a    219    226

UGUGCAAAUCUAUGCAAAACUGA&AAUAUGCUUUAUACUGCUAGACAGGGAUUGGUGUGUUUGCACC

.((((((((.(((.(((..(((.&.....................)))...)))))).)))))))). -19.10

>ENSG0000113300 hs-mir-19a    615    622

UGUGCAAAUCUAUGCAAAACUGA&UAAAAGAAGCUGCAACAGACUUUCUCUGCUCAUGAUUUGCACU

.(((((((((...(((.......&..........................)))....))))))))). -20.90

mir-19a   ENSMUSG00000020362  5687 nt UTR    2 hits 309 607

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>ENSMUSG00000020362 hs-mir-19a    309    316

UGUGCAAAUCUAUGCAAAACUGA&GCCUUGAAAUAGGAAGAUGUGUGAGCAGUGUGCUGUUUGCACAG

(((((((((....(((..((((.&.........................)))).))).))))))))). -
22.10

>ENSMUSG00000020362 hs-mir-19a    607    614

UGUGCAAAUCUAUGCAAAACUGA&GGUAACAAAGCUGCAUCCGACUUUCUCUGCAGUGAUUUGCACU

.(((((((((..((((.......&...........................))))..))))))))). -22.50

mir-19a   ENSRNOG00000002803  2000 nt UTR    2 hits 319 611
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>ENSRNOG00000002803 hs-mir-19a    319    326

UGUGCAAAUCUAUGCAAAACUGA&UGCCUUGAAAUAGGAAGAUGUGUGAACAGUGUGUGUUUGCACAG

(((((((((....(((..((((.&..........................)))).)))))))))))). -
20.20

>ENSRNOG00000002803 hs-mir-19a    611    618

UGUGCAAAUCUAUGCAAAACUGA&GGUAACAAAGUUGCAUCAGACUUUCUCUGCAGUGAUUUGCACU

.(((((((((..(((((((((((&...............))))..)))...))))..))))))))). -22.80

mir-19a   SINFRUG00000136719  2000 nt UTR    2 hits 196 1751

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>SINFRUG00000136719 hs-mir-19a    196    203

UGUGCAAAUCUAUGCAAAACUGA&CCCUUUCUUUGCUCCUUUUUUGGGUUUUUUUUUUUUUUGCACAC

((((((((.......((((((..&.......................))))))......)))))))). -
17.32

>SINFRUG00000136719 hs-mir-19a   1751   1758

UGUGCAAAUCUAUGCAAAACUGA&UUUCCUGGCCCGGACGGGUAGCAUCGCUCGCUUCGUUUGCACAU

((((((((((.((((....(((.&..............)))...)))).)........))))))))). -
19.00
```

```
miRNA: mir-19a

Human predicted target: ENSG00000164463

Mouse predicted target: ENSMUSG00000048249

Rat predicted target: ENSRNOG00000020769

Fugu predicted target: SINFRUG00000139862
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Hs Gene description: ADULT RETINA PROTEIN. [Source:RefSeq;Acc:NM_153607]
     NM_153607

mir-19a   ENSG00000164463     5222 nt UTR    2 hits 959 4350

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>ENSG00000164463 hs-mir-19a    959    966

UGUGCAAAUCUAUGCAAAACUGA&CAACUGAUAUGGCAAACUGCCAGUCUAAGUAAAGUUUUGCACAG

((((((((.((.(((...((((.&....................))))....))).)).)))))))). -
21.30

>ENSG00000164463 hs-mir-19a   4350   4357

UGUGCAAAUCUAUGCAAAACUGA&ACCAUUUCCCAUGGAACUGAGGCCAUUUCCACAACUUUGCACAG

((((((((((((((.........&.........))))))....................)))))))). -
16.75

mir-19a   ENSMUSG00000048249  2000 nt UTR    1 hits 991

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>ENSMUSG00000048249 hs-mir-19a    991    998

UGUGCAAAUCUAUGCAAAACUGA&CAACUGGUAUGGCAGACUGCCAGUCUAAGUAAAGUUUUGCACAG

((((((((.((.(((...((((.&....................))))....))).)).)))))))). -
21.30

mir-19a   ENSRNOG00000020769  3521 nt UTR    2 hits 999 2340

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>ENSRNOG00000020769 hs-mir-19a    999   1006

UGUGCAAAUCUAUGCAAAACUGA&CAACUGGUAUGGCAGACUGCCAGUCUAAGUAAAGUUUUGCACAG

((((((((.((.(((...((((.&....................))))....))).)).)))))))). -
21.30
```

```
>ENSRNOG00000020769 hs-mir-19a   2340   2347

UGUGCAAAUCUAUGCAAAACUGA&CAACUGGUAUGGCAGACUGCCAGUCUAAGUAAAGUUUUGCACAG

((((((((.((.(((...((((.&....................))))....))).)).)))))))). -
21.30

mir-19a   SINFRUG00000139862  2000 nt UTR    2 hits 1514 1592

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>SINFRUG00000139862 hs-mir-19a   1514   1521

UGUGCAAAUCUAUGCAAAACUGA&AGAUAUAUUUGUUUAAAGUUACAGAAAAAAAAAUAUUUGCACAC

(((((((((..........(((.&.....................)))..........))))))))). -
16.65

>SINFRUG00000139862 hs-mir-19a   1592   1599

UGUGCAAAUCUAUGCAAAACUGA&GCAACGAAAUGGCGACCAGCCAGUUAAAGUAAGGUUUUGCACAG

((((((((.((.(((..(((((.&....................)))))...))).)).)))))))). -
22.60




miRNA: mir-19a

Human predicted target: ENSG00000171150

Mouse predicted target: ENSMUSG00000037104

Rat predicted target: ENSRNOG00000015163

Rat predicted target: ENSRNOG00000015169

Fugu predicted target: SINFRUG00000141543

Hs Gene description: CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN 5
(SUPPRESSOR OF CYTOKINE SIGNALING 5) (SOCS-5) (CYTOKINE-INDUCIBLE SH2
PROTEIN 6) (CIS-6). [Source:SWISSPROT;Acc:O75159] NM_014011

mir-19a   ENSG00000171150     4640 nt UTR    1 hits 1212
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>ENSG00000171150 hs-mir-19a   1212   1219

UGUGCAAAUCUAUGCAAAACUGA&UAACUGAACUGAAUUUACAGUUCUGUCCUAGACAUUUUGCACU

.(((((((((((.(((.(((((.&.................))))).)))..))))...))))))). -22.50

mir-19a   ENSMUSG00000037104  2000 nt UTR    1 hits 1132

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>ENSMUSG00000037104 hs-mir-19a   1132   1139

UGUGCAAAUCUAUGCAAAACUGA&CGUGUUGGACUGUGUUCCCGGUUCUGUCCUAGCCAUUUGCACU

.(((((((((((.(((.(((((.&..................))))).)))..)))..)))))))). -21.20

mir-19a   ENSRNOG00000015163  2000 nt UTR    1 hits 1109

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>ENSRNOG00000015163 hs-mir-19a   1109   1116

UGUGCAAAUCUAUGCAAAACUGA&AGUGUUGGACUGUGUUCUCAGUUUUGUCCUAGACCUUUGCACU

.(((((((((((.((((((((((&.................))))))))))..))))..))))))). -26.80

mir-19a   ENSRNOG00000015169  2000 nt UTR    1 hits 1109

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>ENSRNOG00000015169 hs-mir-19a   1109   1116

UGUGCAAAUCUAUGCAAAACUGA&AGUGUUGGACUGUGUUCUCAGUUUUGUCCUAGACCUUUGCACU

.(((((((((((.((((((((((&.................))))))))))..))))..))))))). -26.80

mir-19a   SINFRUG00000141543  2000 nt UTR    1 hits 559

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>SINFRUG00000141543 hs-mir-19a    559    566

UGUGCAAAUCUAUGCAAAACUGA&GACGGCGCUACACCAGGCACAGUCGUUGCUCUCUUUUUGCACAC

((((((((.....((((.((((.&...................))))..))))......)))))))). -
22.60




miRNA: mir-20

Human predicted target: ENSG00000109189

Mouse predicted target: ENSMUSG00000048255

Rat predicted target: ENSRNOG00000002106

Fugu predicted target: SINFRUG00000123610

Hs Gene description: NM_022832

mir-20    ENSG00000109189     4611 nt UTR    3 hits 1488 1789 3367

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>ENSG00000109189 hs-mir-20   1488   1495

UAAAGUGCUUAUAGUGCAGGUAG&AUGUUAGUGGCCAUUUUGCAACAAUGAAGAGGAUAGCACUUUAU

(((((((((.....(((((((..&.........)))....))))..............))))))))). -
19.21

>ENSG00000109189 hs-mir-20   1789   1796

UAAAGUGCUUAUAGUGCAGGUAG&CUGGAAGGUGAGUUUUGAUCUCUUUUUAAGGAGAGGCACUUUC

.((((((((..............&..................................)))))))). -14.70

>ENSG00000109189 hs-mir-20   3367   3374

UAAAGUGCUUAUAGUGCAGGUAG&CUGUACCUUAAUUUUUUAAAAUGUAACCAAUUCAAGCACUUUAA

((((((((((...((((((....&))))))...........................)))))))))). -
20.01
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mir-20    ENSMUSG00000048255  3996 nt UTR    2 hits 1538 1839

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>ENSMUSG00000048255 hs-mir-20   1538   1545

UAAAGUGCUUAUAGUGCAGGUAG&UCAUCAGUGGCCAUCGUGCAGCAGUGAAGAGGAUAGCACUUUAU

(((((((((((.(((((((((..&.........)))....)))).).)))........))))))))). -
19.00

>ENSMUSG00000048255 hs-mir-20   1839   1846

UAAAGUGCUUAUAGUGCAGGUAG&UACAUGGAUGGUGAACCUUCAUUCUUUAAGGAGAGGCACUUUU

.(((((((((..((((.((((..&..............)))).))))...........))))))))). -19.20

mir-20    ENSRNOG00000002106  3862 nt UTR    2 hits 1404 1704

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>ENSRNOG00000002106 hs-mir-20   1404   1411

UAAAGUGCUUAUAGUGCAGGUAG&AUGUCAGUGGCCAUUUUGCAGCAACGAAGAGGAUAGCACUUUAU

(((((((((.....(((((((..&.........)))....))))..............))))))))). -
18.11

>ENSRNOG00000002106 hs-mir-20   1704   1711

UAAAGUGCUUAUAGUGCAGGUAG&UACGUUGGAGGUGAACCUUCAUUCUUCGAGGAGAGGCACUUUU

.(((((((((..((((.((((..&..............)))).))))...........))))))))). -19.20

mir-20    SINFRUG00000123610  2000 nt UTR    2 hits 129 1490

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>SINFRUG00000123610 hs-mir-20    129    136

UAAAGUGCUUAUAGUGCAGGUAG&UGUCCUCUUGCCUUUCUGUCACCUGCAUCUGGACUGCACUUUAA
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((((((((...((((((((((..&....................))))))).)))....)))))))). -
28.80

>SINFRUG00000123610 hs-mir-20   1490   1497

UAAAGUGCUUAUAGUGCAGGUAG&GAGAGCUGCAGUCUGGUGGGCUGUGACCUACGGGGGCACUUUAA

(((((((((((((((.((.((((&.....))))......)).)))))..........)))))))))). -
21.00




miRNA: mir-20

Human predicted target: ENSG00000134323

Mouse predicted target: ENSMUSG00000037169

Rat predicted target: ENSRNOG00000006308

Fugu predicted target: SINFRUG00000128278

Hs Gene description: N-MYC PROTO-ONCOGENE PROTEIN.
[Source:SWISSPROT;Acc:P04198]

mir-20    ENSG00000134323     2907 nt UTR    1 hits 859

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>ENSG00000134323 hs-mir-20    859    866

UAAAGUGCUUAUAGUGCAGGUAG&CUUCAAAAUGUAUAUAUUUAGUGCUGCAUCUUAUAGCACUUUGA

(((((((((((..((((((....&.......................))))))..)).))))))))). -
24.80

mir-20    ENSMUSG00000037169  2911 nt UTR    1 hits 861

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>ENSMUSG00000037169 hs-mir-20    861    868

UAAAGUGCUUAUAGUGCAGGUAG&CUUCAAAAUGUAUAUAUUUAGUGCUGCACCUUAGAGCACUUUGA
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((((((((((...((((((....&.......................))))))....)))))))))). -
26.30

mir-20    ENSRNOG00000006308  2915 nt UTR    3 hits 864 1794 2048

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>ENSRNOG00000006308 hs-mir-20    864    871

UAAAGUGCUUAUAGUGCAGGUAG&UCAAAAUGUGUAUAUUUAGUGCUGCACCUUAGAGCACUUUGA

((((((((((...((((((....&.......................))))))....)))))))))). -
26.30

>ENSRNOG00000006308 hs-mir-20   1794   1801

UAAAGUGCUUAUAGUGCAGGUAG&UCAAAAUGUGUAUAUUUAGUGCUGCACCUUAGAGCACUUUGA

((((((((((...((((((....&.......................))))))....)))))))))). -
26.30

>ENSRNOG00000006308 hs-mir-20   2048   2055

UAAAGUGCUUAUAGUGCAGGUAG&AGCUAUUUCAAUAGGAAUUCAAUGGGUGGUAAAAGCACUUUU

.(((((((((.((.(((..((..&......................))..))).)).))))))))). -18.10

mir-20    SINFRUG00000128278  2000 nt UTR    2 hits 509 1268

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>SINFRUG00000128278 hs-mir-20    509    516

UAAAGUGCUUAUAGUGCAGGUAG&CACCAGCCUGGAAAUCAGGGACAGGGUGUCAGAGGGCACUUUGC

((((((((((....(.(((((..&.....))))).).....................)))))))))). -
19.91

>SINFRUG00000128278 hs-mir-20   1268   1275

UAAAGUGCUUAUAGUGCAGGUAG&ACUUUUAAAAUGUACAUUUAGUGCUGCAACUCAUAGCACUUUU

.((((((((...(((((((....&.......................))))).))...)))))))). -22.50
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miRNA: mir-23a

Human predicted target: ENSG00000104725

Mouse predicted target: ENSMUSG00000022055

Rat predicted target: ENSRNOG00000013658

Fugu predicted target: SINFRUG00000121670

Hs Gene description: NEUROFILAMENT TRIPLET L PROTEIN (68 KDA NEUROFILAMENT
PROTEIN) (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L).
[Source:SWISSPROT;Acc:P07196]

mir-23a   ENSG00000104725     3852 nt UTR    1 hits 264

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>ENSG00000104725 hs-mir-23a    264    271

AUCACAUUGCCAGGGAUUUCC&GCAUGGACCACGCUUAUGAGUUCAGGAUCUACGGCAAUGUGAA

.((((((((((..((((((..&........................))))))..)))))))))). -26.20

mir-23a   ENSMUSG00000022055  2327 nt UTR    1 hits 256

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>ENSMUSG00000022055 hs-mir-23a    256    263

AUCACAUUGCCAGGGAUUUCC&GCAUGGUCCAUGCUUAUGAGUUCAGGAUCUAUGGCAAUGUGAA

.(((((((((((.((((((..&........................)))))).))))))))))). -27.90

mir-23a   ENSRNOG00000013658  2335 nt UTR    1 hits 262

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>ENSRNOG00000013658 hs-mir-23a    262    269

AUCACAUUGCCAGGGAUUUCC&GCAUGGUCCAUGCUUAUGAGUUCAGGAUCUACGGCAAUGUGAA
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.((((((((((..((((((..&........................))))))..)))))))))). -26.20

mir-23a   SINFRUG00000121670  2000 nt UTR    1 hits 1308

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>SINFRUG00000121670 hs-mir-23a   1308   1315

AUCACAUUGCCAGGGAUUUCC&GAGGGGGAAGAGCUGCAAUCCUAUUGUUUUAUGGUAAUGUGAUU

(((((((((((((((((((((&.....))))........)))))).........)))))))))))). -24.40



miRNA: mir-23a

Human predicted target: ENSG00000137942

Mouse predicted target: ENSMUSG00000039735

Rat predicted target: ENSRNOG00000013798

Fugu predicted target: SINFRUG00000120809

Hs Gene description: NM_017737

mir-23a   ENSG00000137942     4245 nt UTR    3 hits 1740 1829 2769

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>ENSG00000137942 hs-mir-23a   1740   1747

AUCACAUUGCCAGGGAUUUCC&UUAGAUAUUGAAUCUCGUUACAGGGUUAUUUAUAUAAUGUGAC

.((((((((((.(((((((..&.........))))))).......)).........)))))))). -16.10

>ENSG00000137942 hs-mir-23a   1829   1836

AUCACAUUGCCAGGGAUUUCC&GCUAUUUUUAUUUUAAAGGUUAGCAAUGAGGAGGAAAUGUGAUC

((((((((.((.......(((&.............................))))).)))))))). -14.51

>ENSG00000137942 hs-mir-23a   2769   2776
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AUCACAUUGCCAGGGAUUUCC&UCUAAUUUCAGAAGAUUCACCUUUUAAAAAAUGCAAAUGUGAA

.(((((((((.(((((((((.&..........))))..)).)))..........)).))))))). -15.20

mir-23a   ENSMUSG00000039735  5380 nt UTR    5 hits 1902 2621 2876 2965
3441

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>ENSMUSG00000039735 hs-mir-23a   1902   1909

AUCACAUUGCCAGGGAUUUCC&UCUGCUCUAGCCUGCAGCCCAGUUACCGACUCUGAAAUGUGAC

.(((((((..(((((......&.............................))))).))))))). -19.10

>ENSMUSG00000039735 hs-mir-23a   2621   2628

AUCACAUUGCCAGGGAUUUCC&CGUUUGGUUCUUUACUGUUGUGAGGGGAGAAAGAGAAUGUGAA

.(((((((..(.....(..((&.......................))..)....)..))))))). -14.70

>ENSMUSG00000039735 hs-mir-23a   2876   2883

AUCACAUUGCCAGGGAUUUCC&UUAGAUAUUAAAUCUCGUUACAGGGUUAUUUAUAUAAUGUGAC

.((((((((((.(((((((..&.........))))))).......)).........)))))))). -15.70

>ENSMUSG00000039735 hs-mir-23a   2965   2972

AUCACAUUGCCAGGGAUUUCC&GCUAUUUUUAUUUCAAAAGUUAGCAAUGAGAAGGAAAUGUGAC

.(((((((.((..........&................................)).))))))). -15.20

>ENSMUSG00000039735 hs-mir-23a   3441   3448

AUCACAUUGCCAGGGAUUUCC&CUGCUGCUGGAACCAAAGAGACUCGGAGCACCUUAAAUGUGAUA

((((((((...(((...((((&........................))))..)))..)))))))). -19.60

mir-23a   ENSRNOG00000013798  5105 nt UTR    5 hits 1674 2358 2612 2701
4695

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>ENSRNOG00000013798 hs-mir-23a   1674   1681

AUCACAUUGCCAGGGAUUUCC&UGCUCUAGCCUGCAGCCCAGUUAAAGACUCUGUGAAAUGUGAC

.(((((((.((((((......&...........................))))).).))))))). -18.90

>ENSRNOG00000013798 hs-mir-23a   2358   2365

AUCACAUUGCCAGGGAUUUCC&AAUUUGGUUCUUUACUGUUUUGGGGGGAGAAGAACAAUGUGAA

.((((((((.......(..((&.......................))..)......)))))))). -17.42

>ENSRNOG00000013798 hs-mir-23a   2612   2619

AUCACAUUGCCAGGGAUUUCC&UUAGAUAUUAAAUCUCGUUACAGGGUUAUUUAUAUAAUGUGAC

.((((((((((.(((((((..&.........))))))).......)).........)))))))). -15.70

>ENSRNOG00000013798 hs-mir-23a   2701   2708

AUCACAUUGCCAGGGAUUUCC&GCUAUUUUUAUUUCAGAAGUUAGCAAUGAGAAGGAAAUGUGAC

.(((((((.((...((((((.&...............))))))...........)).))))))). -15.44

>ENSRNOG00000013798 hs-mir-23a   4695   4702

AUCACAUUGCCAGGGAUUUCC&UGCUCUAGCCUGCAGCCCAGUUAAAGACUCUGUGAAAUGUGAC

.(((((((.((((((......&...........................))))).).))))))). -18.90

mir-23a   SINFRUG00000120809  2000 nt UTR    1 hits 979

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>SINFRUG00000120809 hs-mir-23a    979    986

AUCACAUUGCCAGGGAUUUCC&UUGUGGAAAUCUAAAAACAAACUUGGGAAACCCUGAAUGUGAG

.(((((((..(((((.(((((&.........................))))))))))))))))). -24.80



miRNA: mir-23a
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Human predicted target: ENSG00000151615

Mouse predicted target: ENSMUSG00000031688

Rat predicted target: ENSRNOG00000012167

Fugu predicted target: SINFRUG00000126552

Hs Gene description: POU DOMAIN, CLASS 4, TRANSCRIPTION FACTOR 2 (BRAIN-
SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 3B) (BRN-3B).
[Source:SWISSPROT;Acc:Q12837] NM_004575

mir-23a   ENSG00000151615     3663 nt UTR    4 hits 102 173 463 1665

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>ENSG00000151615 hs-mir-23a    102    109

AUCACAUUGCCAGGGAUUUCC&CUUUUCACUUUUGGCGACUAGAAACAAUUCCAGUAAAUGUGAA

.(((((((....((((((...&.........................))))))....))))))). -17.50

>ENSG00000151615 hs-mir-23a    173    180

AUCACAUUGCCAGGGAUUUCC&GCGAACGAGCGAACAACUGAGCCCAAGCCGGUGAGAAUGUGAA

.((((((((((.(((.(((..&..................)))))).....)))...))))))). -16.00

>ENSG00000151615 hs-mir-23a    463    470

AUCACAUUGCCAGGGAUUUCC&UUCAGGACUAAAACUUUAAACUAGAGUUGAUGCUUAAUGUGAUA

(((((((((.((..(((((..&.......................)))))..))..))))))))). -15.80

>ENSG00000151615 hs-mir-23a   1665   1672

AUCACAUUGCCAGGGAUUUCC&AUUAAAAUAUGCUAUUAAAAUUAAAUGGCUUUUAAAAUGUGAUG

((((((((((((..(((((..&.................)))))...))))......)))))))). -18.60

mir-23a   ENSMUSG00000031688  2000 nt UTR    2 hits 113 490

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>ENSMUSG00000031688 hs-mir-23a    113    120
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```
AUCACAUUGCCAGGGAUUUCC&CUUUCUACUUUGGCUAUCAGAAAACAAUUCCGGUAAAUGUGAA

.((((((((((.((((((...&.........................))))))))).))))))). -21.00

>ENSMUSG00000031688 hs-mir-23a    490    497

AUCACAUUGCCAGGGAUUUCC&UUCAGGACUGAAACUCGAAGCUAGAGUUGAUGCUUAAUGUGAUA

(((((((((.((..(((((..&.......................)))))..))..))))))))). -15.80

mir-23a   ENSRNOG00000012167  3709 nt UTR    2 hits 114 489

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>ENSRNOG00000012167 hs-mir-23a    114    121

AUCACAUUGCCAGGGAUUUCC&UCUUUCUACUUUGGCUAUCAGAAACAAUUCCGGUAAAUGUGAA

.((((((((((.((((((...&.........................))))))))).))))))). -21.00

>ENSRNOG00000012167 hs-mir-23a    489    496

AUCACAUUGCCAGGGAUUUCC&UUCAGGACUGAAACUCGAAGCUAGAGUUGAUGCUUAAUGUGAC

.((((((((.((..(((((..&.......................)))))..))..)))))))). -14.80

mir-23a   SINFRUG00000126552  2000 nt UTR    2 hits 646 1730

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>SINFRUG00000126552 hs-mir-23a    646    653

AUCACAUUGCCAGGGAUUUCC&CUUUGCCCGUCACGCACGUCAUUUUGUGUCCAAAAAUGUGAUC

((((((((.....((((....&...........................))))...)))))))). -16.60

>SINFRUG00000126552 hs-mir-23a   1730   1737

AUCACAUUGCCAGGGAUUUCC&CCCGCUUGCACGCGUGGCCACUUUUUCAGACCUGAAAUGUGAG

.(((((((..((((..(....&...........................)..)))).))))))). -18.50
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miRNA: mir-24

Human predicted target: ENSG00000174151

Mouse predicted target: ENSMUSG00000050639

Rat predicted target: ENSRNOG00000019777

Fugu predicted target: SINFRUG00000125370

mir-24    ENSG00000174151     4596 nt UTR    4 hits 1364 1941 2867 4204

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>ENSG00000174151 hs-mir-24   1364   1371

UGGCUCAGUUCAGCAGGAACAG&GGAUCUCCCUAGAUCAUGGCAAGGCCUGACAACAGCUGAGCCAG

((((((((((...((((.....&........................)))).....)))))))))). -26.80

>ENSG00000174151 hs-mir-24   1941   1948

UGGCUCAGUUCAGCAGGAACAG&CUUGCUCUAAGAGCAAGCAGGCAAUGCCGUAAAGCCUGAGCCU

.((((((((((((((((.....&))))))....))).......................))))))). -20.64

>ENSG00000174151 hs-mir-24   2867   2874

UGGCUCAGUUCAGCAGGAACAG&CCCAAGCCCCGUCUUUUCUGUAACCACCCCUCCUCUGAGCCC

.(((((((....(((((((...&...............)))))))............))))))). -20.73

>ENSG00000174151 hs-mir-24   4204   4211

UGGCUCAGUUCAGCAGGAACAG&AGGUGGUAUUAUGUUCUUGUCCUUCUCUUUCACUGAGCCAG

(((((((((...(((((((((.&...........))))))))).........)))))))))). -28.24

mir-24    ENSMUSG00000050639  2942 nt UTR    3 hits 114 1727 2820

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>ENSMUSG00000050639 hs-mir-24    114    121
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UGGCUCAGUUCAGCAGGAACAG&CACUUCAGAAGUAGAUGAAUUUUUGCACUUCAUGGCUGAGCCAC

((((((((((..(((((((...&...................)))))))......)))))))))). -24.00

>ENSMUSG00000050639 hs-mir-24   1727   1734

UGGCUCAGUUCAGCAGGAACAG&CUUGUUCUCAGAGCACAGAGGCGAUGCCAGAAAGCCUGAGCCU

.(((((((((.(((((((((((&.)))))))................)))..)))...))))))). -23.09

>ENSMUSG00000050639 hs-mir-24   2820   2827

UGGCUCAGUUCAGCAGGAACAG&UUUAAACCUCGCUGUGGGAGAUCCAGGCAUCCUCCCUGAGCCAG

((((((((..(((((((.....&......))).)))).....................)))))))). -25.00

mir-24    ENSRNOG00000019777  2000 nt UTR    2 hits 112 1226

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>ENSRNOG00000019777 hs-mir-24    112    119

UGGCUCAGUUCAGCAGGAACAG&CACUUCAGAAGUAGAUGCAUUUUUGCACUUCAUGGCUGAGCCAC

((((((((((..(((((((...&...................)))))))......)))))))))). -24.00

>ENSRNOG00000019777 hs-mir-24   1226   1233

UGGCUCAGUUCAGCAGGAACAG&UGGGCCCUCUGGAUCCUAAUAAGGACUGAAGACUGCUGAGCCAG

((((((((((((((((((.(((&........)))..))))......).)))).....))))))))). -26.90

mir-24    SINFRUG00000125370  889 nt UTR     1 hits 356

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>SINFRUG00000125370 hs-mir-24    356    363

UGGCUCAGUUCAGCAGGAACAG&AGUCUGGAAAACAGAUUUAUUGUUGCUGUUUUGAGCUGAGCCC

.(((((((((((((((.(((((&...................))))).)))..))))))))))))). -31.90


miRNA: mir-24
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Human predicted target: ENSG00000179905

Mouse predicted target: ENSMUSG00000049932

Rat predicted target: ENSRNOG00000010386

Fugu predicted target: SINFRUG00000150234

Hs Gene description: HISTONE H2A.X (H2A/X). [Source:SWISSPROT;Acc:P16104]
     NM_002105

mir-24    ENSG00000179905     2000 nt UTR    2 hits 154 1037

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>ENSG00000179905 hs-mir-24    154    161

UGGCUCAGUUCAGCAGGAACAG&CCUUUUAAGGGCCACCACCGCCCUCAUGGAAAGAGCUGAGCCGC

(((((((((((..(..((....&.......................))...)...))))))))))). -23.80

>ENSG00000179905 hs-mir-24   1037   1044

UGGCUCAGUUCAGCAGGAACAG&AGAUACCAGCACAAGUCGGUUAAUCCCUGUCUGGACUGAGCCU

.((((((((((((((((.....&.........................)))).))))))))))))). -34.30

mir-24    ENSMUSG00000049932  2878 nt UTR    3 hits 85 766 1780

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>ENSMUSG00000049932 hs-mir-24     85     92

UGGCUCAGUUCAGCAGGAACAG&CCUUUUAAGGGCCACCACCUCCCUCACAGAAAGAGCUGAGCCAC

(((((((((((..((((.....&.....................)))....)...))))))))))). -24.50

>ENSMUSG00000049932 hs-mir-24    766    773

UGGCUCAGUUCAGCAGGAACAG&AGAUACCAGCACAAGCCGGUGAAUCCCUGUCUGGACUGAGCCU

.((((((((((((((((.....&.........................)))).))))))))))))). -34.30

>ENSMUSG00000049932 hs-mir-24   1780   1787
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UGGCUCAGUUCAGCAGGAACAG&CUGGAUGGUGGCCUGCAUAGUCUCUUGCAUGCUAUCUGAGCCAU

((((((((..((((((((....&......................)))))).))....)))))))). -26.70

mir-24    ENSRNOG00000010386  2000 nt UTR    3 hits 87 737 1772

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>ENSRNOG00000010386 hs-mir-24     87     94

UGGCUCAGUUCAGCAGGAACAG&CCUUUUAAGGGCCACCACCUCCCUCACAGAAAGAGCUGAGCCAC

(((((((((((..((((.....&.....................)))....)...))))))))))). -24.50

>ENSRNOG00000010386 hs-mir-24    737    744

UGGCUCAGUUCAGCAGGAACAG&AGAUACCAGCACAAGUCGGUGAAUCCCUGUCUGGACUGAGCCU

.((((((((((((((((.....&.........................)))).)))))))))))). -34.30

>ENSRNOG00000010386 hs-mir-24   1772   1779

UGGCUCAGUUCAGCAGGAACAG&CUGGAUGGUGGCCUGCAUGGUCUCUUGCAUGCUAUCUGAGCCAU

((((((((.((((((((.((..&.......))..))))).)))...............)))))))). -27.79

mir-24    SINFRUG00000150234  2000 nt UTR    2 hits 436 1228

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>SINFRUG00000150234 hs-mir-24    436    443

UGGCUCAGUUCAGCAGGAACAG&UUGCGGUUGAGGCCUACAUGAACACACCAACGGCUCUGAGCCC

.(((((((((((..(((..(((&......)))...)))...)))).............))))))). -19.91

>SINFRUG00000150234 hs-mir-24   1228   1235

UGGCUCAGUUCAGCAGGAACAG&UAGUGGCAAAAGCAGCAUGACACAUUGGGUUUGAACUGAGCCC

.((((((((((((.........&..............................)))))))))))). -24.60
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miRNA: mir-25

Human predicted target: ENSG00000099822

Mouse predicted target: ENSMUSG00000020331

Rat predicted target: ENSRNOG00000008831

Fugu predicted target: SINFRUG00000153577

Hs Gene description: POTASSIUM/SODIUM HYPERPOLARIZATION-ACTIVATED CYCLIC
NUCLEOTIDE-GATED CHANNEL 2 (BRAIN CYCLIC NUCLEOTIDE GATED CHANNEL 2)
(BCNG-2). [Source:SWISSPROT;Acc:Q9UL51] NM_001194

mir-25    ENSG00000099822     2000 nt UTR    1 hits 391

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>ENSG00000099822 hs-mir-25    391    398

CAUUGCACUUGUCUCGGUCUGA&UAGGUGGCCCCGUCCGAGGAGGAUCGUUUUCUAAGUGCAAUA

.((((((((((((((((.(...&............).))))))...........)))))))))). -24.10

mir-25    ENSMUSG00000020331  2462 nt UTR    1 hits 321

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>ENSMUSG00000020331 hs-mir-25    321    328

CAUUGCACUUGUCUCGGUCUGA&AUGUGCGGUGGCCUCCGAGGAAGAAUAUGGAUCAAGUGCAAUA

.((((((((((((((((.(((.&.....)))......))))))...........)))))))))). -25.00

mir-25    ENSRNOG00000008831  2009 nt UTR    1 hits 323

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>ENSRNOG00000008831 hs-mir-25    323    330

CAUUGCACUUGUCUCGGUCUGA&AUGUGCGGUGGCCUCCGAGGAAGAAUAUGGAUCAAGUGCAAUA

.((((((((((((((((.(((.&.....)))......))))))...........)))))))))). -25.00

mir-25    SINFRUG00000153577  2000 nt UTR    1 hits 1401
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>SINFRUG00000153577 hs-mir-25   1401   1408

CAUUGCACUUGUCUCGGUCUGA&GGAUCCCUGGCUGAGGUGGAGGUGCAUGUGAGCGAGUGCAAUU

.((((((((((((((((((...&.........))))))).................))))))))))). -26.29




miRNA: mir-25

Human predicted target: ENSG00000131459

Mouse predicted target: ENSMUSG00000020363

Rat predicted target: ENSRNOG00000002810

Fugu predicted target: SINFRUG00000147825

Hs Gene description: GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE
[ISOMERIZING] 2 (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE 2) (D-
FRUCTOSE-6- PHOSPHATE AMIDOTRANSFERASE 2) (GFAT 2) (GFAT2).
[Source:SWISSPROT;Acc:O94808] NM_005110

mir-25    ENSG00000131459     2874 nt UTR    1 hits 256

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>ENSG00000131459 hs-mir-25    256    263

CAUUGCACUUGUCUCGGUCUGA&UACACAUGGGGAUCAGAGCAGACUUCUCCACUACUGUGCAAUA

.(((((((..((((.(.(((((&............))))).)))))............))))))). -22.64

mir-25    ENSMUSG00000020363  2848 nt UTR    1 hits 250

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>ENSMUSG00000020363 hs-mir-25    250    257

CAUUGCACUUGUCUCGGUCUGA&UUACACAUGGGGAUCAGAGCAGACUUUCCACUACUGUGCAAUA
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.(((((((..((((.(.(((((&.............))))).)))))...........))))))). -22.72

mir-25    ENSRNOG00000002810  2000 nt UTR    1 hits 255

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>ENSRNOG00000002810 hs-mir-25    255    262

CAUUGCACUUGUCUCGGUCUGA&UUACACACGGGGAUGGGAGCAGACUUUCCACUACUGUGCAAUA

.(((((((..((...((((((.&...................))))))....))....))))))). -21.00

mir-25    SINFRUG00000147825  2000 nt UTR    2 hits 1114 1407

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>SINFRUG00000147825 hs-mir-25   1114   1121

CAUUGCACUUGUCUCGGUCUGA&AAGGGAGAGAAUCCUCCAAGAUUUGCAAUGAAGUAGUGCAAUU

.((((((((..((((..(((..&.)))..))))........................)))))))). -18.37

>SINFRUG00000147825 hs-mir-25   1407   1414

CAUUGCACUUGUCUCGGUCUGA&UGGCAGAAAGGUAAUGAACUAAAGUAUUUAUAGUCGUGCAAUA

.(((((((((..((...((((.&...)))).))..)).....................))))))). -16.19



miRNA: mir-25

Human predicted target: ENSG00000146083

Mouse predicted target: ENSMUSG00000034928

Rat predicted target: ENSRNOG00000017641

Fugu predicted target: SINFRUG00000154157

Hs Gene description: NM_014901

mir-25    ENSG00000146083     4316 nt UTR    1 hits 2241
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>ENSG00000146083 hs-mir-25   2241   2248

CAUUGCACUUGUCUCGGUCUGA&UAAAAUGAAAGUUGCUAGUUCUGCUUGACCAAGUAGUGCAAUC

.((((((((...((.((((...&..........................)))).)).)))))))). -21.90

mir-25    ENSMUSG00000034928  4342 nt UTR    2 hits 2269 3585

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>ENSMUSG00000034928 hs-mir-25   2269   2276

CAUUGCACUUGUCUCGGUCUGA&UAAAAUGAAAGUUGCUAGUUCUGCUUGACCAAGUAGUGCAAUC

.((((((((...((.((((...&..........................)))).)).)))))))). -21.90

>ENSMUSG00000034928 hs-mir-25   3585   3592

CAUUGCACUUGUCUCGGUCUGA&UAAAAUGAAAGUUGCUAGUUCUGCUUGACCAAGUAGUGCAAUC

.((((((((...((.((((...&..........................)))).)).)))))))). -21.90

mir-25    ENSRNOG00000017641  4296 nt UTR    2 hits 2222 4158

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>ENSRNOG00000017641 hs-mir-25   2222   2229

CAUUGCACUUGUCUCGGUCUGA&UAAAAUGAAAGUUGCUAGUUCUGCUUGACCAAGUAGUGCAAUC

.((((((((...((.((((...&..........................)))).)).)))))))). -21.90

>ENSRNOG00000017641 hs-mir-25   4158   4165

CAUUGCACUUGUCUCGGUCUGA&UAAAAUGAAAGUUGCUAGUUCUGCUUGACCAAGUAGUGCAAUC

.((((((((...((.((((...&..........................)))).)).)))))))). -21.90

mir-25    SINFRUG00000154157  2000 nt UTR    1 hits 340
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>SINFRUG00000154157 hs-mir-25    340    347

