

Genome: Homo Sapiens | mRNA | miRBase 21 (Jun. 2014), EN

Description: List of transcripts that are targeted by *all* of the l
miRNA's:hsa_miR_378e

Filtering By: Base pair min value: 12 | Folding energy max valu

Gene	Accession number
KIAA1522	
PHC3	ENSG00000173889
VPS53	ENSG00000141252
GPR156	ENSG00000175697
C4orf46	ENSG00000205208
CCNI2	ENSG00000205089
WDR31	ENSG00000148225
OTUB2	ENSG00000089723
ATXN7L3B	ENSG00000253719
SRSF10	ENSG00000188529
DACT2	ENSG00000164488
CACNA2D4	ENSG00000151062
MPP3	ENSG00000161647
SAR1A	ENSG00000079332
GIPC3	ENSG00000179855
PPP1R12B	ENSG00000077157
CRLS1	ENSG00000088766
TOB2	ENSG00000183864
PRR29	ENSG00000224383
PLCB1	ENSG00000182621
NEUROD4	ENSG00000123307
CCDC125	ENSG00000183323
KIAA1958	ENSG00000165185
ZNF599	ENSG00000153896
RBBP9	ENSG00000089050
PAX8	ENSG00000125618
RAPGEF3	ENSG00000079337
CBX5	ENSG00000094916
C14orf177	ENSG00000176605
TMEM245	ENSG00000106771
RPL15	ENSG00000174748
ALDH3A2	ENSG00000072210
TBC1D16	ENSG00000167291
CNTD2	ENSG00000105219
FOXI2	ENSG00000186766

IGF1	ENSG00000017427
AKR1C4	ENSG000000198610
TRIM44	ENSG000000166326
CCSER2	ENSG000000107771
CNTN5	ENSG000000149972
MAPK1	ENSG000000100030
TGFBRAP1	ENSG000000135966
TMPRSS13	ENSG000000137747
RIMS4	ENSG000000101098
HM13	ENSG000000101294
IL17RD	ENSG000000144730
COL6A2	ENSG000000142173
ARL8B	ENSG000000134108

SEMBL 78 (Dec. 2014) and RNA22v2.0

below miRNA identifiers *simultaneously*

e (Kcal/mol): -12 | Min miRNA targets: 1 | p-value < 0

Trascript	Predicted Target Site	cseed - cDNA Region	deltaG
ENST00000373480	4776	3'UTR	-12.50
ENST00000495893	11106	3'UTR	-12.80
ENST00000437048	3899	3'UTR	-16
ENST00000315843	3189	3'UTR	-13.70
ENST00000379205	669	3'UTR	-14.90
ENST00000614847	2581	3'UTR	-16.80
ENST00000341761	3947	3'UTR	-13.30
ENST00000203664	3739	3'UTR	-12.60
ENST00000519948	7005	3'UTR	-15.20
ENST00000343255	1410	3'UTR	-15.60
ENST00000366796	1705	3'UTR	-17.60
ENST00000538450	1215	3'UTR	-27.30
ENST00000398393	2839	3'UTR	-15.50
ENST00000373241	1551	3'UTR	-12.10
ENST00000322315	1190	3'UTR	-17.60
ENST00000391959	5064	3'UTR	-13.30
ENST00000452938	796	3'UTR	-13.60
ENST00000327492	2106	3'UTR	-13.50
ENST00000577953	539	3'UTR	-16.00
ENST00000378641	4177	3'UTR	-16.50
ENST00000242994	1747	3'UTR	-18.90
ENST00000396499	3262	3'UTR	-20.90
ENST00000337530	8406	3'UTR	-13.30
ENST00000329285	2657	3'UTR	-18.60
ENST00000337227	1832	3'UTR	-12.70
ENST00000263334	2054	3'UTR	-13.70
ENST00000395358	2900	3'UTR	-13.00
ENST00000209875	8989	3'UTR	-13.70
ENST00000325812	1148	3'UTR	-15.80
ENST00000374586	7482	3'UTR	-32.00
ENST00000307839	1758	3'UTR	-17.60
ENST00000579855	1976	3'UTR	-13.90
ENST00000340848	1724	3'UTR	-19.60
ENST00000221818	1443	3'UTR	-15.40
ENST00000388920	1230	3'UTR	-23.40

