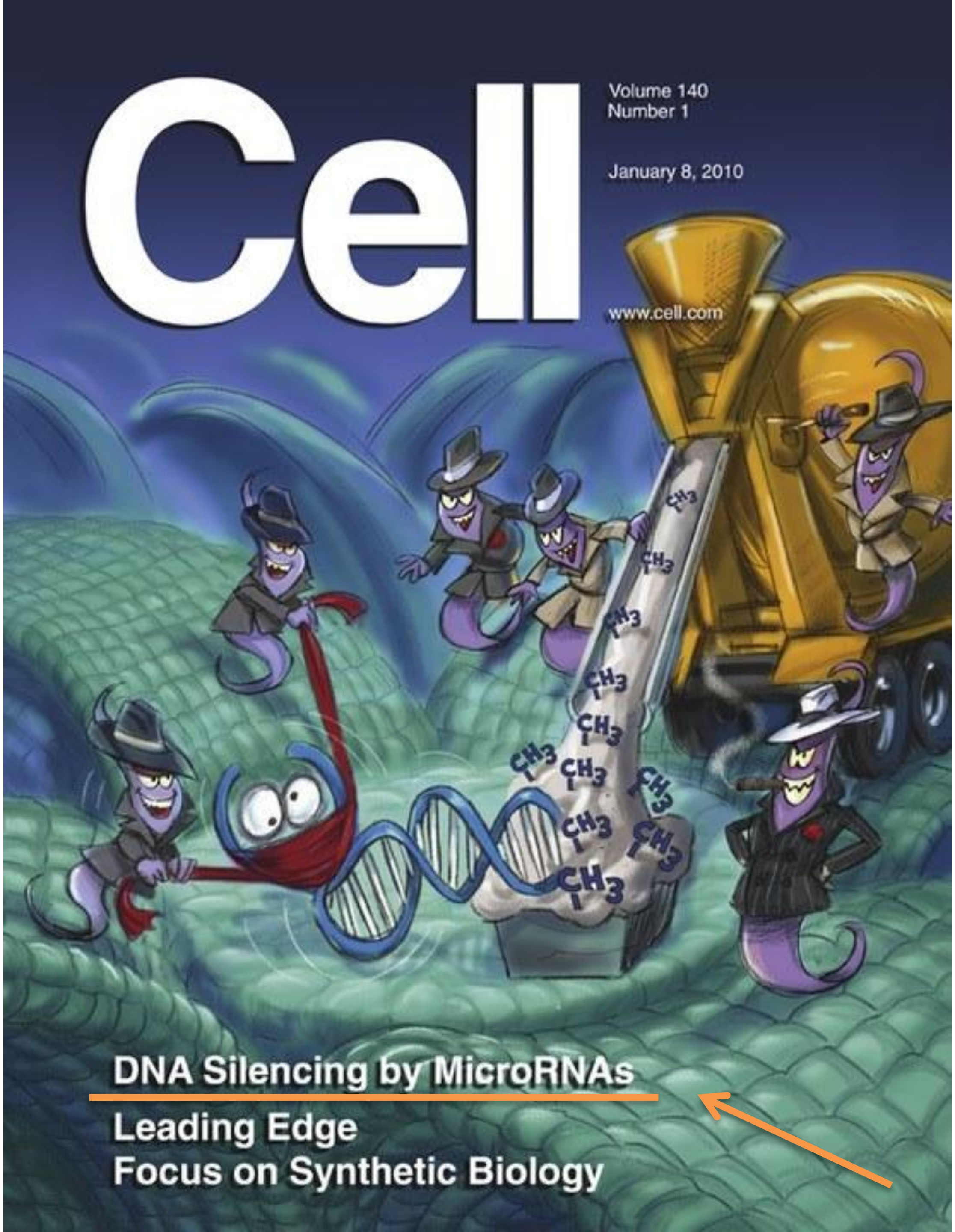
microRNA Targets

Group 11

Ma Ming



Cell

Volume 140
Number 1

January 8, 2010

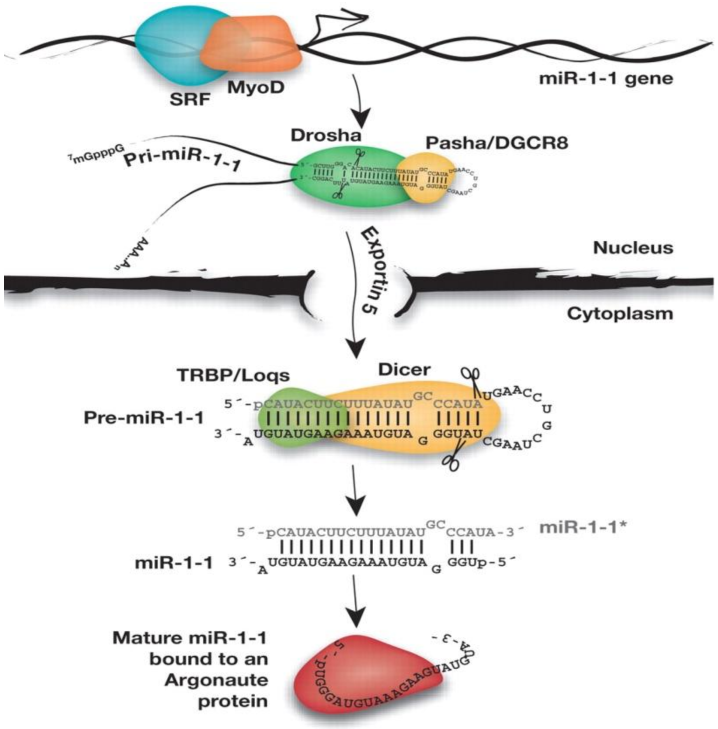
www.cell.com

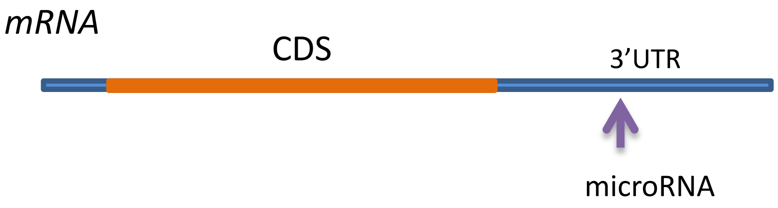
DNA Silencing by MicroRNAs

Leading Edge
Focus on Synthetic Biology

Background

- What is microRNA
- Apoptosis
- High Throughput Screening





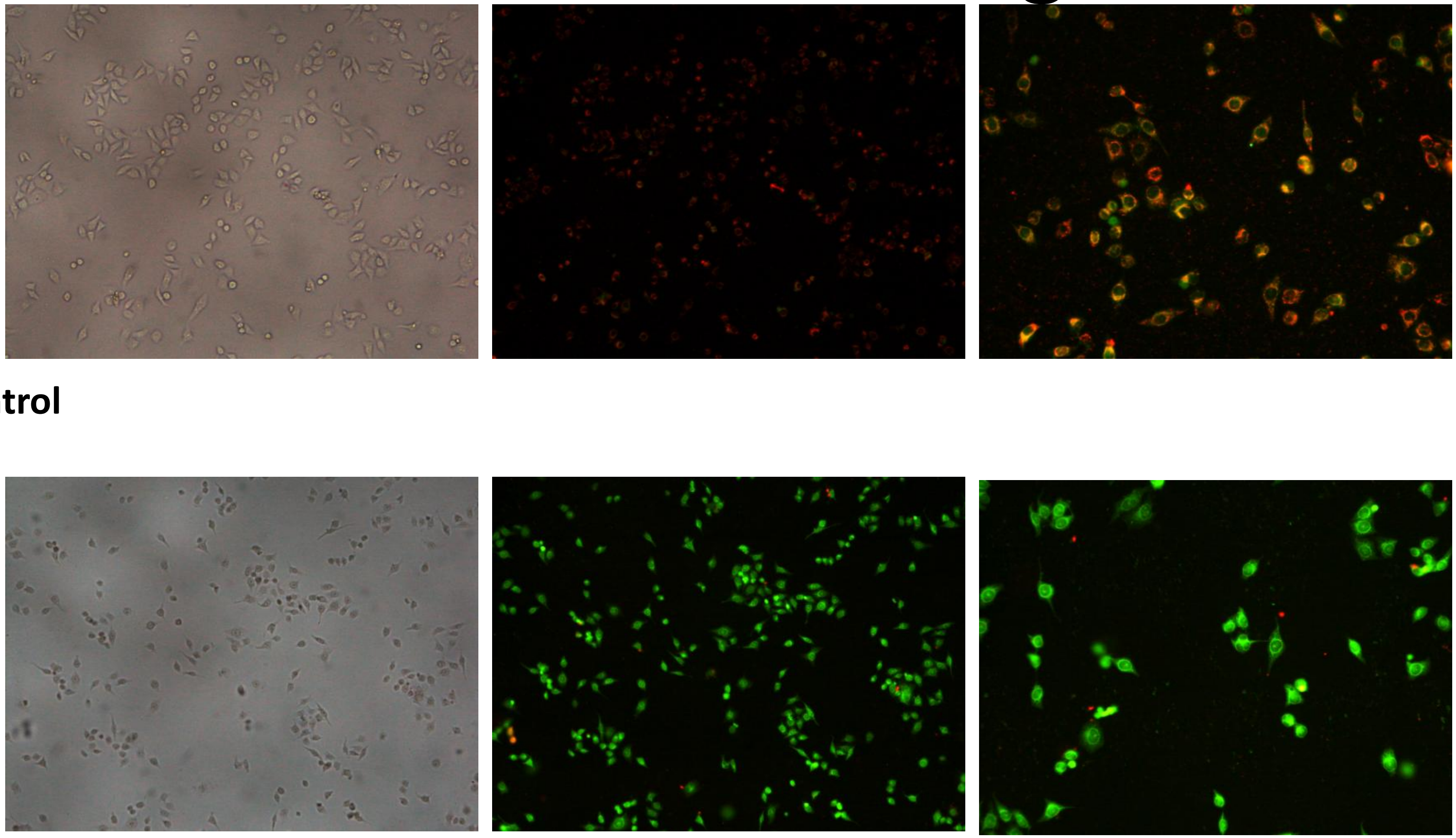
mRNA

CDS

3’UTR

microRNA

Apoptosis Screen Method: JC-1 Staining



NC

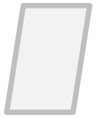
Control

Apoptosis

Alcohol Induced

Screening of miRNAs that Promotes Cellular Apoptosis

HeLa Cells,