CAUUGCACUUGUCUCGGUCUGA&UUCAGCGGGCUGGAGGACGGUGAGCUGCAGAUCUUGUGCAAUGA

(((((((((((((((((((((.&.....)))))))..))))))...............)))))))). -26.76




miRNA: mir-25

Human predicted target: ENSG00000155744

Mouse predicted target: ENSMUSG00000038174

Rat predicted target: ENSRNOG00000011327

Rat predicted target: ENSRNOG00000012078

Fugu predicted target: SINFRUG00000137040

Hs Gene description: NM_173822

mir-25    ENSG00000155744     4800 nt UTR    2 hits 275 506

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>ENSG00000155744 hs-mir-25    275    282

CAUUGCACUUGUCUCGGUCUGA&UGCCUUUUCCAUGCCUUCCUUUCUCCUUGGGUGAUGUGCAAUC

.((((((((..(((.((...((&.....................)).))..)))..).))))))). -17.20

>ENSG00000155744 hs-mir-25    506    513

CAUUGCACUUGUCUCGGUCUGA&GAGAUUCUGCUAUGACUUUGGACUUCUCUGAGUCUGUGCAAUC

.(((((((..(.(((((((..(&.................)..)))).....))).).))))))). -21.10

mir-25    ENSMUSG00000038174  2575 nt UTR    2 hits 256 485
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>ENSMUSG00000038174 hs-mir-25    256    263

CAUUGCACUUGUCUCGGUCUGA&UGCCUUUUCCAUGCCUUCCUUUCUCCUUGGGUGAUGUGCAAUC

.((((((((..(((.((...((&.....................)).))..)))..).))))))). -17.20

>ENSMUSG00000038174 hs-mir-25    485    492

CAUUGCACUUGUCUCGGUCUGA&GAGAUUCUGCUAUGACUUUGGGCUUCUCUGAGCCUGUGCAAUU

.(((((((..(.(((((((..(&.................)..)))).....))))..))))))). -20.10

mir-25    ENSRNOG00000011327  2572 nt UTR    2 hits 257 489

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>ENSRNOG00000011327 hs-mir-25    257    264

CAUUGCACUUGUCUCGGUCUGA&UUUGCCUUUCCCUGCCUUCCUUUCUCUUGGGUGAUGUGCAAUC

.((((((((..(((.((...((&......................)).)).)))..).))))))). -17.30

>ENSRNOG00000011327 hs-mir-25    489    496

CAUUGCACUUGUCUCGGUCUGA&AGAUUCUGCUAUGACUUUGGGCUUUCUCUGAGUCUGUGCAAUU

.(((((((..(.(((((((..(&................)..))))......))).).))))))). -20.10

mir-25    ENSRNOG00000012078  2572 nt UTR    2 hits 257 489

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>ENSRNOG00000012078 hs-mir-25    257    264

CAUUGCACUUGUCUCGGUCUGA&UUUGCCUUUCCCUGCCUUCCUUUCUCUUGGGUGAUGUGCAAUC

.((((((((..(((.((...((&......................)).)).)))..).))))))). -17.30

>ENSRNOG00000012078 hs-mir-25    489    496

CAUUGCACUUGUCUCGGUCUGA&AGAUUCUGCUAUGACUUUGGGCUUUCUCUGAGUCUGUGCAAUU

.(((((((..(.(((((((..(&................)..))))......))).).))))))). -20.10
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mir-25    SINFRUG00000137040  2000 nt UTR    2 hits 531 1416

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>SINFRUG00000137040 hs-mir-25    531    538

CAUUGCACUUGUCUCGGUCUGA&GCGUUUCAUUCCUACCCUUUCAUUCCCGGGCACAUGUGCAAUC

.(((((((.((((((((..(((&...................)))...))))).))).))))))). -24.00

>SINFRUG00000137040 hs-mir-25   1416   1423

CAUUGCACUUGUCUCGGUCUGA&AUGACCUGCUAAUCUCUCAUGUGAUGAUUUUGAAAGUGCAAUU

.(((((((((.((..((((...&.........................))))..))))))))))). -18.50
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miRNA: mir-25

Human predicted target: ENSG00000156052

Mouse predicted target: ENSMUSG00000024639

Rat predicted target: ENSRNOG00000014183

Fugu predicted target: SINFRUG00000134002

Hs Gene description: GUANINE NUCLEOTIDE-BINDING PROTEIN G(Q), ALPHA
SUBUNIT. [Source:SWISSPROT;Acc:P50148]  NM_002072

mir-25    ENSG00000156052     2401 nt UTR    2 hits 1556 1940

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>ENSG00000156052 hs-mir-25   1556   1563

CAUUGCACUUGUCUCGGUCUGA&UGAACCUACCAGGAGAAAUGUUUGGAAUUCUAUAUGUGCAAUU

.(((((((.(((.....((..(&.....................)..)).....))).))))))). -15.80

>ENSG00000156052 hs-mir-25   1940   1947
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CAUUGCACUUGUCUCGGUCUGA&CCUGUAAUUUAACAAACAGACUGCCUGUAGGUAUAGUGCAAUU

.(((((((((..(((((((((.&................))))))).....))..).)))))))). -24.60

mir-25    ENSMUSG00000024639  2342 nt UTR    2 hits 1605 1940

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>ENSMUSG00000024639 hs-mir-25   1605   1612

CAUUGCACUUGUCUCGGUCUGA&CGAUCAUACUAGGAGGGAUGUUUGGAAUUCUCCAUGUGCAAUU

.(((((((.(((((..((.(((&...))).))..)))..................)).))))))). -17.06

>ENSMUSG00000024639 hs-mir-25   1940   1947

CAUUGCACUUGUCUCGGUCUGA&CCUGUAAUUUAAUUAACAGACUGCCUGUAGGUAUAGUGCAAUU

.(((((((((..(((((((((.&................))))))).....))..).)))))))). -24.60

mir-25    ENSRNOG00000014183  2317 nt UTR    2 hits 1570 1906

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>ENSRNOG00000014183 hs-mir-25   1570   1577

CAUUGCACUUGUCUCGGUCUGA&CGAUCAUACUAGGAGAGAUGUUUGGAAUUCUCCAUGUGCAAUU

.(((((((.((((((..((((.&.........)))).))))))...............))))))). -18.19

>ENSRNOG00000014183 hs-mir-25   1906   1913

CAUUGCACUUGUCUCGGUCUGA&CCUGUAAUUUAAUUAACAGACUGCCUGUAGGUACAGUGCAAUU

.(((((((((..(((((((((.&................))))))).....))..).)))))))). -24.60

mir-25    SINFRUG00000134002  2000 nt UTR    1 hits 1199

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>SINFRUG00000134002 hs-mir-25   1199   1206

CAUUGCACUUGUCUCGGUCUGA&AACGUAAGCCUGUAAUUUCCAUUUAUUGAGGCAUAGUGCAAUU

.(((((((((((((((((....&........................))))))))).)))))))). -24.60
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miRNA: mir-25

Human predicted target: ENSG00000157152

Mouse predicted target: ENSMUSG00000009394

Rat predicted target: ENSRNOG00000008157

Fugu predicted target: SINFRUG00000126214

Hs Gene description: SYNAPSIN II. [Source:SWISSPROT;Acc:Q92777]

mir-25    ENSG00000157152     2574 nt UTR    2 hits 798 2261

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>ENSG00000157152 hs-mir-25     798    805

CAUUGCACUUGUCUCGGUCUGA&UAACUAUGAGAUUUUUAAAAAAUGGGGCCGCUGAUGUGCAAUA

.(((((((..(((.((((((.(&.......................).))))))..)))))))))). -23.30

>ENSG00000157152 hs-mir-25   2261   2268

CAUUGCACUUGUCUCGGUCUGA&AGUACCUCUCUUUUGUGACUCUUGUACAGCUUAAUGUGCAAUA

.((((((((((((..((((...&................))))...).))))......))))))). -16.50

mir-25    ENSMUSG00000009394  2752 nt UTR    2 hits 780 2208

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>ENSMUSG00000009394 hs-mir-25    780    787

CAUUGCACUUGUCUCGGUCUGA&UACAAGAUAAAAAAAAAAAAUAAGGGGCCGCCGAUGUGCAAUA

.((((((((((...((((((..&........................)))))).))).))))))). -23.00

>ENSMUSG00000009394 hs-mir-25   2208   2215

CAUUGCACUUGUCUCGGUCUGA&CAUCUCCCUUUUGUGAUUCUCUUGUACAGCUCAAUGUGCAAUA
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.((((((((((....((.(((.&..........................)))))))).))))))). -17.00

mir-25    ENSRNOG00000008157  2750 nt UTR    2 hits 767 2144

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>ENSRNOG00000008157 hs-mir-25    767    774

CAUUGCACUUGUCUCGGUCUGA&GCUAAAGGUUAAAAAAAAAUCAAGGGGCCGCUGAUGUGCAAUA

.(((((((..(((.((((((..&........................))))))..)))))))))). -23.70

>ENSRNOG00000008157 hs-mir-25   2144   2151

CAUUGCACUUGUCUCGGUCUGA&CAUCUCCCUUUUGUGAUUCUCUUGUACAGCUCAAUGUGCAAUA

.((((((((((....((.(((.&..........................)))))))).))))))). -17.00

mir-25    SINFRUG00000126214  2000 nt UTR    1 hits 1359

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>SINFRUG00000126214 hs-mir-25   1359   1366

CAUUGCACUUGUCUCGGUCUGA&GCAUGGUGUCUGUGCGUCUUGUGAGCCGAUGCAAAGUGCAAUA

.((((((((((.(((((....&.........................))))).)).)))))))). -24.90



miRNA: mir-25

Human predicted target: ENSG00000173517

Mouse predicted target: ENSMUSG00000043561

Rat predicted target: ENSRNOG00000016824

Fugu predicted target: SINFRUG00000154075

mir-25    ENSG00000173517     7992 nt UTR    2 hits 850 1308
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>ENSG00000173517 hs-mir-25    850    857

CAUUGCACUUGUCUCGGUCUGA&AGCUGGCAGGGCAUGAGGAGAUGAUUUUCUUGCAUGUGCAAUU

.(((((((.(((((((((((..&........)))).))))..............))).))))))). -20.23

>ENSG00000173517 hs-mir-25   1308   1315

CAUUGCACUUGUCUCGGUCUGA&UGUGUGCAGCCUGUGCUCCCCUUCUAUGGAUAUGUGUGCAAUU

.(((((((.((((((((.(((.&......))).)))..............)))))...))))))). -19.43

mir-25    ENSMUSG00000043561  3319 nt UTR    2 hits 778 1262

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>ENSMUSG00000043561 hs-mir-25    778    785

CAUUGCACUUGUCUCGGUCUGA&AGUUGGCAGGAUAUGAAGAAAUAAUGUCCUUAUGUGUGCAAUU

.(((((((...(((((.((((.&......))))...))).))................))))))). -16.21

>ENSMUSG00000043561 hs-mir-25   1262   1269

CAUUGCACUUGUCUCGGUCUGA&GUUCCCCGUGGAGCCCGGGCUCUCCCGUGAAUUAUGUGCAAUU

.(((((((...((.(((((((.&...............)))).....))).)).....))))))). -19.80

mir-25    ENSRNOG00000016824  2000 nt UTR    2 hits 816 1284

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>ENSRNOG00000016824 hs-mir-25    816    823

CAUUGCACUUGUCUCGGUCUGA&AUAGUGGGCAGGAUAUGAAGAAAUAAUGUCCUUAUGUGCAAUU

.(((((((.(((((..((((..&.....)))).)))))....................))))))). -17.10

>ENSRNOG00000016824 hs-mir-25   1284   1291
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CAUUGCACUUGUCUCGGUCUGA&GUUCCCCAUGAAGCCUGUGCUCUCCCGUGAAUUAUGUGCAAUU

.(((((((...((.(((...((&....................))..))).)).....))))))). -18.30

mir-25    SINFRUG00000154075  2000 nt UTR    1 hits 956

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>SINFRUG00000154075 hs-mir-25    956    963

CAUUGCACUUGUCUCGGUCUGA&CAGCCCUGACCAGGCUUGACUUCUUGUUGGAGCAUGUGCAAUU

.(((((((.((.(((((((((.&..........)))))).............))))).))))))). -22.81



miRNA: mir-26a

Human predicted target: ENSG00000110321

Mouse predicted target: ENSMUSG00000005610

Rat predicted target: ENSRNOG00000011124

Rat predicted target: ENSRNOG00000017168

Fugu predicted target: SINFRUG00000136922

Hs Gene description: EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA, 2;
EUKARYOTIC TRANSLATION INITIATION FACTOR 4G-LIKE 1; P97.
[Source:RefSeq;Acc:NM_001418] NM_001418

mir-26a   ENSG00000110321     2000 nt UTR    2 hits 378 756

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>ENSG00000110321 hs-mir-26a    378    385

UUCAAGUAAUCCAGGAUAGGCU&CACUGAAUACUGUAGAAAUGCACUUUGCUCAGUAAUACUUGAGU

((((((((..(..((..((((.&...................)).))...))..)...)))))))). -15.00

>ENSG00000110321 hs-mir-26a    756    763
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UUCAAGUAAUCCAGGAUAGGCU&UUUUAUAUACUUGUAUCUAUCAAUAAACAUUGUGAUACUUGAU

.(((((((.(((((((((((..&...............))))))........))).))))))))). -16.70

mir-26a   ENSMUSG00000005610  2762 nt UTR    2 hits 380 757

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>ENSMUSG00000005610 hs-mir-26a    380    387

UUCAAGUAAUCCAGGAUAGGCU&CACUGAAUACUGUAGAGAUGCACUUUGCUCAGUAAUACUUGAGU

((((((((..(..((..((((.&...................)).))...))..)...)))))))). -15.00

>ENSMUSG00000005610 hs-mir-26a    757    764

UUCAAGUAAUCCAGGAUAGGCU&UUUUAUAUACUUGUAUCUAUCAAUAAACAUUGUGAUACUUGAU

.(((((((.(((((((((((..&...............))))))........))).))))))))). -16.70

mir-26a   ENSRNOG00000011124  2000 nt UTR    2 hits 379 756

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>ENSRNOG00000011124 hs-mir-26a    379    386

UUCAAGUAAUCCAGGAUAGGCU&CACUGAAUACUGUAGAGAUGCACUUUGCUCAGUAAUACUUGAGU

((((((((..(..((..((((.&...................)).))...))..)...)))))))). -15.00

>ENSRNOG00000011124 hs-mir-26a    756    763

UUCAAGUAAUCCAGGAUAGGCU&UUUUAUAUACUUGUAUCUAUCAAUAAACAUUGUGAUACUUGAAA

((((((((.(((((((((((..&...............))))))........))).)))))))))). -17.60

mir-26a   ENSRNOG00000017168  2762 nt UTR    2 hits 379 756

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>ENSRNOG00000017168 hs-mir-26a    379    386

UUCAAGUAAUCCAGGAUAGGCU&CACUGAAUACUGUAGAGAUGCACUUUGCUCAGUAAUACUUGAGU

((((((((..(..((..((((.&...................)).))...))..)...)))))))). -15.00
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>ENSRNOG00000017168 hs-mir-26a    756    763

UUCAAGUAAUCCAGGAUAGGCU&UUUUAUAUACUUGUAUCUAUCAAUAAACAUUGUGAUACUUGAU

.(((((((.(((((((((((..&...............))))))........))).))))))))). -16.70

mir-26a   SINFRUG00000136922  2000 nt UTR    1 hits 682

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>SINFRUG00000136922 hs-mir-26a    682    689

UUCAAGUAAUCCAGGAUAGGCU&UUCAUAUGAAUAUACCUCUAAUGUAUCUCGGACUGUACUUGAAU

((((((((.(((..((((.(..&.....................).))))..)))...)))))))). -21.30



miRNA: mir-26a

Human predicted target: ENSG00000137193

Mouse predicted target: ENSMUSG00000024014

Rat predicted target: ENSRNOG00000000529

Fugu predicted target: SINFRUG00000138008

Hs Gene description: PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE PIM-1
(EC 2.7.1.37). [Source:SWISSPROT;Acc:P11309] NM_002648

mir-26a   ENSG00000137193     3337 nt UTR    1 hits 478

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>ENSG00000137193 hs-mir-26a    478    485

UUCAAGUAAUCCAGGAUAGGCU&GCCUUCUGUGGGGACUCCGGCUGUGCUGGGAGAAAUACUUGAAC

((((((((.(((((.((((.(.&..................).)))).))))).....)))))))). -24.60

mir-26a   ENSMUSG00000024014  2000 nt UTR    1 hits 450
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>ENSMUSG00000024014 hs-mir-26a    450    457

UUCAAGUAAUCCAGGAUAGGCU&GCCUUCUGUGGGGACUCCGCCUGUGCUGGGAGAAAUACUUGAAC

((((((((.(((((.((((((.&..................)))))).))))).....)))))))). -29.20

mir-26a   ENSRNOG00000000529  2360 nt UTR    1 hits 434

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>ENSRNOG00000000529 hs-mir-26a    434    441

UUCAAGUAAUCCAGGAUAGGCU&CCUUCUGUGGGGACUCUUGUCUGUGCUGGGAGAAAUACUUGAAC

((((((((.(((((.((((((.&..................)))))).))))).....)))))))). -26.20

mir-26a   SINFRUG00000138008  2000 nt UTR    1 hits 397

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>SINFRUG00000138008 hs-mir-26a    397    404