ENST00000337514	6054	3'UTR	-13.30
ENST00000263126	1117	3'UTR	-13.30
ENST00000299413	4081	3'UTR	-12.70
ENST00000372088	4528	3'UTR	-15.50
ENST00000279463	4849	3'UTR	-12.50
ENST00000215832	3316	3'UTR	-13.00
ENST00000393359	3326	3'UTR	-14.20
ENST00000526090	2414	3'UTR	-13.40
ENST00000372851	1122	3'UTR	-17.50
ENST00000398174	1416	3'UTR	-13.80
ENST00000296318	5080	3'UTR	-15.80
ENST00000310645	3319	3'UTR	-14.40
ENST00000256496	814	3'UTR	-17.80

predicted target	targeting miRNA
ACCTGCCACTGAGTTGGGG	ACTGGACTTGGAGTCAGGA
CCCAGGCTTGAGTGCAGC	ACTGGACTTGGAGTCAGGA
TCAGGAGTTTGAGACCAGT	ACTGGACTTGGAGTCAGGA
TCCAGCTTCTGGCCAGA	ACTGGACTTGGAGTCAGGA
GGATGACCTCTGTCCAGC	ACTGGACTTGGAGTCAGGA
CTCTGCCTCCTCCTCCAGT	ACTGGACTTGGAGTCAGGA
CCCAGGCTGGAGTGCAGT	ACTGGACTTGGAGTCAGGA
ACCATGAGAGAGAGTCTAGG	ACTGGACTTGGAGTCAGGA
ACCTGATGTGCTAGTTGTTAGT	ACTGGACTTGGAGTCAGGA
TCAGGAGTTCGAGACCAGC	ACTGGACTTGGAGTCAGGA
ACCTGGCACAGCTCCAGC	ACTGGACTTGGAGTCAGGA
TCCTGTACTIONCAGAGTCCAGA	ACTGGACTTGGAGTCAGGA
GCCTTGGTCTAGCCAGT	ACTGGACTTGGAGTCAGGA
TCCTTTTTCGTTTTAGT	ACTGGACTTGGAGTCAGGA
CTCTGAGACCAAGCCCAGC	ACTGGACTTGGAGTCAGGA
CCCAGGCTGGAGTGCAGT	ACTGGACTTGGAGTCAGGA
AGGTGAATACAGCAGTCCAGT	ACTGGACTTGGAGTCAGGA
TTCACACTCCTAGTTTAGG	ACTGGACTTGGAGTCAGGA
TCCTGGACGGGCCGGA	ACTGGACTTGGAGTCAGGA
ACAAGACTCCCTCCAGT	ACTGGACTTGGAGTCAGGA
CAACTATTCTAAGTCCAGA	ACTGGACTTGGAGTCAGGA
GTCTGAATCTCAAGTCCAGA	ACTGGACTTGGAGTCAGGA
CCCAGGCTGGAGTGCAGT	ACTGGACTTGGAGTCAGGA
ATATATCTCTAAGTCCAGA	ACTGGACTTGGAGTCAGGA
TTTTGGCTGGGTGTGGT	ACTGGACTTGGAGTCAGGA
TCCAGCCCACAAGTCACAGC	ACTGGACTTGGAGTCAGGA
AGGGGAAGAGCCAAGTCCAGT	ACTGGACTTGGAGTCAGGA
TCTTAAGGCTCAAGTCAAGT	ACTGGACTTGGAGTCAGGA
TCCCGCAACATCCCTGAGTCCAGA	ACTGGACTTGGAGTCAGGA
TTCTGACTCCAAGTCCAGA	ACTGGACTTGGAGTCAGGA
TGAAAGCTCCTGGTTCAGT	ACTGGACTTGGAGTCAGGA
GCAGTCCTCTGTAGTCCAGA	ACTGGACTTGGAGTCAGGA
TCCTGTCCAGGCCAGG	ACTGGACTTGGAGTCAGGA
TCTCAGCCTCCAGTCTCCAGT	ACTGGACTTGGAGTCAGGA
CTCTGCCTCTAAGTCCAGC	ACTGGACTTGGAGTCAGGA