946 miRNAs



Chips

First Round Screening

HeLa Cells,
107 miRNAs

96 well plates

Validation

Cell lines

HCT 116 WT

HCT 116 P53 KO

PNAC-1

MCF-7

A549

293T

Detect Apoptosis, Using JC-1

8 miRNAs

mir-X

How to find its Targets ?

Method 1: Targetscan

TargetScanHuman
Prediction of microRNA targets
Release 6.1: March 2012

Search for predicted microRNA targets in mammals

[Go to TargetScanMouse]
[Go to TargetScanWorm]
[Go to TargetScanFly]

1. Select a species Human

AND

2. Enter a human Entrez Gene symbol (e.g. "LIN28A")

AND/OR

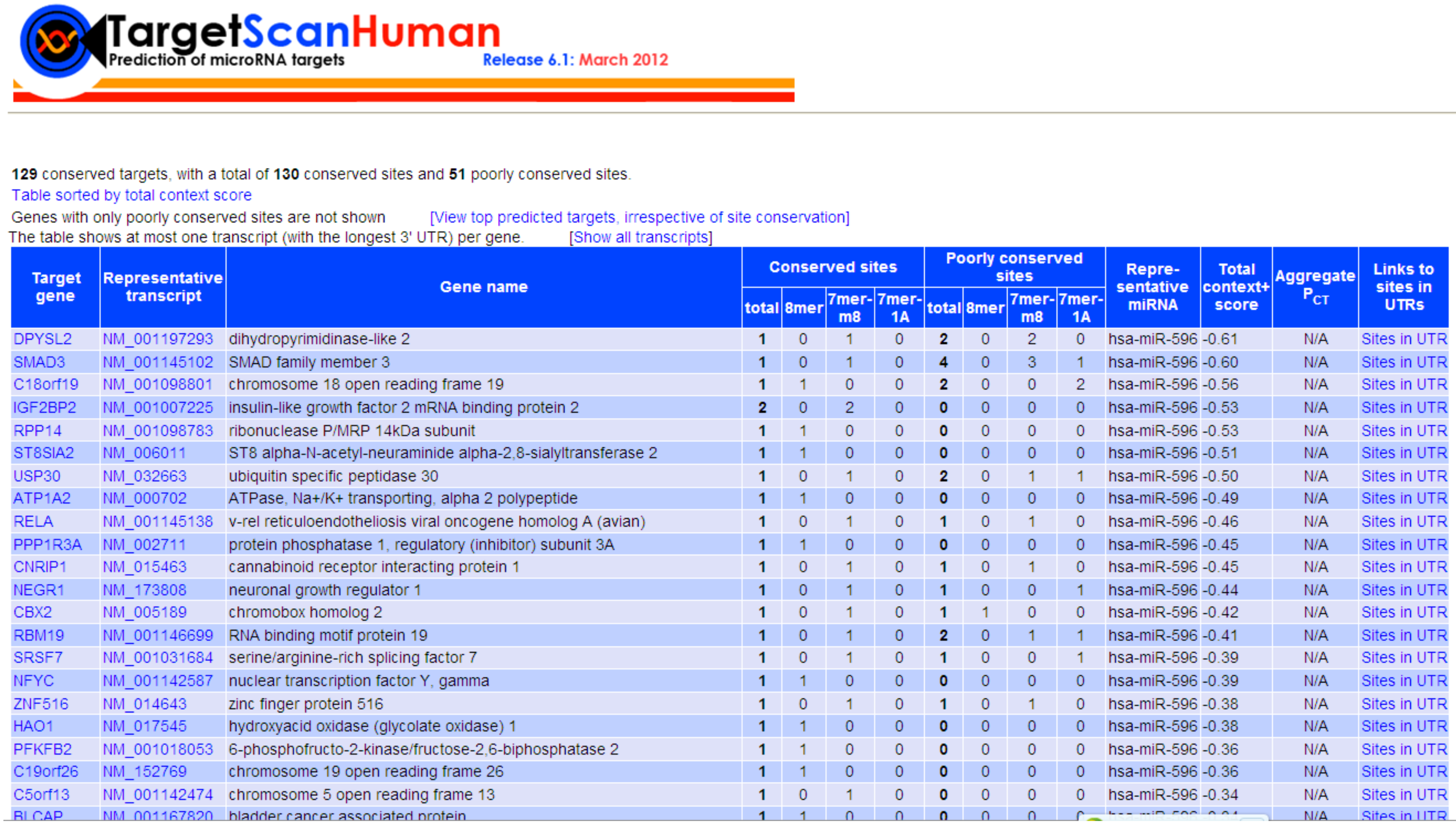
3. Do one of the following:

- Select a broadly conserved* microRNA family Broadly conserved microRNA families
- Select a conserved* microRNA family Conserved microRNA families
- Select a poorly conserved microRNA family Poorly conserved microRNA families Note that these families also include small RNAs that have been misclassified as miRNAs.
- Enter a microRNA name (e.g. "mmu-miR-1")

* broadly conserved = conserved across most vertebrates, usually to zebrafish
conserved = conserved across most mammals, but usually not beyond placental mammals

TargetScan predicts biological targets of miRNAs by searching for the presence of conserved 8mer and 7mer sites that match the seed region of each miRNA (ref. 1). As an option, nonconserved sites are also predicted. Also identified are sites with mismatches in the seed region that are compensated by conserved 3' pairing (ref. 2). In mammals, predictions are ranked based on the predicted efficacy of targeting as calculated using the context+ scores of the sites (ref. 3, 4). As an option, predictions are also ranked by their probability of conserved targeting (P_{CT}, ref. 2).

Method 1: Targetscan



TargetScanHuman
Prediction of microRNA targets
Release 6.1: March 2012

129 conserved targets, with a total of **130** conserved sites and **51** poorly conserved sites.

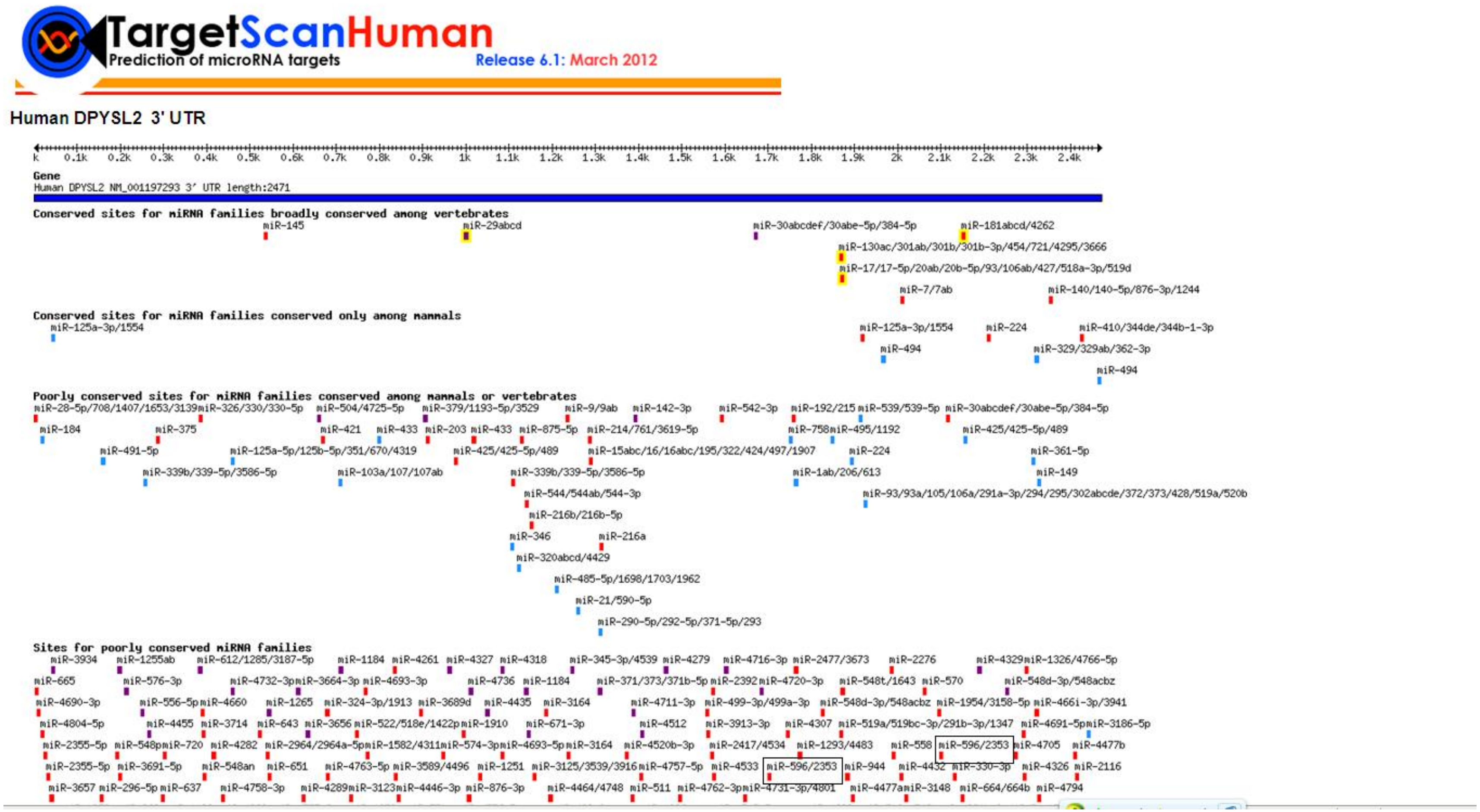
Table sorted by total context score

Genes with only poorly conserved sites are not shown [View top predicted targets, irrespective of site conservation]

The table shows at most one transcript (with the longest 3' UTR) per gene. [Show all transcripts]