UUCAAGUAAUCCAGGAUAGGCU&GAGUGCCUUCUGCAAAUGUGUGAAGAGUCUGACCGUACUUGAAG

((((((((.....((.((((((&.........................)))))).)).)))))))). -21.00
```

miRNA: mir-26a

Human predicted target: ENSG00000163932

Mouse predicted target: ENSMUSG00000021948

Rat predicted target: ENSRNOG00000016346

Fugu predicted target: SINFRUG00000127498

Hs Gene description: PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA). [Source:SWISSPROT;Acc:Q05655]   NM_006254

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mir-26a   ENSG00000163932     2263 nt UTR    1 hits 226

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>ENSG00000163932 hs-mir-26a    226    233

UUCAAGUAAUCCAGGAUAGGCU&GCCUUCGGAGGGAAAUUGUAAAUCCUGUGUUUCAUUACUUGAAU

(((((((((((((((((((((.&)))).................)))))).)....)))))))))). -23.92

mir-26a   ENSMUSG00000021948  2498 nt UTR    1 hits 232

---------1-----------------------------------------------------------------
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>ENSMUSG00000021948 hs-mir-26a    232    239

UUCAAGUAAUCCAGGAUAGGCU&GCCAUCAGAGGGAAACUGUAAAUCCUGUGUUUCAUUACUUGAAU

(((((((((((((((((..((.&.................))..)))))).)....)))))))))). -22.40

mir-26a   ENSRNOG00000016346  2473 nt UTR    1 hits 234

---------1-----------------------------------------------------------------
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>ENSRNOG00000016346 hs-mir-26a    234    241

UUCAAGUAAUCCAGGAUAGGCU&GCCAUCGGAGGGAAACUGUAAAUCCUGUGUGUCAUUACUUGAAU

(((((((((((((((((..((.&.................))..)))))).)....)))))))))). -22.40

mir-26a   SINFRUG00000127498  2000 nt UTR    1 hits 593

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>SINFRUG00000127498 hs-mir-26a    593    600

UUCAAGUAAUCCAGGAUAGGCU&AAACACAGUAAAAAGUAAGUGCUUAUUCGUCAUAUUACUUGAAU

((((((((((...((((((((.&....................)))))))).....)))))))))). -23.60
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miRNA: mir-26a

Human predicted target: ENSG00000170365

Mouse predicted target: ENSMUSG00000031681

Rat predicted target: ENSRNOG00000018483

Fugu predicted target: SINFRUG00000126514

Hs Gene description: MOTHERS AGAINST DECAPENTAPLEGIC HOMOLOG 1 (SMAD 1)
(MOTHERS AGAINST DPP HOMOLOG 1) (MAD-RELATED PROTEIN 1) (TRANSFORMING
GROWTH FACTOR- BETA SIGNALING PROTEIN-1) (BSP-1) (HSMAD1) (JV4-1).
[Source:SWISSPROT;Acc:Q15797] NM_005900

mir-26a   ENSG00000170365     2160 nt UTR    2 hits 46 103

-1--1----------------------------------------------------------------------
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>ENSG00000170365 hs-mir-26a     46     53

UUCAAGUAAUCCAGGAUAGGCU&GCAUCUGCCUCUGGAAAACUAUUGAGCCUUGCAUGUACUUGAAG

((((((((.(((((...((((.&......)))))))))....................)))))))). -21.80

>ENSG00000170365 hs-mir-26a    103    110

UUCAAGUAAUCCAGGAUAGGCU&GACACGAUUGAGAACUGACAAAGGAGCCUUGAUAAUACUUGAC

.((((((((((......(((((&........................))))).)))..))))))). -17.00

mir-26a   ENSMUSG00000031681  3248 nt UTR    2 hits 46 103

-1--1----------------------------------------------------------------------
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>ENSMUSG00000031681 hs-mir-26a     46     53

UUCAAGUAAUCCAGGAUAGGCU&GCUUCCGUCUCUUGCAAACUAUCGAGCCUUGCAUGUACUUGAAG

((((((((...((....(((((&........................)))))....)))))))))). -19.50

>ENSMUSG00000031681 hs-mir-26a    103    110

UUCAAGUAAUCCAGGAUAGGCU&GACAGGAUGGAGACCUGACGAAGGAGCCACGAUAAUACUUGAC

.(((((((.....(....((((&........................)))).).....))))))). -15.60
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mir-26a   ENSRNOG00000018483  2285 nt UTR    2 hits 49 102

-1--1---------------------------------------------------------------------
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>ENSRNOG00000018483 hs-mir-26a     49     56

UUCAAGUAAUCCAGGAUAGGCU&GCUUCUGUCUCUUGCAAACUAUUGGGCCUUGCAUGUACUUGAAG

((((((((...((....(((((&........................)))))....)))))))))). -19.50

>ENSRNOG00000018483 hs-mir-26a    102    109

UUCAAGUAAUCCAGGAUAGGCU&GUCAGACAGGAUGGGGAGCUGUAAAGGAGCCGUGAUACUUGAC

.(((((((.((..((...((((&................)))).........))..))))))))). -16.20

mir-26a   SINFRUG00000126514  2000 nt UTR    2 hits 194 273

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>SINFRUG00000126514 hs-mir-26a    194    201

UUCAAGUAAUCCAGGAUAGGCU&GGGACCAGUGGGGCUGGGCAGGAUGGUUUGAUGUCUACUUGAAG

((((((((((((.(..(((.((&..........)).)))..).)))).........))))))))). -18.60

>SINFRUG00000126514 hs-mir-26a    273    280

UUCAAGUAAUCCAGGAUAGGCU&GGAGUCAAAGAAGUGAGCAUGAUGCAACUGGAAGAUACUUGAU

.(((((((.(((((.((..(((&...............)))...))....)))))...))))))). -19.90



miRNA: mir-27a

Human predicted target: ENSG00000055070

Mouse predicted target: ENSMUSG00000040842

Rat predicted target: ENSRNOG00000009183

Fugu predicted target: SINFRUG00000123544
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Fugu predicted target: SINFRUG00000124328

Hs Gene description: NM_015609

mir-27a   ENSG00000055070     5002 nt UTR    4 hits 122 146 168 198

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>ENSG00000055070 hs-mir-27a    122    129

UUCACAGUGGCUAAGUUCCGCC&GGACUUGAGCAGAGGGAACGACCUGACUUACUUGCACUGUGAU

.(((((((((((((((((....&)))))).))).......................)))))))). -21.45

>ENSG00000055070 hs-mir-27a    146    153

UUCACAGUGGCUAAGUUCCGCC&GACUUACUUGCACUGUGAUCCCCCUUGCUCCGCCCACUGUGAC

.((((((((((..(((......&..........................)))..).))))))))). -21.10

>ENSG00000055070 hs-mir-27a    168    175

UUCACAGUGGCUAAGUUCCGCC&CCUUGCUCCGCCCACUGUGACCUUGAACCCCAUGCACUGUGAC

.((((((((.(...((((....&........................)))).....))))))))). -18.70

>ENSG00000055070 hs-mir-27a    198    205

UUCACAGUGGCUAAGUUCCGCC&CAUGCACUGUGACCUCCCCCCUUCUCCCCCUUCCCACUGUGAU

.(((((((((............&.................................))))))))). -19.50

mir-27a   ENSMUSG00000040842  2000 nt UTR    4 hits 119 143 165 193

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>ENSMUSG00000040842 hs-mir-27a    119    126

UUCACAGUGGCUAAGUUCCGCC&GGACUUGAGCAGAGGGAAUAACCUGACUUACUUGCACUGUGAU

.(((((((((((((((((....&)))))).))).......................)))))))). -21.45

>ENSMUSG00000040842 hs-mir-27a    143    150
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UUCACAGUGGCUAAGUUCCGCC&GACUUACUUGCACUGUGAUCCCCCUUGCUCCGCCCACUGUGAC

.((((((((((..(((......&..........................)))..).))))))))). -21.10

>ENSMUSG00000040842 hs-mir-27a    165    172

UUCACAGUGGCUAAGUUCCGCC&CCUUGCUCCGCCCACUGUGACCUUGAACCCCAUGCACUGUGAC

.((((((((.(...((((....&........................)))).....))))))))). -18.70

>ENSMUSG00000040842 hs-mir-27a    193    200

UUCACAGUGGCUAAGUUCCGCC&CCCAUGCACUGUGACCUCUGCCUCCCCCCCUUCCCACUGUGAU

.((((((((.............&..................................)))))))). -19.50

mir-27a   ENSRNOG00000009183  2530 nt UTR    8 hits 117 141 163 191 641
665 687 715

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>ENSRNOG00000009183 hs-mir-27a    117    124

UUCACAGUGGCUAAGUUCCGCC&GGACUUGAGCAGAGGGAAUAACCUGACUUACUUGCACUGUGAU

.(((((((((((((((((....&)))))).))).......................))))))))). -21.45

>ENSRNOG00000009183 hs-mir-27a    141    148

UUCACAGUGGCUAAGUUCCGCC&GACUUACUUGCACUGUGAUCCCCCUUGCUCCGCCCACUGUGAC

.((((((((((..(((......&..........................)))..).))))))))). -21.10

>ENSRNOG00000009183 hs-mir-27a    163    170

UUCACAGUGGCUAAGUUCCGCC&CCUUGCUCCGCCCACUGUGACCUUGAACCCCAUGCACUGUGAC

.((((((((.(...((((....&........................)))).....))))))))). -18.70

>ENSRNOG00000009183 hs-mir-27a    191    198

UUCACAGUGGCUAAGUUCCGCC&CCCAUGCACUGUGACCUCUGCCUCCCCCCCUUCCCACUGUGAU

.((((((((.............&..................................)))))))). -19.50

>ENSRNOG00000009183 hs-mir-27a    641    648
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UUCACAGUGGCUAAGUUCCGCC&GGACUUGAGCAGAGGGAAUAACCUGACUUACUUGCACUGUGAU

.(((((((((((((((((....&)))))).)))........................)))))))). -21.45

>ENSRNOG00000009183 hs-mir-27a    665    672

UUCACAGUGGCUAAGUUCCGCC&GACUUACUUGCACUGUGAUCCCCCUUGCUCCGCCCACUGUGAC

.((((((((((..(((......&..........................)))..).))))))))). -21.10

>ENSRNOG00000009183 hs-mir-27a    687    694

UUCACAGUGGCUAAGUUCCGCC&CCUUGCUCCGCCCACUGUGACCUUGAACCCCAUGCACUGUGAC

.((((((((.(...((((....&........................)))).....))))))))). -18.70

>ENSRNOG00000009183 hs-mir-27a    715    722

UUCACAGUGGCUAAGUUCCGCC&CCCAUGCACUGUGACCUCUGCCUCCCCCCCUUCCCACUGUGAU

.(((((((((............&.................................))))))))). -19.50

mir-27a   SINFRUG00000123544  2000 nt UTR    2 hits 879 907

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>SINFRUG00000123544 hs-mir-27a    879    886

UUCACAGUGGCUAAGUUCCGCC&GCGCUCUUCUCUUAUACCACCCCGAGUCGGUUGACACUGUGAU

.((((((((........(((..&...........................)))....)))))))). -18.80

>SINFRUG00000123544 hs-mir-27a    907    914

UUCACAGUGGCUAAGUUCCGCC&GGUUGACACUGUGAUCGUGGACGUCUUCUGCUCUCACUGUGAC

.(((((((((...((((((((.&................)))))........))).))))))))). -22.40

mir-27a   SINFRUG00000124328  2000 nt UTR    1 hits 314

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>SINFRUG00000124328 hs-mir-27a    314    321

UUCACAGUGGCUAAGUUCCGCC&CGCUGCGAACGGGCCUUCAGCUCACAUCCCUCUACACUGUGAU
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.((((((((((((((..(((..&.........)))..))).))).............)))))))). -24.41

miRNA: mir-27a

Human predicted target: ENSG00000135373

Mouse predicted target: ENSMUSG00000012350

Rat predicted target: ENSRNOG00000007484

Fugu predicted target: SINFRUG00000151958

Hs Gene description: ETS HOMOLOGOUS FACTOR ISOFORM B; EPITHELIUM-SPECIFIC
ETS FACTOR 3. [Source:RefSeq;Acc:NM_012153]  NM_172233

mir-27a   ENSG00000135373     3861 nt UTR    2 hits 3387 3499

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>ENSG00000135373 hs-mir-27a   3387   3394

UUCACAGUGGCUAAGUUCCGCC&ACCUUCAAGGACAUAUUAUCUACUAUGAACAUUUUACUGUGAGA

((((((((((....((((....&..........................))))...)))))))))). -18.40

>ENSG00000135373 hs-mir-27a   3499   3506

UUCACAGUGGCUAAGUUCCGCC&AUAUGUUGGAUGAGGAUUCUGUUGCCUUAUUGGGAACUGUGAGA

(((((((((((..((.(((.((&.......))....)))..))...))).........)))))))). -22.20

mir-27a   ENSMUSG00000012350  5426 nt UTR    2 hits 2373 2481

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>ENSMUSG00000012350 hs-mir-27a   2373   2380

UUCACAGUGGCUAAGUUCCGCC&CAUAAUAACUAAACCUUCCAGGAUGAGAACAUUUUACUGUGAC

.(((((((((....((((((((&....................)).)).))))...))))))))). -20.00
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>ENSMUSG00000012350 hs-mir-27a   2481   2488

UUCACAGUGGCUAAGUUCCGCC&GUGUCUGCUGGAUGAGAAUUCUGUUGCUUUUUAGAACUGUGAGA

((((((((..(((((.(((((.&......)).))).................))))).)))))))). -20.07

mir-27a   ENSRNOG00000007484  5075 nt UTR    4 hits 2164 2251 4810 4916

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>ENSRNOG00000007484 hs-mir-27a   2164   2171

UUCACAGUGGCUAAGUUCCGCC&AGCAUAAUAACCAAACCUCCCAGGACGAACAUUUUACUGUGAC

.(((((((((....((((..((&......................))..))))...))))))))). -19.70

>ENSRNOG00000007484 hs-mir-27a   2251   2258

UUCACAGUGGCUAAGUUCCGCC&UGUCUUGCUGGAUAAGAAUUCUGUUGCUUUCUAGAACUGUGAGA

((((((((..(((((((((((.&......)).))).............)))...))).)))))))). -18.91

>ENSRNOG00000007484 hs-mir-27a   4810   4817

UUCACAGUGGCUAAGUUCCGCC&ACCUCCCAGGACAUAUCCUCUCAGGCGAACAUUUUACUGUGAC

.(((((((((....(((.((((&.......................)))))))...))))))))). -22.40

>ENSRNOG00000007484 hs-mir-27a   4916   4923

UUCACAGUGGCUAAGUUCCGCC&UGUCUUGCUGGAUAAGAAUUCUGUUGCUUUCUAGAACUGUGAGA

((((((((..(((((((((((.&......)).))).............)))...))).)))))))). -18.91

mir-27a   SINFRUG00000151958  2000 nt UTR    2 hits 69 378

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>SINFRUG00000151958 hs-mir-27a     69     76

UUCACAGUGGCUAAGUUCCGCC&GUUGACGAUUUAGUAUGCGUUUGAUAUUUUUACCACUGUGAU

.(((((((((..(((.(((((.&...............)))...))....)))..))))))))). -21.80
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>SINFRUG00000151958 hs-mir-27a    378    385

UUCACAGUGGCUAAGUUCCGCC&AUGUAUUCAGUGUGUGUUGAGUGUGUGUUAUUUAUACUGUGAAA

(((((((((..(((((..(((.&........................)))..))))))))))))))). -20.40




miRNA: mir-29b

Human predicted target: ENSG00000071575

Mouse predicted target: ENSMUSG00000020601

Rat predicted target: ENSRNOG00000004110

Fugu predicted target: SINFRUG00000143157

Hs Gene description: GS3955 PROTEIN. [Source:RefSeq;Acc:NM_021643]
     NM_021643

mir-29b   ENSG00000071575     2610 nt UTR    2 hits 1758 1862

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>ENSG00000071575 hs-mir-29b   1758   1765

UAGCACCAUUUGAAAUCAGUGUU&AGAGAAGGUUUUUUUUUUUUUUAACAUUCUGAAGAUGGUGCUGU

(((((((((((....((((((((&......................))))..)))))))))))))))). -
22.90

>ENSG00000071575 hs-mir-29b   1862   1869

UAGCACCAUUUGAAAUCAGUGUU&GGUUGGUGACAUGCAUGGUGGGGAUCUAUGGCCUCUGGUGCUU

.(((((((......(((((((((&.......)))))...))))................))))))). -15.85

mir-29b   ENSMUSG00000020601  3879 nt UTR    3 hits 1701 1805 3766

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>ENSMUSG00000020601 hs-mir-29b   1701   1708
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UAGCACCAUUUGAAAUCAGUGUU&GAAGAUACAGAGAGAGGGUUUUUACAUUCAGAAGAUGGUGCUGU

(((((((((((......(((((.&.......................)))))....))))))))))). -
21.60

>ENSMUSG00000020601 hs-mir-29b   1805   1812

UAGCACCAUUUGAAAUCAGUGUU&GAUUGGAAACAUGCAUGAUGGGGACUAAUGGCCUCUGGUGCUU

.(((((((...((..(((..(((&......................)))...)))..))))))))). -17.10

>ENSMUSG00000020601 hs-mir-29b   3766   3773

UAGCACCAUUUGAAAUCAGUGUU&GCAAGAGGAAACACAGAGCUCUUUUGACUUGGGAGUGGUGCUAG

(((((((((((((..((.(((((&.........))))).))..))...........))))))))))). -
24.10

mir-29b   ENSRNOG00000004110  3884 nt UTR    2 hits 1702 1806

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>ENSRNOG00000004110 hs-mir-29b   1702   1709

UAGCACCAUUUGAAAUCAGUGUU&GAAGAUACAGAGAAAGGGUUUUUACAUUCAGAAGAUGGUGCUGU

(((((((((((......(((((.&.......................)))))....))))))))))). -
21.60

>ENSRNOG00000004110 hs-mir-29b   1806   1813

UAGCACCAUUUGAAAUCAGUGUU&GAUUGGUAACAUGCAUGAUGGGGACUAAUGGCCUCUGGUGCUU

.(((((((...((..(((..(((&......................)))...)))..))))))))). -17.10

mir-29b   SINFRUG00000143157  2000 nt UTR    2 hits 302 1509

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>SINFRUG00000143157 hs-mir-29b    302    309

UAGCACCAUUUGAAAUCAGUGUU&AAUUUUUAUUUCUUUUGGAUCUGUUUGGUUUUAUGUGGUGCUC

.((((((((.(((((((((....&........................))))))))).)))))))). -24.70
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>SINFRUG00000143157 hs-mir-29b   1509   1516

UAGCACCAUUUGAAAUCAGUGUU&UGCUUUUUUCCUUCCCCUGAUCAACUUUUUAAGUUGGUGCUGA

(((((((((((((((((((....&................)))))......)))))).)))))))). -
22.00




miRNA: mir-29b

Human predicted target: ENSG00000080573

Mouse predicted target: ENSMUSG00000004098

Rat predicted target: ENSRNOG00000020525

Fugu predicted target: SINFRUG00000127082

Fugu predicted target: SINFRUG00000146544

Hs Gene description: COLLAGEN ALPHA 3(V) CHAIN (FRAGMENTS).
[Source:SWISSPROT;Acc:P25940] NM_015719

mir-29b   ENSG00000080573     2850 nt UTR    3 hits 52 385 663

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>ENSG00000080573 hs-mir-29b     52     59

UAGCACCAUUUGAAAUCAGUGUU&AGGGACCAUGAGGAGCCCCAGAAUGGGGUGCAUUUGGUGCUGA

((((((((..((...(((.....&.......................)))....))..)))))))). -
21.00

>ENSG00000080573 hs-mir-29b    385    392

UAGCACCAUUUGAAAUCAGUGUU&CUCCUCACUCCUCCGUCGCUGCCCUUCACACCUUUUGGUGCUAC

((((((((..((((..(((((..&................)))))...)))).......)))))))). -
22.10

>ENSG00000080573 hs-mir-29b    663    670
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UAGCACCAUUUGAAAUCAGUGUU&GACCAAGAUGUUGGGGGGGUGAAUCAGGAUCCUAAUGGUGCUGC

((((((((((.....((((..((&......))..))))...................)))))))))). -
19.55

mir-29b   ENSMUSG00000004098  2000 nt UTR    3 hits 57 334 586

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>ENSMUSG00000004098 hs-mir-29b     57     64

UAGCACCAUUUGAAAUCAGUGUU&GGAAGGAAGCUGAAGGGAGCCCCACAUGGGCUCCUUGGUGCUGA

((((((((...((..((((((..&......................))).)))..))..)))))))). -
22.30

>ENSMUSG00000004098 hs-mir-29b    334    341

UAGCACCAUUUGAAAUCAGUGUU&CCACCCCUGCCUCUCCACCCCUCCACCAGGCCUUUUGGUGCUAU

((((((((..........(((..&.......................)))..........)))))))). -
18.11

>ENSMUSG00000004098 hs-mir-29b    586    593

UAGCACCAUUUGAAAUCAGUGUU&GGACCAAGAUGUUGGGCAUAAAUCAGGAUCCUACAUGGUGCUGC

(((((((((.((..(((.(((((&..............))))).......)))..)).))))))))). -
19.40

mir-29b   ENSRNOG00000020525  2786 nt UTR    3 hits 52 333 585

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>ENSRNOG00000020525 hs-mir-29b     52     59

UAGCACCAUUUGAAAUCAGUGUU&GAAGGAAGCUAAAGGGAGCCCCAUGUGGGGCUAUGUGGUGCUGA

(((((((((......((((((..&.....................))).)))......))))))))). -
20.40

>ENSRNOG00000020525 hs-mir-29b    333    340

UAGCACCAUUUGAAAUCAGUGUU&CCACCCCUGCCUCUCCACCCCUCCACCAGGCCCUUUGGUGCUAU
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((((((((..........(((..&.......................)))........)))))))). -
18.11

>ENSRNOG00000020525 hs-mir-29b    585    592

UAGCACCAUUUGAAAUCAGUGUU&GGACCAAGAUGUUGGGCACAAAUCAGGAUCCUAAAUGGUGCUGC

((((((((((((..(((.(((((&..............)))))).......)))..)))))))))))). -
24.40

mir-29b   SINFRUG00000127082  2000 nt UTR    1 hits 584

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>SINFRUG00000127082 hs-mir-29b    584    591

UAGCACCAUUUGAAAUCAGUGUU&UUGUUGUGAAAUGUAUAUUAGUUUGUAAUUAAUCAUGGUGCUAU

(((((((((((((...(((....&......................)))...))))..))))))))). -
18.10

mir-29b   SINFRUG00000146544  2000 nt UTR    2 hits 960 1097

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>SINFRUG00000146544 hs-mir-29b    960    967

UAGCACCAUUUGAAAUCAGUGUU&UUUGGGUUUGUGUGACUGAUGAUUUGCUCUGCCAUGGUGCUAA

(((((((((..(((((((..(((&..............)))...))))))).)......))))))))). -
21.60

>SINFRUG00000146544 hs-mir-29b   1097   1104

UAGCACCAUUUGAAAUCAGUGUU&AUUGCUCUUUCAGCUGAAAUAACGUCCUUAGAGACUGGUGCUU

.(((((((.((....(((((...&............)))))...............)).))))))). -17.71
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miRNA: mir-29b

Human predicted target: ENSG00000119772

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Mouse predicted target: ENSMUSG00000020661

Rat predicted target: ENSRNOG00000012555

Fugu predicted target: SINFRUG00000135438

Hs Gene description: DNA (CYTOSINE-5)-METHYLTRANSFERASE 3A (EC 2.1.1.37)
(DNMT3A) (DNA METHYLTRANSFERASE HSAIIIA) (DNA MTASE HSAIIIA) (M.HSAIIIA).
[Source:SWISSPROT;Acc:Q9Y6K1] NM_175630

mir-29b   ENSG00000119772     3303 nt UTR    4 hits 862 1305 2998 3256

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>ENSG00000119772 hs-mir-29b    862    869

UAGCACCAUUUGAAAUCAGUGUU&GGUACUGUUAACUACUGUACAACCCGACUUCAUAAUGGUGCUU

.(((((((((((((.((.(.(((&....................)))).)).)))).))))))))). -22.20

>ENSG00000119772 hs-mir-29b   1305   1312

UAGCACCAUUUGAAAUCAGUGUU&CACCUGGAGCAAAUAAAAAAACAUACAAAACGUACUGGUGCUU

.(((((((((((...((((.((.&.))))))..)))).......................))))))). -17.54

>ENSG00000119772 hs-mir-29b   2998   3005

UAGCACCAUUUGAAAUCAGUGUU&CCUCUGCCCCCUCAGUGGAGUCCCUGUGCUAACUGUGGUGCUC

.((((((((.......(((....&.......................)))........)))))))). -18.76

>ENSG00000119772 hs-mir-29b   3256   3263

UAGCACCAUUUGAAAUCAGUGUU&UUUCCCAGCGGCCCAAGCUCCACCGGAACUGGGCCUGGUGCUC

.(((((((...(...(((((...&...........................))))).).))))))). -18.80

mir-29b   ENSMUSG00000020661  3103 nt UTR    2 hits 825 1252

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>ENSMUSG00000020661 hs-mir-29b    825    832

UAGCACCAUUUGAAAUCAGUGUU&GGUACUGUUAACUACUGUACAUCCCGACUUCAUAAUGGUGCUU
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.(((((((((((((.((.((((.&..................))))...)).)))).))))))))). -22.30

>ENSMUSG00000020661 hs-mir-29b   1252   1259

UAGCACCAUUUGAAAUCAGUGUU&CACCUGGAGCAAAUAAAAAAACAUACAAAAUGUACUGGUGCUU

.(((((((((((...((((.((.&.))))))..))))......................))))))). -17.54

mir-29b   ENSRNOG00000012555  2000 nt UTR    2 hits 811 1281

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>ENSRNOG00000012555 hs-mir-29b    811    818

UAGCACCAUUUGAAAUCAGUGUU&GGUACUGUUAACUACUGUACAUCCCAACUUCAUAAUGGUGCUU

.(((((((((((((..(((((((&.........))).))))...........)))).))))))))). -21.22

>ENSRNOG00000012555 hs-mir-29b   1281   1288

UAGCACCAUUUGAAAUCAGUGUU&CACCUGGAGCAAAUAAAAAAACAUACAAAACGUACUGGUGCUU

.(((((((((((...((((.((.&.))))))..))))......................))))))). -17.54

mir-29b   SINFRUG00000135438  2000 nt UTR    2 hits 459 647

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>SINFRUG00000135438 hs-mir-29b    459    466

UAGCACCAUUUGAAAUCAGUGUU&AAUAAAGGUACUACUGUAAUAUGGUUACAACACCAUGGUGCUC

.(((((((((((.(((((.((((&.................))))))))).)))....)))))))). -19.60

>SINFRUG00000135438 hs-mir-29b    647    654

UAGCACCAUUUGAAAUCAGUGUU&UUUUAUGCAUUUUACAGCUUUUCUACAGUUUGUACUGGUGCUC

.(((((((...............&...................................))))))). -15.20




miRNA: mir-29b
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Human predicted target: ENSG00000132510

Mouse predicted target: ENSMUSG00000018476

Mouse predicted target: ENSMUSG00000046383

Rat predicted target: ENSRNOG00000010142

Fugu predicted target: SINFRUG00000131193

Fugu predicted target: SINFRUG00000148279

mir-29b   ENSG00000132510     3275 nt UTR    3 hits 744 1690 1696

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>ENSG00000132510 hs-mir-29b    744    751

UAGCACCAUUUGAAAUCAGUGUU&CCACCCGUCCGCCCGCGGCUCCAGCCGGGUUCUCAUGGUGCUC

.((((((((..(((..(.((...&.......................)).)..)))..)))))))). -20.90

>ENSG00000132510 hs-mir-29b   1690   1697

UAGCACCAUUUGAAAUCAGUGUU&GAAUCUGCUGGUGGCUGCCUUCAAUCUUCUCCUGCUGGUGCUGG

((((((((.(((((..((((...&.............))))..)))))...........)))))))). -
21.90

>ENSG00000132510 hs-mir-29b   1696   1703

UAGCACCAUUUGAAAUCAGUGUU&GCUGGUGGCUGCCUUCAAUCUUCUCCUGCUGGUGCUGGUGCUAG

((((((((......((((((...&...........................))))))..)))))))). -
22.20

mir-29b   ENSMUSG00000018476  2147 nt UTR    2 hits 782 1743

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>ENSMUSG00000018476 hs-mir-29b    782    789

UAGCACCAUUUGAAAUCAGUGUU&GUCUCCGCCCGCCCGCGGCUCCAGCCGGGCUCUCAUGGUGCUC

.((((((((..((..((.((...&.......................)).))..))..)))))))). -20.00
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>ENSMUSG00000018476 hs-mir-29b   1743   1750

UAGCACCAUUUGAAAUCAGUGUU&GCUGGUGGCUGUUUUCAAUCUCCUCUUGCUGGCACUGGUGCUGG

((((((((.((((((.((((...&.......)))).)))))).................)))))))). -
23.17

mir-29b   ENSMUSG00000046383  2002 nt UTR    1 hits 1921

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>ENSMUSG00000046383 hs-mir-29b   1921   1928

UAGCACCAUUUGAAAUCAGUGUU&UGCGCGCCGUCGCAGCGCGGCCUACAGGGCGUGGUGGUGCUAG

(((((((((((((.....((((.&.))))....)))....................)))))))))). -
20.59

mir-29b   ENSRNOG00000010142  2000 nt UTR    2 hits 776 1729

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>ENSRNOG00000010142 hs-mir-29b    776    783

UAGCACCAUUUGAAAUCAGUGUU&GUCUCCGCCCGCCCGCGGCUCCAGCCGGGUUCUCAUGGUGCUC

.((((((((..(((..(.((...&.......................)).)..)))..)))))))). -20.90

>ENSRNOG00000010142 hs-mir-29b   1729   1736

UAGCACCAUUUGAAAUCAGUGUU&GCUGGUGGCUGUUUUCAAUCUCCUCUUGUUGGCGCUGGUGCUGG

((((((((.((((((.((((...&.......)))).)))))).................)))))))). -
23.17

mir-29b   SINFRUG00000131193  2000 nt UTR    1 hits 39

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>SINFRUG00000131193 hs-mir-29b     39     46

UAGCACCAUUUGAAAUCAGUGUU&CUCACUCAGCGUUUCAUCAUAUUUUGUGCUAAAAAUGGUGCUU

.(((((((((((((((.((((..&..))))....))))).................)))))))))). -19.92
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mir-29b   SINFRUG00000148279  2000 nt UTR    2 hits 279 1105

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>SINFRUG00000148279 hs-mir-29b    279    286

UAGCACCAUUUGAAAUCAGUGUU&CCAGGCGGCCACCAACACACCAGUUUACUCUCAGAUGGUGCUU

.(((((((((((((((..((((.&................))))..))).....)))))))))))). -24.70

>SINFRUG00000148279 hs-mir-29b   1105   1112

UAGCACCAUUUGAAAUCAGUGUU&GAUUUUAUAAGAUGCGUUGAACAUAACAGGAUAGAUGGUGCUAA

((((((((((((......(((((&...................))))).......)))))))))))). -
22.62




miRNA: mir-29b

Human predicted target: ENSG00000138779

Mouse predicted target: ENSMUSG00000040943

Rat predicted target: ENSRNOG00000012350

Fugu predicted target: SINFRUG00000143809

mir-29b   ENSG00000138779     5282 nt UTR    3 hits 447 596 1151

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>ENSG00000138779 hs-mir-29b    447    454

UAGCACCAUUUGAAAUCAGUGUU&UAGUAUUACAGUGACAGGAAUCUUAAAAUACCAUCUGGUGCUGA

((((((((..((...(((.(((.&.......))).))).................))..)))))))). -
19.25

>ENSG00000138779 hs-mir-29b    596    603

UAGCACCAUUUGAAAUCAGUGUU&GGAAAACACUGAAUUUGUUUGGAUGUUCUAAGAAAUGGUGCUAA
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((((((((((((((.((((((((&....)))))))).)))...............))))))))))). -
27.59

>ENSG00000138779 hs-mir-29b   1151   1158

UAGCACCAUUUGAAAUCAGUGUU&UCAAGGAAUACGUUAGUCCACAAAACAUGUUUUCUGGUGCUC

.(((((((...((((...(((((&.......................)))))..))))))))))). -20.00

mir-29b   ENSMUSG00000040943  2877 nt UTR    4 hits 398 557 1055 1161

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>ENSMUSG00000040943 hs-mir-29b    398    405

UAGCACCAUUUGAAAUCAGUGUU&ACACAGCGCUGUAGUAGAGCAGUUGCAGGAUCAUCUGGUGCUGA

((((((((..(((...(((((((&....)))))))...................)))..)))))))). -
24.25

>ENSMUSG00000040943 hs-mir-29b    557    564

UAGCACCAUUUGAAAUCAGUGUU&CAAAACACUGAAUCUGUUUGGGUGUUAACAUUAAAUGGUGCUAC

(((((((((((((..((((((((&...))))))))...................))))))))))))). -
27.80

>ENSMUSG00000040943 hs-mir-29b   1055   1062

UAGCACCAUUUGAAAUCAGUGUU&GAUAUGCUAGUCCACAGAAAACAAAUAACAGUUUUUGGUGCUC

.(((((((...........((((&...................))))............))))))). -16.50

>ENSMUSG00000040943 hs-mir-29b   1161   1168

UAGCACCAUUUGAAAUCAGUGUU&AAGAACGUCUGUUAAUUGCAGGUGAUAAUUAGCCUUGGUGCUGC

((((((((((((....(((((((&...)))).)))......))))..............)))))))). -
18.21

mir-29b   ENSRNOG00000012350  2000 nt UTR    2 hits 556 1107

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>ENSRNOG00000012350 hs-mir-29b    556    563
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UAGCACCAUUUGAAAUCAGUGUU&CAAAACACUGAAUUUGUUUGGGUGUUAACAUUAAAUGGUGCUAC

(((((((((((((..((((((((&...)))))))).......................))))))))))))). -
27.80

>ENSRNOG00000012350 hs-mir-29b   1107   1114

UAGCACCAUUUGAAAUCAGUGUU&GUGAAUGGAUAGGCUAGUCUACAAAACACGUUUCCUGGUGCUU

.(((((((...(((((..(((((&........................)))))))))).))))))). -21.10

mir-29b   SINFRUG00000143809  2000 nt UTR    3 hits 241 665 875

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>SINFRUG00000143809 hs-mir-29b    241    248

UAGCACCAUUUGAAAUCAGUGUU&GGCAAAUUCUGCAACACACACCUUGUCAAAAUAUCUGGUGCUU

.((((((((((((.....((((.&.................))))....))))).....))))))). -20.20

>SINFRUG00000143809 hs-mir-29b    665    672

UAGCACCAUUUGAAAUCAGUGUU&CUGCUUUGUUUAUGCAAAAAUGAACUUUCUUGUGUUGGUGCUC

.(((((((...(((((((.(((.&.............)))....)))..))))......))))))). -18.60

>SINFRUG00000143809 hs-mir-29b    875    882

UAGCACCAUUUGAAAUCAGUGUU&CUGGACUGUGAAUAUUACAUGUGUUAUUAUGUCUGUGGUGCUU

.((((((((..((...((((.(.&..).))))......................)).)))))))). -17.97
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```
miRNA: mir-29b

Human predicted target: ENSG00000171215

Mouse predicted target: ENSMUSG00000034832

Rat predicted target: ENSRNOG00000011387

Fugu predicted target: SINFRUG00000143809
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mir-29b   ENSG00000171215     2395 nt UTR    5 hits 53 1070 1084 1101 1471

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>ENSG00000171215 hs-mir-29b     53     60

UAGCACCAUUUGAAAUCAGUGUU&UACCUCAGCGUCGGGCCUGGCCCGAGCUGUCUCUGUGGUGCUU

.((((((((..((...((((...&.........................))))..)).)))))))). -21.70

>ENSG00000171215 hs-mir-29b   1070   1077

UAGCACCAUUUGAAAUCAGUGUU&AAACAGGAAGUUGAACCCAAGCUGUGAAAGCCAGUGGUGCUC

.(((((((((.(....((((...&...................)))).......).))))))))). -20.80

>ENSG00000171215 hs-mir-29b   1084   1091

UAGCACCAUUUGAAAUCAGUGUU&ACCCAAGCUGUGAAAAGCCAGUGGUGCUCUGUGCAUGGUGCUGU

(((((((((..((.((((.((..&..................)).))))..)).....))))))))). -
22.40

>ENSG00000171215 hs-mir-29b   1101   1108

UAGCACCAUUUGAAAUCAGUGUU&CCAGUGGUGCUCUGUGCAUGGUGCUGUGCGGAGCCUGGUGCUGU

((((((((((((....(((..((&...................))..)))..))))...)))))))). -
22.00

>ENSG00000171215 hs-mir-29b   1471   1478

UAGCACCAUUUGAAAUCAGUGUU&CUGGUGCAUUCAUUCGGUUCUUUGAAAUGAGAAUGUGGUGCUU

.((((((((.(((((((((....&)))))...))))......................)))))))). -18.90

mir-29b   ENSMUSG00000034832  2000 nt UTR    2 hits 51 1367

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>ENSMUSG00000034832 hs-mir-29b     51     58

UAGCACCAUUUGAAAUCAGUGUU&GUACCUCAGCGUCGGGCCCGGCCCGAGCUGCUCUGUGGUGCUU

.((((((((..((...((((...&..........................)))).)).)))))))). -20.60
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>ENSMUSG00000034832 hs-mir-29b   1367   1374

UAGCACCAUUUGAAAUCAGUGUU&GGUGCAUUCAUUCAGCUCUUUGAAAAUGAGAACGUUGGUGCUU

.(((((((.(((((...(((((.&...)))))..))))).................... ))))))). -16.70

mir-29b   ENSRNOG00000011387  3807 nt UTR    2 hits 540 2751

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>ENSRNOG00000011387 hs-mir-29b    540    547

UAGCACCAUUUGAAAUCAGUGUU&CAUGCUCUACACAACAGCCUGAACCCGGCCUACGGUGGUGCUGA

((((((((((((...((((.(((&...............)))))))...))......)))))))))). -
20.70

>ENSRNOG00000011387 hs-mir-29b   2751   2758

UAGCACCAUUUGAAAUCAGUGUU&CAUGCUCUACACAACAGCCUGAACCCGGCCUACGGUGGUGCUGA

((((((((((((...((((.(((&...............)))))))...))......)))))))))). -
20.70

mir-29b   SINFRUG00000143809  2000 nt UTR    3 hits 241 665 875

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>SINFRUG00000143809 hs-mir-29b    241    248

UAGCACCAUUUGAAAUCAGUGUU&GGCAAAUUCUGCAACACACACCUUGUCAAAAUAUCUGGUGCUU

.((((((((((((.....((((.&.................))))....)))))).....))))))). -20.20

>SINFRUG00000143809 hs-mir-29b    665    672

UAGCACCAUUUGAAAUCAGUGUU&CUGCUUUGUUUAUGCAAAAAUGAACUUUCUUGUGUUGGUGCUC

.(((((((...(((((((.(((.&.............)))....)))..)))).......))))))). -18.60

>SINFRUG00000143809 hs-mir-29b    875    882

UAGCACCAUUUGAAAUCAGUGUU&CUGGACUGUGAAUAUUACAUGUGUUAUUAUGUCUGUGGUGCUU
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.((((((((..((...((((.(.&..).)))).......................)).)))))))). -17.97



miRNA: mir-30b

Human predicted target: ENSG00000108604

Mouse predicted target: ENSMUSG00000020710

Rat predicted target: ENSRNOG00000010557

Fugu predicted target: SINFRUG00000136799

Hs Gene description: SWI/SNF-RELATED MATRIX-ASSOCIATED ACTIN-DEPENDENT
REGULATOR OF CHROMATIN D2; RSC6P; MAMMALIAN CHROMATIN REMODELING COMPLEX
BRG1-ASSOCIATED FACTOR 60B; SWP73-LIKE PROTEIN; CHROMATIN REMODELING
COMPLEX BAF60B SUBUNIT; SWI/SNF COMPLEX 60 KDA SUBUNIT B.
[Source:RefSeq;Acc:NM_003077]

mir-30b   ENSG00000108604     2854 nt UTR    1 hits 316

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>ENSG00000108604 hs-mir-30b    316    323

UGUAAACAUCCUACACUCAGC&AAGACAUUUCCGAACCAAAGGCUGCUGGGUUUGCAUGUUUACAG

(((((((((.(...(((((((&.......................)))))))..).))))))))). -23.10

mir-30b   ENSMUSG00000020710  2879 nt UTR    1 hits 339

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>ENSMUSG00000020710 hs-mir-30b    339    346

UGUAAACAUCCUACACUCAGC&CAGACAUUUCCAAACCAAAGGCUGCUGGGUUUGCAUGUUUACAG

(((((((((.(...(((((((&.......................)))))))..).))))))))). -23.10

mir-30b   ENSRNOG00000010557  2889 nt UTR    1 hits 331

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>ENSRNOG00000010557 hs-mir-30b    331    338

UGUAAACAUCCUACACUCAGC&CAGACAUUUCCGAACCAAAGGCUGCUGGGUUUGCAUGUUUACAG

(((((((((.(...(((((((&.......................)))))))..).))))))))). -23.10

mir-30b   SINFRUG00000136799  2000 nt UTR    2 hits 636 906

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>SINFRUG00000136799 hs-mir-30b    636    643

UGUAAACAUCCUACACUCAGC&AAACGCCACGUGGUGUCUUAUUUUGAAAGGGUUUAUGUUUACC

.((((((((((((((((....&...........))))))............)))...)))))))). -15.50

>SINFRUG00000136799 hs-mir-30b    906    913

UGUAAACAUCCUACACUCAGC&AUUAGUCAGAUUUUUCCUUUAGUCUCCUCUGGGAAUGUUUACAU

(((((((((((((........&.............................)))).))))))))). -18.00



miRNA: mir-30b

Human predicted target: ENSG00000109586

Mouse predicted target: ENSMUSG00000031608

Rat predicted target: ENSRNOG00000012037

Fugu predicted target: SINFRUG00000140751

Hs Gene description: POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE 7; UDP-
N-ACETYL-ALPHA-D-GALACTOSAMINE. [Source:RefSeq;Acc:NM_017423]    NM_017423

mir-30b   ENSG00000109586     4249 nt UTR    3 hits 185 221 2628

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>ENSG00000109586 hs-mir-30b    185    192
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UGUAAACAUCCUACACUCAGC&UGUGAUUUUACAAUAACAUUAUCAUCUGCAGUUACUGUUUACAA

((((((((......((((((.&.........................))).)))...)))))))). -14.30

>ENSG00000109586 hs-mir-30b    221    228

UGUAAACAUCCUACACUCAGC&GUUUACAAGACUGCUUUUACCUUAAACUUUGUAGAUGUUUACAU

((((((((((.((((......&.............................)))))))))))))). -19.40

>ENSG00000109586 hs-mir-30b   2628   2635

UGUAAACAUCCUACACUCAGC&GCCUAUUAGAAGCAAACAUGCCUUCAAAUCAAAUUUGUUUACAA

((((((((.............&...................................)))))))). -12.30

mir-30b   ENSMUSG00000031608  3587 nt UTR    2 hits 361 395

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>ENSMUSG00000031608 hs-mir-30b    361    368

UGUAAACAUCCUACACUCAGC&UGUGAUUUUACAAUAACAUUAUCAUCUGCAGUGACUGUUUACAA

((((((((.....(((((((.&.........................))).))))..)))))))). -17.30

>ENSMUSG00000031608 hs-mir-30b    395    402

UGUAAACAUCCUACACUCAGC&CUGUUUACAAAACUGCUCUUACCUUAAACUCUAGAUGUUUACAU

((((((((((...........&.................................)))))))))). -16.30

mir-30b   ENSRNOG00000012037  2180 nt UTR    2 hits 191 225

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>ENSRNOG00000012037 hs-mir-30b    191    198

UGUAAACAUCCUACACUCAGC&GUGAUUUUUACAAUAAUAUUAUCAUCUGCAGUUACUGUUUACAA

((((((((......((((((.&.........................))).)))...)))))))). -14.30

>ENSRNOG00000012037 hs-mir-30b    225    232

UGUAAACAUCCUACACUCAGC&CUGUUUACAAAACUGCUCUUACCUUAAACUCUAGAUGUUUACAU
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((((((((((...........&.................................)))))))))). -16.30

mir-30b   SINFRUG00000140751  2000 nt UTR    2 hits 149 1572

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>SINFRUG00000140751 hs-mir-30b    149    156

UGUAAACAUCCUACACUCAGC&UCCACAUGUUUAAAUGUAGGGGACAAAUGUUUCUGUGUUUACU

.((((((((((((((......&..............))))))..............)))))))). -17.73

>SINFRUG00000140751 hs-mir-30b   1572   1579

UGUAAACAUCCUACACUCAGC&CGGUGCAUUAUGGGGCUUCAUCAUUGUGUUCUUCCUGUUUACAU

(((((((((((((((((....&.)))).....))))).....................)))))))). -14.85



miRNA: mir-30b

Human predicted target: ENSG00000114353

Mouse predicted target: ENSMUSG00000032562

Rat predicted target: ENSRNOG00000016592

Fugu predicted target: SINFRUG00000136406

Hs Gene description: GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2
SUBUNIT (ADENYLATE CYCLASE-INHIBITING G ALPHA PROTEIN).
[Source:SWISSPROT;Acc:P04899] NM_002070

mir-30b   ENSG00000114353     2567 nt UTR    2 hits 405 682

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>ENSG00000114353 hs-mir-30b    405    412

UGUAAACAUCCUACACUCAGC&CCCAACACCAGCCCCUGCCCCAGCCCAAGUCCAAAUGUUUACAG

(((((((((.....(((..((&......................))...)))....))))))))). -13.70
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>ENSG00000114353 hs-mir-30b    682    689

UGUAAACAUCCUACACUCAGC&CUUCCAAGUGACUCCGUGCCUUGAGUGUGUCUGCGUGUUUACAC

(((((((((.((((((((((.&....................))))))))))...).)))))))). -23.10

mir-30b   ENSMUSG00000032562  2992 nt UTR    4 hits 398 683 1880 2165

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>ENSMUSG00000032562 hs-mir-30b    398    405

UGUAAACAUCCUACACUCAGC&GCUUUGUCCAACACCAGCCCUGACCCAAGUCCAAAUGUUUACAG

(((((((((.((....((((.&...................))))....)).....))))))))). -14.10

>ENSMUSG00000032562 hs-mir-30b    683    690

UGUAAACAUCCUACACUCAGC&CUUUCCAGCGAUUCCGUGCCUUGAGUGUGUCUGCGUGUUUACAC

(((((((((.((((((((((.&....................))))))))))...).)))))))). -23.10

>ENSMUSG00000032562 hs-mir-30b   1880   1887

UGUAAACAUCCUACACUCAGC&GCUUUGUCCAACACCAGCCCUGACCCAAGUCCAAAUGUUUACAG

(((((((((.((....((((.&...................))))....)).....))))))))). -14.10

>ENSMUSG00000032562 hs-mir-30b   2165   2172

UGUAAACAUCCUACACUCAGC&CUUUCCAGCGAUUCCGUGCCUUGAGUGUGUCUGCGUGUUUACAC

(((((((((.((((((((((.&....................))))))))))...).)))))))). -23.10

mir-30b   ENSRNOG00000016592  2294 nt UTR    2 hits 1202 1486

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>ENSRNOG00000016592 hs-mir-30b   1202   1209

UGUAAACAUCCUACACUCAGC&GCUUUGUCCAACACCAGCCCUGACCCAAGUCCAAAUGUUUACAG

(((((((((.((....((((.&...................))))....)).....))))))))). -14.10

>ENSRNOG00000016592 hs-mir-30b   1486   1493
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UGUAAACAUCCUACACUCAGC&CUUUCCAGUGAUUCCGUGCCUUGAGUGUUUCUGCCUGUUUACAC

((((((((..(.((((((((.&....................))))))))....)..)))))))). -21.30

mir-30b   SINFRUG00000136406  2000 nt UTR    2 hits 784 1749

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>SINFRUG00000136406 hs-mir-30b    784    791

UGUAAACAUCCUACACUCAGC&CUUUAUAUAUAUAUAUAUGUUUGUGCCUUGAUAUCUGUUUACAC

((((((((((...(((..(((&..................))).)))....))....)))))))). -11.70

>SINFRUG00000136406 hs-mir-30b   1749   1756

UGUAAACAUCCUACACUCAGC&AGAUGCAGACAGUAAAGACAUUGGAAGGUCAGGUAUGUUUACAA

((((((((((((((..((((.&....................))))...)).))).))))))))). -19.40



miRNA: mir-30b

Human predicted target: ENSG00000132130

Mouse predicted target: ENSMUSG00000018698

Rat predicted target: ENSRNOG00000002812

Fugu predicted target: SINFRUG00000142325

Hs Gene description: LIM/HOMEOBOX PROTEIN LHX1 (HOMEOBOX PROTEIN LIM-1).
[Source:SWISSPROT;Acc:P48742] NM_005568

mir-30b   ENSG00000132130     2000 nt UTR    2 hits 845 1028

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>ENSG00000132130 hs-mir-30b    845    852

UGUAAACAUCCUACACUCAGC&AAAAAAAAAAGACUAUUGAACUAAAAACAGUCAACUGUUUACGU
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((((((((.............&...................................)))))))). -11.30

>ENSG00000132130 hs-mir-30b   1028   1035

UGUAAACAUCCUACACUCAGC&CUUUCGGCUCACUGUGCUAGUAUGUAAAAAGGUGUUGUUUACAC

((((((((.((((((..((((&...............))).)..)))....)))...)))))))). -17.70

mir-30b   ENSMUSG00000018698  2170 nt UTR    2 hits 938 1119

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>ENSMUSG00000018698 hs-mir-30b    938    945

UGUAAACAUCCUACACUCAGC&AAAAAGAAAAGACUAUCGAACUAAAAACAGUCAACUGUUUACGU

((((((((.............&...................................)))))))). -11.30

>ENSMUSG00000018698 hs-mir-30b   1119   1126

UGUAAACAUCCUACACUCAGC&CUUGCGGCUCACUGUGCUAGUAUGUAAAAAGGUGUUGUUUACAC

((((((((.((((((..((((&...............))).)..)))....)))...)))))))). -17.70

mir-30b   ENSRNOG00000002812  2086 nt UTR    2 hits 943 1126

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>ENSRNOG00000002812 hs-mir-30b    943    950

UGUAAACAUCCUACACUCAGC&AAAAAAAAAAGACUAUUGAACUAAAAACAGUCAACUGUUUACGU

((((((((.............&...................................)))))))). -11.30

>ENSRNOG00000002812 hs-mir-30b   1126   1133

UGUAAACAUCCUACACUCAGC&CUUGCGGCUCACUGUGCUAGUAUGUAAAAAGGUGUUGUUUACAC

((((((((.((((((..((((&...............))).)..)))....)))...)))))))). -17.70

mir-30b   SINFRUG00000142325  2000 nt UTR    2 hits 920 1095

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>SINFRUG00000142325 hs-mir-30b    920    927
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UGUAAACAUCCUACACUCAGC&CACAACACACUUAACUGUUACAUUUGUGGCACUGAUGUUUACGA

(((((((((((((((......&........................)))))....)))))))))). -18.80

>SINFRUG00000142325 hs-mir-30b   1095   1102

UGUAAACAUCCUACACUCAGC&CAUUUUCAGCUAUUUACAACCUUGUUUAUUUGCAUUGUUUACC

.(((((((.............&...................................))))))). -10.70



miRNA: mir-30b

Human predicted target: ENSG00000136052

Mouse predicted target: ENSMUSG00000034591

Rat predicted target: ENSRNOG00000008713

Fugu predicted target: SINFRUG00000137981

Hs Gene description: NM_032148

mir-30b   ENSG00000136052     2000 nt UTR    1 hits 277

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>ENSG00000136052 hs-mir-30b    277    284

UGUAAACAUCCUACACUCAGC&UCCAGCUCUGAAAUUAAUUAGGAAAGAAUAUAGGAUGUUUACAG

(((((((((((((........&..............................))))))))))))). -22.50

mir-30b   ENSMUSG00000034591  2000 nt UTR    1 hits 271

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>ENSMUSG00000034591 hs-mir-30b    271    278

UGUAAACAUCCUACACUCAGC&UCACAUUCUAAAGUUAAUUAGGAAAGAAUUUAGGAUGUUUACAA

(((((((((((((........&..............................))))))))))))). -22.40
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mir-30b   ENSRNOG00000008713  2000 nt UTR    1 hits 274

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>ENSRNOG00000008713 hs-mir-30b    274    281

UGUAAACAUCCUACACUCAGC&UCACACUCUAAAGUCAAUUAGGGAAGAAUAUAGGAUGUUUACAA

(((((((((((((........&..............................))))))))))))). -22.50

mir-30b   SINFRUG00000137981  2000 nt UTR    2 hits 662 1787

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>SINFRUG00000137981 hs-mir-30b    662    669

UGUAAACAUCCUACACUCAGC&GGGGGUAGUUAAUCAGCGUUUGCAUGCUAAUCACCUGUUUACAG

((((((((..((((.(((...&))).))))..........................)))))))). -15.15

>SINFRUG00000137981 hs-mir-30b   1787   1794

UGUAAACAUCCUACACUCAGC&AAUAUGGUCACAUGCUAACACAGUGAAGAGAAUUCUGUUUACC

.(((((((((((.((((.(((&.............))).....)))).)).))....))))))). -15.20



miRNA: mir-30b

Human predicted target: ENSG00000185112

Mouse predicted target: ENSMUSG00000046546

Rat predicted target: ENSRNOG00000001728

Fugu predicted target: SINFRUG00000124355

Hs Gene description: NM_153690

mir-30b   ENSG00000185112     2445 nt UTR    2 hits 519 609
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>ENSG00000185112 hs-mir-30b    519    526

UGUAAACAUCCUACACUCAGC&UAGCCCUUGGUUCUUUUUGGUGCAAGAAUUCUGGCUGUUUACC

.(((((((.((..(((.(((.&................))))))..........)).))))))). -14.30

>ENSG00000185112 hs-mir-30b    609    616

UGUAAACAUCCUACACUCAGC&UGGGGGGUGGGGGGAGAUGAAAGAGAGUCGCGUUUUGUUUACAG

((((((((((((((.((((..&))))..)))))).......................)))))))). -20.90

mir-30b   ENSMUSG00000046546  2846 nt UTR    4 hits 487 577 1366 1391

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>ENSMUSG00000046546 hs-mir-30b    487    494

UGUAAACAUCCUACACUCAGC&CUGCCCCCAGUUCUUUCGGAUAGGGGAGCUUGGGCUGUUUACC

.(((((((.((((..(((...&.........................)))..)))).))))))). -20.30

>ENSMUSG00000046546 hs-mir-30b    577    584

UGUAAACAUCCUACACUCAGC&CUUGGGGGGGGGGGCAGUGUAUGAAAGUCGUGUUUUGUUUACAG

((((((((((((...(((((.&.)))))...))))......................)))))))). -18.04

>ENSMUSG00000046546 hs-mir-30b   1366   1373

UGUAAACAUCCUACACUCAGC&UUUGGAGAGGUCAGUGUAAAUUCAACUGCCCACGCUGUUUACAC

((((((((...((((((....&............)))))).................)))))))). -13.85

>ENSMUSG00000046546 hs-mir-30b   1391   1398

UGUAAACAUCCUACACUCAGC&CUGCCCACGCUGUUUACACGAGUCACGUGGAUGGCUGUUUACU

.(((((((.((..(((.((((&........))))..............)))...)).))))))). -19.46

mir-30b   ENSRNOG00000001728  2000 nt UTR    3 hits 511 604 1397

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>ENSRNOG00000001728 hs-mir-30b    511    518
UGUAAACAUCCUACACUCAGC&CUGCCCCCAGUUCUUUUGGAUAUGAGAGCUUGGGCUGUUUACC
.(((((((.((((..(((...&.........................)))..)))).))))))). -20.50
>ENSRNOG00000001728 hs-mir-30b    604    611
UGUAAACAUCCUACACUCAGC&UGGGGGGCGGAGGGCGGGGUAUGAAAGUUGUGUUUUGUUUACAG
(((((((((((..(.(((.((&......)).))).)..)))................)))))))). -19.09
>ENSRNOG00000001728 hs-mir-30b   1397   1404
UGUAAACAUCCUACACUCAGC&AAUUCAACUGCCCACACUGUUUAGACGUGUAUGGCUGUUUACU
.(((((((.(((((((((...&.......................)).))))).)).))))))). -21.70
mir-30b   SINFRUG00000124355  2000 nt UTR    2 hits 329 1397
-------------1-----------------------------------------1------------------
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>SINFRUG00000124355 hs-mir-30b    329    336
UGUAAACAUCCUACACUCAGC&UGGGAAUCCGAGCGGCAGGUUUUGGGGACGCUGCGUGUUUACAA
((((((((((((.(.(((...&.........))).)..)))...............))))))))). -18.46
>SINFRUG00000124355 hs-mir-30b   1397   1404
UGUAAACAUCCUACACUCAGC&UGAGAUGAGAGAUUAUUUAAAUGAAUCCACCAACUUGUUUACAU
((((((((((((.((((((..&)))).)))).)).......................)))))))). -15.00
```

```
miRNA: mir-34
Human predicted target: ENSG00000117308
Mouse predicted target: ENSMUSG00000028671
Rat predicted target: ENSRNOG00000009712
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Fugu predicted target: SINFRUG00000129461

Hs Gene description: UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2)
(GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE).
[Source:SWISSPROT;Acc:Q14376] NM_000403

mir-34    ENSG00000117308     2350 nt UTR    2 hits 510 1507

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>ENSG00000117308 hs-mir-34    510    517

UGGCAGUGUCUUAGCUGGUUGU&ACAUGGAGACAGAAGACGAGACACAACUCCUCCCCCACUGCCU

.(((((((....((..((((((&......................))))))).))....))))))). -21.80

>ENSG00000117308 hs-mir-34   1507   1514

UGGCAGUGUCUUAGCUGGUUGU&CUCCCCAUGGCACUGGAGUAUGGCCAGGUCCUUGGCACUGCCAU

((((((((((..(.(((((..(&...................)..))))).)....)))))))))). -31.60

mir-34    ENSMUSG00000028671  2319 nt UTR    2 hits 1443 1880

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>ENSMUSG00000028671 hs-mir-34   1443   1450

UGGCAGUGUCUUAGCUGGUUGU&CUCCCCGUGGCACUGAAGGAUGGCCAGGUCCUUGGCACUGCCAU

((((((((((..(.(((((..(&...................)..))))).)....)))))))))). -31.80

>ENSMUSG00000028671 hs-mir-34   1880   1887

UGGCAGUGUCUUAGCUGGUUGU&AGGAGACUGCUGGAGGCUUGAAGGGAGCAGGUGGGCACUGCCU

.((((((((((.(.(((.((.(&......................).)).))).))))))))))). -27.40

mir-34    ENSRNOG00000009712  2319 nt UTR    2 hits 1438 1902

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>ENSRNOG00000009712 hs-mir-34   1438   1445

UGGCAGUGUCUUAGCUGGUUGU&CUCGCCGUGGCAUUGAAGGAUGGCCAGGUCCUUGGCACUGCCAU
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((((((((((..(.(((((..(&...................)..))))).)....)))))))))). -31.80

>ENSRNOG00000009712 hs-mir-34   1902   1909

UGGCAGUGUCUUAGCUGGUUGU&AGGAGACUGCUGGAGGCUUGAAGGGAGCAGGUGGGCACUGCCC

.((((((((((.(.(((.((.(&......................).)).))).)))))))))))). -27.00

mir-34    SINFRUG00000129461  2000 nt UTR    1 hits 1991

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>SINFRUG00000129461 hs-mir-34   1991   1998

UGGCAGUGUCUUAGCUGGUUGU&GUCUUCUCCUCCAGGCAGCCUCAGAGGUGGUUCAACACUGCCGA

((((((((((((....((((((&..............))))))....))).......))))))))). -26.41



miRNA: mir-34

Human predicted target: ENSG00000148400

Mouse predicted target: ENSMUSG00000026923

Rat predicted target: ENSRNOG00000019322

Fugu predicted target: SINFRUG00000127119

Hs Gene description: NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR
(NOTCH 1) (HN1) (TRANSLOCATION-ASSOCIATED NOTCH PROTEIN TAN-1).
[Source:SWISSPROT;Acc:P46531] NM_017617

mir-34    ENSG00000148400     3627 nt UTR    4 hits 909 2299 2398 2714

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>ENSG00000148400 hs-mir-34    909    916

UGGCAGUGUCUUAGCUGGUUGU&CACACGGAGGCAUCCUACCCUUUUCUGGGGAAAGACACUGCCU

.(((((((((((..(..(....&........................)..)...))))))))))). -25.90
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>ENSG00000148400 hs-mir-34   2299   2306
UGGCAGUGUCUUAGCUGGUUGU&GCCAGCCUCACACAAGGGUGGGCCCCUUCUCUCCCCACUGCCU
.(((((((((((.((((((...&)))))).......))))..................))))))). -21.86
>ENSG00000148400 hs-mir-34   2398   2405
UGGCAGUGUCUUAGCUGGUUGU&GUGGGGAGUCUGAGAUCCCUCUUUGGAUUGCAAAGCACUGCCU
.(((((((((((((((..(..(&)..)..)).)))))....................)))))))). -21.55
>ENSG00000148400 hs-mir-34   2714   2721
UGGCAGUGUCUUAGCUGGUUGU&CAUCACUCAGUACAGCCACAGACAGCCUGAGCGUCCACUGCCAA
((((((((.((((((((.((((&.................)))).)))).))))....)))))))). -28.20
mir-34    ENSMUSG00000026923  3625 nt UTR    3 hits 187 458 800
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>ENSMUSG00000026923 hs-mir-34    187    194
UGGCAGUGUCUUAGCUGGUUGU&AGUAUUUAUUUAUGUACUUUUAUUUUCCACAGAAACACUGCCU
.((((((((.((.(.(((....&..........................)))).)).)))))))). -21.60
>ENSMUSG00000026923 hs-mir-34    458    465
UGGCAGUGUCUUAGCUGGUUGU&AACUGCCAUGGCCAGAAUUGCCCCUCCCCCACACUCACUGCCC
.(((((((......(((((..(&.......)..)))))....................))))))). -23.57
>ENSMUSG00000026923 hs-mir-34    800    807
UGGCAGUGUCUUAGCUGGUUGU&UAAGCCAUGCAGGGUGUGGUGCCUCCUAGAGAAAACACUGCCU
.((((((((((..(((((((..&..))))).))..))....................)))))))). -25.05
mir-34    ENSRNOG00000019322  2384 nt UTR    3 hits 193 523 890
-------1------------1--------------1--------------------------------------
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>ENSRNOG00000019322 hs-mir-34    193    200
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UGGCAGUGUCUUAGCUGGUUGU&AGUAUUUAUUUAUGUACUUUUAUUUUCCACAGAAACACUGCCU

.((((((((.((.(.(((....&..........................)))).)).)))))))). -21.60

>ENSRNOG00000019322 hs-mir-34    523    530

UGGCAGUGUCUUAGCUGGUUGU&AGAUUUCCCCUCCCCAGAUGCCUGCUACCCCACUCACUGCCC

.(((((((...((((.(((...&...................))).)))).......))))))). -23.50

>ENSRNOG00000019322 hs-mir-34    890    897

UGGCAGUGUCUUAGCUGGUUGU&AAGCCAAGUGGGGUGUGGUGCCUCCUGGAGAAUGACACUGCCU

.(((((((((((..((((..((&...................))..)).))..)).))))))))). -25.50

mir-34    SINFRUG00000127119  2000 nt UTR    1 hits 1164

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>SINFRUG00000127119 hs-mir-34   1164   1171

UGGCAGUGUCUUAGCUGGUUGU&CAGAGUAACACCGCCCUCUGGUGUUUACUAGGUGACACUGCCAU

((((((((((..(.(((((...&..........................))))).))))))))))). -26.90



miRNA: mir-34

Human predicted target: ENSG00000168758

Mouse predicted target: ENSMUSG00000026121

Rat predicted target: ENSRNOG00000016254

Fugu predicted target: SINFRUG00000125424

Hs Gene description: SEMA DOMAIN, IMMUNOGLOBULIN DOMAIN (IG),
TRANSMEMBRANE DOMAIN TM. [Source:RefSeq;Acc:NM_017789] NM_017789

mir-34    ENSG00000168758     2884 nt UTR    2 hits 162 465
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>ENSG00000168758 hs-mir-34    162    169

UGGCAGUGUCUUAGCUGGUUGU&ACCCGGCCAUGAGGACCUGCUCUGCUCAGCACGGGCACUGCCAC

(((((((((((..((((((.((&..................))...)).))))..))))))))))). -30.60

>ENSG00000168758 hs-mir-34    465    472

UGGCAGUGUCUUAGCUGGUUGU&GGGAAGGGGUCGUAUCACUUUGUCUCUCCUACCCCCACUGCCC

.(((((((...(((..((....&........................))..)))....))))))). -17.40

mir-34    ENSMUSG00000026121  2000 nt UTR    2 hits 119 164

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>ENSMUSG00000026121 hs-mir-34    119    126

UGGCAGUGUCUUAGCUGGUUGU&GACAUGGCAGGGGCACUUGCUCUGCCUGGGACAGACACUGCCC

.((((((((((...(((((.((&..................))...))).))...)))))))))). -25.70

>ENSMUSG00000026121 hs-mir-34    164    171

UGGCAGUGUCUUAGCUGGUUGU&CAUUUGCCCGGCCGUGAGGACCUGCUCAGCAUGGGCACUGCCAC

(((((((((((..((((((.((&...................))..)).))))..))))))))))). -30.80

mir-34    ENSRNOG00000016254  2862 nt UTR    1 hits 136

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>ENSRNOG00000016254 hs-mir-34    136    143

UGGCAGUGUCUUAGCUGGUUGU&CAUUUGCCCAGCCAUGAGGACCUGCUCAGCAUGGGCACUGCCAC

(((((((((((..((((((.((&...................))..)).))))..))))))))))). -30.80

mir-34    SINFRUG00000125424  2000 nt UTR    3 hits 1158 1174 1644

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>SINFRUG00000125424 hs-mir-34   1158   1165

UGGCAGUGUCUUAGCUGGUUGU&UUAUAUCUUAAUGUUUGGAGAGGGAGGAAAACUUGCACUGCCAA

((((((((((((..(..(....&..............)..)..)))...........))))))))). -21.40

>SINFRUG00000125424 hs-mir-34   1174   1181

UGGCAGUGUCUUAGCUGGUUGU&GGAGAGGGAGGAAAACUUGCACUGCCAAGAACGGACACUGCCC

.((((((((((...(((((.((&....................)).)))).)...)))))))))). -28.20

>SINFRUG00000125424 hs-mir-34   1644   1651

UGGCAGUGUCUUAGCUGGUUGU&AGUCAAAUAUUCUGCAUUGAUGUUGACUAAUUGCACACUGCCC

.((((((((..(((.(((((..&........................))))).))).)))))))). -21.40




miRNA: mir-34

Human predicted target: ENSG00000179036

Mouse predicted target: ENSMUSG00000020894

Rat predicted target: ENSRNOG00000006989

Fugu predicted target: SINFRUG00000131186

Hs Gene description: VESICLE-ASSOCIATED MEMBRANE PROTEIN 2 (VAMP-2)
(SYNAPTOBREVIN 2). [Source:SWISSPROT;Acc:P19065]  NM_014232

mir-34    ENSG00000179036     3727 nt UTR    6 hits 1129 1256 1309 3456
3583 3636

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>ENSG00000179036 hs-mir-34   1129   1136

UGGCAGUGUCUUAGCUGGUUGU&AGAGGGGUGGCUACCAGUGUGUGUGUGGGGGUCAUCACUGCCU

.(((((((.(((.((((((.((&.........)).))))))..........)))....))))))). -25.80
```