CCCAGGCTGGAGTGCAGT	ACTGGACTTGGAGTCAGGA
TCCTGCTTGGCAACTTCAGC	ACTGGACTTGGAGTCAGGA
GAAGTGCTTGGAGTCTCGGC	ACTGGACTTGGAGTCAGGA
CCCTCCCCATCTCCAGT	ACTGGACTTGGAGTCAGGA
TCCTGAAAGAATAGTTTCAGA	ACTGGACTTGGAGTCAGGA
TCCTCACCACCCAGCCAGG	ACTGGACTTGGAGTCAGGA
GTCTTCCTCATGCAGTCCAGA	ACTGGACTTGGAGTCAGGA
CCCTGAAGAATGGAGCCAGA	ACTGGACTTGGAGTCAGGA
ATGTGGCTGCAGTCCAGA	ACTGGACTTGGAGTCAGGA
GCCCGAGCCTCTCAGGGCCAGA	ACTGGACTTGGAGTCAGGA
TCCAGTCCAGGCCAGG	ACTGGACTTGGAGTCAGGA
GCTGCGGCTGCATCTTCCAGT	ACTGGACTTGGAGTCAGGA
TCCTGAAGTCTTCCAGT	ACTGGACTTGGAGTCAGGA

Base Pairs in putative heteroduplex	Span of Target
12	20
12	18
13	19
14	17
12	18
14	21
14	18
13	20
17	23
14	19
14	18
18	21
14	18
15	18
14	19
14	18
13	21
12	19
14	16
12	17
13	19
16	20
14	18
12	19
15	17
14	20
12	21
17	19
17	24
18	19
13	19
12	20
15	17
16	21
16	19

14	18
16	20
12	20
13	18
13	21
14	20
13	21
13	20
14	18
15	22
14	17
14	21
14	17

P-Value
0.041400
0.030300
0.038700
0.007400
0.040100
0.012700
0.000297
0.041300
0.007270
0.016100
0.049400
0.026000
0.038000
0.035500
0.029800
0.000482
0.024100
0.002720
0.005180
0.009070
0.048900
0.029000
0.000015
0.007490
0.012100
0.005450
0.032700
0.043200
0.017000
0.000001
0.040600
0.037400
0.036000
0.029500
0.039000

0.000829
0.029200
0.018900
0.011300
0.041900
0.035100
0.008420
0.041200
0.043700
0.027500
0.011900
0.029800
0.025700

Genome: Homo Sapiens | mRNA | miRBase 21 (Jun. 2014), ENSEMBL 78 (Dec. 2014) and RNA2
 Description: List of transcripts that are targeted by *all* of the below miRNA identifiers *simultaneous*
 miRNA's: hsa-miR-708-3p
 Filtering By: Base pair min value: 12 | Folding energy max value (Kcal/mol): -12 | Min miRNA target

Gene	Accession number	Trascript	Predicted Target Site	seed - cDNA Region
VIM	ENSG00000026025	ENST00000469543	1831	3'UTR
SPRED1	ENSG00000166068	ENST00000299084	5506	3'UTR
EMP1	ENSG00000134531	ENST00000256951	4801	3'UTR
STXBP4	ENSG00000166263	ENST00000376352	8798	3'UTR
SIX1	ENSG00000126778	ENST00000247182	1411	3'UTR
ANK3	ENSG00000151150	ENST00000280772	16605	3'UTR
FUT2	ENSG00000176920	ENST00000425340	1668	3'UTR
NWD1	ENSG00000188039	ENST00000438489	2564	3'UTR
REPS2	ENSG00000169891	ENST00000303843	6445	3'UTR
AK4	ENSG00000162433	ENST00000395334	1312	3'UTR
FGFR2	ENSG00000066468	ENST00000356226	3446	3'UTR
MXI1	ENSG00000119950	ENST00000332674	2730	3'UTR
RPP25	ENSG00000178718	ENST00000322177	2378	3'UTR
EIF4E3	ENSG00000163412	ENST00000425534	9630	3'UTR
ZNF720	ENSG00000197302	ENST00000316491	1412	3'UTR
IFIT1	ENSG00000185745	ENST00000546318	2338	3'UTR
PURA	ENSG00000185129	ENST00000331327	4622	3'UTR
GRIA3	ENSG00000125675	ENST00000611689	756	3'UTR
YPEL2	ENSG00000175155	ENST00000312655	4202	3'UTR
PDP2	ENSG00000172840	ENST00000311765	4707	3'UTR