Target gene	Representative transcript	Gene name	Conserved sites				Poorly conserved sites				Representative miRNA	Total context+ score	Aggregate P_{CT}	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A				
DPYSL2	NM_001197293	dihydropyrimidinase-like 2	**1**	0	1	0	**2**	0	2	0	hsa-miR-596	-0.61	N/A	Sites in UTR
SMAD3	NM_001145102	SMAD family member 3	**1**	0	1	0	**4**	0	3	1	hsa-miR-596	-0.60	N/A	Sites in UTR
C18orf19	NM_001098801	chromosome 18 open reading frame 19	**1**	1	0	0	**2**	0	0	2	hsa-miR-596	-0.56	N/A	Sites in UTR
IGF2BP2	NM_001007225	insulin-like growth factor 2 mRNA binding protein 2	**2**	0	2	0	**0**	0	0	0	hsa-miR-596	-0.53	N/A	Sites in UTR
RPP14	NM_001098783	ribonuclease P/MRP 14kDa subunit	**1**	1	0	0	**0**	0	0	0	hsa-miR-596	-0.53	N/A	Sites in UTR
ST8SIA2	NM_006011	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-596	-0.51	N/A	Sites in UTR
USP30	NM_032663	ubiquitin specific peptidase 30	**1**	0	1	0	**2**	0	1	1	hsa-miR-596	-0.50	N/A	Sites in UTR
ATP1A2	NM_000702	ATPase, Na+/K+ transporting, alpha 2 polypeptide	**1**	1	0	0	**0**	0	0	0	hsa-miR-596	-0.49	N/A	Sites in UTR
RELA	NM_001145138	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	**1**	0	1	0	**1**	0	1	0	hsa-miR-596	-0.46	N/A	Sites in UTR
PPP1R3A	NM_002711	protein phosphatase 1, regulatory (inhibitor) subunit 3A	**1**	1	0	0	**0**	0	0	0	hsa-miR-596	-0.45	N/A	Sites in UTR
CNRIP1	NM_015463	cannabinoid receptor interacting protein 1	**1**	0	1	0	**1**	0	1	0	hsa-miR-596	-0.45	N/A	Sites in UTR
NEGR1	NM_173808	neuronal growth regulator 1	**1**	0	1	0	**1**	0	0	1	hsa-miR-596	-0.44	N/A	Sites in UTR
CBX2	NM_005189	chromobox homolog 2	**1**	0	1	0	**1**	1	0	0	hsa-miR-596	-0.42	N/A	Sites in UTR
RBM19	NM_001146699	RNA binding motif protein 19	**1**	0	1	0	**2**	0	1	1	hsa-miR-596	-0.41	N/A	Sites in UTR
SRSF7	NM_001031684	serine/arginine-rich splicing factor 7	**1**	0	1	0	**1**	0	0	1	hsa-miR-596	-0.39	N/A	Sites in UTR
NFYC	NM_001142587	nuclear transcription factor Y, gamma	**1**	1	0	0	**0**	0	0	0	hsa-miR-596	-0.39	N/A	Sites in UTR
ZNF516	NM_014643	zinc finger protein 516	**1**	0	1	0	**1**	0	1	0	hsa-miR-596	-0.38	N/A	Sites in UTR
HAO1	NM_017545	hydroxyacid oxidase (glycolate oxidase) 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-596	-0.38	N/A	Sites in UTR
PFKFB2	NM_001018053	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-596	-0.36	N/A	Sites in UTR
C19orf26	NM_152769	chromosome 19 open reading frame 26	**1**	1	0	0	**0**	0	0	0	hsa-miR-596	-0.36	N/A	Sites in UTR
C5orf13	NM_001142474	chromosome 5 open reading frame 13	**1**	0	1	0	**0**	0	0	0	hsa-miR-596	-0.34	N/A	Sites in UTR
BLCAP	NM_001167820	bladder cancer associated protein	**1**	1	0	0	**0**	0	0	[illegible]	[illegible]	[illegible]	N/A	Sites in UTR

Method 1: Targetscan



TargetScanHuman
Prediction of microRNA targets
Release 6.1: March 2012

Human DPYSL2 3' UTR

Gene
Human DPYSL2 NM_001197293 3' UTR length:2471

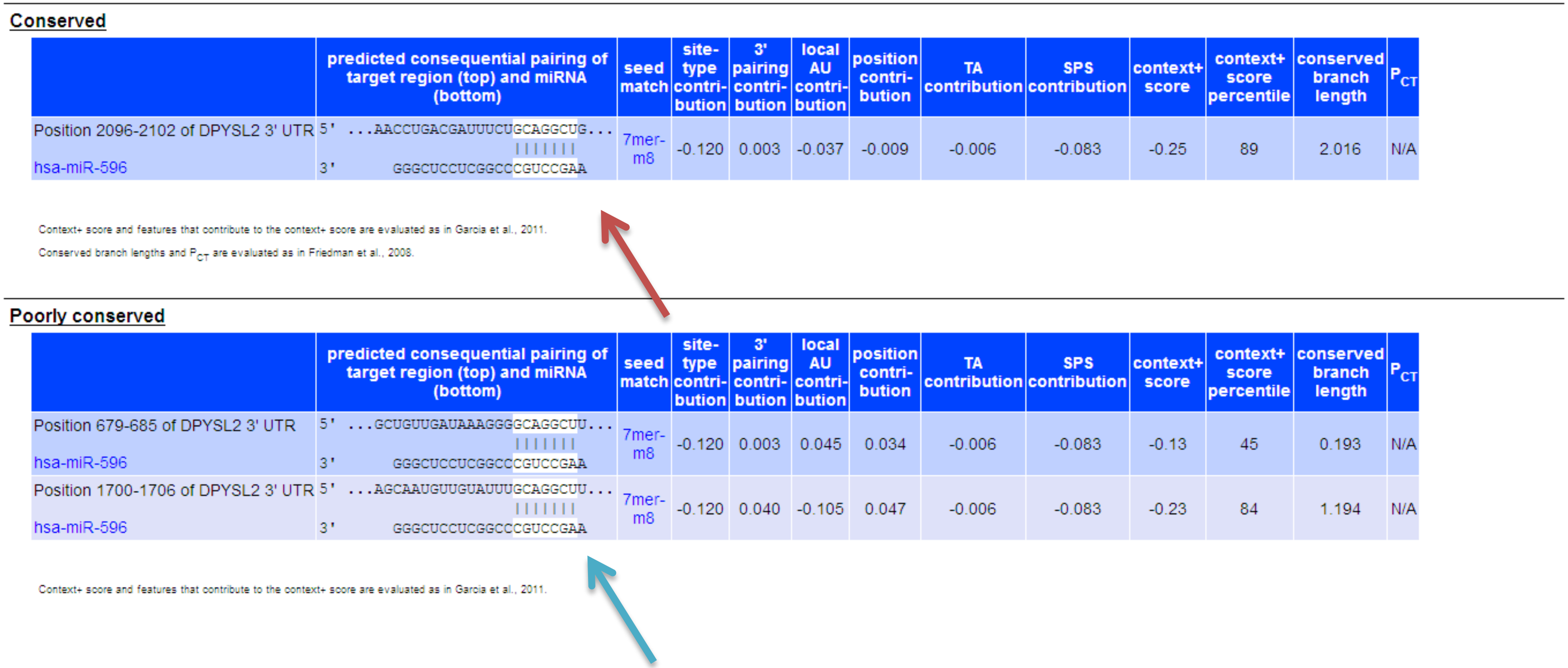
Conserved sites for miRNA families broadly conserved among vertebrates

Conserved sites for miRNA families conserved only among mammals

Poorly conserved sites for miRNA families conserved among mammals or vertebrates

Sites for poorly conserved miRNA families

Method 1: Targetscan



Conserved

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contri-bution	3' pairing contri-bution	local AU contri-bution	position contri-bution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P_{CT}
Position 2096-2102 of DPYSL2 3' UTR hsa-miR-596	5' ...AACCUGACGAUUUCUGCAGGCUG... ||||||| 3' GGGCUCCUCGGCCCGUCCGAA	7mer-m8	-0.120	0.003	-0.037	-0.009	-0.006	-0.083	-0.25	89	2.016	N/A

Context+ score and features that contribute to the context+ score are evaluated as in Garcia et al., 2011.

Conserved branch lengths and P_{CT} are evaluated as in Friedman et al., 2008.