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>ENSG00000179036 hs-mir-34   1256   1263

UGGCAGUGUCUUAGCUGGUUGU&AACCCUCCUCCCCAAUUUGGGGGGUGUUGCCCCAUCACUGCCC

.(((((((.(((..(..((((.&............))))..)..)))...........))))))). -18.70

>ENSG00000179036 hs-mir-34   1309   1316

UGGCAGUGUCUUAGCUGGUUGU&ACUGCCCCCCCUGAAUUUAGGGUGGGGGUACUAGUCACUGCCAA

((((((((.....((((((...&.............................)))))))))))))). -22.80

>ENSG00000179036 hs-mir-34   3456   3463

UGGCAGUGUCUUAGCUGGUUGU&AGAGGGGUGGCUACCAGUGUGUGUGUGGGGGUCAUCACUGCCU

.(((((((.(((.((((((.((&.........)).))))))..........)))....))))))). -25.80

>ENSG00000179036 hs-mir-34   3583   3590

UGGCAGUGUCUUAGCUGGUUGU&AACCCUCCUCCCCAAUUUGGGGGGUGUUGCCCCAUCACUGCCC

.(((((((.(((..(..((((.&............))))..)..)))...........))))))). -18.70

>ENSG00000179036 hs-mir-34   3636   3643

UGGCAGUGUCUUAGCUGGUUGU&ACUGCCCCCCCUGAAUUUAGGGUGGGGGUACUAGUCACUGCCAA

((((((((.....((((((...&.............................)))))))))))))). -22.80

mir-34    ENSMUSG00000020894  3731 nt UTR    3 hits 1116 1246 1298

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>ENSMUSG00000020894 hs-mir-34   1116   1123