!2v2.0

s/y

sts: 1 | p-value < 0.05

deltaG	predicted target	targeting miRNA
-16.80	CTGGATTCACTCCCTCTGGTTG	CAACTAGACTGTGAGCTTCTAG
-12.10	GACGGAGTTTCACTCTTGTTG	CAACTAGACTGTGAGCTTCTAG
-18.90	CTTCCAGCTTTCAGTCTAGCTTG	CAACTAGACTGTGAGCTTCTAG
-18.30	TTAGAGGCTTGAAATCTGGTTC	CAACTAGACTGTGAGCTTCTAG
-13.70	ACCCAGGCACCCAGTCTGAGTTC	CAACTAGACTGTGAGCTTCTAG
-16.50	GCATCAGCTCACGTTTGGCTG	CAACTAGACTGTGAGCTTCTAG
-12.30	GCCCAGGTCCAGGGTCAGTTA	CAACTAGACTGTGAGCTTCTAG
-13.20	CAACAGGCCCCAGAGCTGGTTC	CAACTAGACTGTGAGCTTCTAG
-18.30	TCCTCAGCTCACATGTCTTGTTT	CAACTAGACTGTGAGCTTCTAG
-16.50	ACTTCAGCTCCAGCTGGTTT	CAACTAGACTGTGAGCTTCTAG
-14.10	GCAGGCAGCACAGCAGACTAGTTA	CAACTAGACTGTGAGCTTCTAG
-14.90	TTAGCAGTGCAGTTGAGTTG	CAACTAGACTGTGAGCTTCTAG
-12.70	CTGGCCTCAGAGGCTGTTG	CAACTAGACTGTGAGCTTCTAG
-13.30	ATGGAAAAATCACTGGCCTAGTTC	CAACTAGACTGTGAGCTTCTAG
-12.30	AAAGGAGTAGCAAAGGTCAGTTC	CAACTAGACTGTGAGCTTCTAG
-14.00	ACAGAAGACTCACTCCTTGGCTG	CAACTAGACTGTGAGCTTCTAG
-19.10	CTTGAAAGTCTCACTTTCTAGTTG	CAACTAGACTGTGAGCTTCTAG
-13.00	AAAGAAGTTCAGCCTGGGTG	CAACTAGACTGTGAGCTTCTAG
-13.60	AATCAGAATCACGTTTTAGTTG	CAACTAGACTGTGAGCTTCTAG
-15.90	CTATGTTGCTCAGGCTGGTTG	CAACTAGACTGTGAGCTTCTAG

Base Pairs in putative heteroduplex	Span of Target	P-Value
18	22	0.012700
16	21	0.000040
16	23	0.003890
17	22	0.032800
15	23	0.000008
15	21	0.000982
13	21	0.038000
14	21	0.001100
15	23	0.023600
14	20	0.002770
16	24	0.022300
18	20	0.015100
16	19	0.00153
17	24	0.015900
16	23	0.021300
16	23	0.002060
19	24	0.005070
16	20	0.033900
13	23	0.000195
18	21	0.047000

Genome: Homo Sapiens | mRNA | miRBase 21 (Jun. 2014), ENSEMBL 78 (Dec. 2014) and RNA22v2.0

Description: List of transcripts that are targeted by *all* of the below miRNA identifiers *simultaneously*

miRNA's: hsa-miR-4508

Filtering By: Base pair min value: 12 | Folding energy max value (Kcal/mol): -12 | Min miRNA targets: 1 | p-value < 0.05