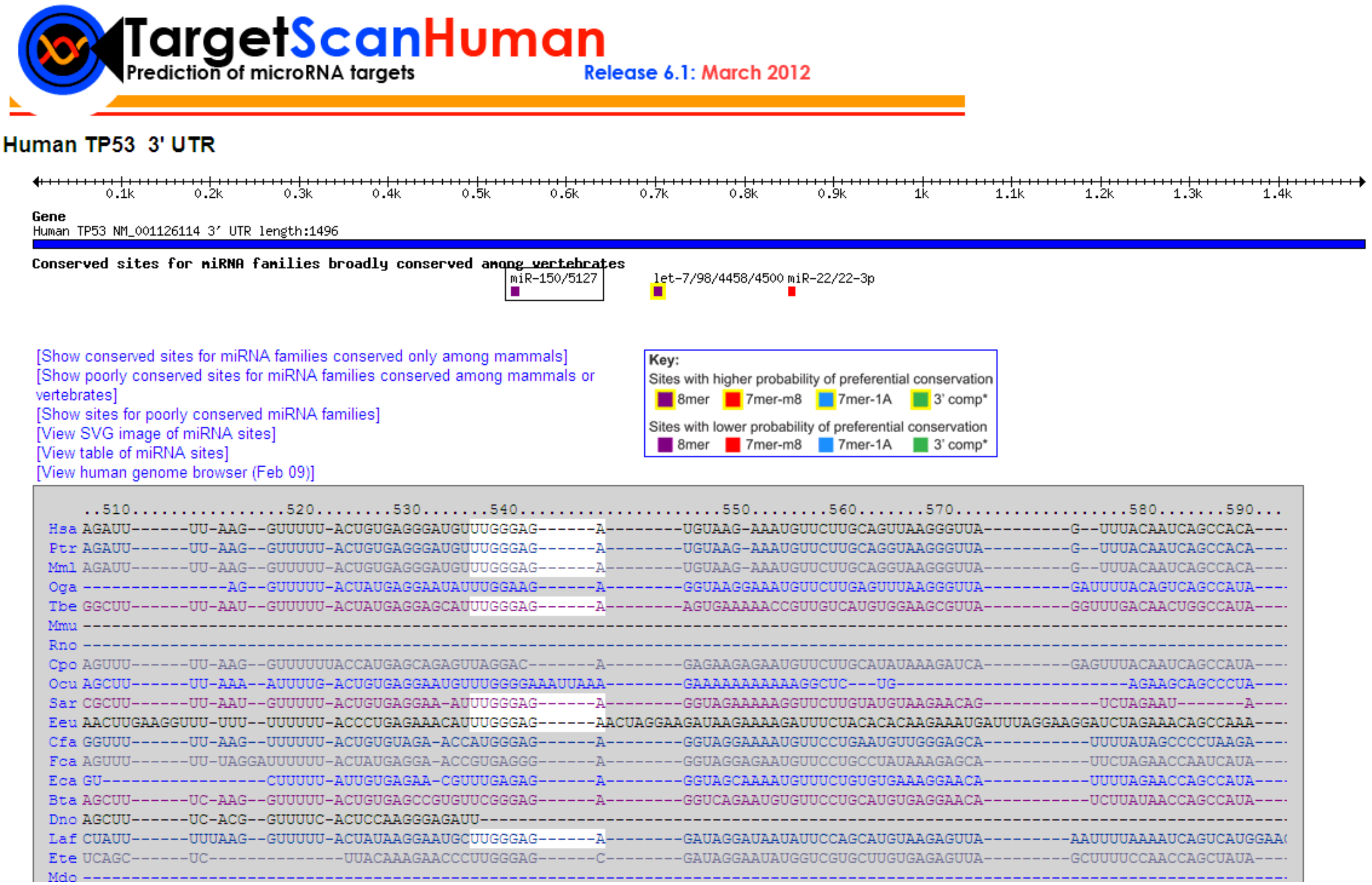
Poorly conserved

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contri-bution	3' pairing contri-bution	local AU contri-bution	position contri-bution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P_{CT}
Position 679-685 of DPYSL2 3' UTR hsa-miR-596	5' ...GCUGUUGAUAAAGGGGCAGGCUU... ||||||| 3' GGGCUCCUCGGCCCGUCCGAA	7mer-m8	-0.120	0.003	0.045	0.034	-0.006	-0.083	-0.13	45	0.193	N/A
Position 1700-1706 of DPYSL2 3' UTR hsa-miR-596	5' ...AGCAAUGUUGUAUUUGCAGGCUU... ||||||| 3' GGGCUCCUCGGCCCGUCCGAA	7mer-m8	-0.120	0.040	-0.105	0.047	-0.006	-0.083	-0.23	84	1.194	N/A

Context+ score and features that contribute to the context+ score are evaluated as in Garcia et al., 2011.

Mutant Design

Method 1: Targetscan



TargetScanHuman
Prediction of microRNA targets
Release 6.1: March 2012

Human TP53 3' UTR

Gene
Human TP53 NM_001126114 3' UTR length:1496

Conserved sites for miRNA families broadly conserved among vertebrates

[Show conserved sites for miRNA families conserved only among mammals]
[Show poorly conserved sites for miRNA families conserved among mammals or vertebrates]
[Show sites for poorly conserved miRNA families]
[View SVG image of miRNA sites]
[View table of miRNA sites]
[View human genome browser (Feb 09)]

Key:
Sites with higher probability of preferential conservation
■ 8mer ■ 7mer-m8 ■ 7mer-1A ■ 3' comp*
Sites with lower probability of preferential conservation
■ 8mer ■ 7mer-m8 ■ 7mer-1A ■ 3' comp*

```
    ..510.................520.........530.......540......................550.........560.......570...................580.......590...
Hsa AGAUU------UU-AAG--GUUUUU-ACUGUGAGGGAUGUUUGGGAG------A--------UGUAAG-AAAUGUUCUUGCAGUUAAGGGUUA---------G--UUUACAAUCAGCCACA---
Ptr AGAUU------UU-AAG--GUUUUU-ACUGUGAGGGAUGUUUGGGAG------A--------UGUAAG-AAAUGUUCUUGCAGGUAAGGGUUA---------G--UUUACAAUCAGCCACA---
Mml AGAUU------UU-AAG--GUUUUU-ACUGUGAGGGAUGUUUGGGAG------A--------UGUAAG-AAAUGUUCUUGCAGGUAAGGGUUA---------G--UUUACAAUCAGCCACA---
Oga ---------------AG--GUUUUU-ACUAUGAGGAAUAUUUGGAAG------A--------GGUAAGGAAAUGUUCUUGAGUUUAAGGGUUA---------GAUUUUACAGUCAGCCAUA---
Tbe GGCUU------UU-AAU--GUUUUU-ACUAUGAGGAGCAUUUGGGAG------A--------AGUGAAAAACCGUUGUCAUGUGGAAGCGUUA---------GGUUUGACAACUGGCCAUA---
Mmu ---------------------------------------------------------------------------------------------------------------------------
Rno ---------------------------------------------------------------------------------------------------------------------------
Cpo AGUUU------UU-AAG--GUUUUUUACCAUGAGCAGAGUUAGGAC-------A--------GAGAAGAGAAUGUUCUUGCAUAUAAAGAUCA---------GAGUUUACAAUCAGCCAUA---
Ocu AGCUU------UU-AAA--AUUUUG-ACUGUGAGGAAUGUUUGGGGAAAUUAAA--------GAAAAAAAAAAAGGCUC---UG-----------------------AGAAGCAGCCCUA---
Sar CGCUU------UU-AAU--GUUUUU-ACUGUGAGGAA-AUUUGGGAG------A--------GGUAGAAAAAGGUUCUUGUAUGUAAGAACAG------------UCUAGAAU-------A---
Eeu AACUUGAAGGUUU-UUU--UUUUUU-ACCCUGAGAAACAUUUGGGAG------AACUAGGAAGAUAAGAAAAGAUUUCUACACACAAGAAAUGAUUUAGGAAGGAUCUAGAAACAGCCAAA---
Cfa GGUUU------UU-AAG--UUUUUU-ACUGUGUAGA-ACCAUGGGAG------A--------GGUAGGAAAAUGUUCCUGAAUGUUGGGAGCA-----------UUUUAUAGCCCCUAAGA---
Fca AGUUU------UU-UAGGAUUUUUU-ACUAUGAGGA-ACCGUGAGGG------A--------GGUAGGAGAAUGUUCCUGCCUAUAAAGAGCA-----------UUCUAGAACCAAUCAUA---
Eca GU-----------------CUUUUU-AUUGUGAGAA-CGUUUGAGAG------A--------GGUAGCAAAAUGUUUCUGUGUGAAAGGAACA-----------UUUUAGAACCAGCCAUA---
Bta AGCUU------UC-AAG--GUUUUU-ACUGUGAGCCGUGUUCGGGAG------A--------GGUCAGAAUGUGUUCCUGCAUGUGAGGAACA-----------UCUUAUAACCAGCCAUA---
Dno AGCUU------UC-ACG--GUUUUC-ACUCCAAGGGAGAUU----------------------------------------------------------------------------------
Laf CUAUU------UUUAAG--GUUUUU-ACUAUAAGGAAUGCUUGGGAG------A--------GAUAGGAUAAUAUUCCAGCAUGUAAGAGUUA---------AAUUUUAAAAUCAGUCAUGGAA(
Ete UCAGC------UC--------------UUACAAAGAACCCUUGGGAG------C--------GAUAGGAAUAUGGUCGUGCUUGUGAGAGUUA---------GCUUUUCCAACCAGCUAUA---
Mdo ---------------------------------------------------------------------------------------------------------------------------
```
]