UGGCAGUGUCUUAGCUGGUUGU&UUUGAGGAGGGGUGGCUCCAGUGUGUGGGGGUCAUCACUGCCU

.(((((((((((.(((((..((&..............)).))))).....))))....))))))). -24.40

>ENSMUSG00000020894 hs-mir-34   1246   1253

UGGCAGUGUCUUAGCUGGUUGU&UCCUCCCCAGUCUGGGGGGGGGGUAUUACCCCCAUCACUGCCC

.(((((((((((((((((....&......)))).))))))..................))))))). -25.16
```

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>ENSMUSG00000020894 hs-mir-34   1298   1305

UGGCAGUGUCUUAGCUGGUUGU&GACUGCCCCCUGUAUUCAGGUGGGGUACUAGUCACUGCCAA

((((((((.....((((((...&............................)))))))))))))). -22.80

mir-34    ENSRNOG00000006989  4248 nt UTR    4 hits 1629 1761 1813 2899

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>ENSRNOG00000006989 hs-mir-34   1629   1636

UGGCAGUGUCUUAGCUGGUUGU&UGAGGAGGGGUGGCUCUAGUGUGUGGGGGUCAUCACUGCCU

.(((((((.(((.(((((..((&............)).))))).......)))....))))))). -21.40

>ENSRNOG00000006989 hs-mir-34   1761   1768

UGGCAGUGUCUUAGCUGGUUGU&CCUCCCCAAUCCUGGGGGGGGUAUUACCCCCCAUCACUGCCC

.(((((((((((((..(((((.&......))))))))))).................))))))). -21.16

>ENSRNOG00000006989 hs-mir-34   1813   1820

UGGCAGUGUCUUAGCUGGUUGU&GACUGCCCCCUGUAUUCAGGUGGGGUACUAGUCACUGCCAA

((((((((.....((((((...&............................)))))))))))))). -22.80

>ENSRNOG00000006989 hs-mir-34   2899   2906

UGGCAGUGUCUUAGCUGGUUGU&GGUUGCCCUCUGUAUUCAGGUCAUGAGGGACUAGUCACUGCCAG

((((((((.....(((((((.(&.........................).))))))))))))))). -24.50

mir-34    SINFRUG00000131186  2000 nt UTR    2 hits 903 1844

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>SINFRUG00000131186 hs-mir-34    903    910

UGGCAGUGUCUUAGCUGGUUGU&GUAAUUGUCUAAAGCUGCCCCCCUUCCCCCCCCCACUGCCC

.(((((((...(((((......&............)))))................))))))). -18.10

>SINFRUG00000131186 hs-mir-34   1844   1851
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UGGCAGUGUCUUAGCUGGUUGU&CUGGUGCGUUUUUUGUAAUUCCGCUGUGCGUUAUACACUGCCAA

(((((((((....((((((...&......................)))).)).....))))))))). -23.20



miRNA: mir-96

Human predicted target: ENSG00000103365

Mouse predicted target: ENSMUSG00000030872

Rat predicted target: ENSRNOG00000018599

Fugu predicted target: SINFRUG00000145164

Hs Gene description: ADP-RIBOSYLATION FACTOR BINDING PROTEIN GGA2 (GOLGI-
LOCALIZED, GAMMA EAR-CONTAINING, ARF-BINDING PROTEIN 2) (GAMMA-ADAPTIN
RELATED PROTEIN 2) (VEAR) (VHS DOMAIN AND EAR DOMAIN OF GAMMA-ADAPTIN).
[Source:SWISSPROT;Acc:Q9UJY4] NM_138640

mir-96    ENSG00000103365     2000 nt UTR    1 hits 90

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>ENSG00000103365 hs-mir-96     90     97

UUUGGCACUAGCACAUUUUUGC&UCUAGUCAGGACUAAUCACGGUGUUUCAGUGCGGAGUGCCAAGA

(((((((((.((((........&............................))))..))))))))). -25.40

mir-96    ENSMUSG00000030872  2923 nt UTR    1 hits 83

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>ENSMUSG00000030872 hs-mir-96     83     90

UUUGGCACUAGCACAUUUUUGC&CUGUCUGGUCGGGACUUGUUGUAAUGUAGUGCAGAGUGCCAAGG

(((((((((.((((....((((&....................))))....))))..))))))))). -24.40

mir-96    ENSRNOG00000018599  2000 nt UTR    1 hits 87
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>ENSRNOG00000018599 hs-mir-96     87     94

UUUGGCACUAGCACAUUUUUGC&CUGUCUGGUUGGACUCCUUGUAAUGUCGUGCAGAGUGCCAAGA

(((((((((.((((....((((&...................))))....))))..))))))))). -24.40

mir-96    SINFRUG00000145164  2000 nt UTR    1 hits 925

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>SINFRUG00000145164 hs-mir-96    925    932

UUUGGCACUAGCACAUUUUUGC&CUAUGUACAUUUGUGUAACAGGGGUGUUAGAUAAAGUGCCAAAU

((((((((((((((.((.((((&..............)))).))..)))))......))))))))). -21.20




miRNA: mir-96

Human predicted target: ENSG00000103723

Mouse predicted target: ENSMUSG00000025586

Rat predicted target: ENSRNOG00000019161

Fugu predicted target: SINFRUG00000122270

Hs Gene description: CYTOPLASMIC POLYADENYLATION ELEMENT BINDING PROTEIN;
CYTOPLASMIC POLYADENYLATION ELEMENT-BINDING PROTEIN.
[Source:RefSeq;Acc:NM_030594] NM_030594

mir-96    ENSG00000103723     2319 nt UTR    1 hits 1183

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>ENSG00000103723 hs-mir-96   1183   1190

UUUGGCACUAGCACAUUUUUGC&CCACAAAAACUACUUGCCCCUCCUAGGGAAGCUGUGUGCCAAAG

((((((((((((..........&..............................)))).)))))))). -21.90
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mir-96    ENSMUSG00000025586  2898 nt UTR    2 hits 41 1107

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>ENSMUSG00000025586 hs-mir-96     41     48

UUUGGCACUAGCACAUUUUUGC&CAGCUAGAGGAGCUGGCCUUGCCCAGUGUCCUGUGGUGCCAAAG

(((((((((((.(((((...((&....................))..))))).)..)))))))))). -20.60

>ENSMUSG00000025586 hs-mir-96   1107   1114

UUUGGCACUAGCACAUUUUUGC&AUUUAACGAUUACUUGCCUCUCUUAGGGAAGCUGUGUGCCAAAG

((((((((((((..........&..............................)))).)))))))). -21.90

mir-96    ENSRNOG00000019161  3299 nt UTR    2 hits 1103 2340

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>ENSRNOG00000019161 hs-mir-96   1103   1110

UUUGGCACUAGCACAUUUUUGC&AUUUAGUUACUACUUGCCCCUCUUAGGGAAGCUGUGUGCCAAAG

((((((((((((..........&..............................)))).)))))))). -21.90

>ENSRNOG00000019161 hs-mir-96   2340   2347

UUUGGCACUAGCACAUUUUUGC&AUUUAGUUACUACUUGCCCCUCUUAGGGAAGCUGUGUGCCAAAG

((((((((((((..........&..............................)))).)))))))). -21.90

mir-96    SINFRUG00000122270  2000 nt UTR    1 hits 1131

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>SINFRUG00000122270 hs-mir-96   1131   1138

UUUGGCACUAGCACAUUUUUGC&CCUGUUCCAGUUGGAUAUAAAUGCAUAAAUAAGCUGUGCCAAAG

((((((((.(((..((((.(((&......................))).))))..))))))))))). -23.90
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```
miRNA: mir-96

Human predicted target: ENSG00000169992

Mouse predicted target: ENSMUSG00000019462

Rat predicted target: ENSRNOG00000015430

Fugu predicted target: SINFRUG00000131198

Fugu predicted target: SINFRUG00000131199

Fugu predicted target: SINFRUG00000146652

Hs Gene description: NEUROLIGIN 2. [Source:SPTREMBL;Acc:Q8NFZ4]

mir-96    ENSG00000169992     2212 nt UTR    3 hits 1066 1111 1639

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>ENSG00000169992 hs-mir-96   1066   1073

UUUGGCACUAGCACAUUUUUGC&AGCCUUUUCCCCAGGCCUCAGAGCAUUGCUCAUCCGUGCCAAAC

((((((((.((((...(((((.&..................)))))...)))).....)))))))). -19.50

>ENSG00000169992 hs-mir-96   1111   1118

UUUGGCACUAGCACAUUUUUGC&GGGUAGGUGGAUUUGAGCGGAAAGACUCCCAAAAUGUGCCAAGA

((((((((..((.((..((..(&......)..))..)).)).................)))))))). -20.21

>ENSG00000169992 hs-mir-96   1639   1646

UUUGGCACUAGCACAUUUUUGC&AGAGUCCUCAUCUGCUGGCAUUUUGUGGGGUGUUAGUGCCAAAC

((((((((((((((.....(((&.................))).........)))))))))))))). -27.44

mir-96    ENSMUSG00000019462  2000 nt UTR    3 hits 1242 1281 1821

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>ENSMUSG00000019462 hs-mir-96   1242   1249
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UUUGGCACUAGCACAUUUUUGC&GCCUUUUCCUCAGUCCUUGAGAUCAUUGCUCAUCCGUGCCAAAC
((((((((.((((.(((((...&..................)))))...)))).....)))))))). -17.80
>ENSMUSG00000019462 hs-mir-96   1281   1288
UUUGGCACUAGCACAUUUUUGC&CAAACUGGGUAGAUGGGUUGGGAGACUCUCAAAAUGUGCCAAGG
((((((((((((.(((((....&..........))))).))))...............)))))))). -17.66
>ENSMUSG00000019462 hs-mir-96   1821   1828
UUUGGCACUAGCACAUUUUUGC&UCUUCAUGUAUUGUUUGGCUUUCUGAGGGAUGUUAGUGCCAAAC
(((((((((((((..((((.((&.................)).....))))..))))))))))))). -24.70
mir-96    ENSRNOG00000015430  2000 nt UTR    2 hits 1226 1799
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>ENSRNOG00000015430 hs-mir-96   1226   1233
UUUGGCACUAGCACAUUUUUGC&GCCUUUUCCUCAGACCUUGAGAUCAUUGCUCAUCCGUGCCAAAC
((((((((.((((.(((((...&..................)))))...)))).....)))))))). -17.80
>ENSRNOG00000015430 hs-mir-96   1799   1806
UUUGGCACUAGCACAUUUUUGC&UCUCCAUGUGUUGUUUGGCUUUCUGAGGGAUGUUAGUGCCAAAC
(((((((((((((..((((.((&.................)).....))))..))))))))))))). -24.70
mir-96    SINFRUG00000131198  2000 nt UTR    1 hits 1320
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>SINFRUG00000131198 hs-mir-96   1320   1327
UUUGGCACUAGCACAUUUUUGC&AGCAGAGGGUAACAUGAUCCAGACUGUUAUUGACAGUGCCAAU
.((((((((..((..(((((((&.)))))))......................))..)))))))). -19.75
mir-96    SINFRUG00000131199  2000 nt UTR    2 hits 1051 1148
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>SINFRUG00000131199 hs-mir-96   1051   1058

UUUGGCACUAGCACAUUUUUGC&GAUAUUCUGAUAUCUCGUUUUUACCAGCAUUCUUGGUGCCAAGU

(((((((((((........(((&..........................)))...))))))))))). -18.30

>SINFRUG00000131199 hs-mir-96   1148   1155

UUUGGCACUAGCACAUUUUUGC&CAACUUGACUGUCAAAGAUUUACCAUCAUAAAAAAGUGCCAAGC

(((((((((.............&..................................))))))))). -17.20

mir-96    SINFRUG00000146652  2000 nt UTR    3 hits 549 641 1009

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>SINFRUG00000146652 hs-mir-96    549    556

UUUGGCACUAGCACAUUUUUGC&UUAAAACACUGAUCUCAUUUUUACCAGCGUUCUUGGUGCCAAGU

(((((((((((...........&................................))))))))))). -18.50

>SINFRUG00000146652 hs-mir-96    641    648

UUUGGCACUAGCACAUUUUUGC&AAAAUAUUAAGAGAAGCUGUGUGUUCUUAUAAGAAGUGCCAAAC

((((((((((((((((....((&...............)).))))))).........))))))))). -23.10

>SINFRUG00000146652 hs-mir-96   1009   1016

UUUGGCACUAGCACAUUUUUGC&GUUGUUUGUUUGAUUCUCUGAGUCCUGGCAGCCAUGUGCCAAGA

((((((((..((.......(((&...........................)))))...)))))))). -17.11
```

```
miRNA: mir-100

Human predicted target: ENSG00000132510

Mouse predicted target: ENSMUSG00000018476

Rat predicted target: ENSRNOG00000010142
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Fugu predicted target: SINFRUG00000131193

Fugu predicted target: SINFRUG00000148279

mir-100   ENSG00000132510     3275 nt UTR    1 hits 320

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>ENSG00000132510 hs-mir-100    320    327

AACCCGUAGAUCCGAACUUGUG&ACAAGGACCAGGCUCCGGCGGCGGCGGGGGUCACAUACGGGUUC

((((((((((((((..(((((.&)))))..)...................)))))...)))))))). -22.50

mir-100   ENSMUSG00000018476  2147 nt UTR    1 hits 319

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>ENSMUSG00000018476 hs-mir-100    319    326

AACCCGUAGAUCCGAACUUGUG&ACAAGGACCAGGCUCCGGCGGCGGCGGGGGUCACAUACGGGUUC

((((((((((((((..(((((.&)))))..)...................)))))...)))))))). -22.50

mir-100   ENSRNOG00000010142  2000 nt UTR    1 hits 308

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>ENSRNOG00000010142 hs-mir-100    308    315

AACCCGUAGAUCCGAACUUGUG&ACAAGGACCAGGCUCCGGCGGCGGCGGGGGUCACAUACGGGUUC

((((((((((((((..(((((.&)))))..)...................)))))...)))))))). -22.50

mir-100   SINFRUG00000131193  2000 nt UTR    1 hits 1440

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>SINFRUG00000131193 hs-mir-100   1440   1447

AACCCGUAGAUCCGAACUUGUG&AAAAAAAAAUCCUACUUUUGUCAGCUUCUCUAAAAUACGGGUUA

((((((((.....(((.(((..&.....................))).))).......)))))))). -17.50
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mir-100   SINFRUG00000148279  2000 nt UTR    1 hits 642

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>SINFRUG00000148279 hs-mir-100    642    649

AACCCGUAGAUCCGAACUUGUG&AAAAAACGUACAAAUGGUCGGAAUGCUUCAAAUCAUACGGGUUU

(((((((((((((((..(((((&........)))))....))))).........)).)))))))). -23.10




miRNA: mir-100

Human predicted target: ENSG00000163376

Mouse predicted target: ENSMUSG00000030031

Rat predicted target: ENSRNOG00000013390

Fugu predicted target: SINFRUG00000125449

Hs Gene description: T-CELL ACTIVATION KELCH REPEAT PROTEIN.
[Source:RefSeq;Acc:NM_032505] NM_032505

mir-100   ENSG00000163376     4825 nt UTR    1 hits 379

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>ENSG00000163376 hs-mir-100    379    386

AACCCGUAGAUCCGAACUUGUG&GUCUAAACUUGUUUGAUGUGACUUUUAAUUUUAAAUACGGGUA

.(((((((....(((((..((.&......))..)))))....................))))))). -18.05

mir-100   ENSMUSG00000030031  2000 nt UTR    1 hits 358

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>ENSMUSG00000030031 hs-mir-100    358    365

AACCCGUAGAUCCGAACUUGUG&GACAUCCAAACUGGUUAACGUGACUUUCUUUUAACUACGGGUA
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.((((((((.((((((((.((.&.........)).))))..)).))...........)))))))). -18.70

mir-100   ENSRNOG00000013390  2000 nt UTR    1 hits 362

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>ENSRNOG00000013390 hs-mir-100    362    369

AACCCGUAGAUCCGAACUUGUG&AAUCCAAACUGGUUAACGUGACUUUUUAUUUUAAAUACGGUA

.(((((((..((((((((.((.&.......)).))))..)).))..............))))))). -16.69

mir-100   SINFRUG00000125449  2000 nt UTR    1 hits 441

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>SINFRUG00000125449 hs-mir-100    441    448

AACCCGUAGAUCCGAACUUGUG&CAGAAAUGGCUAUAUAUAAACUCAAACUAUAUAACUACGGUA

.((((((((.............&.................................)))))))). -18.90



miRNA: mir-101

Human predicted target: ENSG00000124788

Mouse predicted target: ENSMUSG00000046876

Rat predicted target: ENSRNOG00000016998

Fugu predicted target: SINFRUG00000136920

Fugu predicted target: SINFRUG00000149524

Hs Gene description: ATAXIN-1 (SPINOCEREBELLAR ATAXIA TYPE 1 PROTEIN).
[Source:SWISSPROT;Acc:P54253]

mir-101   ENSG00000124788     9219 nt UTR    3 hits 58 1000 1174

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>ENSG00000124788 hs-mir-101     58     65

UACAGUACUGUGAUAACUGA&CGUGGCUCUCCCUUAUCAUUUGUAUCCAGAUUACUGUACUGUAG

((((((((.(((((..(((.&..........................)))))))).)))))))). -21.20

>ENSG00000124788 hs-mir-101   1000   1007

UACAGUACUGUGAUAACUGA&UUGAGUUUGCGAAAUCUUUUUGUCUUUGAACUCUAGUACUGUU

.(((((((((.((.......&...............................))))))))))). -15.90

>ENSG00000124788 hs-mir-101   1174   1181

UACAGUACUGUGAUAACUGA&UUUAUUACCAAGCAUCUUGGUCUCUCAUUCAACAAGUACUGUAU

(((((((((.(((....(((&........................))).)))...))))))))). -18.30

mir-101   ENSMUSG00000046876  2589 nt UTR    3 hits 59 1030 1215

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>ENSMUSG00000046876 hs-mir-101     59     66

UACAGUACUGUGAUAACUGA&CGGGGCCUCCUUUUACUGUCUGUAUCCAGAUUACUGUACUGUAG

((((((((.(((((..(((.&..........................)))))))).)))))))). -21.20

>ENSMUSG00000046876 hs-mir-101   1030   1037

UACAGUACUGUGAUAACUGA&UGUGCCGGCAGCAUCUUUUCUGUAUUUUAGGUCUAGUACUGUU

.(((((((((.(((..((((&..........................)))))))))))))))). -17.90

>ENSMUSG00000046876 hs-mir-101   1215   1222

UACAGUACUGUGAUAACUGA&UUCUUAACCAAGCAUCUUGGUCUGUCAUUCAACAAGUACUGUAU

(((((((((((((((((..(&.................)..)).)))))).....))))))))). -20.90

mir-101   ENSRNOG00000016998  2534 nt UTR    3 hits 60 989 1111
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>ENSRNOG00000016998 hs-mir-101     60     67

UACAGUACUGUGAUAACUGA&CGUGGGCCCCGUUUGCUGUCUGUAUCCAGAUUACUGUACUGUAG

((((((((.(((((..(((.&..........................)))))))).)))))))). -21.20

>ENSRNOG00000016998 hs-mir-101    989    996

UACAGUACUGUGAUAACUGA&CAGCUGGCAGCAUAAUUGUCCACCUCUUAGGUCUAGUACUGUU

.(((((((((.(((....((&........................))....))))))))))))). -17.90

>ENSRNOG00000016998 hs-mir-101   1111   1118

UACAGUACUGUGAUAACUGA&UUCUUAACCAAGCACCUUGUUCUGUCAUUCAACAAGUACUGUAU

(((((((((.(((..((.((&....................)).))...)))...))))))))). -19.10

mir-101   SINFRUG00000136920  2000 nt UTR    1 hits 1042

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>SINFRUG00000136920 hs-mir-101   1042   1049

UACAGUACUGUGAUAACUGA&GUGAGUAUAGAUAUUCUAAUCCUCAUGUAGUGUAUGUACUGUAU

((((((((.(((...((((.&...........................)))).))))))))))). -17.40

mir-101   SINFRUG00000149524  2000 nt UTR    1 hits 923

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>SINFRUG00000149524 hs-mir-101    923    930

UACAGUACUGUGAUAACUGA&CUGUCCACAUUUGUUUAUGUCUCUUUAUCUACGCAGUACUGUAU

((((((((((((........&...............................)))))))))))). -23.20



miRNA: mir-101
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Human predicted target: ENSG00000127314

Mouse predicted target: ENSMUSG00000020200

Rat predicted target: ENSRNOG00000007048

Fugu predicted target: SINFRUG00000129510

Hs Gene description: RAS-RELATED PROTEIN RAP-1 (GTP-BINDING PROTEIN SMG
P21B). [Source:SWISSPROT;Acc:P09526]    NM_015646

mir-101   ENSG00000127314     3273 nt UTR    2 hits 309 965

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>ENSG00000127314 hs-mir-101    309    316

UACAGUACUGUGAUAACUGA&UUCAUCCACCAAUGUUGUACAUGUAUGAAAAUGGUGUACUGUAU

((((((((.((((((((...&.............))))).))).............)))))))). -16.44

>ENSG00000127314 hs-mir-101    965    972

UACAGUACUGUGAUAACUGA&GUAACGUUUUGGUUGAGAUGUUAAAUGGUGGACGAGUACUGUGG

(((((((((.((...(((..&..........................)))...))))))))))). -17.50

mir-101   ENSMUSG00000020200  3340 nt UTR    4 hits 305 961 2865 3178

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>ENSMUSG00000020200 hs-mir-101    305    312

UACAGUACUGUGAUAACUGA&UUCAUCCACCAAUGUUGUACAUGUAUGAAAAUGGUGUACUGUAU

((((((((.((((((((...&.............))))).))).............)))))))). -16.44

>ENSMUSG00000020200 hs-mir-101    961    968

UACAGUACUGUGAUAACUGA&GUAACGUUUCGGUUGAGAUGUUAACUGGUGGACGAGUACUGUGG

((((((((((..((((((((&........)))))))................)).))))))))). -18.17

>ENSMUSG00000020200 hs-mir-101   2865   2872
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UACAGUACUGUGAUAACUGA&AGACUUUAUCUUGCUGUUUCCUUUCGUUCUUUAUUGUACUGUU

.(((((((.((((.(((.((&.......................)))))..)))).))))))). -15.50

>ENSMUSG00000020200 hs-mir-101   3178   3185

UACAGUACUGUGAUAACUGA&UUCAUCCACCAAUGUUGUACAUGUAUGAAAAUGGUGUACUGUAU

((((((((.((((((((...&.............))))).))).............)))))))). -16.44

mir-101   ENSRNOG00000007048  3254 nt UTR    4 hits 310 966 2796 3114

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>ENSRNOG00000007048 hs-mir-101    310    317

UACAGUACUGUGAUAACUGA&UUCAUCCACCAAUGUUGUACAUGUAUGAAAAUGGUGUACUGUAU

((((((((.((((((((...&.............))))).))).............)))))))). -16.44

>ENSRNOG00000007048 hs-mir-101    966    973

UACAGUACUGUGAUAACUGA&GUAACGUUUUGGUUGAGAUGUUAAAUGGUGGACGAGUACUGUGG

(((((((((.((...(((..&..........................)))...))))))))))). -17.50

>ENSRNOG00000007048 hs-mir-101   2796   2803

UACAGUACUGUGAUAACUGA&AACCUUUAUCUUAGUGUUUCCUUUCAUUCUUUAUUGUACUGUU

.(((((((.((((..(.(((&.......................))).)..)))).))))))). -15.80

>ENSRNOG00000007048 hs-mir-101   3114   3121

UACAGUACUGUGAUAACUGA&UUCAUCCACCAAUGUUGUACAUGUAUGAAAAUGGUGUACUGUAU

((((((((.((((((((...&.............))))).))).............)))))))). -16.44

mir-101   SINFRUG00000129510  2000 nt UTR    2 hits 1467 1905

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>SINFRUG00000129510 hs-mir-101   1467   1474

UACAGUACUGUGAUAACUGA&UGAUGGCCCUGUUGCCCCAGGGUGAGGGAAGAUGUGUACUGUGC
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((((((((........((..&.........................))........)))))))). -14.49

>SINFRUG00000129510 hs-mir-101   1905   1912

UACAGUACUGUGAUAACUGA&CUGCUGUUGAGUGUUGAGUACUGCAGUACUUAGAAGUACUGUU

.((((((((.(((..((((.&.......................))))..)))..)))))))). -18.60




miRNA: mir-101

Human predicted target: ENSG00000170242

Mouse predicted target: ENSMUSG00000045151

Rat predicted target: ENSRNOG00000016651

Fugu predicted target: SINFRUG00000136891

Fugu predicted target: SINFRUG00000136901

Hs Gene description: NM_017944

mir-101   ENSG00000170242     2393 nt UTR    1 hits 205

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>ENSG00000170242 hs-mir-101    205    212

UACAGUACUGUGAUAACUGA&UUGACUCGGAAUCAUGUUGUGCACUAUAGUCAAAUGUACUGUAA

((((((((.(((((((((((&...........))).))))).)))...........)))))))). -20.40

mir-101   ENSMUSG00000045151  3265 nt UTR    1 hits 198

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>ENSMUSG00000045151 hs-mir-101    198    205

UACAGUACUGUGAUAACUGA&UUGACUUGGAAUCAUGUUGUGCACUAUGGUCAGAUGUACUGUAA

((((((((.(((((((((((&...........))).))))).)))...........)))))))). -20.40
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mir-101   ENSRNOG00000016651  3229 nt UTR    1 hits 199

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>ENSRNOG00000016651 hs-mir-101    199    206

UACAGUACUGUGAUAACUGA&UUGACUUGGAAUCAUGUUGUGCACUAUAGUCAGAUGUACUGUAA

((((((((.(((((((((((&...........))).))))).)))...........)))))))). -20.40

mir-101   SINFRUG00000136891  2000 nt UTR    1 hits 480

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>SINFRUG00000136891 hs-mir-101    480    487

UACAGUACUGUGAUAACUGA&CAGCUCAGAAACUCUGUUGUGCACUAUAGUGUAUUGUACUGUAA

((((((((.((((((((.((&............)).))))).)))...........)))))))). -19.40

mir-101   SINFRUG00000136901  2000 nt UTR    1 hits 188

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>SINFRUG00000136901 hs-mir-101    188    195

UACAGUACUGUGAUAACUGA&CAGCUCAGAAACUCUGUUGUGCACUAUAGUGUAUUGUACUGUAA

((((((((.((((((((.((&............)).))))).)))...........)))))))). -19.40



miRNA: mir-103

Human predicted target: ENSG00000141433

Mouse predicted target: ENSMUSG00000024256

Rat predicted target: ENSRNOG00000014921

Fugu predicted target: SINFRUG00000134427
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Hs Gene description: PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE
PRECURSOR (PACAP) [CONTAINS: PACAP-RELATED PEPTIDE (PRP-48); PITUITARY
ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE-27 (PACAP-27) (PACAP27);
PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE-38 (PACAP-38)
(PACAP38)]. [Source:SWISSPROT;Acc:P18509]    NM_001117

mir-103   ENSG00000141433     3418 nt UTR    2 hits 1921 2120

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>ENSG00000141433 hs-mir-103   1921   1928

AGCAGCAUUGUACAGGGCUAUGA&AAACAGAAUUGGAUUUGCAUUCCCAGGCGGGAUGGAUGCUGCC

.((((((((((...(((..(((.&.................))).)))..))......)))))))). -21.20

>ENSG00000141433 hs-mir-103   2120   2127

AGCAGCAUUGUACAGGGCUAUGA&CCACGAAUCACAGAUGGCUAUUUAGUGGCCCUACAAUGCUGCA

.(((((((((((..(((((((..&........................)))))))))))))))))). -34.30

mir-103   ENSMUSG00000024256  2000 nt UTR    2 hits 1400 1821

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>ENSMUSG00000024256 hs-mir-103   1400   1407

AGCAGCAUUGUACAGGGCUAUGA&CCAAUCUUUGUCAUAUUAGAAUGUGUAGUGUUCCAAUGCUGCUC

((((((((((...((.(((((..&........................))))).)).)))))))))). -
24.20

>ENSMUSG00000024256 hs-mir-103   1821   1828

AGCAGCAUUGUACAGGGCUAUGA&AACAACUGUAUUUGCAUUCCCAGGUGGGUGGAUGGAUGCUGCC

.((((((((.(((.(((..(((.&..............))).)))......)))....)))))))). -20.40

mir-103   ENSRNOG00000014921  2000 nt UTR    2 hits 1437 1880

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>ENSRNOG00000014921 hs-mir-103   1437   1444
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AGCAGCAUUGUACAGGGCUAUGA&CCAAUCUUUGUCAUAUUAGAAUGUGUAGUGUUCCAAUGCUGCUC

((((((((((...((.(((((..&........................))))).)).)))))))))). -
24.20

>ENSRNOG00000014921 hs-mir-103   1880   1887

AGCAGCAUUGUACAGGGCUAUGA&AAAAACUGUAUUUGCAUUCCCAGGCGGGUGGAUGGAUGCUGCC

.((((((((((...(((..(((.&..............))).)))..)).........)))))))). -20.80

mir-103   SINFRUG00000134427  2000 nt UTR    2 hits 423 1197

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>SINFRUG00000134427 hs-mir-103    423    430

AGCAGCAUUGUACAGGGCUAUGA&GAAAUAAAUAGUUUAAAAGACAAUCAAUGUGCUGAAUGCUGCUU

(((((((((((((((((((((..&.......))))))).............))))).))))))))). -
23.61

>SINFRUG00000134427 hs-mir-103   1197   1204

AGCAGCAUUGUACAGGGCUAUGA&GAAAUAAAUAGUUUAAAAGACAAUCAAUGUGCUGAAUGCUGCUU

(((((((((((((((((((((..&.......))))))).............)))))..))))))))). -
23.61




miRNA: mir-122a

Human predicted target: ENSG00000139514

Mouse predicted target: ENSMUSG00000041313

Rat predicted target: ENSRNOG00000000924

Fugu predicted target: SINFRUG00000142273

Hs Gene description: HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-
1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL
LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).
[Source:SWISSPROT;Acc:P30825] NM_003045
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mir-122a  ENSG00000139514     3866 nt UTR    2 hits 1091 1364

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>ENSG00000139514 hs-mir-122a   1091   1098

UGGAGUGUGACAAUGGUGUUUGU&GAAAUUGAAAUCAAUCCACAGUCCAUGAAAUUGUGACACUCCAC

((((((((.(((((.(((.((((&.................))))..)))...))))).)))))))). -
25.80

>ENSG00000139514 hs-mir-122a   1364   1371

UGGAGUGUGACAAUGGUGUUUGU&CUGGGUCGGGGCCUGCGGCCAGCACCAUUUCACACACACUCCU

.((((((((..(((((((((.((&.................)).))))))))).....)))))))). -29.30

mir-122a  ENSMUSG00000041313  2358 nt UTR    1 hits 331

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>ENSMUSG00000041313 hs-mir-122a    331    338

UGGAGUGUGACAAUGGUGUUUGU&CCCUCCCUGGGACCACCCUGGCAUCGCCCAUGUGCACACUCCAG

((((((((((((..((((..(((&....................))).))))..))).))))))))). -
28.70

mir-122a  ENSRNOG00000000924  2309 nt UTR    1 hits 325

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>ENSRNOG00000000924 hs-mir-122a    325    332

UGGAGUGUGACAAUGGUGUUUGU&CCUUCCCUGGGACCACCCUGCGUACACUCAUACGUACACUCCAG

(((((((((...(((((((.(((&...................))).)))).)))...))))))))). -
26.50

mir-122a  SINFRUG00000142273  2000 nt UTR    1 hits 935

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>SINFRUG00000142273 hs-mir-122a    935    942

UGGAGUGUGACAAUGGUGUUUGU&CAUGGACACACUGACGGGAAAUGAGCACACACACCACACUCCC

.((((((((......(((((..(&....................)..))))).......)))))))). -25.30



miRNA: mir-124a

Human predicted target: ENSG00000070882

Mouse predicted target: ENSMUSG00000029822

Rat predicted target: ENSRNOG00000010011

Fugu predicted target: SINFRUG00000137005

Hs Gene description: OXYSTEROL BINDING PROTEIN-RELATED PROTEIN 3 (OSBP-
RELATED PROTEIN 3) (ORP-3). [Source:SWISSPROT;Acc:Q9H4L5]   NM_145321

mir-124a  ENSG00000070882     5643 nt UTR    3 hits 336 656 1053

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>ENSG00000070882 hs-mir-124a    336    343

UUAAGGCACGCGGUGAAUGCCA&UUUCCAAAGGUUAGGGAAGAUUCCAAUUAAAUUUAUGCCUUAU

.(((((((..............&...................................))))))). -13.70

>ENSG00000070882 hs-mir-124a    656    663

UUAAGGCACGCGGUGAAUGCCA&GAAGCAUUUGAACUUGUUCCUCCCUAUAGUUCUAUUGCCUUAU

.(((((((.(((((((((((..&...))))))..))).))..................))))))). -16.21

>ENSG00000070882 hs-mir-124a   1053   1060

UUAAGGCACGCGGUGAAUGCCA&ACCAUAUUUUAGAUCUUGUAUAAAAAGUUGCCAUCUGCCUUAU

.(((((((...((..(......&.............................)..))...))))))). -18.40
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mir-124a  ENSMUSG00000029822  2258 nt UTR    2 hits 336 1027

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>ENSMUSG00000029822 hs-mir-124a    336    343

UUAAGGCACGCGGUGAAUGCCA&AAUUUUCCAGAGGUAAGGGGGAAAUUUCAAAUUUAUGCCUUAU

.(((((((.....((((..((.&...................))....))))......))))))). -18.50

>ENSMUSG00000029822 hs-mir-124a   1027   1034

UUAAGGCACGCGGUGAAUGCCA&CGCCCUUUUGACCUUGUAUAGCCAGUUUGACCAUCUGCCUUAU

.(((((((...(((.((.((..&....................))....)).)))...))))))). -18.60

mir-124a  ENSRNOG00000010011  2000 nt UTR    3 hits 342 641 1040

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>ENSRNOG00000010011 hs-mir-124a    342    349

UUAAGGCACGCGGUGAAUGCCA&AAUUUUCCAAAGGUAAGGGGGAAAAUUCAGAUUUAUGCCUUAU

.(((((((.....(((((.((.&...................))...)))))......))))))). -19.20

>ENSRNOG00000010011 hs-mir-124a    641    648

UUAAGGCACGCGGUGAAUGCCA&CAACCGGAAGAAGUCUUCUCUCCCUCGAGUUCUGUUGCCUUAU

.(((((((.((((.........&...............................))))))))))). -16.90

>ENSRNOG00000010011 hs-mir-124a   1040   1047

UUAAGGCACGCGGUGAAUGCCA&CGUACUUUUGACCUUGUAUAGAGAGUUUGACCAUCUGCCUUAU

.(((((((...(((.((.....&..........................)).)))...))))))). -17.80

mir-124a  SINFRUG00000137005  2000 nt UTR    2 hits 118 379

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>SINFRUG00000137005 hs-mir-124a    118    125
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UUAAGGCACGCGGUGAAUGCCA&AAUGGACAUACUUUCAAUCCUGUUUAUUGCACUUUUGCCUUAAC

((((((((.(((((((((....&.....................)))))))))).....)))))))). -21.00

>SINFRUG00000137005 hs-mir-124a    379    386

UUAAGGCACGCGGUGAAUGCCA&CUGUUUAAGUUCAUAUGUAUUCAGCACUUGCCCGAUGCCUUAC

.(((((((((.((..(.(((..&.......................))).)..)))).))))))). -25.60




miRNA: mir-124a

Human predicted target: ENSG00000110422

Mouse predicted target: ENSMUSG00000027177

Rat predicted target: ENSRNOG00000011358

Fugu predicted target: SINFRUG00000121575

Fugu predicted target: SINFRUG00000133436

Hs Gene description: HOMEODOMAIN INTERACTING PROTEIN KINASE 3;
HOMEODOMAIN-INTERACTING PROTEIN KINASE 3. [Source:RefSeq;Acc:NM_005734]
     NM_005734

mir-124a  ENSG00000110422     2737 nt UTR    1 hits 550

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>ENSG00000110422 hs-mir-124a    550    557

UUAAGGCACGCGGUGAAUGCCA&AUCUCAGCUGCAUUGUAAACCGUUCCUACACAUAGUGCCUUAAA

((((((((((((((.(((((..&.........)))))....))))).........))))))))). -26.10

mir-124a  ENSMUSG00000027177  2090 nt UTR    1 hits 564

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>ENSMUSG00000027177 hs-mir-124a    564    571
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UUAAGGCACGCGGUGAAUGCCA&ACUCUCAGCUGCAUUGUAACCGUUCCCACACAUAGUGCCUUAAA

((((((((((((((.(((((..&..........)))))...)))))...........))))))))). -26.70

mir-124a  ENSRNOG00000011358  2072 nt UTR    1 hits 566

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>ENSRNOG00000011358 hs-mir-124a    566    573

UUAAGGCACGCGGUGAAUGCCA&AUCUCAGCUGCAUUGUAAACCGUUCCCACACAUAGUGCCUUAAA

((((((((((((((.(((((..&.........)))))....)))))...........))))))))). -26.10

mir-124a  SINFRUG00000121575  2000 nt UTR    1 hits 698

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>SINFRUG00000121575 hs-mir-124a    698    705

UUAAGGCACGCGGUGAAUGCCA&ACUCGCUGCAUUGUCUAACCUGUCCCCAACCAUAGUGCCUUAC

.(((((((((((((((......&..))))))).........................)))))))). -23.21

mir-124a  SINFRUG00000133436  2000 nt UTR    1 hits 564

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>SINFRUG00000133436 hs-mir-124a    564    571

UUAAGGCACGCGGUGAAUGCCA&UUUGGGAGGCAGAACUCGUUACUGCUCCUCCUCAGUGCCUUAC

.(((((((((((((((.((((.&.......))))......))))))).........)))))))). -28.30



miRNA: mir-124a

Human predicted target: ENSG00000163403

Mouse predicted target: ENSMUSG00000035158

Rat predicted target: ENSRNOG00000008651
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Rat predicted target: ENSRNOG00000008658

Fugu predicted target: SINFRUG00000141734

Hs Gene description: MICROPHTHALMIA-ASSOCIATED TRANSCRIPTION FACTOR.
[Source:SWISSPROT;Acc:O75030]

mir-124a  ENSG00000163403     2000 nt UTR    2 hits 485 1585

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>ENSG00000163403 hs-mir-124a    485    492

UUAAGGCACGCGGUGAAUGCCA&UUUUCCAUUUUAUAAAUGUAUUGAUUCAUUGGUACUGCCUUAAA

((((((((..((((((((....&.......................))))))))....)))))))). -21.00

>ENSG00000163403 hs-mir-124a   1585   1592

UUAAGGCACGCGGUGAAUGCCA&GCAAGUGGCAUAAAGCAUAUCCAUUCAGAAUGAAGUGCCUUAAA

(((((((((...(((.((((((&.....))))))....)))................))))))))). -24.11

mir-124a  ENSMUSG00000035158  2527 nt UTR    2 hits 548 1640

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>ENSMUSG00000035158 hs-mir-124a    548    555

UUAAGGCACGCGGUGAAUGCCA&UUUCUCGCUUUCUAAAUGCGGCAAUUUCCUGGUACUGCCUUAAA

((((((((..(((..((((((.&...................)))).))..)))....)))))))). -24.00

>ENSMUSG00000035158 hs-mir-124a   1640   1647

UUAAGGCACGCGGUGAAUGCCA&CUGUGUGGCAUAAAGCAUACCCUUUCAGAAUGAAGUGCCUUAAA

(((((((((...(((.((((((&.....))))))....)))................))))))))). -24.11

mir-124a  ENSRNOG00000008651  2000 nt UTR    1 hits 469

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>ENSRNOG00000008651 hs-mir-124a    469    476
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UUAAGGCACGCGGUGAAUGCCA&UUCAGAAAGAGAACUGUGGUCAAGCAUUCUGUCUGUGCCUUAAU

((((((((((....((((((..&.......................))))))....)))))))))). -26.30

mir-124a  ENSRNOG00000008658  2835 nt UTR    2 hits 958 2046

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>ENSRNOG00000008658 hs-mir-124a    958    965

UUAAGGCACGCGGUGAAUGCCA&UUUCUCACUUUAUAAAUGUGUCGAUUCCCUGGUACUGCCUUAAA

((((((((..(((.((((((((&................)).))..)))).)))....)))))))). -18.10

>ENSRNOG00000008658 hs-mir-124a   2046   2053

UUAAGGCACGCGGUGAAUGCCA&GCGAGCGGCAUAAAACUUAUCCUUUCAGAAUGAAGUGCCUUAAA

(((((((((..(((..(((((.&......)))))...))).................))))))))). -24.31

mir-124a  SINFRUG00000141734  2000 nt UTR    2 hits 555 1447

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>SINFRUG00000141734 hs-mir-124a    555    562

UUAAGGCACGCGGUGAAUGCCA&CUCCUCGUGUCUUAGAUGAAACUUGAACGUGUUGAUGCCUUAU

.(((((((((((..........&...........................))))....))))))). -17.40

>SINFRUG00000141734 hs-mir-124a   1447   1454

UUAAGGCACGCGGUGAAUGCCA&GACGCGACCUCCUUAUGCAUUAAGUCCAUAAUUAGUGCCUUAU

.((((((((..((..(((((..&................)))))....)).......)))))))). -21.50
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miRNA: mir-125b

Human predicted target: ENSG00000068724

Mouse predicted target: ENSMUSG00000036918

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Rat predicted target: ENSRNOG00000014879

Fugu predicted target: SINFRUG00000131832

Fugu predicted target: SINFRUG00000141548

Hs Gene description: TETRATRICOPEPTIDE REPEAT PROTEIN 7 (TPR REPEAT
PROTEIN 7) (FRAGMENT). [Source:SWISSPROT;Acc:Q9ULT0]

mir-125b  ENSG00000068724     3407 nt UTR    3 hits 97 1469 2785

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>ENSG00000068724 hs-mir-125b     97    104

UCCCUGAGACCCUAACUUGUGA&UCAGGGUGGGGCAACAGUGGCAUCAGGUGCGGGGCCUCAGGGAA

((((((((.((((.(((((((.&....................)).)))))..)))).)))))))). -33.00

>ENSG00000068724 hs-mir-125b   1469   1476

UCCCUGAGACCCUAACUUGUGA&GAAAAGUAAAGAAAAAGCAAAUGCUGUUGGUUUAUCUCAGGGU

.((((((((..(((((..((..&......................)).)))))....)))))))). -22.60

>ENSG00000068724 hs-mir-125b   2785   2792

UCCCUGAGACCCUAACUUGUGA&CGAAUGUUGGAGAGUCACGCAGCGGUGGAGACCUGCUCAGGGC

.(((((((...((.((((((((&..............)))))....)))..)).....))))))). -21.30

mir-125b  ENSMUSG00000036918   3693 nt UTR    2 hits 106 488

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>ENSMUSG00000036918 hs-mir-125b     106    113

UCCCUGAGACCCUAACUUGUGA&GGGGGCAGGGAAGGGCGUGUGUCCAGAUGUGGGGCCUCAGGGAA

((((((((.(((((.(((((..&....)))))....................))))).)))))))). -30.40

>ENSMUSG00000036918 hs-mir-125b     488    495

UCCCUGAGACCCUAACUUGUGA&UGCCGGAGAGCCCCGGAUACAUUUCCCCAUCCGAUCUCAGGGC
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.((((((((.............&..................................)))))))). -18.50

mir-125b  ENSRNOG00000014879  2000 nt UTR    1 hits 73

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>ENSRNOG00000014879 hs-mir-125b     73     80

UCCCUGAGACCCUAACUUGUGA&GGGGGCAGGGAAGGCACCAUCCGGAUGUGGGGGCCUCAGGAA

((((((((.(((((.(((((..&....)))))...................)))))..)))))))). -30.25

mir-125b  SINFRUG00000131832  2000 nt UTR    1 hits 500

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>SINFRUG00000131832 hs-mir-125b    500    507

UCCCUGAGACCCUAACUUGUGA&GCCGUGGGAGGAGAAAACACGGCUGGAUCGCGGUCCUCAGGGAC

((((((((((((((.(.((((.&.................))))).))).....))).)))))))). -25.40

mir-125b  SINFRUG00000141548  2000 nt UTR    1 hits 1907

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>SINFRUG00000141548 hs-mir-125b   1907   1914

UCCCUGAGACCCUAACUUGUGA&UGUCUGAACGGAGGAGGAGAGUAUGUCCUGUUUCCUCAGGGC

.(((((((..(((..(((((..&.......)))))...))).................))))))). -19.81



miRNA: mir-128

Human predicted target: ENSG00000055070

Mouse predicted target: ENSMUSG00000040842

Rat predicted target: ENSRNOG00000009183

Fugu predicted target: SINFRUG00000123544
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Fugu predicted target: SINFRUG00000124328

Hs Gene description: NM_015609

mir-128   ENSG00000055070     5002 nt UTR    4 hits 121 145 167 197

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>ENSG00000055070 hs-mir-128    121    128

UCACAGUGAACCGGUCUCUUUU&UGGACUUGAGCAGAGGGAACGACCUGACUUACUUGCACUGUGAU

((((((((....((((((((((&............))))))..))))...........)))))))). -21.76

>ENSG00000055070 hs-mir-128    145    152

UCACAGUGAACCGGUCUCUUUU&UGACUUACUUGCACUGUGAUCCCCCUUGCUCCGCCCACUGUGAC

((((((((...(((........&..............................)))..)))))))). -19.30

>ENSG00000055070 hs-mir-128    167    174

UCACAGUGAACCGGUCUCUUUU&CCCUUGCUCCGCCCACUGUGACCUUGAACCCCAUGCACUGUGAC

((((((((....((..((....&.........................))..))....)))))))). -20.20

>ENSG00000055070 hs-mir-128    197    204

UCACAGUGAACCGGUCUCUUUU&CCAUGCACUGUGACCUCCCCCCUUCUCCCCCUUCCCACUGUGAU

((((((((....((((.(....&.........).))))....................)))))))). -18.25

mir-128   ENSMUSG00000040842  2000 nt UTR    4 hits 118 142 164 192

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>ENSMUSG00000040842 hs-mir-128    118    125

UCACAGUGAACCGGUCUCUUUU&UGGACUUGAGCAGAGGGAAUAACCUGACUUACUUGCACUGUGAU

((((((((....((((((((((&............)))))).......))))......)))))))). -20.51

>ENSMUSG00000040842 hs-mir-128    142    149
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UCACAGUGAACCGGUCUCUUUU&UGACUUACUUGCACUGUGAUCCCCCUUGCUCCGCCCACUGUGAC

((((((((...(((........&..............................)))..)))))))). -19.30

>ENSMUSG00000040842 hs-mir-128    164    171

UCACAGUGAACCGGUCUCUUUU&CCCUUGCUCCGCCCACUGUGACCUUGAACCCCAUGCACUGUGAC

((((((((....((..((....&.........................))..))....)))))))). -20.20

>ENSMUSG00000040842 hs-mir-128    192    199

UCACAGUGAACCGGUCUCUUUU&CCCCAUGCACUGUGACCUCUGCCUCCCCCCCUUCCCACUGUGAU

((((((((....((((.(....&...........).))))..................)))))))). -18.35

mir-128   ENSRNOG00000009183  2530 nt UTR    8 hits 116 140 162 190 640
664 686 714

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>ENSRNOG00000009183 hs-mir-128    116    123

UCACAGUGAACCGGUCUCUUUU&UGGACUUGAGCAGAGGGAAUAACCUGACUUACUUGCACUGUGAU

((((((((....((((((((((&............)))))).......)))).......)))))))). -20.51

>ENSRNOG00000009183 hs-mir-128    140    147

UCACAGUGAACCGGUCUCUUUU&UGACUUACUUGCACUGUGAUCCCCCUUGCUCCGCCCACUGUGAC

((((((((...(((........&..............................)))..)))))))). -19.30

>ENSRNOG00000009183 hs-mir-128    162    169

UCACAGUGAACCGGUCUCUUUU&CCCUUGCUCCGCCCACUGUGACCUUGAACCCCAUGCACUGUGAC

((((((((....((..((....&.........................))..))....)))))))). -20.20

>ENSRNOG00000009183 hs-mir-128    190    197

UCACAGUGAACCGGUCUCUUUU&CCCCAUGCACUGUGACCUCUGCCUCCCCCCCUUCCCACUGUGAU

((((((((....((((.(....&...........).))))..................)))))))). -18.35

>ENSRNOG00000009183 hs-mir-128    640    647
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UCACAGUGAACCGGUCUCUUUU&UGGACUUGAGCAGAGGGAAUAACCUGACUUACUUGCACUGUGAU

((((((((....((((((((((&............)))))).......))))......)))))))). -20.51

>ENSRNOG00000009183 hs-mir-128    664    671

UCACAGUGAACCGGUCUCUUUU&UGACUUACUUGCACUGUGAUCCCCCUUGCUCCGCCCACUGUGAC

((((((((...(((........&..............................)))..)))))))). -19.30

>ENSRNOG00000009183 hs-mir-128    686    693

UCACAGUGAACCGGUCUCUUUU&CCCUUGCUCCGCCCACUGUGACCUUGAACCCCAUGCACUGUGAC

((((((((....((..((....&.........................))..))....)))))))). -20.20

>ENSRNOG00000009183 hs-mir-128    714    721

UCACAGUGAACCGGUCUCUUUU&CCCCAUGCACUGUGACCUCUGCCUCCCCCCUUCCCACUGUGAU

((((((((....((((.(....&...........).))))..................)))))))). -18.35

mir-128   SINFRUG00000123544  2000 nt UTR    2 hits 878 906

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>SINFRUG00000123544 hs-mir-128    878    885

UCACAGUGAACCGGUCUCUUUU&CGCGCUCUUCUCUUAUACCACCCCGAGUCGGUUGACACUGUGAU

((((((((((((((.(((....&........................)))))))))..)))))))). -27.00

>SINFRUG00000123544 hs-mir-128    906    913

UCACAGUGAACCGGUCUCUUUU&CGGUUGACACUGUGAUCGUGGACGUCUUCUGCUCUCACUGUGAC

(((((((((.((((((.(....&...........).))))).)..............))))))))). -20.76

mir-128   SINFRUG00000124328  2000 nt UTR    1 hits 313

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>SINFRUG00000124328 hs-mir-128    313    320

UCACAGUGAACCGGUCUCUUUU&CCGCUGCGAACGGGCCUUCAGCUCACAUCCCUCUACACUGUGAU
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((((((((....(((((.(((.&.......))).)))))...................)))))))). -18.70



miRNA: mir-128

Human predicted target: ENSG00000070444

Mouse predicted target: ENSMUSG00000000282

Rat predicted target: ENSRNOG00000002894

Fugu predicted target: SINFRUG00000136074

Hs Gene description: MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST
MNT). [Source:SWISSPROT;Acc:Q99583]     NM_020310

mir-128   ENSG00000070444     4136 nt UTR    2 hits 614 2563

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>ENSG00000070444 hs-mir-128    614    621

UCACAGUGAACCGGUCUCUUUU&GGCCUCAGCCUGGGGCUCUCUGACCCGGUUGCAGUCACUGUGAU

((((((((((((((((......&.....................)))).))).....))))))))). -25.90

>ENSG00000070444 hs-mir-128   2563   2570

UCACAGUGAACCGGUCUCUUUU&CCAGAGGUGGCCCUUGUUUACAGUGAGGACUCGGCCACUGUGU

.(((((((..((((((.(((..&........................)))))).))).))))))). -23.70

mir-128   ENSMUSG00000000282  4381 nt UTR    4 hits 321 589 780 2119

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>ENSMUSG00000000282 hs-mir-128    321    328

UCACAGUGAACCGGUCUCUUUU&CGCUCCAUCUCCCUGUUUUGUCCCCUGGAAGUCUGCACUGUGGC

((((((((....((..(((...&..........................)))..))..)))))))). -18.00
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>ENSMUSG00000000282 hs-mir-128    589    596

UCACAGUGAACCGGUCUCUUUU&GGCCUGGGCCUGGGCCACUCUGACCCACCUGUGGUCACUGUGAU

(((((((((.(((((((.....&.....))))).)).....................))))))))). -23.95

>ENSMUSG00000000282 hs-mir-128    780    787

UCACAGUGAACCGGUCUCUUUU&GGUGUGGACCAGCAAGGGCUCUAGGAGCUAAGGUACACUGUGGA

((((((((.(((((.(((((..&......................)))))))..))).)))))))). -24.40

>ENSMUSG00000000282 hs-mir-128   2119   2126

UCACAGUGAACCGGUCUCUUUU&AAAGAGGUGGCCCUUGUUUACAGUGAGGACUUGGUCACUGUGU

.((((((((.((((((.(((..&........................))))))).)))))))))). -24.60

mir-128   ENSRNOG00000002894  4278 nt UTR    2 hits 330 2015

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>ENSRNOG00000002894 hs-mir-128    330    337

UCACAGUGAACCGGUCUCUUUU&ACCUCCCUGCUUUGUCCCCCCCCCCAGGAAGUCUGCACUGUGGC

((((((((....((..((((..&.........................))))..))..)))))))). -18.70

>ENSRNOG00000002894 hs-mir-128   2015   2022

UCACAGUGAACCGGUCUCUUUU&AAAGAGGUGGCCCUUGUUUACAGUGAGGACUUGGUCACUGUGU

.((((((((.((((((.(((..&........................))))))).)))))))))). -24.60

mir-128   SINFRUG00000136074  2000 nt UTR    1 hits 1106

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>SINFRUG00000136074 hs-mir-128   1106   1113

UCACAGUGAACCGGUCUCUUUU&AUGUGUUUUAUUCAGUACUAUUUUAGGCCAGGCAGCACUGUGAA

((((((((..(((((((.....&........................))))).))...)))))))). -25.40
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miRNA: mir-131

Human predicted target: ENSG00000015153

Mouse predicted target: ENSMUSG00000022634

Rat predicted target: ENSRNOG00000004773

Rat predicted target: ENSRNOG00000005254

Fugu predicted target: SINFRUG00000122248

Fugu predicted target: SINFRUG00000152392

Hs Gene description: YY1 ASSOCIATED FACTOR 2.
[Source:RefSeq;Acc:NM_005748] NM_005748

mir-131   ENSG00000015153     3555 nt UTR    1 hits 703

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>ENSG00000015153 hs-mir-131    703    710

UAAAGCUAGAUAACCGAAAGU&CUAGCGGACUAGUAAACAAUAAAACAUUGAUUAUUUAGCUUUAU

(((((((((((((.(((....&..........................))).))))))))))))). -19.50

mir-131   ENSMUSG00000022634  3109 nt UTR    1 hits 691

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>ENSMUSG00000022634 hs-mir-131    691    698

UAAAGCUAGAUAACCGAAAGU&ACUGUUCACUAGUAGACAGUACGACGUGGCUUGUUUAGCUUUC

.(((((((((((((((...((&.......................)).))).))))))))))))). -19.70

mir-131   ENSRNOG00000004773  2000 nt UTR    1 hits 697

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>ENSRNOG00000004773 hs-mir-131    697    704

UAAAGCUAGAUAACCGAAAGU&CUAGCUGAAUAGUAAACAAUAAAACACGGACUGUGUAGCUUUC

.(((((((.(((.(((.....&..........................)))..))).))))))). -17.60

mir-131   ENSRNOG00000005254  3403 nt UTR    2 hits 652 1683

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>ENSRNOG00000005254 hs-mir-131    652    659

UAAAGCUAGAUAACCGAAAGU&UUUCAAAGCCUCGGUUUGUUGUACUGUUUACUAGGUAGCUUUC

.((((((((((((((((....&..........)))))).)))...............))))))). -15.66

>ENSRNOG00000005254 hs-mir-131   1683   1690

UAAAGCUAGAUAACCGAAAGU&CUAGCUGAAUAGUAAACAAUAAAACACGGACUGUGUAGCUUUC

.(((((((.(((.(((.....&..........................)))..))).))))))). -17.60

mir-131   SINFRUG00000122248  2000 nt UTR    1 hits 1409

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>SINFRUG00000122248 hs-mir-131   1409   1416

UAAAGCUAGAUAACCGAAAGU&UGAUUACCAUAUGUGAUGUUACCCCGCUGCUUCAUUAGCUUUU

.((((((((............&..................................)))))))). -11.70

mir-131   SINFRUG00000152392  2000 nt UTR    1 hits 1911

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>SINFRUG00000152392 hs-mir-131   1911   1918

UAAAGCUAGAUAACCGAAAGU&GACGUCGGGAGAAUAGCUGCUCAGAAACUUGCGGCUAGCUUUU

.((((((((....(((.((((&..........................)))).))))))))))). -18.60
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miRNA: mir-131

Human predicted target: ENSG00000120549

Mouse predicted target: ENSMUSG00000036617

Rat predicted target: ENSRNOG00000008666

Fugu predicted target: SINFRUG00000139197

mir-131   ENSG00000120549     3350 nt UTR    1 hits 460

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>ENSG00000120549 hs-mir-131    460    467

UAAAGCUAGAUAACCGAAAGU&GAUACUAUAAUAUUUCCUUUUAUUUUAGUGUUAUUUAGCUUUAU

(((((((((((((((.(((((&.....................))))).).)))))))))))))). -21.40

mir-131   ENSMUSG00000036617  3314 nt UTR    1 hits 466

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>ENSMUSG00000036617 hs-mir-131    466    473

UAAAGCUAGAUAACCGAAAGU&UAUAUUAUGAUAUUUUCUUUUAUUUUAGUGUUAUUUAGCUUUAU

(((((((((((((((.(((((&.....................))))).).)))))))))))))). -21.40

mir-131   ENSRNOG00000008666  3304 nt UTR    1 hits 459

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>ENSRNOG00000008666 hs-mir-131    459    466

UAAAGCUAGAUAACCGAAAGU&UAUAUUACGAUAUUUUCUUUUAUUUUAGUGUUAUUUAGCUUUAU

(((((((((((((((.(((((&.....................))))).).)))))))))))))). -21.40

mir-131   SINFRUG00000139197  2000 nt UTR    2 hits 88 1521

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>SINFRUG00000139197 hs-mir-131     88     95

UAAAGCUAGAUAACCGAAAGU&GCAGUGUGAAUAAUCAGUUUCAGCGGCGCAGGAAGUAGCUUUAC

((((((((.....((....((&.........................))...))...)))))))). -13.20

>SINFRUG00000139197 hs-mir-131   1521   1528

UAAAGCUAGAUAACCGAAAGU&UGCAUGGUCUUGUAUAAUAUUUCACCAACAUCUGGUAGCUUUU

.(((((((.....(((.....&................................)))))))))). -11.10



miRNA: mir-135b

Human predicted target: ENSG00000053254

Mouse predicted target: ENSMUSG00000033713

Rat predicted target: ENSRNOG00000004709

Fugu predicted target: SINFRUG00000137365

Hs Gene description: CHECKPOINT SUPPRESSOR 1 (FORKHEAD BOX PROTEIN N3).
[Source:SWISSPROT;Acc:O00409] NM_005197

mir-135b  ENSG00000053254     3029 nt UTR    3 hits 211 780 2620

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>ENSG00000053254 hs-mir-135b    211    218

UAUGGCUUUUUAUUCCUAUGUGAU&UGGACCCUUAAGAAUUUAUUUUUAAAGGAGAUUGAAGCCAUAG

(((((((((...(((((.......&.........................)))))...))))))))). -
22.00

>ENSG00000053254 hs-mir-135b    780    787

UAUGGCUUUUUAUUCCUAUGUGAU&AUUCUGUUCUAUUAAAUUAAGAAAAUGUUCCAAAAGCCAUAA

((((((((((..............&...............................)))))))))). -
16.20
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>ENSG00000053254 hs-mir-135b   2620   2627

UAUGGCUUUUUAUUCCUAUGUGAU&GUUCCCUCCGUCUCCCCAGACAUCUGACACCCUAAAAGCCAUC

.(((((((((...((..((((...&...................))))..))......))))))))). -
16.50

mir-135b  ENSMUSG00000033713  2310 nt UTR    2 hits 236 798

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>ENSMUSG00000033713 hs-mir-135b    236    243

UAUGGCUUUUUAUUCCUAUGUGAU&GGACCCUUAAAAUUUUUUCUGUUUAAAGGAGAUUGAAGCCAUAG

(((((((((...(((((.......&..........................)))))...))))))))). -
22.00

>ENSMUSG00000033713 hs-mir-135b    798    805

UAUGGCUUUUUAUUCCUAUGUGAU&GAGUUCUGCUCUAUGUUAAAUUAAGAAGACUUCCAAAGCCAUAA

(((((((((...(((.((..((((&..............))))...)).))).......))))))))). -
15.60

mir-135b  ENSRNOG00000004709  3495 nt UTR    3 hits 217 720 1863

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>ENSRNOG00000004709 hs-mir-135b    217    224

UAUGGCUUUUUAUUCCUAUGUGAU&UGGACCCUUAAGAAUUUUCUGUUUAAAGGAGAUUGAAGCCAUAG

(((((((((...(((((.......&..........................)))))...))))))))). -
22.00

>ENSRNOG00000004709 hs-mir-135b    720    727

UAUGGCUUUUUAUUCCUAUGUGAU&GUUCUGCUCUAUGUUAAAUCAAGAAGACGUUCCAAAAGCCAUAA

((((((((((.((..((...((((&.................))))...))..))...)))))))))). -
17.70

>ENSRNOG00000004709 hs-mir-135b   1863   1870
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UAUGGCUUUUUAUUCCUAUGUGAU&GUUCUGCUCUAUGUUAAAUCAAGAAGACGUUCCAAAAGCCAUAA