Gene	Accession number	Trascript	Predicted Target Site	seed - cDNA Region	deltaG
ANXA11	ENSG00000122359	ENST00000372231	3284	3'UTR	-22.00
BOK	ENSG00000176720	ENST00000318407	991	3'UTR	-18.50
PLCB2	ENSG00000137841	ENST00000543785	1271	3'UTR	-20.20
FOXN3	ENSG00000053254	ENST00000261302	2091	3'UTR	-17.20
ARHGAP39	ENSG00000147799	ENST00000276826	4553	3'UTR	-26.50
NAPA	ENSG00000105402	ENST00000595227	861	3'UTR	-20.30
SLC43A3	ENSG00000134802	ENST00000352187	2258	3'UTR	-22.30
CC2D1A	ENSG00000132024	ENST00000318003	3225	3'UTR	-32.80
NFIX	ENSG00000008441	ENST00000592199	1484	CDS, 3'UTR	-17.20
SLC12A4	ENSG00000124067	ENST00000316341	3500	3'UTR	-26.90
ADD1	ENSG00000087274	ENST00000398123	2190	3'UTR	-23.50
FGD6	ENSG00000180263	ENST00000343958	7963	3'UTR	-16.30
FARSB	ENSG00000116120	ENST00000281828	3233	3'UTR	-23.10
MSC	ENSG00000178860	ENST00000325509	1727	3'UTR	-21.90
CST3	ENSG00000101439	ENST00000398409	630	3'UTR	-14.70
NXPH3	ENSG00000182575	ENST00000328741	2064	3'UTR	-14.00
LRRC10	ENSG00000198812	ENST00000361484	1891	3'UTR	-20.60
DNM1L	ENSG00000087470	ENST00000381000	3523	3'UTR	-18.60
TMEM63B	ENSG00000137216	ENST00000259746	3054	3'UTR	-14.40
VWA1	ENSG00000179403	ENST00000338660	1392	3'UTR	-24.00
ZG16	ENSG00000174992	ENST00000400752	917	3'UTR	-14.90
Orai2	ENSG00000160991	ENST00000478730	2501	3'UTR	-28.20
PAX2	ENSG00000075891	ENST00000355243	2150	3'UTR	-33.60

predicted target	targeting miRNA
TTCGAGACCCAGCCTGGC	GCGGGGCTGGGCGCGCG
GAGGCCCTCAGCACCCGA	GCGGGGCTGGGCGCGCG
CCACAGCCACAGCTCTGC	GCGGGGCTGGGCGCGCG
CGGCCACCAGTCCTCGA	GCGGGGCTGGGCGCGCG
AAAGCCCCAGCCCTGC	GCGGGGCTGGGCGCGCG
AGCCCCCAGTGCCCGT	GCGGGGCTGGGCGCGCG
CCTGGGCCCAGTCTCAGC	GCGGGGCTGGGCGCGCG
CGGGCCCCAGCCCCGC	GCGGGGCTGGGCGCGCG
AGCAGTCTCAGTCTTGG	GCGGGGCTGGGCGCGCG
TGCTTGCTGGCCCTGT	GCGGGGCTGGGCGCGCG
AGCCCCAGACCCAGCCCCGG	GCGGGGCTGGGCGCGCG
TGCACCACCAGGCCTGG	GCGGGGCTGGGCGCGCG
TGTGGGCCTGCAGTCCCAGC	GCGGGGCTGGGCGCGCG
TCTCCGCCCCGCTCCTGC	GCGGGGCTGGGCGCGCG
TGTATTCCCACCCCTGG	GCGGGGCTGGGCGCGCG
TGTGTGTCTGTCTGT	GCGGGGCTGGGCGCGCG
CCCGCCTCAGCCTGC	GCGGGGCTGGGCGCGCG
TGCACTCCAGCCTTGG	GCGGGGCTGGGCGCGCG
TGTTCCCCCCCCTCCGT	GCGGGGCTGGGCGCGCG
CGGCCCCATCCCCGC	GCGGGGCTGGGCGCGCG
TGAGGGCAAGGCCTAGT	GCGGGGCTGGGCGCGCG
CGGGCGCCTGTAGCCCCAGC	GCGGGGCTGGGCGCGCG
AGCGCGGCCAGCCCCGG	GCGGGGCTGGGCGCGCG

Base Pairs in putative heteroduplex	Span of Target	P-Value	
13	18	0.020300	
12	18	0.010700	
12	18	0.001310	
13	17	0.047400	
13	16	0.019300	
14	17	0.001880	
14	18	0.006860	
15	17	0.023500	
13	17	0.013400	
14	17	0.021800	
13	20	0.007850	
12	17	0.010500	
16	20	0.012900	
12	18	0.023200	
12	17	0.015600	
15	15	0.000663	
13	15	0.037400	
14	16	0.009050	
13	17	0.014000	
14	15	0.001540	
12	17	0.021000	
16	20	0.016700	
15	18	0.030600	