Method 2: mirbase

Latest miRBase blog posts

miRBase, Wikipedia and community annotation — By sam (April 20, 2012)

Many miRBase entry pages have a new "community annotation" section (see, for example, dme-mir-10). This section incorporates information about specific microRNA families and sequences taken directly from the free, online encyclopedia, Wikipedia. In total, over 4500 miRBase entries currently include information from Wikipedia. We show the summary paragraph from the Wikipedia page, the full page, [...]

MicroRNA Wikipedia pages in need of attention — By sam ()

The following Wikipedia pages about microRNA sequences and families could do with some loving care. Please take a look, and consider adding information about microRNA function, evolution, discovery, and references. Feel free to comment here, or email us at the usual address, if you make changes worthy of removing pages from this list. lin-4_microRNA_precursor lsy-6_microRNA [...]

miRNA count: 18226 entries

Release 18: November 2011

Search by miRNA name or keyword

Download published miRNA data

Download page | FTP site

This site is featured in:

NetWatch - *Science* 303:1741 (2004)

Highlights, Web watch - *Nature Reviews Genetics* 5:244 (2004)

miRBase: the microRNA database

miRBase provides the following services:

- The miRBase database is a searchable database of published miRNA sequences and annotation. Each entry in the miRBase Sequence database represents a predicted hairpin portion of a miRNA transcript (termed mir in the database), with information on the location and sequence of the mature miRNA sequence (termed miR). Both hairpin and mature sequences are available for searching and browsing, and entries can also be retrieved by name, keyword, references and annotation. All sequence and annotation data are also available for download.
- The miRBase Registry provides miRNA gene hunters with unique names for novel miRNA genes prior to publication of results. Visit the help pages for more information about the naming service.
- The miRBase Targets database and pipeline has been rebranded as microCosm, and is now hosted at the EBI. The microCosm resource continues to be maintained by the Enright group. miRBase currently links miRNAs to targets predicted by microCosm, TargetScan and Pictar, and aims to provide a more extensive target prediction aggregation service in the future.

To receive email notification of data updates and feature changes please subscribe to the miRBase announcements mailing list. Any queries about the website or naming service should be directed at mirbase@manchester.ac.uk.

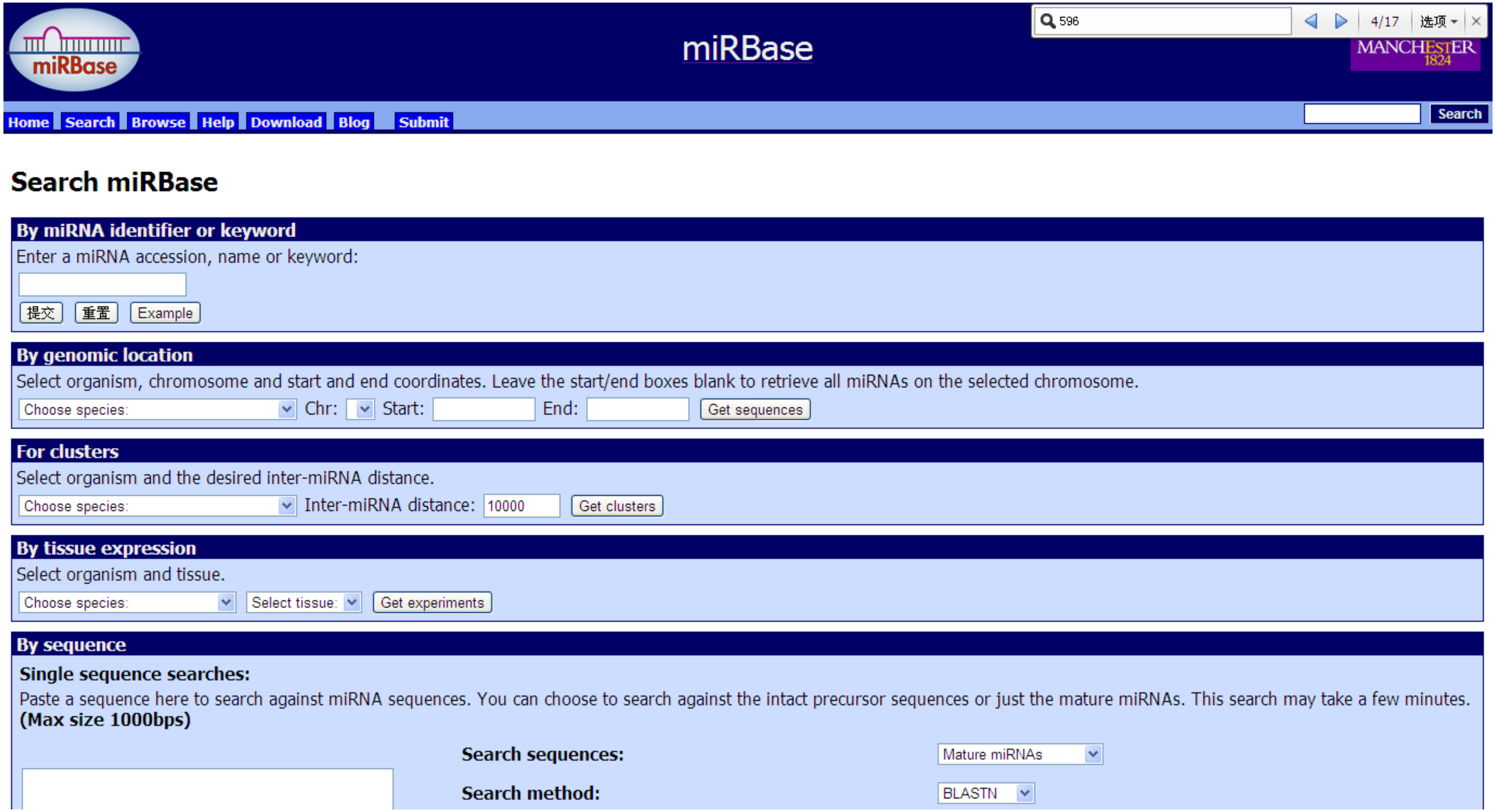
miRBase is hosted and maintained in the Faculty of Life Sciences at the University of Manchester with funding from the BBSRC, and was previously hosted and supported by the Wellcome Trust Sanger Institute.