((((((((((.((..((...((((&.................))))...))..))...)))))))))). -
17.70

mir-135b  SINFRUG00000137365  2000 nt UTR    1 hits 291

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>SINFRUG00000137365 hs-mir-135b    291    298

UAUGGCUUUUUAUUCCUAUGUGAU&UGUCUUUGUUGUUUUGUUGUUUAAAAGGGGAUGAAAGCCAUAA

((((((((((.((((((.......&..........................)))))))))))))))). -
23.70




miRNA: mir-135b

Human predicted target: ENSG00000145925

Mouse predicted target: ENSMUSG00000025867

Mouse predicted target: ENSMUSG00000033615

Rat predicted target: ENSRNOG00000000105

Fugu predicted target: SINFRUG00000121517

Fugu predicted target: SINFRUG00000145582

Hs Gene description: COMPLEXIN 2 (SYNAPHIN 1) (921-L).
[Source:SWISSPROT;Acc:Q13329] NM_006651

mir-135b  ENSG00000145925     2183 nt UTR    2 hits 1741 1927

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>ENSG00000145925 hs-mir-135b   1741   1748

UAUGGCUUUUUAUUCCUAUGUGAU&AAUCCCACUGCAAUGGACCCAGGCAGCGCCCCAGGAAGCCAUGC
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(((((((((((.......(((...&......................))).......))))))))))). -
18.34

>ENSG00000145925 hs-mir-135b   1927   1934

UAUGGCUUUUUAUUCCUAUGUGAU&AGACAUGUGUCUUCUCUGUCCGUUUCCAAUAGGUAAAGCCAUAU

(((((((((.....(((((..((.&........................))..))))).))))))))). -
20.40

mir-135b  ENSMUSG00000025867  2000 nt UTR    2 hits 1756 1941

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>ENSMUSG00000025867 hs-mir-135b   1756   1763

UAUGGCUUUUUAUUCCUAUGUGAU&AAUGCUACUGGACAGACCCAGGCAGUACCCUAGGAAGCCAUGC

((((((((((((.(((((.(((..&.....))))))))..................)))))))))))). -
20.71

>ENSMUSG00000025867 hs-mir-135b   1941   1948

UAUGGCUUUUUAUUCCUAUGUGAU&AGACAGACGUCUUCCCUGUCCGUUUCCAAUAGUUAAAGCCAUAU

((((((((((((((...(((.(((&.................))))))....)))))..))))))))). -
17.70

mir-135b  ENSMUSG00000033615  3569 nt UTR    2 hits 110 1246

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>ENSMUSG00000033615 hs-mir-135b    110    117

UAUGGCUUUUUAUUCCUAUGUGAU&GGGAGCAGAUGCAGCCCCCCUACCCCCGCAAAAAUAAGCCAUAG

(((((((((((.(((((.......&))))).)))..........................)))))))). -
16.36

>ENSMUSG00000033615 hs-mir-135b   1246   1253

UAUGGCUUUUUAUUCCUAUGUGAU&CAUUGACCUUCAUGACCUUACAUAGCUCUUUAGAGAAGCCAUAA

(((((((((((....((((((((.&.................)))))))).......))))))))))). -
24.20
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mir-135b  ENSRNOG00000000105  2000 nt UTR    2 hits 1689 1875

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>ENSRNOG00000000105 hs-mir-135b   1689   1696

UAUGGCUUUUUAUUCCUAUGUGAU&AAUGCUACUGGGACAGACCCAGGCAGUGCCCCAGGAAGCCAUGC

(((((((((((..(((((.(((..&.....))))))))...................))))))))))). -
19.30

>ENSRNOG00000000105 hs-mir-135b   1875   1882

UAUGGCUUUUUAUUCCUAUGUGAU&AGACAGACGUCUUCCCUGUCCGUUUCCAAUAGUUAAAGCCAUAU

((((((((((((((...(((.(((&.................))))))....)))))..))))))))). -
17.70

mir-135b  SINFRUG00000121517  2000 nt UTR    2 hits 1493 1663

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>SINFRUG00000121517 hs-mir-135b   1493   1500

UAUGGCUUUUUAUUCCUAUGUGAU&GUUUUUUUAGCUCAGAUAGGACUUUUCACUAGACGAAGCCAUAU

(((((((((....((((((.(((.&...........))).)))))).............))))))))). -
23.43

>SINFRUG00000121517 hs-mir-135b   1663   1670

UAUGGCUUUUUAUUCCUAUGUGAU&GGCUGACGUAAACACAGAGAACACGUAUGUAGAAGAAGCCAUU

.((((((((((...(.((((((..&.....................)))))).)...)))))))))). -
23.50

mir-135b  SINFRUG00000145582  2000 nt UTR    1 hits 235

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>SINFRUG00000145582 hs-mir-135b    235    242

UAUGGCUUUUUAUUCCUAUGUGAU&ACGUGAAACGUGACAUAUAUCAAGAUACAGAGUAUAAGCCAUAU
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((((((((..(((((.(((.((((&..................))))..)))..))))).)))))))). -19.70

miRNA: mir-135b

Human predicted target: ENSG00000158186

Mouse predicted target: ENSMUSG00000032470

Rat predicted target: ENSRNOG00000014060

Fugu predicted target: SINFRUG00000121799

Hs Gene description: RAS-RELATED PROTEIN M-RAS (RAS-RELATED PROTEIN R-RAS3). [Source:SWISSPROT;Acc:O14807]   NM_012219

mir-135b ENSG00000158186   2178 nt UTR   2 hits 365 1131

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>ENSG00000158186 hs-mir-135b   365   372

UAUGGCUUUUUAUUCCUAUGUGAU&UGUGGAAGUGUUUAUCCACAUACAAAGUACAAAACAAGCCAUGA

((((((((..((((..((((((..&................))))))...))))......)))))))). -18.30

>ENSG00000158186 hs-mir-135b   1131   1138

UAUGGCUUUUUAUUCCUAUGUGAU&CAAUACUGUUAUCACUAAAACAGCACCAAGACCUGAAGCCAUC

.((((((((..........(((((&..........)))))...................)))))))). -15.55

mir-135b ENSMUSG00000032470 2425 nt UTR   3 hits 313 1016 1857

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>ENSMUSG00000032470 hs-mir-135b   313   320

UAUGGCUUUUUAUUCCUAUGUGAU&UAUGGAAGUGCUUACCCACAUACAACGCACCAGACAAGCCAUGA

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((((((((........((((((..&................)))))).............)))))))). -
17.20

>ENSMUSG00000032470 hs-mir-135b   1016   1023

UAUGGCUUUUUAUUCCUAUGUGAU&GCUCAAUACUAUUAUCUCAGAAGCCCCAGGACCUGAAGCCAUU

.((((((((....((((.((.(((&.............))).))........))))...)))))))). -
18.30

>ENSMUSG00000032470 hs-mir-135b   1857   1864

UAUGGCUUUUUAUUCCUAUGUGAU&AUGCUCUACACUCAGGGCAGCAGCCACUGCCAGAGAAGCCAUGU

(((((((((((..((((..(((..&........)))..))))...............))))))))))). -
21.33

mir-135b  ENSRNOG00000014060  2480 nt UTR    3 hits 318 1011 1814

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>ENSRNOG00000014060 hs-mir-135b    318    325

UAUGGCUUUUUAUUCCUAUGUGAU&UGGAAGUGCUUUUAUCCACAUUCAACGCACCAGACAAGCCAUGA

((((((((.........(((((..&................)))))..............)))))))). -
16.50

>ENSRNOG00000014060 hs-mir-135b   1011   1018

UAUGGCUUUUUAUUCCUAUGUGAU&CCGAAGGCACUGCUGUCUGGGAAGCCCCAGGACUGAAGCCAUC

.((((((((...((((((...(((&..............))))))))).........)))))))). -
18.04

>ENSRNOG00000014060 hs-mir-135b   1814   1821

UAUGGCUUUUUAUUCCUAUGUGAU&AUAGUCCACACUCAGGGCAGCAGCCACUGCCAGAGAAGCCAUGU

(((((((((((..((((..(((..&........)))..))))...............))))))))))). -
21.33

mir-135b  SINFRUG00000121799  2000 nt UTR    1 hits 1169

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>SINFRUG00000121799 hs-mir-135b   1169   1176

UAUGGCUUUUUAUUCCUAUGUGAU&UCUGGUGCCGUAGCCCUGGGACCCGCCGGGCCCGAAGCCAUGU

(((((((((....((((..(((..&......................))).))))...))))))))). -
20.40




miRNA: mir-135b

Human predicted target: ENSG00000172845

Mouse predicted target: ENSMUSG00000027109

Mouse predicted target: ENSMUSG00000041788

Rat predicted target: ENSRNOG00000019263

Fugu predicted target: SINFRUG00000140785

Hs Gene description: TRANSCRIPTION FACTOR SP3 (SPR-2) (FRAGMENT).
[Source:SWISSPROT;Acc:Q02447]

mir-135b  ENSG00000172845     3411 nt UTR    2 hits 633 886

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>ENSG00000172845 hs-mir-135b    633    640

UAUGGCUUUUUAUUCCUAUGUGAU&ACUCUAGGGAUAGUCACCUUUUAAAUCCUGUUGAAAGCCAUGU

((((((((((((((((((......&....))))))....................)))))))))))). -
21.09

>ENSG00000172845 hs-mir-135b    886    893

UAUGGCUUUUUAUUCCUAUGUGAU&CUUGUUUCCAAAAACCAUGUCUCCCAGGGCCUUAAAAGCCAUC

.(((((((((...((((..(.(((&..................))).)..))))....))))))))). -
19.70

mir-135b  ENSMUSG00000027109  3632 nt UTR    2 hits 628 910
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>ENSMUSG00000027109 hs-mir-135b    628    635

UAUGGCUUUUUAUUCCUAUGUGAU&CCUUUAGGGAUAGUCACCUUUUAAAUCCUGUUGAAAGCCAUGU

((((((((((((((((((......&....)))))).....................)))))))))))). -
21.19

>ENSMUSG00000027109 hs-mir-135b    910    917

UAUGGCUUUUUAUUCCUAUGUGAU&AAAAAAAAAAAAAAAAUAUGUCUGCCAGGGCCUUAAAAGCCAUC

.(((((((((...((((....(((&..................)))....))))....))))))))). -
19.20

mir-135b  ENSMUSG00000041788  2000 nt UTR    1 hits 1252

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>ENSMUSG00000041788 hs-mir-135b   1252   1259

UAUGGCUUUUUAUUCCUAUGUGAU&UUAGUUGUAGGCAAUGAAGUUUAUGUGGGUUGCAAAAGCCAUAG

((((((((((....(((((((((.&....................)))))))))....)))))))))). -
25.50

mir-135b  ENSRNOG00000019263  3628 nt UTR    2 hits 630 900

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>ENSRNOG00000019263 hs-mir-135b    630    637

UAUGGCUUUUUAUUCCUAUGUGAU&CCUUUAGGGAUAGUCACCUUUUAAAUCCUGUUGAAAGCCAUGU

((((((((((((((((((......&....)))))).....................)))))))))))). -
21.19

>ENSRNOG00000019263 hs-mir-135b    900    907

UAUGGCUUUUUAUUCCUAUGUGAU&CUUGUUUCCAAAAAAUAUGUCUGCCAGGGCCUUAAAAGCCAUC

.(((((((((...((((....(((&..................)))....))))....))))))))). -
19.20
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mir-135b  SINFRUG00000140785  2000 nt UTR    1 hits 1182

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>SINFRUG00000140785 hs-mir-135b   1182   1189

UAUGGCUUUUUAUUCCUAUGUGAU&ACAUGUAUGUUAUCUUAUUUUCACAUUGUUCAUAGAAGCCAUU

.(((((((((.......((((((.&....................)))))).......))))))))). -
21.94




miRNA: mir-135b

Human predicted target: ENSG00000173153

Mouse predicted target: ENSMUSG00000024955

Rat predicted target: ENSRNOG00000021139

Fugu predicted target: SINFRUG00000131162

Hs Gene description: STEROID HORMONE RECEPTOR ERR1 (ESTROGEN-RELATED
RECEPTOR, ALPHA) (ERR-ALPHA) (ESTROGEN RECEPTOR-LIKE 1).
[Source:SWISSPROT;Acc:P11474] NM_004451

mir-135b  ENSG00000173153     2779 nt UTR    2 hits 228 267

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>ENSG00000173153 hs-mir-135b    228    235

UAUGGCUUUUUAUUCCUAUGUGAU&UGUGUCCAGGCUCUGGGCACAGUGCUGCCCCUUGCAAGCCAUAA

((((((((..........((((..&.................))))..............)))))))). -
16.45

>ENSG00000173153 hs-mir-135b    267    274

UAUGGCUUUUUAUUCCUAUGUGAU&CAUAACGUGCCCCCAGAGUGUAGGGGGCCUUGCGGAAGCCAUAG

((((((((((..((((((..(...&.................)..)))))).......)))))))))). -
22.40
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mir-135b  ENSMUSG00000024955  2773 nt UTR    2 hits 237 278

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>ENSMUSG00000024955 hs-mir-135b    237    244

UAUGGCUUUUUAUUCCUAUGUGAU&GAAUGCCCAGGUGUGGGCACAGUGCUGCCCCUUGCAAGCCAUAA

(((((((((((((.(((..((...&....))..))).)))))..................)))))))). -
16.46

>ENSMUSG00000024955 hs-mir-135b    278    285

UAUGGCUUUUUAUUCCUAUGUGAU&UAACGUGCCCCCCAAGAGUGUUGGGGGCCUCGCGGAAGCCAUAG

((((((((((..((((((......&.....................))))))......)))))))))). -
19.30

mir-135b  ENSRNOG00000021139  2765 nt UTR    4 hits 226 269 935 978

---------11--------------------------1-1----------------------------------
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>ENSRNOG00000021139 hs-mir-135b    226    233

UAUGGCUUUUUAUUCCUAUGUGAU&GAAUGCCCAGGUGUGGGCACAGUGCUGCCCCUUGCAAGCCAUAA

(((((((((((((.(((..((...&....))..))).)))))..................)))))))). -
16.46

>ENSRNOG00000021139 hs-mir-135b    269    276

UAUGGCUUUUUAUUCCUAUGUGAU&ACGUGCCCCUCCCAGAGUGUCGGGGGCCUUGCGGAAGCCAUAG

((((((((((....(((...((((&..................)))).)))......)))))))))). -
19.40

>ENSRNOG00000021139 hs-mir-135b    935    942

UAUGGCUUUUUAUUCCUAUGUGAU&GAAUGCCCAGGUGUGGGCACAGUGCUGCCCCUUGCAAGCCAUAA

(((((((((((((.(((..((...&....))..))).)))))..................)))))))). -
16.46

>ENSRNOG00000021139 hs-mir-135b    978    985
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UAUGGCUUUUUAUUCCUAUGUGAU&ACGUGCCCCCUCCCAGAGUGUCGGGGGCCUUGCGGAAGCCAUAG

((((((((((....(((...((((&...................)))).)))......)))))))))). -
19.40

mir-135b  SINFRUG00000131162  2000 nt UTR    3 hits 484 1117 1456

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>SINFRUG00000131162 hs-mir-135b    484    491

UAUGGCUUUUUAUUCCUAUGUGAU&GCUGAACGUGGACCGGGAGGAGUUUGUUAUGCUAAAAGCCAUC

.(((((((((.((((((.......&.................))))))..........))))))))). -
19.30

>SINFRUG00000131162 hs-mir-135b   1117   1124

UAUGGCUUUUUAUUCCUAUGUGAU&CGUACCCAUGCACAAACUCUUCCUGGAGAUGCUGGAAGCCAUGA

(((((((((((((..(((((((..&..........)))).........)))..)))..)))))))))). -
20.30

>SINFRUG00000131162 hs-mir-135b   1456   1463

UAUGGCUUUUUAUUCCUAUGUGAU&AAAUAAACAUAAACAAUGGAACAUGUAACUCCUGAAAGCCAUAG

((((((((((......((((((..&.....................))))))......)))))))))). -
20.80
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miRNA: mir-137

Human predicted target: ENSG00000142178

Mouse predicted target: ENSMUSG00000024042

Rat predicted target: ENSRNOG00000001189

Fugu predicted target: SINFRUG00000135301

Hs Gene description: PROBABLE SERINE/THREONINE PROTEIN KINASE SNF1LK (EC 2.7.1.-). [Source:SWISSPROT;Acc:P57059] NM_173354

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mir-137   ENSG00000142178     4227 nt UTR    2 hits 104 1894

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>ENSG00000142178 hs-mir-137    104    111

UAUUGCUUAAGAAUACGCGUAG&UGGCCUCAAAGCCAAGAACUUUCUAGAAGCGAAAUAAGCAAUAC

(((((((((......(((.(((&......................)))...)))...))))))))). -15.50

>ENSG00000142178 hs-mir-137   1894   1901

UAUUGCUUAAGAAUACGCGUAG&AAAGGCCUCAGAAACCAUUGUGUGUUUCCUCUUUGAAGCAAUGA

(((((((((((((((((((...&..................)))))))....))))..)))))))). -19.00

mir-137   ENSMUSG00000024042  3967 nt UTR    2 hits 77 147

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>ENSMUSG00000024042 hs-mir-137     77     84

UAUUGCUUAAGAAUACGCGUAG&CCACCCCCCCCAACCGUGGCCGAUUGACUCUUCCAAGCAAUAA

((((((((((((((.((((...&...............))))....))....))))..)))))))). -15.60

>ENSMUSG00000024042 hs-mir-137    147    154

UAUUGCUUAAGAAUACGCGUAG&GGACUCAAAAGCCAAGAACUUUCUAGACGUGAAACAAGCAAUAC

((((((((.....((((..(((&......................)))..))))....)))))))). -15.40

mir-137   ENSRNOG00000001189  3642 nt UTR    2 hits 54 123

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>ENSRNOG00000001189 hs-mir-137     54     61

UAUUGCUUAAGAAUACGCGUAG&ACCCCUGCCCCCCACCCCACGGAUGGACUCUUCCAAGCAAUAA

((((((((((((...(((((..&...................)))..))...))))..)))))))). -15.30

>ENSRNOG00000001189 hs-mir-137    123    130
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UAUUGCUUAAGAAUACGCGUAG&GGACUCAAAAGCCAAGAACUUUCUAGACGUGAAACAAGCAAUAU

((((((((.....((((..(((&......................)))..))))....)))))))). -15.50

mir-137   SINFRUG00000135301  2000 nt UTR    2 hits 800 843

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>SINFRUG00000135301 hs-mir-137    800    807

UAUUGCUUAAGAAUACGCGUAG&ACUGGUGUGUUAUCUUCUGUUAUAAGCUAAAUACCAAGCAAUAA

((((((((((((((((((.(((&.)))))))))..))))...................)))))))). -17.50

>SINFRUG00000135301 hs-mir-137    843    850

UAUUGCUUAAGAAUACGCGUAG&ACCAAACUCUAGAAAAAAGAGUCAGACAGACAGAAAAGCAAUAA

((((((((..............&...................................)))))))). -12.60




miRNA: mir-137

Human predicted target: ENSG00000169764

Mouse predicted target: ENSMUSG00000001891

Rat predicted target: ENSRNOG00000008079

Fugu predicted target: SINFRUG00000128752

Hs Gene description: UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE 2 (EC
2.7.7.9) (UDP- GLUCOSE PYROPHOSPHORYLASE 2) (UDPGP 2) (UGPASE 2).
[Source:SWISSPROT;Acc:Q16851]

mir-137   ENSG00000169764     2335 nt UTR    2 hits 328 1677

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>ENSG00000169764 hs-mir-137    328    335

UAUUGCUUAAGAAUACGCGUAG&UUUGAAUUGCUUGUGAUUUCAAAAAUAAAGCAGUGAAGCAAUAC
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((((((((.(((.((((.((((&......)))).)))).)))...............)))))))). -13.03

>ENSG00000169764 hs-mir-137   1677   1684

UAUUGCUUAAGAAUACGCGUAG&UUGGUCACUGAAACAAAAAUUGAAUUCCUAAAUCCAAGCAAUC

.(((((((..............&...................................))))))). -10.80

mir-137   ENSMUSG00000001891  2878 nt UTR    2 hits 178 1645

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>ENSMUSG00000001891 hs-mir-137    178    185

UAUUGCUUAAGAAUACGCGUAG&UGCAAUGAGCUUUUAGUCUAAGGAAAGCAUAGAUGAAGCAAUAC

((((((((.....((.((.(((&.................)))......)).))....)))))))). -13.60

>ENSMUSG00000001891 hs-mir-137   1645   1652

UAUUGCUUAAGAAUACGCGUAG&UUGGUCAUUAAAACAAAAACUGAAUUCCUAAAUCCAAGCAAUC

.(((((((..............&...................................))))))). -10.80

mir-137   ENSRNOG00000008079  2000 nt UTR    2 hits 176 1543

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>ENSRNOG00000008079 hs-mir-137    176    183

UAUUGCUUAAGAAUACGCGUAG&UGCAAUGAGCUUUUAGUCUAAGGAAAGCCUAAACAAAGCAAUAC

((((((((..............&...................................)))))))). -12.30

>ENSRNOG00000008079 hs-mir-137   1543   1550

UAUUGCUUAAGAAUACGCGUAG&UUGGUCACUAAAACAAAAACUGAAUUUCUAAAUCCAAGCAAUC

.(((((((..............&...................................))))))). -10.80

mir-137   SINFRUG00000128752  2000 nt UTR    1 hits 1377

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>SINFRUG00000128752 hs-mir-137   1377   1384

UAUUGCUUAAGAAUACGCGUAG&UGGUUUCAGUGAGAAUACUUGAGACGUGGACCUGAAAGCAAUAA

((((((((.((....(((((..&.......................)))))...))..)))))))). -19.20



miRNA: mir-138

Human predicted target: ENSG00000114993

Mouse predicted target: ENSMUSG00000034930

Rat predicted target: ENSRNOG00000009022

Fugu predicted target: SINFRUG00000154952

Hs Gene description: RHOTEKIN. [Source:RefSeq;Acc:NM_033046]     NM_033046

mir-138   ENSG00000114993     2381 nt UTR    2 hits 441 2363

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>ENSG00000114993 hs-mir-138    441    448

AGCUGGUGUUGUGAAUC&CUAGACCUGCCUCACAUCAUCCCUGGAGCAUAGUUCACCAGCUG

((((((((.(((((...&...........))))).......................)))))))). -21.15

>ENSG00000114993 hs-mir-138   2363   2370

AGCUGGUGUUGUGAAUC&AGUACAAUGUUGGGACCCUUUGCUGGGAUGUCAAACACCAGCA

.(((((((((.((((((&..........................))).))))))))))))). -22.40

mir-138   ENSMUSG00000034930  2355 nt UTR    2 hits 1532 2069

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>ENSMUSG00000034930 hs-mir-138   1532   1539

AGCUGGUGUUGUGAAUC&UGCUUCUACAGGGAAAGGGUGAGAGGUGGCUCUUUCACCAGCUC
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((((((((....((..(&...........................)..))...)))))))). -18.80

>ENSMUSG00000034930 hs-mir-138   2069   2076

AGCUGGUGUUGUGAAUC&GUCUGGGAGAUGGUAGAUUCCAACUUCUGGAUUCACACCAGCG

.((((((((...(((((&.............................))))))))))))). -22.40

mir-138   ENSRNOG00000009022  2331 nt UTR    2 hits 1697 1960

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>ENSRNOG00000009022 hs-mir-138   1697   1704

AGCUGGUGUUGUGAAUC&GUCCCUAGACCUCCUGACCUGGUGUCAGGCAGACACACCAGCUA

(((((((((.((.....&................................))))))))))). -20.80

>ENSRNOG00000009022 hs-mir-138   1960   1967

AGCUGGUGUUGUGAAUC&AUCUGGGAGAUGGUAGGCUCCAACUUCUGGAUUCACACCAGCG

.((((((((...(((((&.............................))))))))))))). -22.40

mir-138   SINFRUG00000154952  2000 nt UTR    2 hits 1136 1412

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>SINFRUG00000154952 hs-mir-138   1136   1143

AGCUGGUGUUGUGAAUC&GCCAGCGUGACGUCCGACAGCGACAGCCACUGCAGCACCAGCC

.(((((((((((.....&...............................))))))))))). -24.30

>SINFRUG00000154952 hs-mir-138   1412   1419

AGCUGGUGUUGUGAAUC&CAGACCACGCUGUCCUGCUCCAGCUCCACCUCCAGCACCAGCUC

(((((((((((.((...&..............................))))))))))))). -24.40



miRNA: mir-140
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Human predicted target: ENSG00000034677

Mouse predicted target: ENSMUSG00000022280

Rat predicted target: ENSRNOG00000009658

Fugu predicted target: SINFRUG00000139353

Hs Gene description: RING FINGER PROTEIN 19 (DORFIN) (DOUBLE RING-FINGER
PROTEIN) (P38 PROTEIN). [Source:SWISSPROT;Acc:Q9NV58]  NM_015435

mir-140   ENSG00000034677     2000 nt UTR    1 hits 398

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>ENSG00000034677 hs-mir-140    398    405

AGUGGUUUUACCCUAUGGUAG&GGCUUUAGGGAUAAGUGGUUAGUGAUAUUUUAUUGAAACCACUA

(((((((((((((((.(((..&.))).))))).......................)))))))))). -23.40

mir-140   ENSMUSG00000022280  3435 nt UTR    1 hits 391

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>ENSMUSG00000022280 hs-mir-140    391    398

AGUGGUUUUACCCUAUGGUAG&AGGCUUAGGGAUGAGUGGUUAGUGACAUUUUAUUGAAACCACUA

(((((((((((((((.(((..&..)))))))).......................)))))))))). -21.90

mir-140   ENSRNOG00000009658  3003 nt UTR    1 hits 382

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>ENSRNOG00000009658 hs-mir-140    382    389

AGUGGUUUUACCCUAUGGUAG&AGGCUUAGGGAUAAGUGGUUAGUGACAUUUUAUUGAAACCACUA

(((((((((((((((.(((..&..)))))))).......................)))))))))). -21.90

mir-140   SINFRUG00000139353  2000 nt UTR    2 hits 550 631

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>SINFRUG00000139353 hs-mir-140    550    557

AGUGGUUUUACCCUAUGGUAG&CAUGUGAGAGGGGCGUGAAAUUGGUCUUUCUUUGCAAACCACA

.(((((((..((((.......&........)))).......................))))))). -16.71

>SINFRUG00000139353 hs-mir-140    631    638

AGUGGUUUUACCCUAUGGUAG&CGGGCAGAUGGUGCAGCCUCCUGUCUGUUUAAACAAAACCACUG

(((((((((.....(((((((&...................))).)))).....))))))))). -16.30



miRNA: mir-140

Human predicted target: ENSG00000126562

Mouse predicted target: ENSMUSG00000035112

Rat predicted target: ENSRNOG00000020476

Fugu predicted target: SINFRUG00000154207

Hs Gene description: PROTEIN KINASE, LYSINE DEFICIENT 4; PUTATIVE PROTEIN
KINASE WNK4. [Source:RefSeq;Acc:NM_032387]

mir-140   ENSG00000126562     2112 nt UTR    2 hits 1072 1499

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>ENSG00000126562 hs-mir-140   1072   1079

AGUGGUUUUACCCUAUGGUAG&UCGUAACAACUGCGUCCCUGGAAGGUGAAGGGGGUAAACCACA

.(((((((.(((((...((((&.........)))).................))))))))))))). -22.15

>ENSG00000126562 hs-mir-140   1499   1506

AGUGGUUUUACCCUAUGGUAG&UAGAAGGUGUAACCAUCUGGGGAGGUAGGUUCAGGAAACCACA

.((((((((.(((.(((((..&...........)))))..)))..............)))))))). -24.14

mir-140   ENSMUSG00000035112  2022 nt UTR    2 hits 1061 1440
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>ENSMUSG00000035112 hs-mir-140   1061   1068

AGUGGUUUUACCCUAUGGUAG&CCUUAAGAGUCGGGGCCCCUGGGAGGUGAAGGGGUAAACCACA

.(((((((.(((((.......&..............................)))))))))))). -22.40

>ENSMUSG00000035112 hs-mir-140   1440   1447

AGUGGUUUUACCCUAUGGUAG&UAGAAGGUGUAACCAUCUGACGGAGUGGGUUCAGGAAACCACA

.((((((((((((.(((((..&...........)))))..........))))....)))))))). -22.60

mir-140   ENSRNOG00000020476  2000 nt UTR    2 hits 1154 1534

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>ENSRNOG00000020476 hs-mir-140   1154   1161

AGUGGUUUUACCCUAUGGUAG&CCCCUUAACAUUGGGCCCCUGGGAGGUGAAGAGGUAAACCACA

.(((((((((((((..(((..&..............)))....)).)))).......))))))). -19.81

>ENSRNOG00000020476 hs-mir-140   1534   1541

AGUGGUUUUACCCUAUGGUAG&UAGAAGGUGUAACCAUCUGGCGGGGUGGGUUCAGGAAACCACA

.((((((((((((((((((..&...........))))).....)))))........)))))))). -24.20

mir-140   SINFRUG00000154207  839 nt UTR     1 hits 368

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>SINFRUG00000154207 hs-mir-140    368    375

AGUGGUUUUACCCUAUGGUAG&AAAUGAUGAUUCAGGUUGACUUCUGCCUGGAUUAAAACCACG

.(((((((((..(((.(((((&......................))))))))..))))))))). -24.60


miRNA: mir-140
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Human predicted target: ENSG00000143816

Mouse predicted target: ENSMUSG00000000126

Rat predicted target: ENSRNOG00000003066

Fugu predicted target: SINFRUG00000147642

Hs Gene description: WNT-14 PROTEIN PRECURSOR.
[Source:SWISSPROT;Acc:O14904] NM_003395

mir-140   ENSG00000143816     2522 nt UTR    2 hits 912 1210

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>ENSG00000143816 hs-mir-140    912    919

AGUGGUUUUACCCUAUGGUAG&GGCUGCCCCAACACCAGCACUGUCUUCAGAGACUCAAACCACUA

((((((((....((..(((((&..)))))......................))....)))))))). -16.05

>ENSG00000143816 hs-mir-140   1210   1217

AGUGGUUUUACCCUAUGGUAG&CUCCUAACCCUGCCUCUGAUCUGCUUAGUUGUUUGAAACCACUA

((((((((((..(...(((((&....................))))).....)..)))))))))). -20.80

mir-140   ENSMUSG00000000126  2001 nt UTR    2 hits 575 835

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>ENSMUSG00000000126 hs-mir-140    575    582

AGUGGUUUUACCCUAUGGUAG&CAGCCUGAUGCCAGCACUGUCUUCUUCAGAGAGCCAAACCACUA

((((((((..(.((.(((((.&........)))))................)).)..)))))))). -18.03

>ENSMUSG00000000126 hs-mir-140    835    842

AGUGGUUUUACCCUAUGGUAG&UCAUCGUCCCCCCCUCCUUUGCUUGCUCUAGUUUGAAACCACUA

((((((((((..(((.(((((&......................))))).)))..)))))))))). -23.10

mir-140   ENSRNOG00000003066  4058 nt UTR    2 hits 550 807
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>ENSRNOG00000003066 hs-mir-140    550    557

AGUGGUUUUACCCUAUGGUAG&CAGCAGCCUGACGCCAGCACUGUCUUCAGAGAGCCAAACCACUA

((((((((..(.((.((((..&............)))).............)).)..)))))))). -17.14

>ENSRNOG00000003066 hs-mir-140    807    814

AGUGGUUUUACCCUAUGGUAG&UUCAUACUCCCUCCUCGUCUGCUUGCUCUAGUUUGAAACCACUA

((((((((((..(((.(((((&......................))))).)))..)))))))))). -23.10

mir-140   SINFRUG00000147642  2000 nt UTR    2 hits 565 833

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>SINFRUG00000147642 hs-mir-140    565    572

AGUGGUUUUACCCUAUGGUAG&UACUAUAUAAGCCACUUAUCUAACGAUGUUAAAACAAACCACUA

((((((((.....(((.((((&...................))).).))).......)))))))). -13.80

>SINFRUG00000147642 hs-mir-140    833    840

AGUGGUUUUACCCUAUGGUAG&CAGCCUUGAACGAAGCAGAGUUCAGGGAAUGACUUAAACCACUA

((((((((..((((.......&.......................))))........)))))))). -17.60



miRNA: mir-142as

Human predicted target: ENSG00000104388

Mouse predicted target: ENSMUSG00000050754

Mouse predicted target: ENSMUSG00000047187

Rat predicted target: ENSRNOG00000005963

Fugu predicted target: SINFRUG00000143003
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Hs Gene description: RAS-RELATED PROTEIN RAB-2A.
[Source:SWISSPROT;Acc:P08886] NM_002865

mir-142as ENSG00000104388     2301 nt UTR    1 hits 289

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>ENSG00000104388 hs-mir-142as    289    296

UGUAGUGUUUCCUACUUUAUGG&UCUUGUGCCCUUAACUACGAACUGAAUUGUAUUAAACACUACAA

((((((((((..(((.......&............................)))..)))))))))). -18.80

mir-142as ENSMUSG00000050754  2000 nt UTR    1 hits 281

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>ENSMUSG00000050754 hs-mir-142as    281    288

UGUAGUGUUUCCUACUUUAUGG&UCUUGUGCCAUUAACUACGAGCUGAAUUGUAUUAGACACUACAA

((((((((((..(((...((((&.......)))).................)))..)))))))))). -18.85

mir-142as ENSMUSG00000047187  2162 nt UTR    2 hits 284 822

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>ENSMUSG00000047187 hs-mir-142as    284    291

UGUAGUGUUUCCUACUUUAUGG&UCUUGUGCCCUUAACUACGAGCUGAAUUGUAUUAAACACUACAA

((((((((((..(((.......&............................)))..)))))))))). -18.80

>ENSMUSG00000047187 hs-mir-142as    822    829

UGUAGUGUUUCCUACUUUAUGG&UGUAAUGAGUGGGACGGGCAGAAACAGAAACUCCAACACUACAC

(((((((((((((((((.....&......))))))))....................))))))))). -22.65

mir-142as ENSRNOG00000005963  3227 nt UTR    3 hits 288 824 2382

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>ENSRNOG00000005963 hs-mir-142as    288    295

UGUAGUGUUUCCUACUUUAUGG&CUUGUGCCCUUAACUACGAGCUGAAUUGUAUUAAAACACUACAA

((((((((((..(((.......&...........................)))...)))))))))). -17.30

>ENSRNOG00000005963 hs-mir-142as    824    831

UGUAGUGUUUCCUACUUUAUGG&GGUGUAAUGAGUGGGAAGGGCAGACACAAACUCCAACACUACGC

(((((((((((((((((.....&........))))))))..................))))))))). -22.06

>ENSRNOG00000005963 hs-mir-142as   2382   2389

UGUAGUGUUUCCUACUUUAUGG&ACUGAAUCUGUAGUGUUUCCAUUGUUCUGCUUGAGACACUACAC

(((((((((((.......((((&..................))))..........))))))))))). -20.53

mir-142as SINFRUG00000143003  2000 nt UTR    1 hits 738

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>SINFRUG00000143003 hs-mir-142as    738    745

UGUAGUGUUUCCUACUUUAUGG&CUGACUCUGUCCUUUUGUUGAUUUGCAUUCAAGGAACACUACAA

(((((((((((...........&................................))))))))))). -19.20



miRNA: mir-142as

Human predicted target: ENSG00000104866

Mouse predicted target: ENSMUSG00000051403

Rat predicted target: ENSRNOG00000017692

Fugu predicted target: SINFRUG00000123919

mir-142as ENSG00000104866     2718 nt UTR    1 hits 142

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>ENSG00000104866 hs-mir-142as    142    149

UGUAGUGUUUCCUACUUUAUGG&GGGGGCCAUUCUGGGGCCCCCUCCCCCCACAGCAACACUACAA

((((((((((((((....((((&.....))))..)))))..................))))))))). -19.76

mir-142as ENSMUSG00000051403  2494 nt UTR    2 hits 119 689

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>ENSMUSG00000051403 hs-mir-142as    119    126

UGUAGUGUUUCCUACUUUAUGG&AGACCAGGCAGAGCAUCCCAAGCCUCGCCACAACAACACUACAG

(((((((((.............&..................................))))))))). -15.30

>ENSMUSG00000051403 hs-mir-142as    689    696

UGUAGUGUUUCCUACUUUAUGG&AGACCAGGCAGAGCAUCCCAAGCCUCGCCACAACAACACUACAG

(((((((((.............&..................................))))))))). -15.30

mir-142as ENSRNOG00000017692  2597 nt UTR    1 hits 1439

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>ENSRNOG00000017692 hs-mir-142as   1439   1446

UGUAGUGUUUCCUACUUUAUGG&GCACCCCCCUCUCUAUGAACCCACACCUCAGGAGCACACUACAG

(((((((((((((......(((&....................)))......))))).)))))))). -22.00

mir-142as SINFRUG00000123919  2000 nt UTR    2 hits 187 1412

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>SINFRUG00000123919 hs-mir-142as    187    194

UGUAGUGUUUCCUACUUUAUGG&CUCAAGCAAGGGCACACGGUCCUUCACGCACCCACACACUACAG

((((((((..............&...................................)))))))). -14.40

>SINFRUG00000123919 hs-mir-142as   1412   1419

UGUAGUGUUUCCUACUUUAUGG&UGAAAAGAACUUUAUCAAGCUAUCUCUCUCCAUCCACACUACAU
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((((((((..............&...................................)))))))). -14.20



miRNA: mir-142s

Human predicted target: ENSG00000069849

Mouse predicted target: ENSMUSG00000032412

Rat predicted target: ENSRNOG00000011501

Fugu predicted target: SINFRUG00000151188

Fugu predicted target: SINFRUG00000151191

Hs Gene description: SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN
(SODIUM/POTASSIUM- DEPENDENT ATPASE BETA-3 SUBUNIT) (ATPB-3).
[Source:SWISSPROT;Acc:P54709] NM_001679

mir-142s  ENSG00000069849     2839 nt UTR    1 hits 335

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>ENSG00000069849 hs-mir-142s    335    342

CCCAUAAAGUAGAAAGCACUAC&UGUCUAAAGCUUAAUAUGCCGUGCUAUGUAAAUAUUUUAUGGA

.((((((((((...(((((...&....................))))).......)))))))))). -20.80

mir-142s  ENSMUSG00000032412  2000 nt UTR    1 hits 329

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>ENSMUSG00000032412 hs-mir-142s    329    336

CCCAUAAAGUAGAAAGCACUAC&CGUCUAAAGCUUCAUGUGCUGGGCUGUGUACAUAUUUUAUGGA

.((((((((((...(((((...&...............)))))............)))))))))). -20.16

mir-142s  ENSRNOG00000011501  2836 nt UTR    1 hits 326
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>ENSRNOG00000011501 hs-mir-142s    326    333

CCCAUAAAGUAGAAAGCACUAC&UGUCUAAAGCUUCAUGUGCUGUGCUGUGUAAAUAUUUUAUGGA

.((((((((((...(((((...&....................))))).......)))))))))). -21.60

mir-142s  SINFRUG00000151188  2000 nt UTR    1 hits 459

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>SINFRUG00000151188 hs-mir-142s    459    466

CCCAUAAAGUAGAAAGCACUAC&CUUCCUGCUGUCAGGGGGAGAACGCUGUUCUCGUCUUUAUGGGA

(((((((((.(((((((.....&.......................))).))))...))))))))). -23.40

mir-142s  SINFRUG00000151191  2000 nt UTR    1 hits 1299

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>SINFRUG00000151191 hs-mir-142s   1299   1306

CCCAUAAAGUAGAAAGCACUAC&CUUCCUGCUGUCAGGGGGAGAACGCUGUUCUCGUCUUUAUGGGA

(((((((((.(((((((.....&.......................))).))))...))))))))). -23.40



miRNA: mir-145

Human predicted target: ENSG00000109189

Mouse predicted target: ENSMUSG00000048255

Rat predicted target: ENSRNOG00000002106

Fugu predicted target: SINFRUG00000123610

Hs Gene description: NM_022832

mir-145   ENSG00000109189     4611 nt UTR    2 hits 1506 2962
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>ENSG00000109189 hs-mir-145   1506   1513

GUCCAGUUUUCCCAGGAAUCCCUU&CAACAAUGAAGAGGAUAGCACUUUAUCUAGAUGAAAACUGGAUU

(((((((((((.(.((((((((((&........))).)))).........))).)..))))))))))). -
22.80

>ENSG00000109189 hs-mir-145   2962   2969

GUCCAGUUUUCCCAGGAAUCCCUU&AUUUCAUGGGCAUGCCUAAUAAUGAUCUAUGUUCUAACUGGAG

.(((((((..(((((((((.....&))))).)))).........................))))))). -
18.33

mir-145   ENSMUSG00000048255  3996 nt UTR    1 hits 1556

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>ENSMUSG00000048255 hs-mir-145   1556   1563

GUCCAGUUUUCCCAGGAAUCCCUU&CAGCAGUGAAGAGGAUAGCACUUUAUCUAGGUGAAAACUGGACU

(((((((((((((.((((((((((&........))).)))).........))).)).))))))))))). -
30.20

mir-145   ENSRNOG00000002106  3862 nt UTR    1 hits 1422

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>ENSRNOG00000002106 hs-mir-145   1422   1429

GUCCAGUUUUCCCAGGAAUCCCUU&CAGCAACGAAGAGGAUAGCACUUUAUCUAGGUGAAAACUGGACU

(((((((((((((.((((((((((&........))).)))).........))).)).))))))))))). -
30.20

mir-145   SINFRUG00000123610  2000 nt UTR    2 hits 709 1137
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>SINFRUG00000123610 hs-mir-145    709    716

GUCCAGUUUUCCCAGGAAUCCCUU&AAGCUGAAGAUGGGACACAAACAUGACUGCCCCAUAACUGGAA

.(((((((....(((..(((((..&...........))))........)..)))......))))))). -
19.60

>SINFRUG00000123610 hs-mir-145   1137   1144

GUCCAGUUUUCCCAGGAAUCCCUU&ACCUUUUUGGGUGAAGUUGUGAGGAACACGUGCCAAACUGGAG

.(((((((((((((.((..(((..&........)))....)).)).))).........)))))))). -
22.80




miRNA: mir-145

Human predicted target: ENSG00000114993

Mouse predicted target: ENSMUSG00000034930

Rat predicted target: ENSRNOG00000009022

Fugu predicted target: SINFRUG00000154952

Hs Gene description: RHOTEKIN. [Source:RefSeq;Acc:NM_033046]     NM_033046

mir-145   ENSG00000114993     2381 nt UTR    1 hits 236

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>ENSG00000114993 hs-mir-145    236    243

GUCCAGUUUUCCCAGGAAUCCCUU&CUCGCUGGGACCUCCCUAAACCCUUCCUGGAAGAAAACUGGAA

.(((((((((((((((((((((..&......)))).............)))))))..)))))))))). -
33.01

mir-145   ENSMUSG00000034930  2355 nt UTR    1 hits 235
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>ENSMUSG00000034930 hs-mir-145    235    242

GUCCAGUUUUCCCAGGAAUCCCUU&CUGGCUAGGAUUCCCCUAAGCGCUUCCUGGGAGAAAACUGGAA

.(((((((((((((((((.(.(((&.................))).).)))))))..)))))))))). -
30.10

mir-145   ENSRNOG00000009022  2331 nt UTR    2 hits 50 222

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>ENSRNOG00000009022 hs-mir-145     50     57

GUCCAGUUUUCCCAGGAAUCCCUU&AAGAGGAUGGCCAAGAGAGAAAAUGACCCAAGGACAACUGGACU

((((((((.(((..((.(((((((&))).))))...................))..))).)))))))). -
25.45

>ENSRNOG00000009022 hs-mir-145    222    229

GUCCAGUUUUCCCAGGAAUCCCUU&CUAGGACCCCCCCCCCCAAGCGCUUCCUGGGAGAAAACUGGAA

.(((((((((((((((((.(.(((&.................))).).)))))))..)))))))))). -
30.20

mir-145   SINFRUG00000154952  2000 nt UTR    1 hits 1708

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>SINFRUG00000154952 hs-mir-145   1708   1715

GUCCAGUUUUCCCAGGAAUCCCUU&GUGGGACAGGUGUCAAGGAGGUCCCUCUGGAGUAAAACUGGAA

.(((((((((((((((.(((((((&..............)))).)))...))))).).))))))))). -
26.80




miRNA: mir-145

Human predicted target: ENSG00000151702
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Mouse predicted target: ENSMUSG00000016087

Rat predicted target: ENSRNOG00000008904

Fugu predicted target: SINFRUG00000153677

Hs Gene description: FRIEND LEUKEMIA INTEGRATION 1 TRANSCRIPTION FACTOR
(FLI-1 PROTO- ONCOGENE) (ERGB TRANSCRIPTION FACTOR).
[Source:SWISSPROT;Acc:Q01543] NM_002017

mir-145   ENSG00000151702     3428 nt UTR    3 hits 100 485 525

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>ENSG00000151702 hs-mir-145    100    107

GUCCAGUUUUCCCAGGAAUCCCUU&UCAACAGGACAUAUGUGGCCUUGAAGGGAAGACAAAACUGGAUG

((((((((((....(...((((((&.......................))))))...))))))))))). -
22.60

>ENSG00000151702 hs-mir-145    485    492

GUCCAGUUUUCCCAGGAAUCCCUU&AUCUAAUUUUAGGAGGACCAAAUUCAGUGGAUGGCAACUGGAA

.(((((((.(((((.((((.((((&............)))).....))))..)))..)).))))))). -
20.60

>ENSG00000151702 hs-mir-145    525    532

GUCCAGUUUUCCCAGGAAUCCCUU&GAACAUUGAUUGUAAGGCCAGUGAAGUUUUCACCCAACUGGAA

.((((((((((.(.((....((((&.............)))))).).)))..........))))))). -
15.00

mir-145   ENSMUSG00000016087  2126 nt UTR    3 hits 97 503 544

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>ENSMUSG00000016087 hs-mir-145     97    104

GUCCAGUUUUCCCAGGAAUCCCUU&CUCUAAAAGGCACAGUAGCCUUGAAGAGAUAAGAAAACUGGAUG

((((((((((((.(((....((((&......))))........))).).........))))))))))). -
20.80
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>ENSMUSG00000016087 hs-mir-145    503    510

GUCCAGUUUUCCCAGGAAUCCCUU&AUCUUAUCUUCGGAGGACUCAAUUCAGUGGAUGGCAACUGGAA

.(((((((.(((((.((((.((((&............)))).....))))..)))..)).))))))). -
20.60

>ENSMUSG00000016087 hs-mir-145    544    551

GUCCAGUUUUCCCAGGAAUCCCUU&AACACUGGCUCUGAGGCCAGUGAAGUUUUUUGCCCAACUGGAA

.(((((((....((((((.(((((&............))))........).))))))...))))))). -
16.20

mir-145   ENSRNOG00000008904  2000 nt UTR    3 hits 102 536 576

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>ENSRNOG00000008904 hs-mir-145    102    109

GUCCAGUUUUCCCAGGAAUCCCUU&CUCUAAAAGAUGCUGUAGCUUUGAAGAGAUAAGAAAACUGGAUG

(((((((((((......(((.(((&.......................))).)))..))))))))))). -
19.90

>ENSRNOG00000008904 hs-mir-145    536    543

GUCCAGUUUUCCCAGGAAUCCCUU&AUCUUUUCUUAGGAGGACUUAAUUCAGCGGAUGGCAACUGGAA

.(((((((.(((...((((.((((&............)))).....))))...)))....))))))). -
20.60

>ENSRNOG00000008904 hs-mir-145    576    583

GUCCAGUUUUCCCAGGAAUCCCUU&GAACACCGGCUGGGAGGCUGGUGAAGUCCCUGCCCAACUGGAA

.((((((((((((((...((((..&...........))))..)))).)))..........))))))). -
26.20

mir-145   SINFRUG00000153677  2000 nt UTR    3 hits 189 556 594

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>SINFRUG00000153677 hs-mir-145    189    196
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GUCCAGUUUUCCCAGGAAUCCCUU&GAAGAUUUUUCUAUUGUUUUUAAGAAUCUAUGAACAACUGGAUG

(((((((((((...(((.((....&.......................)).)))..))).)))))))). -
18.20

>SINFRUG00000153677 hs-mir-145    556    563

GUCCAGUUUUCCCAGGAAUCCCUU&AGAUGAACUUUUCUCAGCACUGAAUGAAAUGAGGCAACUGGAA

.(((((((..((((..........&.............................)).)).))))))). -
16.00

>SINFRUG00000153677 hs-mir-145    594    601

GUCCAGUUUUCCCAGGAAUCCCUU&UGGAAUGUGCCAUUCAUGCUUUUGGUUAUCCUCCAAACUGGAA

.((((((((....((((..((...&.......................))...))))..)))))))). -
19.60




miRNA: mir-153

Human predicted target: ENSG00000011114

Mouse predicted target: ENSMUSG00000041702

Rat predicted target: ENSRNOG00000008531

Fugu predicted target: SINFRUG00000125067

Hs Gene description: NM_018167

mir-153   ENSG00000011114     2000 nt UTR    1 hits 1760

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>ENSG00000011114 hs-mir-153   1760   1767

UUGCAUAGUCACAAAAGUGA&UAAAAAACUAUGAAUCACUCACACUCACUCGAAAACUAUGCAGG

(((((((((......(((((&........................)))))....))))))))). -19.10

mir-153   ENSMUSG00000041702  2000 nt UTR    1 hits 1545
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>ENSMUSG00000041702 hs-mir-153   1545   1552

UUGCAUAGUCACAAAAGUGA&CACAUAGCUAGGAAUCACUUACACUCACUCUAAAACUAUGCAGG

(((((((((......(((((&........................))))).....))))))))). -19.10

mir-153   ENSRNOG00000008531  2805 nt UTR    1 hits 1723

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>ENSRNOG00000008531 hs-mir-153   1723   1730

UUGCAUAGUCACAAAAGUGA&CAUUUAACUAGGAAUCACUUACACUCACUCUAAAACUAUGCAGG

(((((((((......(((((&........................))))).....))))))))). -19.10

mir-153   SINFRUG00000125067  2000 nt UTR    1 hits 1910

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>SINFRUG00000125067 hs-mir-153   1910   1917

UUGCAUAGUCACAAAAGUGA&UGGCCGGGCUUUUACUGGAGACGUGACUUUGGUGUCUAUGCAAG

((((((((.(((.(((((.(&.......................).))))).))).)))))))). -23.40



miRNA: mir-153

Human predicted target: ENSG00000169946

Mouse predicted target: ENSMUSG00000022306

Rat predicted target: ENSRNOG00000004109

Fugu predicted target: SINFRUG00000124894

Hs Gene description: ZINC FINGER PROTEIN, MULTITYPE 2; FRIEND OF GATA2;
TRANSCRIPTION FACTOR GATA4, MODULATOR OF; ZINC FINGER PROTEIN 409.
[Source:RefSeq;Acc:NM_012082] NM_012082
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mir-153   ENSG00000169946     2000 nt UTR    1 hits 957

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>ENSG00000169946 hs-mir-153    957    964

UUGCAUAGUCACAAAAGUGA&UUCUGAUAGAAAUAAUUUCUCAACAAAUGUUGUUACUAUGCAU

.((((((((.((((...(((&...................))).......)))).)))))))). -18.50

mir-153   ENSMUSG00000022306  3019 nt UTR    1 hits 972

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>ENSMUSG00000022306 hs-mir-153    972    979

UUGCAUAGUCACAAAAGUGA&UUCUGAUAGAAAUAAUUUCUCAACAAAUGUUGUUACUAUGCAU

.((((((((.((((...(((&...................))).......)))).)))))))). -18.50

mir-153   ENSRNOG00000004109  2000 nt UTR    1 hits 973

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>ENSRNOG00000004109 hs-mir-153    973    980

UUGCAUAGUCACAAAAGUGA&UCUGAUAGAAAAUAAUUUCUCAACAAAUGUUGUUACUAUGCAU

.((((((((.((((...(((&...................))).......)))).)))))))). -18.50

mir-153   SINFRUG00000124894  2000 nt UTR    1 hits 1007

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>SINFRUG00000124894 hs-mir-153   1007   1014

UUGCAUAGUCACAAAAGUGA&AUUAUGGGAGAAAAUGUUUCUUAAAAACGUUGUUGCUAUGCAU

.((((((((.((((......&.............................)))).)))))))). -18.90
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miRNA: mir-181a

Human predicted target: ENSG00000144677

Mouse predicted target: ENSMUSG00000038995

Rat predicted target: ENSRNOG00000011393

Fugu predicted target: SINFRUG00000130306

Hs Gene description: NUCLEAR LIM INTERACTOR-INTERACTING FACTOR 1 (NLI-
INTERACTING FACTOR 1) (NIF-LIKE PROTEIN) (YA22 PROTEIN) (HYA22).
[Source:SWISSPROT;Acc:O15194] NM_005808

mir-181a  ENSG00000144677     5601 nt UTR    4 hits 120 406 1972 3469

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>ENSG00000144677 hs-mir-181a    120    127

AACAUUCAACGCUGUCGGUGAGU&GAAAGUGAGGAUACUCCGUGCUCCAGGCCACAGGGUGAAUGUG

.(((((((.(.((((.(((((((&...................))))...))))))).)))))))). -24.90

>ENSG00000144677 hs-mir-181a    406    413

AACAUUCAACGCUGUCGGUGAGU&CUCAGAAUCUCUUUCCUACAGGAUGAAGUGCCUUUUGAAUGUUA

((((((((((.((((.((.(((.&........)))...)).)))))............))))))))). -
19.20

>ENSG00000144677 hs-mir-181a   1972   1979

AACAUUCAACGCUGUCGGUGAGU&GUAGUCAUUAAAUGAACCCACUGCCUUAAAUGUCUUGAAUGUUG

(((((((((.((.(.(((((.((&...............)).))))).)......)).))))))))). -
19.40

>ENSG00000144677 hs-mir-181a   3469   3476

AACAUUCAACGCUGUCGGUGAGU&GGUGUCUGGGUAGUCAUGGAUUUCUGCUGGACAUUUGAAUGUG

.(((((((((((.(((.((((.(&...........).)))).)))....)).).....)))))))). -17.90
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mir-181a  ENSMUSG00000038995  5349 nt UTR    3 hits 115 432 3351

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>ENSMUSG00000038995 hs-mir-181a    115    122

AACAUUCAACGCUGUCGGUGAGU&CAGCCCAGGAAGACUCCGUGCUCCGGGCCACAGGGUGAAUGUC

.(((((((.(.((((.(((((((&...................))))...))))))).)))))))). -24.30

>ENSMUSG00000038995 hs-mir-181a    432    439

AACAUUCAACGCUGUCGGUGAGU&UCAGAAUCUCUUUCCUACAGGAUGAAGUGCCUUUUUGAAUGUUA

((((((((((.((((.((.(((.&.......)))...)).))))).............))))))))). -
19.11

>ENSMUSG00000038995 hs-mir-181a   3351   3358

AACAUUCAACGCUGUCGGUGAGU&GGUGUCUGGGGAGUUACAGUUUUCUGCUGGAUGUUUGAAUGUG

.((((((((.((..((((((((.&.....................))).)))))..)))))))))). -18.10

mir-181a  ENSRNOG00000011393  2000 nt UTR    2 hits 123 445

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>ENSRNOG00000011393 hs-mir-181a    123    130

AACAUUCAACGCUGUCGGUGAGU&GAGCCUGGGAAGACUCCACGCUUUGGGCCACAAGGUGAAUGUC

.(((((((.(..(((.(((((((&...................))))...)))))).).))))))). -18.10

>ENSRNOG00000011393 hs-mir-181a    445    452

AACAUUCAACGCUGUCGGUGAGU&CAGAAUCUCUUUCCUACAAGAUGAAGUGCCUUUUUUGAAUGUUA

(((((((((((((((.((.(((.&......)))...)).))).......)))......))))))))). -
17.11

mir-181a  SINFRUG00000130306  2000 nt UTR    2 hits 519 1606

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>SINFRUG00000130306 hs-mir-181a    519    526

AACAUUCAACGCUGUCGGUGAGU&UGUGACUCUUUUCUAACUGAAUGAAGUGCCUUGUGUGAAUGUUG

((((((((.((((.(((((((((&....)))).......)))))....)))).......)))))))). -
20.11

>SINFRUG00000130306 hs-mir-181a   1606   1613

AACAUUCAACGCUGUCGGUGAGU&UUUGUUUUUUUUUCCUAGAUAAUACUGAAACAACUUGAAUGUUG

(((((((((.....((((((...&......................))))))......))))))))). -
19.10




miRNA: mir-181a

Human predicted target: ENSG00000164463

Mouse predicted target: ENSMUSG00000048249

Rat predicted target: ENSRNOG00000020769

Fugu predicted target: SINFRUG00000139862

Hs Gene description: ADULT RETINA PROTEIN. [Source:RefSeq;Acc:NM_153607]
     NM_153607

mir-181a  ENSG00000164463     5222 nt UTR    3 hits 736 984 4518

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>ENSG00000164463 hs-mir-181a    736    743

AACAUUCAACGCUGUCGGUGAGU&AAUGUUUUUUUGUUCCAACUCUUUUUCAGAUUUUUUGAAUGUA

.((((((((..(((.....((((&.................)))).....))).....)))))))). -18.50

>ENSG00000164463 hs-mir-181a    984    991

AACAUUCAACGCUGUCGGUGAGU&UAAGUAAAGUUUUGCACAGCUUACAUGAUACUGUAUGAAUGUA

.((((((((((.(((((((((((&..................)))))).))))).))).))))))). -23.70
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>ENSG00000164463 hs-mir-181a   4518   4525

AACAUUCAACGCUGUCGGUGAGU&UUUUUUAAUACUUCAAACACAUUGGGAUGUAACAAUGAAUGUC

.((((((((((.(.((((((.((&................)).)))))).)))).....))))))). -15.80

mir-181a  ENSMUSG00000048249  2000 nt UTR    2 hits 766 1016

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>ENSMUSG00000048249 hs-mir-181a    766    773

AACAUUCAACGCUGUCGGUGAGU&AUGUCUUUUUGUUCCAACUCUUUUUCAGAUUUUUUUGAAUGUA

.((((((((..(((.....((((&................)))).....)))......)))))))). -17.90

>ENSMUSG00000048249 hs-mir-181a   1016   1023

AACAUUCAACGCUGUCGGUGAGU&UAAGUAAAGUUUUGCACAGCUUACAUGAUACUGUAUGAAUGUA

.((((((((((.(((((((((((&..................)))))).))))).))).))))))). -23.70

mir-181a  ENSRNOG00000020769  3521 nt UTR    4 hits 779 1024 2120 2365

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>ENSRNOG00000020769 hs-mir-181a    779    786

AACAUUCAACGCUGUCGGUGAGU&AAUGUCUUUUUGUUCCAACUCUUUUUCAGAUUUUUUGAAUGUA

.((((((((..(((.....((((&.................)))).....))).....)))))))). -18.50

>ENSRNOG00000020769 hs-mir-181a   1024   1031

AACAUUCAACGCUGUCGGUGAGU&UAAGUAAAGUUUUGCACAGCUUACAUGAUACUGUAUGAAUGUA

.((((((((((.(((((((((((&..................)))))).))))).))).))))))). -23.70

>ENSRNOG00000020769 hs-mir-181a   2120   2127

AACAUUCAACGCUGUCGGUGAGU&AAUGUCUUUUUGUUCCAACUCUUUUUCAGAUUUUUUGAAUGUA

.((((((((..(((.....((((&.................)))).....))).....)))))))). -18.50

>ENSRNOG00000020769 hs-mir-181a   2365   2372
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AACAUUCAACGCUGUCGGUGAGU&UAAGUAAAGUUUUGCACAGCUUACAUGAUACUGUAUGAAUGUA

.((((((((((.(((((((((((&..................)))))).))))).))).))))))). -23.70

mir-181a  SINFRUG00000139862  2000 nt UTR    3 hits 1290 1346 1618

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>SINFRUG00000139862 hs-mir-181a   1290   1297

AACAUUCAACGCUGUCGGUGAGU&GAGAGAGCUCCCUCACAUUCAAGGUUGUUUGUUAGUGAAUGUG

.((((((((((((....(((((.&...........)))))......))).)).......))))))). -17.81

>SINFRUG00000139862 hs-mir-181a   1346   1353

AACAUUCAACGCUGUCGGUGAGU&UUGUGAGGUUUUGUUUCAGUUGUCUGAAGAUAUUCUGAAUGUA

.(((((((....((((..(.((.&.......................)).).))))...))))))). -14.00

>SINFRUG00000139862 hs-mir-181a   1618   1625

AACAUUCAACGCUGUCGGUGAGU&AAGUAAGGUUUUGCACAGCUUACCUGACGCCGUAUUGAAUGUA

.((((((((((.(((((((((((&.................))))))).)))).))..)))))))). -27.00



miRNA: mir-184

Human predicted target: ENSG00000129244

Mouse predicted target: ENSMUSG00000041329

Rat predicted target: ENSRNOG00000011227

Fugu predicted target: SINFRUG00000133968

Hs Gene description: SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 CHAIN
(SODIUM/POTASSIUM- DEPENDENT ATPASE BETA-2 SUBUNIT).
[Source:SWISSPROT;Acc:P14415] NM_001678

mir-184   ENSG00000129244     3485 nt UTR    1 hits 1266
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>ENSG00000129244 hs-mir-184   1266   1273

UGGACGGAGAACUGAUAAGGGU&CCAGGGAGCUCUGGGGGAGGGGCGGCCAUUCUGGCUCCGUCCC

.((((((((....((....(((&........................)))..))...)))))))). -24.20

mir-184   ENSMUSG00000041329  3506 nt UTR    1 hits 655

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>ENSMUSG00000041329 hs-mir-184    655    662

UGGACGGAGAACUGAUAAGGGU&UUUGUAGCUCAGUACAAGUUGGUUCUGUGGCCUUUUCCGUCCU

.((((((((((......((..(&.....................)..))......)))))))))). -22.10

mir-184   ENSRNOG00000011227  2434 nt UTR    1 hits 660

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>ENSRNOG00000011227 hs-mir-184    660    667

UGGACGGAGAACUGAUAAGGGU&UUUGUAGCUCACUACAGGUUGGUUCUGUGGCCUUUUCCGUCCU

.((((((((((......((..(&.....................)..))......)))))))))). -22.10

mir-184   SINFRUG00000133968  2000 nt UTR    1 hits 1652

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>SINFRUG00000133968 hs-mir-184   1652   1659

UGGACGGAGAACUGAUAAGGGU&UGGAGUGCUCGCAUCGGUGUCUGGCCUAAUCCUGCUCCGUCCU

.((((((((.((((((..((((&......))))..))))))................)))))))). -28.73
```