References

If you make use of the data presented here, please cite the following articles in addition to the primary data sources:

miRBase: integrating microRNA annotation and deep-sequencing data

Method 2: mirbase



Search miRBase

By miRNA identifier or keyword

Enter a miRNA accession, name or keyword:

By genomic location

Select organism, chromosome and start and end coordinates. Leave the start/end boxes blank to retrieve all miRNAs on the selected chromosome.

For clusters

Select organism and the desired inter-miRNA distance.

Choose species: Inter-miRNA distance: 10000

By tissue expression

Select organism and tissue.

By sequence

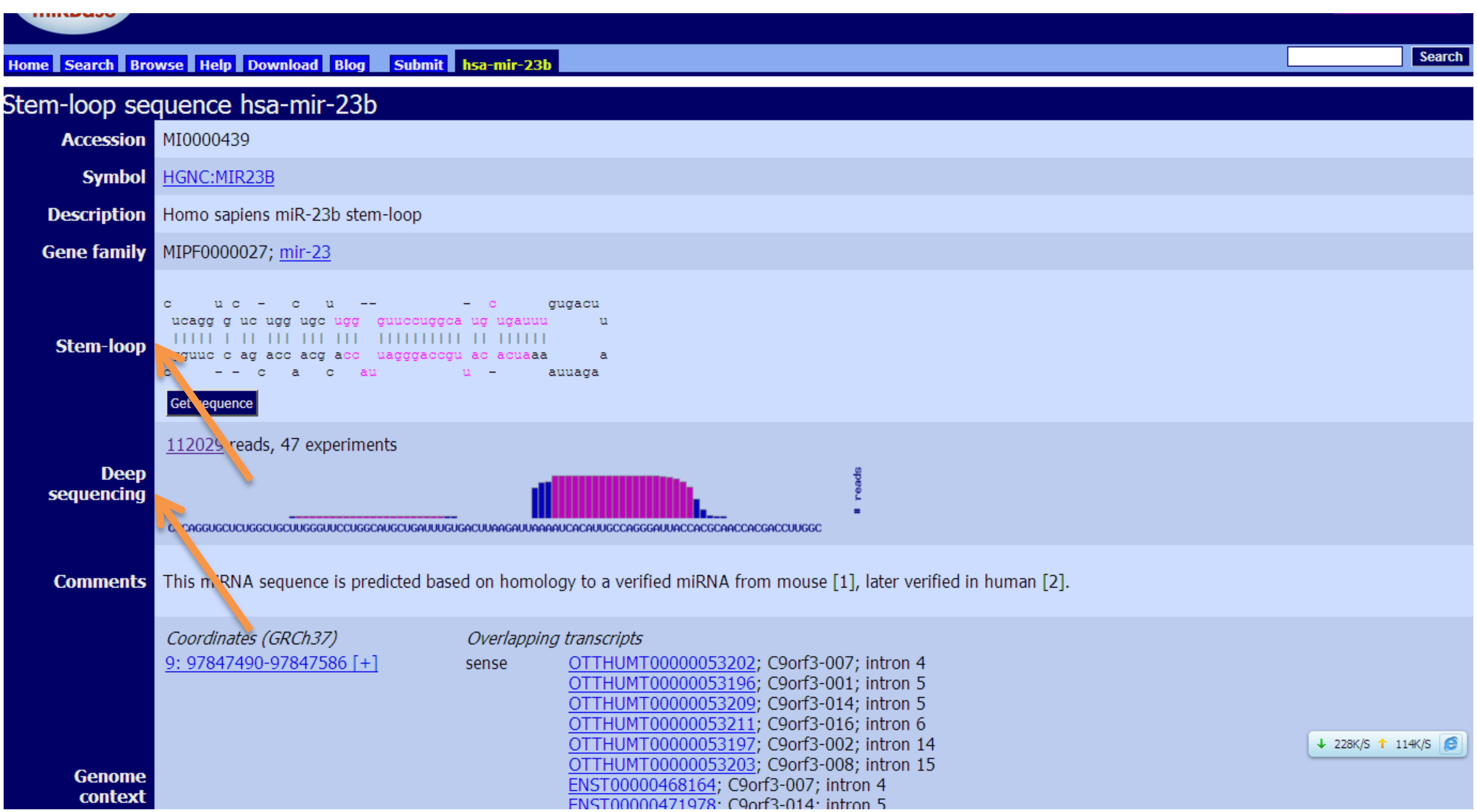
Single sequence searches:

Paste a sequence here to search against miRNA sequences. You can choose to search against the intact precursor sequences or just the mature miRNAs. This search may take a few minutes. **(Max size 1000bps)**

Search sequences: Mature miRNAs

Search method: BLASTN

Method 2: mirbase



Stem-loop sequence hsa-mir-23b

Accession	MI0000439
Symbol	HGNC:MIR23B
Description	Homo sapiens miR-23b stem-loop
Gene family	MIPF0000027; mir-23

Stem-loop

```
c     u c  -   c   u   --            -  c      gugacu
 ucagg g uc ugg ugc ugg  guuccuggca ug ugauuu      u
 ||||| | || ||| ||| |||  |||||||||| || ||||||
  guuc c ag acc acg acc  uagggaccgu ac acuaaa      a
c     - -  c   a   c   au            u  -      auuaga
```

Get sequence

Deep sequencing

112029 reads, 47 experiments

Comments

This miRNA sequence is predicted based on homology to a verified miRNA from mouse [1], later verified in human [2].