miRNA: mir-190

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Human predicted target: ENSG00000109046

Mouse predicted target: ENSMUSG00000017677

Rat predicted target: ENSRNOG00000012929

Fugu predicted target: SINFRUG00000137329

Hs Gene description: WD REPEAT AND SOCS BOX CONTAINING PROTEIN 1 (WSB-1)
(SOCS BOX- CONTAINING WD PROTEIN SWIP-1). [Source:SWISSPROT;Acc:Q9Y6I7]
     NM_134265

mir-190   ENSG00000109046     3264 nt UTR    2 hits 187 2260

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>ENSG00000109046 hs-mir-190    187    194

UGAUAUGUUUGAUAUAUUAGGU&AAAAUAUUAUUUAUAGACAAUAGAAGUAUUUCUGAACAUAUCAA

(((((((((((..(((((....&........................)))))...))))))))))). -16.40

>ENSG00000109046 hs-mir-190   2260   2267

UGAUAUGUUUGAUAUAUUAGGU&UUCAUAUCAUUGCAUUAUUUUUGCUUUCCACACCAACAUAUCC

.((((((((((((((.......&...)))))).........................)))))))). -13.51

mir-190   ENSMUSG00000017677  2000 nt UTR    1 hits 191

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>ENSMUSG00000017677 hs-mir-190    191    198

UGAUAUGUUUGAUAUAUUAGGU&AAAGCAUUAUUUAUACACCAUAGAAAUAUUUCUGAACAUAUCAU

(((((((((((..(((((.(((&................))).....)))))...))))))))))). -16.30

mir-190   ENSRNOG00000012929  2767 nt UTR    1 hits 83

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>ENSRNOG00000012929 hs-mir-190     83     90

UGAUAUGUUUGAUAUAUUAGGU&GCAUUAUUUAUACACCAUUGGAGAAAUAUUUCUGAACAUAUCAU
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((((((((((((..(((((....&........................)))))...))))))))))). -16.20

mir-190   SINFRUG00000137329  2000 nt UTR    1 hits 1209

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>SINFRUG00000137329 hs-mir-190   1209   1216

UGAUAUGUUUGAUAUAUUAGGU&CGUAUACGACGUGUAUAUAGUUUUAAUUUGUAUAAACAUAUCAC

((((((((((((((.((((((.&.....................)))))).))).))))))))))). -18.20




miRNA: mir-194

Human predicted target: ENSG00000055609

Mouse predicted target: ENSMUSG00000028935

Rat predicted target: ENSRNOG00000007997

Fugu predicted target: SINFRUG00000148483

Hs Gene description: MYELOID/LYMPHOID OR MIXED-LINEAGE LEUKEMIA 3; ALR-
LIKE PROTEIN. [Source:RefSeq;Acc:NM_021230]  NM_021230

mir-194   ENSG00000055609     2248 nt UTR    2 hits 722 747

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>ENSG00000055609 hs-mir-194    722    729

UGUAACAGCAACUCCAUGUGGA&UUUUUAAAUAAAGUUAGAAGAAAGCCAAGCUGCUGCUGUUACC

.(((((((((.(......(((.&........................)))....).))))))))). -20.30

>ENSG00000055609 hs-mir-194    747    754

UGUAACAGCAACUCCAUGUGGA&CAAGCUGCUGCUGUUACCUGCAGAACUAACAAACCCUGUUACU

.(((((((........((..(.&.................)..)).............))))))). -14.50
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mir-194   ENSMUSG00000028935  2001 nt UTR    2 hits 715 740

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>ENSMUSG00000028935 hs-mir-194    715    722

UGUAACAGCAACUCCAUGUGGA&UUUUAAAUAAAAGUUAGAAGAAAGCCAAGCUGCUGCUGUUACC

.(((((((((.(......(((.&........................)))....).))))))))). -20.30

>ENSMUSG00000028935 hs-mir-194    740    747

UGUAACAGCAACUCCAUGUGGA&CAAGCUGCUGCUGUUACCUGCAGAACUAACAAACCCUGUUACU

.(((((((........((..(.&.................)..)).............))))))). -14.50

mir-194   ENSRNOG00000007997  2000 nt UTR    2 hits 717 742

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>ENSRNOG00000007997 hs-mir-194    717    724

UGUAACAGCAACUCCAUGUGGA&UUUUAAAUAAAAGUUAGAAGAAAGCCAAGCUGCUGCUGUUACC

.(((((((((.(......(((.&........................)))....).))))))))). -20.30

>ENSRNOG00000007997 hs-mir-194    742    749

UGUAACAGCAACUCCAUGUGGA&CAAGCUGCUGCUGUUACCUGCAGAACUAACAAACCCUGUUACU

.(((((((........((..(.&.................)..)).............))))))). -14.50

mir-194   SINFRUG00000148483  727 nt UTR     1 hits 632

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>SINFRUG00000148483 hs-mir-194    632    639

UGUAACAGCAACUCCAUGUGGA&CGUUGCUAUUGUUUUUGGAGAUCGAGGAAGACAUGCUGUUACU

.(((((((((.(((((.((((.&.....))))......))))).............))))))))). -21.94
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miRNA: mir-194

Human predicted target: ENSG00000123159

Mouse predicted target: ENSMUSG00000019433

Rat predicted target: ENSRNOG00000003864

Fugu predicted target: SINFRUG00000141873

Hs Gene description: RGS19-INTERACTING PROTEIN 1 (GAIP C-TERMINUS
INTERACTING PROTEIN GIPC) (RGS-GAIP INTERACTING PROTEIN) (TAX INTERACTION
PROTEIN 2) (TIP-2). [Source:SWISSPROT;Acc:O14908] NM_005716

mir-194   ENSG00000123159     2654 nt UTR    1 hits 481

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>ENSG00000123159 hs-mir-194    481    488

UGUAACAGCAACUCCAUGUGGA&CACCCCUCCUGAGAGGAGCCCCCUCCCUGUGGAGCCUGUUACC

.(((((((...(((((((.(((&.......................))).))))))).))))))). -24.10

mir-194   ENSMUSG00000019433  2521 nt UTR    2 hits 623 1014

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>ENSMUSG00000019433 hs-mir-194    623    630

UGUAACAGCAACUCCAUGUGGA&AUCUCCCACCUGAGGGGAGCCCUCUCAGUUGGGGUCUGUUACC

.(((((((..((((((..((((&......................)).))..))))))))))))). -21.10

>ENSMUSG00000019433 hs-mir-194   1014   1021

UGUAACAGCAACUCCAUGUGGA&GAGAGCCCCGUGUGUGGCAGCAAGGCCUGUUGCCCUGUUACC

.(((((((((((((((..(((.&........)))..)).))..........))))..))))))). -19.80

mir-194   ENSRNOG00000003864  2391 nt UTR    2 hits 562 960

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>ENSRNOG00000003864 hs-mir-194    562    569
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UGUAACAGCAACUCCAUGUGGA&CUUCUCCCACCUGACAGGAGCUCCUCAGUUGGGUUCUGUUACC

.(((((((.(((((..((.(((&.....................))).))...)))))))))))). -22.70

>ENSRNOG00000003864 hs-mir-194    960    967

UGUAACAGCAACUCCAUGUGGA&CACCUAACCCCUCUGUGGCAGCAAAGCCUGUUGCGCUGUUACAG

((((((((((((.(((((.((.&.........)).).))))...........)))..))))))))). -20.80

mir-194   SINFRUG00000141873  2000 nt UTR    1 hits 267

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>SINFRUG00000141873 hs-mir-194    267    274

UGUAACAGCAACUCCAUGUGGA&AGGUGGUUCCGGUGCGUGCCUGAACCUCCAUCUUGCUGUUACAG

(((((((((((......(((((&..........................))))).))))))))))). -22.30



miRNA: mir-194

Human predicted target: ENSG00000175220

Mouse predicted target: ENSMUSG00000027247

Rat predicted target: ENSRNOG00000016610

Fugu predicted target: SINFRUG00000138340

Hs Gene description: RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING
PROTEIN RHOOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42
GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP). [Source:SWISSPROT;Acc:Q07960]
     NM_004308

mir-194   ENSG00000175220     3957 nt UTR    2 hits 165 866

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>ENSG00000175220 hs-mir-194    165    172
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UGUAACAGCAACUCCAUGUGGA&UCUGUCCAGCCCGCCUCACGGCCCUGGCGGCCUCGCUGUUACC

.((((((((..(.((((((((.&...............)))))....))).).....)))))))). -20.80

>ENSG00000175220 hs-mir-194    866    873

UGUAACAGCAACUCCAUGUGGA&GCAGAUCAUCAGCCUUCAUGUUCUUGUGGACCUGUCUGUUACGG

((((((((((..((((((.(((&....................))).))))))..)).)))))))). -22.20

mir-194   ENSMUSG00000027247  3426 nt UTR    1 hits 190

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>ENSMUSG00000027247 hs-mir-194    190    197

UGUAACAGCAACUCCAUGUGGA&CUCUGCCCGUCCCACCUUACCGGCCCUGGAGGCCUCUGUUACC

.(((((((...(((((.((((.&...........))))...........)))))....))))))). -22.50

mir-194   ENSRNOG00000016610  2000 nt UTR    1 hits 192

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>ENSRNOG00000016610 hs-mir-194    192    199

UGUAACAGCAACUCCAUGUGGA&CCCUCUGUCCAUCCCACCUUACCGGCCCUGGAGGCCUGUUACC

.(((((((...(((((.(((((&.......)))))................)))))..))))))). -21.73

mir-194   SINFRUG00000138340  2000 nt UTR    1 hits 833

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>SINFRUG00000138340 hs-mir-194    833    840

UGUAACAGCAACUCCAUGUGGA&GCUGUAGCUGAAGUAGCUGUAGAAUAGGAGCUGAGCUGUUACAC

(((((((((..((((.((..(.&................)..)).....))))....))))))))). -22.90
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miRNA: mir-199a

Human predicted target: ENSG00000116273

Mouse predicted target: ENSMUSG00000047777

Rat predicted target: ENSRNOG00000009046

Fugu predicted target: SINFRUG00000155548

Hs Gene description: NM_153812

mir-199a  ENSG00000116273     4360 nt UTR    1 hits 1252

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>ENSG00000116273 hs-mir-199a   1252   1259

CCCAGUGUUCAGACUACCUGUUC&UGGAAGAACUCUGCUCGAGGGCAGGGUGCCCUGGAACACUGGU

.(((((((((((....(((((((&..................))))))).....)).))))))))). -29.00

mir-199a  ENSMUSG00000047777  3921 nt UTR    2 hits 684 918

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>ENSMUSG00000047777 hs-mir-199a    684    691

CCCAGUGUUCAGACUACCUGUUC&UCCCCACAAUACAGCCCAAAGUAUUUGCCACUGUUACACUGGGU

((((((((.((((((..((((..&..........)))).....)))........)))..)))))))). -
21.00

>ENSMUSG00000047777 hs-mir-199a    918    925

CCCAGUGUUCAGACUACCUGUUC&GCCCUGGUCUGAGUGAGGGCUGGCUCAGCUCCUGGACACUGGU

.(((((((((((.((.((.((((&................)))).))...))...))))))))))). -25.50

mir-199a  ENSRNOG00000009046  3640 nt UTR    2 hits 821 2347

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>ENSRNOG00000009046 hs-mir-199a    821    828

CCCAGUGUUCAGACUACCUGUUC&GUCCUGAUCUGGGUGAGGGCUGGCUCAGCUCCUGGACACUGGU

.(((((((((((.((.((.((((&................)))).))...))...))))))))))). -25.50

>ENSRNOG00000009046 hs-mir-199a   2347   2354

CCCAGUGUUCAGACUACCUGUUC&GUCCUGAUCUGGGUGAGGGCUGGCUCAGCUCCUGGACACUGGU

.(((((((((((.((.((.((((&................)))).))...))...))))))))))). -25.50

mir-199a  SINFRUG00000155548  2000 nt UTR    1 hits 296

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>SINFRUG00000155548 hs-mir-199a    296    303

CCCAGUGUUCAGACUACCUGUUC&GUAGCGGCUAACUGUUGGGACUCGGUGUCUUGUGAACACUGGA

.(((((((((((((.(((.((((&.................))))..))))))...))))))))))). -28.80



miRNA: mir-205

Human predicted target: ENSG00000134686

Mouse predicted target: ENSMUSG00000028796

Rat predicted target: ENSRNOG00000006004

Fugu predicted target: SINFRUG00000121521

Hs Gene description: POLYHOMEOTIC 2-LIKE; EARLY DEVELOPMENT REGULATOR 2-
LIKE. [Source:RefSeq;Acc:NM_004427]     NM_004427

mir-205   ENSG00000134686     3239 nt UTR    1 hits 1184

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>ENSG00000134686 hs-mir-205   1184   1191

UCCUUCAUUCCACCGGAGUCUG&CUAUUCCCCACCCACACCCCCAGGCAGGUUGGAAAUGAAGGAC
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((((((((((((((...(((((&....................)))))..))).)).))))))))). -27.10
mir-205   ENSMUSG00000028796  3220 nt UTR    1 hits 1164
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>ENSMUSG00000028796 hs-mir-205   1164   1171
UCCUUCAUUCCACCGGAGUCUG&UAACCCCUUCCCCAUACCUCCAGGCAGGGUUGGAAAUGAAGGAC
((((((((((((((...(((((&....................)))))..))).)).))))))))). -27.10
mir-205   ENSRNOG00000006004  3046 nt UTR    3 hits 993 1365 1960
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>ENSRNOG00000006004 hs-mir-205    993   1000
UCCUUCAUUCCACCGGAGUCUG&UGCCCUUUUCCCCAUACCUCCAGGCAGGGUUGGAAAUGAAGGAC
((((((((((((((...(((((&....................)))))..))).)).))))))))). -27.10
>ENSRNOG00000006004 hs-mir-205   1365   1372
UCCUUCAUUCCACCGGAGUCUG&UGCCCUUUUCCCCAUACCUCCAGGCAGGGUUGGAAAUGAAGGAC
((((((((((((((...(((((&....................)))))..))).)).))))))))). -27.10
>ENSRNOG00000006004 hs-mir-205   1960   1967
UCCUUCAUUCCACCGGAGUCUG&CAGCUGCUAGCUGGGAUUGGCUGGCUGCCUCGUGUAUGAAGGU
.(((((((..(((.((((((..&......................)))).))..))).))))))). -21.70
mir-205   SINFRUG00000121521  2000 nt UTR    1 hits 310
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>SINFRUG00000121521 hs-mir-205    310    317
UCCUUCAUUCCACCGGAGUCUG&GAUUUUGAGAGAGCUGCUGUCAACUCCUGGUUUGAAUGAAGGU
.((((((((.(((((((((...&......................))))).)))..))))))))). -26.90
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miRNA: mir-214

Human predicted target: ENSG00000140332

Mouse predicted target: ENSMUSG00000032280

Rat predicted target: ENSRNOG00000013013

Fugu predicted target: SINFRUG00000141146

Hs Gene description: TRANSDUCIN-LIKE ENHANCER PROTEIN 3 (ESG3).
[Source:SWISSPROT;Acc:Q04726] NM_005078

mir-214   ENSG00000140332     3822 nt UTR    4 hits 529 694 2661 3398

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>ENSG00000140332 hs-mir-214    529    536

ACAGCAGGCACAGACAGGCAG&CCCCUUCCCACCGGAAACUCUGAGUGUGUAUUUCGCCUGCUGUA

((((((((((((.((...(((&...................))).)).))).....))))))))). -26.00

>ENSG00000140332 hs-mir-214    694    701

ACAGCAGGCACAGACAGGCAG&AGUGUGGAAAAGGCAACCAGGUUGGCCGUAAGGUGCCUGCUGG

.((((((((((..((.(((..&........................)))))...)))))))))). -33.00

>ENSG00000140332 hs-mir-214   2661   2668

ACAGCAGGCACAGACAGGCAG&UAUUUUGUCAAAGUCAUUCUCAGCACAAACAAUUGCCUGCUGUC

((((((((((..(((.(((((&....)))))...))).................)))))))))). -23.75

>ENSG00000140332 hs-mir-214   3398   3405

ACAGCAGGCACAGACAGGCAG&GCACUGAGCCUCUCUGCACGUGCUUCCUCCUUCCUCCUGCUGC

.((((((((..((((.((((..&.......)))).)))).................)))))))). -25.30

mir-214   ENSMUSG00000032280  3765 nt UTR    3 hits 490 1368 2613
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>ENSMUSG00000032280 hs-mir-214    490    497

ACAGCAGGCACAGACAGGCAG&GAACCCCAUCCCACCAUUGCUCGCCGUGGAUUUUGCCUGCUGUA

((((((((((....(((((((&..................)).))).)).....)))))))))). -28.20

>ENSMUSG00000032280 hs-mir-214   1368   1375

ACAGCAGGCACAGACAGGCAG&UGUUUUAUUAAAGAAAAGCUAAAGACCGUGUGAGCCCUGCUGG

.((((((((.((.((.((...&.........................)))).)).).))))))). -23.60

>ENSMUSG00000032280 hs-mir-214   2613   2620

ACAGCAGGCACAGACAGGCAG&UAAUGUAUCAAGGUCACUGUCGGUCACACCGGUAACCUGCUGUC

((((((((.((.(((.(((((&................))))).)))......))..)))))))). -25.30

mir-214   ENSRNOG00000013013  3661 nt UTR    2 hits 475 1329

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>ENSRNOG00000013013 hs-mir-214    475    482

ACAGCAGGCACAGACAGGCAG&AGGCCCCUUCCCACCAGUGCUCGCCGUGUAUUUUGCCUGCUGUA

((((((((((...((((((((&...................)).))).)))....)))))))))). -29.90

>ENSRNOG00000013013 hs-mir-214   1329   1336

ACAGCAGGCACAGACAGGCAG&UGUUUUAUUAAAGAAAAGCUAAAGACCGUGUGAGCCCUGCUGG

.((((((((.((.((.((...&.........................)))).)).).))))))). -23.60

mir-214   SINFRUG00000141146  2000 nt UTR    1 hits 545

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>SINFRUG00000141146 hs-mir-214    545    552

ACAGCAGGCACAGACAGGCAG&CUUAUUUUAUUAAGUGUUAAAAACCCGUCUGAAUGCCUGCUGUG
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(((((((((((((((.((...&.......................)).)))))..)))))))))). -32.30


miRNA: mir-218

Human predicted target: ENSG00000075240

Mouse predicted target: ENSMUSG00000035900

Rat predicted target: ENSRNOG00000016951

Rat predicted target: ENSRNOG00000016968

Fugu predicted target: SINFRUG00000149385

mir-218   ENSG00000075240     4536 nt UTR    2 hits 807 1609

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>ENSG00000075240 hs-mir-218    807    814

UUGUGCUUGAUCUAACCAUGU&UGGGGACCAGUAAGGGCACAGGAUGGUGCAGGUAAAAGCACAU

.(((((((.((((.(((((.(&....................).)))))..))))..))))))). -21.70

>ENSG00000075240 hs-mir-218   1609    1616

UUGUGCUUGAUCUAACCAUGU&GGUGCUUUGGGGGAGCUGCGCCGAUCACCAGAUUAAGCACAU

.((((((((((((........&.............................)))))))))))). -21.50

mir-218   ENSMUSG00000035900  4090 nt UTR    3 hits 278 711 1359

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>ENSMUSG00000035900 hs-mir-218    278    285

UUGUGCUUGAUCUAACCAUGU&GAUGGCACACAAGACACUGGUCCUCAGGCCCUGCUAAGCACAGC

(((((((((.(((.(((((((&.............))).))))....)))......))))))))). -16.30
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>ENSMUSG00000035900 hs-mir-218    711    718

UUGUGCUUGAUCUAACCAUGU&UCCUGUGAGGGCCCAGACUGGCGUAGUGUCGGCAAAAGCACAC

.(((((((...(..(((((((&....................)))).).))..)...))))))). -17.70

>ENSMUSG00000035900 hs-mir-218   1359   1366

UUGUGCUUGAUCUAACCAUGU&CUGGGGGUGGGAAGGGCUUGCCAGGCAACCAGAUCAAGCACAC

.((((((((((((..((((.(&....).))))....................)))))))))))). -24.25

mir-218   ENSRNOG00000016951  2000 nt UTR    1 hits 441

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>ENSRNOG00000016951 hs-mir-218    441    448

UUGUGCUUGAUCUAACCAUGU&CUAUUCUGUAAAGAUUGGGAAGACAGUCAUGAGUCAAGCACAGU

(((((((((((((..(((...&...............)))..))..........))))))))))). -21.70

mir-218   ENSRNOG00000016968  2000 nt UTR    3 hits 271 678 1361

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>ENSRNOG00000016968 hs-mir-218    271    278

UUGUGCUUGAUCUAACCAUGU&GAUGGCACACAAGACACUGGACCUCAGGCCCUGCUAAGCACAGC

(((((((((......((.((.&........................))))......))))))))). -15.40

>ENSRNOG00000016968 hs-mir-218    678    685

UUGUGCUUGAUCUAACCAUGU&GUGUCCGGCGAGGGUCCAGAAUGGCGCGUCGGCAAAAGCACAC

.(((((((.......((((((&.........................)))).))...))))))). -15.60

>ENSRNOG00000016968 hs-mir-218   1361   1368

UUGUGCUUGAUCUAACCAUGU&CUGGGGGUGGGAAGGGCUCGCCAGGCAACCAGAUCAAGCACAC

.((((((((((((..((((.(&....).))))....................)))))))))))). -24.25

mir-218   SINFRUG00000149385  2000 nt UTR    2 hits 916 1859
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>SINFRUG00000149385 hs-mir-218    916    923

UUGUGCUUGAUCUAACCAUGU&ACAGUUAGCCAGCGCAGGUCACAUCCGGCUGGUCCAAGCACAGC

(((((((((..(((.((((((&....................))))..)).)))..))))))))). -22.50

>SINFRUG00000149385 hs-mir-218   1859   1866

UUGUGCUUGAUCUAACCAUGU&UUGAAGAACGGCUCCGAAGAGCUGCAAUCAGAACAAAGCACAGA

((((((((..(((........&.............................)))...)))))))). -16.10




miRNA: mir-218

Human predicted target: ENSG00000119547

Mouse predicted target: ENSMUSG00000045991

Rat predicted target: ENSRNOG00000018299

Fugu predicted target: SINFRUG00000154314

Hs Gene description: ONE CUT DOMAIN FAMILY MEMBER 2 (ONECUT-2
TRANSCRIPTION FACTOR) (OC-2). [Source:SWISSPROT;Acc:O95948] NM_004852

mir-218   ENSG00000119547     2109 nt UTR    3 hits 116 768 876

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>ENSG00000119547 hs-mir-218    116    123

UUGUGCUUGAUCUAACCAUGU&GGAUUCCUAGCUGGGGCCCUUCACUGGUGAUUUGAAAGCACAAU

((((((((......((((.((&......................)))))).......)))))))). -19.22

>ENSG00000119547 hs-mir-218    768    775

UUGUGCUUGAUCUAACCAUGU&AAAAAACCAGUCAGUUCACUUGCGCUCAAAGUAUCAAGCACAAC
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(((((((((((((........&.............................)).))))))))))). -20.50

>ENSG00000119547 hs-mir-218    876    883

UUGUGCUUGAUCUAACCAUGU&UGAAGUCAUUAGGGAAUUGAUGAGAAUAUGGCUUCAAGCACAU

.(((((((((.....((((((&.........................))))))..))))))))). -22.60

mir-218   ENSMUSG00000045991  2000 nt UTR    3 hits 175 824 948

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>ENSMUSG00000045991 hs-mir-218    175    182

UUGUGCUUGAUCUAACCAUGU&AGAUUCUUAGCUGGGGCCCUUCACUGGUGACUUGAAAGCACAAU

((((((((......((((.((&......................)))))).......)))))))). -19.22

>ENSMUSG00000045991 hs-mir-218    824    831

UUGUGCUUGAUCUAACCAUGU&CAAAAAAAAGUCAAUUCACUUGAGCUCAAAGUAUCAAGCACAAC

(((((((((((((........&.............................)).))))))))))). -20.50

>ENSMUSG00000045991 hs-mir-218    948    955

UUGUGCUUGAUCUAACCAUGU&UGAAGUCAUUAGGGAAUUAUUGGGAAUAUGGCUUCAAGCACAU

.(((((((((.....((((((&.........................))))))..))))))))). -22.60

mir-218   ENSRNOG00000018299  2000 nt UTR    3 hits 157 806 930

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>ENSRNOG00000018299 hs-mir-218    157    164

UUGUGCUUGAUCUAACCAUGU&AGAUUCUUAACUGGGGCCCUUCACUGGUGACUUGAAAGCACAAU

((((((((......((((.((&......................)))))).......)))))))). -19.22

>ENSRNOG00000018299 hs-mir-218    806    813

UUGUGCUUGAUCUAACCAUGU&AAAAAAAAAGUCAAUUCACUUGAGCUCAAAGUAUCAAGCACAAC

(((((((((((((........&.............................)).))))))))))). -20.50
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>ENSRNOG00000018299 hs-mir-218    930    937

UUGUGCUUGAUCUAACCAUGU&UGAAGUCAUUAGGGAAUUAUUGGGAAUAUGGCUUCAAGCACAC

.(((((((((.....((((((&.........................))))))..))))))))). -22.50

mir-218   SINFRUG00000154314  2000 nt UTR    2 hits 791 928

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>SINFRUG00000154314 hs-mir-218    791    798

UUGUGCUUGAUCUAACCAUGU&UGAUUUGACUCUUUAAAGAUGAAUGCUAAUGAUGCAAGCACAAA

((((((((((((....(((..&......................))).....))).))))))))). -19.70

>SINFRUG00000154314 hs-mir-218    928    935

UUGUGCUUGAUCUAACCAUGU&GGUGCAUCUAUACAACAAAUGUGAGCACAAUUUUGAAGCACAU

.(((((((.(........(((&........................)))......).))))))). -13.34



miRNA: mir-218

Human predicted target: ENSG00000149582

Mouse predicted target: ENSMUSG00000002032

Rat predicted target: ENSRNOG00000014218

Fugu predicted target: SINFRUG00000152666

Hs Gene description: NM_032780

mir-218   ENSG00000149582     3254 nt UTR    2 hits 550 801

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>ENSG00000149582 hs-mir-218    550    557

UUGUGCUUGAUCUAACCAUGU&CACAGAAACCAACCCCUGACCCAGCGGUACCGGCCAAGCACAAA
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(((((((((..(..(((.((.&.....................))..)))...)..))))))))). -21.80

>ENSG00000149582 hs-mir-218    801    808

UUGUGCUUGAUCUAACCAUGU&AGCUAUGCAUCAUUUUCCUACGGCGUUAGCACUUUAAGCACAU

.(((((((((.(((((..(((&...................)))..)))))....))))))))). -19.90

mir-218   ENSMUSG00000002032  3196 nt UTR    2 hits 547 784

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>ENSMUSG00000002032 hs-mir-218    547    554

UUGUGCUUGAUCUAACCAUGU&GCUCAGGAACCAGCCCCUUGCCCAGGGACCUGGCCAAGCACAAA

(((((((((..(...((.((.&......................)).))....)..))))))))). -20.90

>ENSMUSG00000002032 hs-mir-218    784    791

UUGUGCUUGAUCUAACCAUGU&AGCUCUGCAUCGUUUUGUACAAGUGUCUGCAUUUUAAGCACAU

.(((((((((...(((.((((&......)))).)))...................))))))))). -16.45

mir-218   ENSRNOG00000014218  3122 nt UTR    4 hits 494 731 1611 1848

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>ENSRNOG00000014218 hs-mir-218    494    501

UUGUGCUUGAUCUAACCAUGU&GCUCAGGAACCAGCCCCUCACCCAGGGACCUGGCCAAGCACAAA

(((((((((..(...((.((.&......................)).))....)..))))))))). -20.90

>ENSRNOG00000014218 hs-mir-218    731    738

UUGUGCUUGAUCUAACCAUGU&UAGCAAUGUAUCAUUUUGUACAGUGUCCUCAUAUUAAGCACAU

.((((((((((..........&................................)))))))))). -16.30

>ENSRNOG00000014218 hs-mir-218   1611   1618

UUGUGCUUGAUCUAACCAUGU&GCUCAGGAACCAGCCCCUCACCCAGGGACCUGGCCAAGCACAAA

(((((((((..(...((.((.&......................)).))....)..))))))))). -20.90
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>ENSRNOG00000014218 hs-mir-218   1848   1855

UUGUGCUUGAUCUAACCAUGU&UAGCAAUGUAUCAUUUUGUACAGUGUCCUCAUAUUAAGCACAU

.((((((((((..........&................................)))))))))). -16.30

mir-218   SINFRUG00000152666  2000 nt UTR    2 hits 1717 1867

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>SINFRUG00000152666 hs-mir-218   1717   1724

UUGUGCUUGAUCUAACCAUGU&UGUUAGGUGGCUUUUGUGGCUUCAGUUUUGACUGGAAGCACAAU

((((((((.(((((((.....&.))))))).........................)))))))). -15.99

>SINFRUG00000152666 hs-mir-218   1867   1874

UUGUGCUUGAUCUAACCAUGU&UGUGGAAAUAUAUUUUUCCUCCAUUAACUUAAAAAAAGCACAU

.(((((((....(((((((..&.)))).......................)))....))))))). -13.60




miRNA: mir-218

Human predicted target: ENSG00000162105

Mouse predicted target: ENSMUSG00000037541

Rat predicted target: ENSRNOG00000020806

Fugu predicted target: SINFRUG00000153210

Hs Gene description: SH3 AND MULTIPLE ANKYRIN REPEAT DOMAINS PROTEIN 2
(SHANK2). [Source:SWISSPROT;Acc:Q9UPX8] NM_012309

mir-218   ENSG00000162105     7013 nt UTR    3 hits 764 1713 6238

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>ENSG00000162105 hs-mir-218    764    771
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UUGUGCUUGAUCUAACCAUGU&AAGGUGGCCAAGCAGAUGUCACAUGGAGUUAGUCAAAGCACAAA

((((((((((.((((((((((&....................))))))..)))))).)))))))). -24.70

>ENSG00000162105 hs-mir-218   1713   1720

UUGUGCUUGAUCUAACCAUGU&UACUGCAAGUUUAAAUAGUUGUACAGAUAGUUUAUAAGCACAAU

(((((((((..(((....(((&......................)))..)))....))))))))). -15.90

>ENSG00000162105 hs-mir-218   6238   6245

UUGUGCUUGAUCUAACCAUGU&ACACAUAGCCCCUGCAGCCCUGCAGAGGUGGCCACAAGCACAAG

(((((((((.....(((.(((&.....................)))..))).....))))))))). -22.00

mir-218   ENSMUSG00000037541  2000 nt UTR    2 hits 675 1395

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>ENSMUSG00000037541 hs-mir-218    675    682

UUGUGCUUGAUCUAACCAUGU&AGGGUGGCCAAAAUGAAGUCACACGGAGUUAGUCAAAGCACAAA

((((((((((.(((((..(((&......................)))..))))))).)))))))). -22.30

>ENSMUSG00000037541 hs-mir-218   1395   1402

UUGUGCUUGAUCUAACCAUGU&UACUGCAAGUUUAAAUAUGUGUACAGAUAGUUCAUAAGCACAAU

(((((((((((((.(((((((&..............))))).))..))))......))))))))). -18.40

mir-218   ENSRNOG00000020806  2000 nt UTR    3 hits 687 755 1603

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>ENSRNOG00000020806 hs-mir-218    687    694

UUGUGCUUGAUCUAACCAUGU&AGGGUGGCCAAACUGAAGUCACACGGAGUUAGUCAAAGCACAAA

((((((((((.(((((..(((&......................)))..))))))).)))))))). -22.30

>ENSRNOG00000020806 hs-mir-218    755    762

UUGUGCUUGAUCUAACCAUGU&GCCUGGCCAUAGAGCCAGCCAAUGUGUGGCUGCCCAAGCACAC
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.((((((((..(...(((..(&........................)..)))..)..)))))))). -19.70

>ENSRNOG00000020806 hs-mir-218   1603   1610

UUGUGCUUGAUCUAACCAUGU&UACUGCAAGUUUAAAUACGUGUACAGAUAGUUCAUAAGCACAAU

(((((((((((((...(((((&................)))))...))))......))))))))). -19.10

mir-218   SINFRUG00000153210  2000 nt UTR    1 hits 1360

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>SINFRUG00000153210 hs-mir-218   1360   1367

UUGUGCUUGAUCUAACCAUGU&AAGAGGGUCACUUUAAGCCCAGUAACAUGCAUCUCAAGCACAAG

((((((((((......(((((&........................)))))....))))))))))). -21.60



miRNA: mir-219

Human predicted target: ENSG00000070610

Mouse predicted target: ENSMUSG00000028467

Rat predicted target: ENSRNOG00000016364

Fugu predicted target: SINFRUG00000130115

Hs Gene description: BILE ACID BETA-GLUCOSIDASE.
[Source:RefSeq;Acc:NM_020944]

mir-219   ENSG00000070610     2000 nt UTR    1 hits 97

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>ENSG00000070610 hs-mir-219     97    104

UGAUUGUCCAAACGCAAUUCU&UCCCCUCUGAACCUCCUGCAACCCUGAGCCAUCAGGACAAUCAU

(((((((((....((......&...........................)).....))))))))). -19.00
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mir-219   ENSMUSG00000028467  2260 nt UTR    1 hits 81

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>ENSMUSG00000028467 hs-mir-219     81     88

UGAUUGUCCAAACGCAAUUCU&UUCCUCCCACAAGUCCUGCAGCCCUGAGCCAAUAGGACAAUCGC

(((((((((....((......&...........................)).....))))))))). -18.20

mir-219   ENSRNOG00000016364  2288 nt UTR    1 hits 124

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>ENSRNOG00000016364 hs-mir-219    124    131

UGAUUGUCCAAACGCAAUUCU&UCCUUCCCACAAGUCCUGCAGCCCUGAGCCAAUAGGACAAUCAU

(((((((((....((......&...........................)).....))))))))). -19.00

mir-219   SINFRUG00000130115  2000 nt UTR    1 hits 1097

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>SINFRUG00000130115 hs-mir-219   1097   1104

UGAUUGUCCAAACGCAAUUCU&UAUCAACUUCUCACUUAUGUGUUUUAUAAAAAAUUGACAAUCAU

((((((((.(((((((.....&.................))))))))...........)))))))). -17.50



miRNA: mir-219

Human predicted target: ENSG00000171656

Mouse predicted target: ENSMUSG00000013089

Rat predicted target: ENSRNOG00000001785

Fugu predicted target: SINFRUG00000148138
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Hs Gene description: ETS-RELATED PROTEIN ERM (ETS TRANSLOCATION VARIANT
5). [Source:SWISSPROT;Acc:P41161]  NM_004454

mir-219   ENSG00000171656     4318 nt UTR    1 hits 343

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>ENSG00000171656 hs-mir-219    343    350

UGAUUGUCCAAACGCAAUUCU&UCAGGUUAGUACCCGCAAAACGGGACAUAGUAUGUGACAAUCU

.(((((((((.((....((((&.....................))))....)).)).))))))). -17.20

mir-219   ENSMUSG00000013089  2000 nt UTR    1 hits 323

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>ENSMUSG00000013089 hs-mir-219    323    330

UGAUUGUCCAAACGCAAUUCU&CAGGGUUAGCGCCCAUGAAAGGGGACCGAGUGUAUGACAAUCU

.(((((((...((((..((((&....................))))....))))..))))))). -16.50

mir-219   ENSRNOG00000001785  3995 nt UTR    2 hits 297 2125

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>ENSRNOG00000001785 hs-mir-219    297    304

UGAUUGUCCAAACGCAAUUCU&UUCAGGUUAGCGCCCAUGAGAGGGGACCGAGUUAUGACAAUCU

.(((((((..(((.(..((((&..................))))..).....)))..))))))). -16.10

>ENSRNOG00000001785 hs-mir-219   2125   2132

UGAUUGUCCAAACGCAAUUCU&UUCAGGUUAGCGCCCAUGAGAGGGGACCGAGUUAUGACAAUCU

.(((((((..(((.(..((((&..................))))..).....)))..))))))). -16.10

mir-219   SINFRUG00000148138  2000 nt UTR    2 hits 276 1660

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>SINFRUG00000148138 hs-mir-219    276    283

UGAUUGUCCAAACGCAAUUCU&UUAAAAACCUAAAGAGCUGUUACAUCUCUGUCUGUGACAAUCU

.(((((((((.(((((.((((&............)))).))).........)).)).))))))). -16.90

>SINFRUG00000148138 hs-mir-219   1660   1667

UGAUUGUCCAAACGCAAUUCU&UUUAUAAUACUAUAAGUUAGAUUCCUGACAGGGUGGACAAUCU

.(((((((((..(.((..(((&..................)))....))...)..))))))))). -20.90



miRNA: mir-219

Human predicted target: ENSG00000179361

Mouse predicted target: ENSMUSG00000004661

Rat predicted target: ENSRNOG00000019677

Fugu predicted target: SINFRUG00000125291

Hs Gene description: DEAD RINGER-LIKE 2; DEAD RINGER DROSOPHILA HOMOLOG 2;
BRIGHT AND DEAD RINGER HOMOLOG. [Source:RefSeq;Acc:NM_006465]    NM_006465

mir-219   ENSG00000179361     4357 nt UTR    1 hits 313

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>ENSG00000179361 hs-mir-219    313    320

UGAUUGUCCAAACGCAAUUCU&CCCCAGCCACCUCCCAGCUCAGGGCACAGUGUAUCGACAAUCU

.(((((((...((((......&............................))))...))))))). -17.60

mir-219   ENSMUSG00000004661  2002 nt UTR    1 hits 1485

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>ENSMUSG00000004661 hs-mir-219   1485   1492
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UGAUUGUCCAAACGCAAUUCU&UUCCCCAACCACCUCCCAACCCAGAGUAGUAUAUCGACAAUCU

.(((((((.....((.(((((&......................))))).)).....))))))). -16.80

mir-219   ENSRNOG00000019677  4077 nt UTR    1 hits 212

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>ENSRNOG00000019677 hs-mir-219    212    219

UGAUUGUCCAAACGCAAUUCU&UUCCCCAGCCACCUCCCAUCCCAGAGUAGUAUAUCGACAAUCU

.(((((((.....((.(((((&......................))))).)).....))))))). -16.80

mir-219   SINFRUG00000125291  2000 nt UTR    1 hits 1347

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>SINFRUG00000125291 hs-mir-219   1347   1354

UGAUUGUCCAAACGCAAUUCU&GUGUUGUUUAAUUUAUCUGCUGAAGUCUGUCCGUGGACAAUCAA

((((((((((...(((.(((.&.....................)))...)))...)))))))))). -22.70



miRNA: mir-221

Human predicted target: ENSG00000112183

Mouse predicted target: ENSMUSG00000038132

Rat predicted target: ENSRNOG00000016925

Fugu predicted target: SINFRUG00000136995

Hs Gene description: NM_153020

mir-221   ENSG00000112183     3747 nt UTR    2 hits 403 1214
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>ENSG00000112183 hs-mir-221    403    410

AGCUACAUUGUCUGCUGGGUUUC&AAUCUAGUUGAACCAGGGAAUACAGAGCGAGCAAUAUGUAGCUU

((((((((((..((((..(((((&.................))).))..))))..))..)))))))). -
22.50

>ENSG00000112183 hs-mir-221   1214   1221

AGCUACAUUGUCUGCUGGGUUUC&UUCAUCUCAUGGCAUAAAUUAUUUAGUAAGUCUAGAUGUAGCG

.((((((((..(((((((((...&....................)))))))).)....)))))))). -20.60

mir-221   ENSMUSG00000038132  2000 nt UTR    2 hits 493 1307

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>ENSMUSG00000038132 hs-mir-221    493    500

AGCUACAUUGUCUGCUGGGUUUC&AAUCUAGUUGAACCAGGGAAUACGGAGUGAGCAAUAUGUAGCUU

(((((((((((..(((.(((((.&.........)))))...........)))..)))..)))))))). -
20.70

>ENSMUSG00000038132 hs-mir-221   1307   1314

AGCUACAUUGUCUGCUGGGUUUC&UUCAUCUCAUGGCAUAAGUUAUUCAGUAGGUCUAGAUGUAGCA

.((((((((.((((((((((..(&.................)..))))))))))....)))))))). -26.40

mir-221   ENSRNOG00000016925  2400 nt UTR    3 hits 370 716 1532

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>ENSRNOG00000016925 hs-mir-221    370    377

AGCUACAUUGUCUGCUGGGUUUC&AAUCUAGCUGAACCAGGGAAUACGGAGUGCACAAUAUGUAGCUU

((((((((..((.((((((((..&)))))))).))........................)))))))). -
21.77

>ENSRNOG00000016925 hs-mir-221    716    723
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AGCUACAUUGUCUGCUGGGUUUC&AAUCUAGCUGAACCAGGGAAUACGGAGUGCACAAUAUGUAGCUU

((((((((..((.((((((((..&)))))))).))........................)))))))). -
21.77

>ENSRNOG00000016925 hs-mir-221   1532   1539

AGCUACAUUGUCUGCUGGGUUUC&UUCAUCUCAUGGCAUAAGUUAUUCAGUAGGUCUAGAUGUAGCA

.((((((((.((((((((((..(&.................)..))))))))))....)))))))). -26.40

mir-221   SINFRUG00000136995  2000 nt UTR    1 hits 123

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>SINFRUG00000136995 hs-mir-221    123    130

AGCUACAUUGUCUGCUGGGUUUC&GGGCUGUACGAUGGGUGUCACCUCCCGGUUUUUUAAUGUAGCA

.(((((((((...((((((....&.......................))))))....))))))))). -26.60



miRNA: mir-221

Human predicted target: ENSG00000117016

Mouse predicted target: ENSMUSG00000032890

Rat predicted target: ENSRNOG00000011171

Rat predicted target: ENSRNOG00000011337

Fugu predicted target: SINFRUG00000149709

Hs Gene description: NM_014747

mir-221   ENSG00000117016     7837 nt UTR    5 hits 510 613 2278 3590 4418

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>ENSG00000117016 hs-mir-221    510    517
AGCUACAUUGUCUGCUGGGUUUC&UUGACUCUCCCGGCUCUGCCACUGUUUUCUGAGAAAUGUAGCA
.((((((((.(((((((((....&........)))))).................))))))))))). -24.82
>ENSG00000117016 hs-mir-221    613    620
AGCUACAUUGUCUGCUGGGUUUC&GGCAGCUCUUCCUGCCACUGAAUGCGUUCUGCAGCAUGUAGCA
.(((((((.(.((((.(..(...&.........................)..).))))))))))))). -22.20
>ENSG00000117016 hs-mir-221   2278   2285
AGCUACAUUGUCUGCUGGGUUUC&GUUAGUGACCCACAGGACAGUAUAGAUGUUUGUGGAUGUAGCA
.((((((((((((..((((((..&......))))))..))))................)))))))). -25.79
>ENSG00000117016 hs-mir-221   3590   3597
AGCUACAUUGUCUGCUGGGUUUC&AUAAAGACCUCCAAGGGUACUUCUUUGGAAAUGAAAUGUAGCA
.((((((((.((((((((((((.&....)))))).....))).........))).....)))))))). -19.60
>ENSG00000117016 hs-mir-221   4418   4425
AGCUACAUUGUCUGCUGGGUUUC&GGACCUUGUUCUCUGAUAAAGGGCUUAAUCUUUCCAUGUAGCA
.(((((((((((.((.((((((.&)))))).)).....)))).................))))))). -19.52
mir-221   ENSMUSG00000032890  2000 nt UTR    2 hits 456 564
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>ENSMUSG00000032890 hs-mir-221    456    463
AGCUACAUUGUCUGCUGGGUUUC&CUUUGCCUCUCCCAGCAUUGCUGCUUUUUUGAGGAAUGUAGCA
.((((((((.(((((((((....&..........))))))).................))))))))))). -25.16
>ENSMUSG00000032890 hs-mir-221    564    571
AGCUACAUUGUCUGCUGGGUUUC&CACUGGUGGUCAUCCCAUUGAAUGCACUCCACAGCAUGUAGCA
.(((((((.(.(((.(((((...&.........................)).))))))))))))))). -21.60
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mir-221   ENSRNOG00000011171  2199 nt UTR    2 hits 468 576

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>ENSRNOG00000011171 hs-mir-221    468    475

AGCUACAUUGUCUGCUGGGUUUC&UUGCCUCUCCCAGCAUUGCUGCUCUUUUUUGAGGAAUGUAGCA

.((((((((.(((((((((....&........)))))))..................))))))))))). -25.02

>ENSRNOG00000011171 hs-mir-221    576    583

AGCUACAUUGUCUGCUGGGUUUC&CGAUGGUGGUCAACCCAUUGAACGCACUCCACAGCAUGUAGCA

.((((((((((.(((((((((..&...........))))))......)))....)))..))))))). -22.20

mir-221   ENSRNOG00000011337  2000 nt UTR    2 hits 468 576

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>ENSRNOG00000011337 hs-mir-221    468    475

AGCUACAUUGUCUGCUGGGUUUC&UUGCCUCUCCCAGCAUUGCUGCUCUUUUUUGAGGAAUGUAGCA

.((((((((.(((((((((....&........)))))))..................))))))))))). -25.02

>ENSRNOG00000011337 hs-mir-221    576    583

AGCUACAUUGUCUGCUGGGUUUC&CGAUGGUGGUCAACCCAUUGAACGCACUCCACAGCAUGUAGCA

.((((((((((.(((((((((..&...........))))))......)))....)))..))))))). -22.20

mir-221   SINFRUG00000149709  2000 nt UTR    2 hits 222 442

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>SINFRUG00000149709 hs-mir-221    222    229

AGCUACAUUGUCUGCUGGGUUUC&UUUUAGGCACGACGCAGAUAUGAUUUUAUGAGAACAUGUAGCA

.(((((((((((((((.(((((.&....)))).).).)))))))...............))))))). -22.36

>SINFRUG00000149709 hs-mir-221    442    449

AGCUACAUUGUCUGCUGGGUUUC&AAUAGGCGAGCUAGUACACAAUAUAAAGUAUAGAUAUGUAGCA
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.((((((((((.((((((.((..&.......)).)))))).)))...............))))))). -21.26



miRNA: mir-221

Human predicted target: ENSG00000129757

Mouse predicted target: ENSMUSG00000037664

Rat predicted target: ENSRNOG00000020559

Fugu predicted target: SINFRUG00000123421

Hs Gene description: CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-
DEPENDENT KINASE INHIBITOR P57) (P57KIP2). [Source:SWISSPROT;Acc:P49918]
     NM_000076

mir-221   ENSG00000129757     2286 nt UTR    3 hits 86 450 1328

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>ENSG00000129757 hs-mir-221     86     93

AGCUACAUUGUCUGCUGGGUUUC&GUUGGAAGGGCGCUGGGCCUCGGCUGGGACCGUUCAUGUAGCA

.(((((((.(((((((((((((.&..............))))).))))..)))).....))))))). -25.80

>ENSG00000129757 hs-mir-221    450    457

AGCUACAUUGUCUGCUGGGUUUC&GUUGGAAGGGCGCUGGGCCUCGGCUGGGACCGUUCAUGUAGCA

.(((((((.(((((((((((((.&..............))))).))))..)))).....))))))). -25.80

>ENSG00000129757 hs-mir-221   1328   1335

AGCUACAUUGUCUGCUGGGUUUC&ACCUGCGGGGCUGCAGAAAGACAAGCCUGGACUUCAUGUAGCC

.((((((((((((.((((((..(&......)..))).)))..)))))............))))))). -23.70

mir-221   ENSMUSG00000037664  2313 nt UTR    2 hits 95 493

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>ENSMUSG00000037664 hs-mir-221     95    102

AGCUACAUUGUCUGCUGGGUUUC&GAAGAACUCUGGGCUUCGGCUGGGACCUUUCGUUCAUGUAGCA

.(((((((.(..((..((((..(&.....................)..))))..))..)))))))). -23.00

>ENSMUSG00000037664 hs-mir-221    493    500

AGCUACAUUGUCUGCUGGGUUUC&GAAGAACUCUGGGCUUCGGCUGGGACCUUUCGUUCAUGUAGCA

.(((((((.(..((..((((..(&.....................)..))))..))..)))))))). -23.00

mir-221   ENSRNOG00000020559  2000 nt UTR    1 hits 188

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>ENSRNOG00000020559 hs-mir-221    188    195

AGCUACAUUGUCUGCUGGGUUUC&GAAGAACUCUGGGCUUCGGCUGGGACCUUUCAUUCAUGUAGCA

.(((((((.(..((..((((..(&.....................)..))))..))..)))))))). -23.70

mir-221   SINFRUG00000123421  2000 nt UTR    1 hits 1170

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>SINFRUG00000123421 hs-mir-221   1170   1177

AGCUACAUUGUCUGCUGGGUUUC&AAAAAAUAUCGGCGAAUGACUUCUAACCAGUACAAAUGUAGCA

.((((((((...((((((.....&..........................))))))..)))))))). -25.20
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miRNA: mir-223

Human predicted target: ENSG00000135945

Mouse predicted target: ENSMUSG00000026082

Rat predicted target: ENSRNOG00000018623

Fugu predicted target: SINFRUG00000153974

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Hs Gene description: REV1-LIKE; REV1 PROTEIN; REV1 (YEAST HOMOLOG)- LIKE.
[Source:RefSeq;Acc:NM_016316] NM_016316

mir-223   ENSG00000135945     2000 nt UTR    1 hits 1636

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>ENSG00000135945 hs-mir-223   1636   1643

UGUCAGUUUGUCAAAUACCCCAA&GAGUGAACAGGCACAUUGGAACUGUGGGGACAUGUAACUGACC

.(((((((...((....(((((.&........................)))))...)).))))))). -21.90

mir-223   ENSMUSG00000026082  2300 nt UTR    1 hits 1224

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>ENSMUSG00000026082 hs-mir-223   1224   1231

UGUCAGUUUGUCAAAUACCCCAA&GGGUGAGUGCAGGCACGCUGGACUGUGGGGCGGGGAACUGACC

.((((((((.((.....(((((.&.........................))))).)).)))))))). -24.40

mir-223   ENSRNOG00000018623  2000 nt UTR    1 hits 1082

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>ENSRNOG00000018623 hs-mir-223   1082   1089

UGUCAGUUUGUCAAAUACCCCAA&AGGUGAGUGCAGGCACGCUGGACUGUGGGGCGGGGAACUGACC

.((((((((.((.....(((((.&.........................))))).)).)))))))). -24.40

mir-223   SINFRUG00000153974  2000 nt UTR    1 hits 1923

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>SINFRUG00000153974 hs-mir-223   1923   1930

UGUCAGUUUGUCAAAUACCCCAA&UACUAUUUAGGGUACAAAAAAAAGUGUUGAUCGUUAACUGACC

.(((((((.(((((.(((((...&.........)))))............)))))....))))))). -20.52
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