Genome context

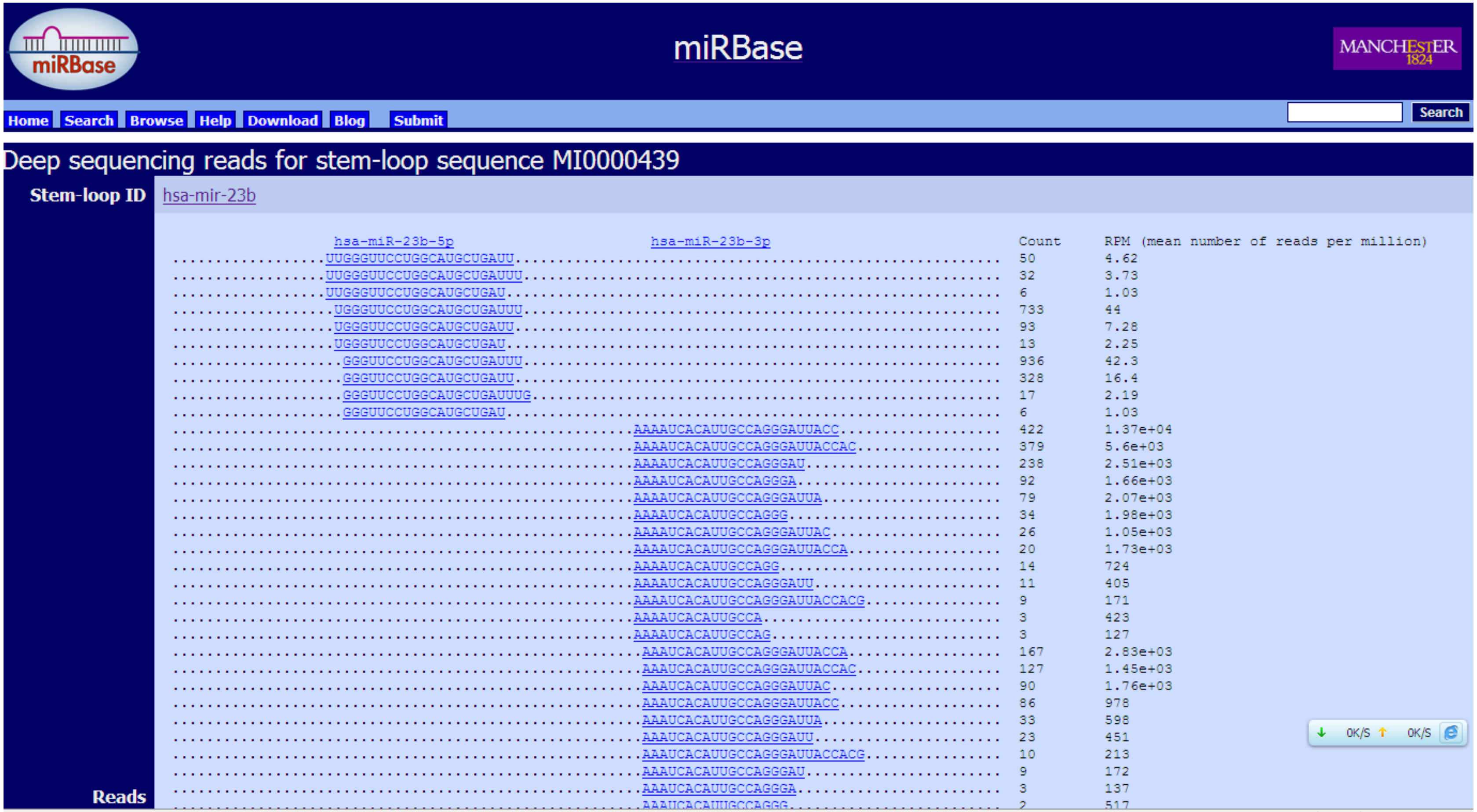
Coordinates (GRCh37)

9: 97847490-97847586 [+]

Overlapping transcripts

sense	OTTHUMT00000053202	C9orf3-007; intron 4
	OTTHUMT00000053196	C9orf3-001; intron 5
	OTTHUMT00000053209	C9orf3-014; intron 5
	OTTHUMT00000053211	C9orf3-016; intron 6
	OTTHUMT00000053197	C9orf3-002; intron 14
	OTTHUMT00000053203	C9orf3-008; intron 15
	ENST00000468164	C9orf3-007; intron 4
	ENST00000471978	C9orf3-014; intron 5

Method 2: mirbase



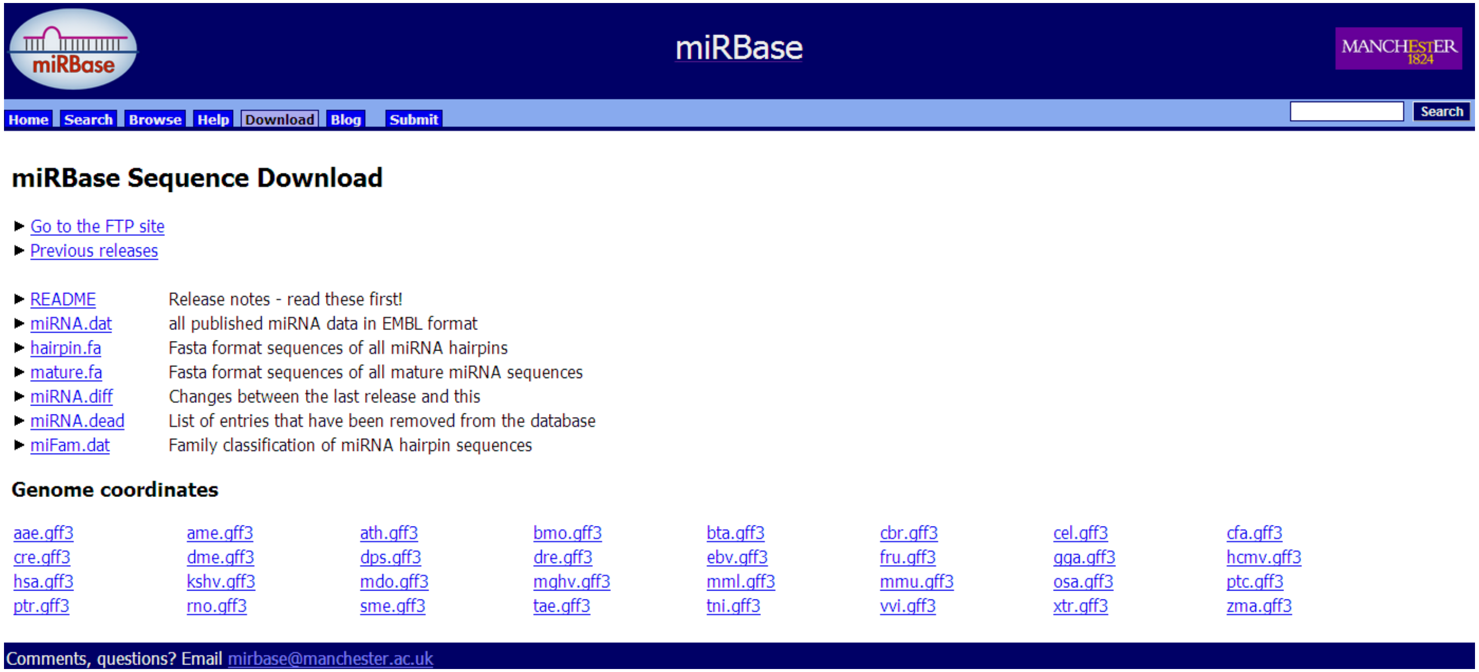
Deep sequencing reads for stem-loop sequence MI0000439

Stem-loop ID hsa-mir-23b

Reads

```
                   hsa-miR-23b-5p                       hsa-miR-23b-3p                             Count     RPM (mean number of reads per million)
..................UUGGGUUCCUGGCAUGCUGAUU.........................................................  50        4.62
..................UUGGGUUCCUGGCAUGCUGAUUU........................................................  32        3.73
..................UUGGGUUCCUGGCAUGCUGAU..........................................................  6         1.03
...................UGGGUUCCUGGCAUGCUGAUUU........................................................  733       44
...................UGGGUUCCUGGCAUGCUGAUU.........................................................  93        7.28
...................UGGGUUCCUGGCAUGCUGAU..........................................................  13        2.25
....................GGGUUCCUGGCAUGCUGAUUU........................................................  936       42.3
....................GGGUUCCUGGCAUGCUGAUU.........................................................  328       16.4
....................GGGUUCCUGGCAUGCUGAUUUG.......................................................  17        2.19
....................GGGUUCCUGGCAUGCUGAU..........................................................  6         1.03
......................................................AAAAUCACAUUGCCAGGGAUUACC...................  422       1.37e+04
......................................................AAAAUCACAUUGCCAGGGAUUACCAC.................  379       5.6e+03
......................................................AAAAUCACAUUGCCAGGGAU.......................  238       2.51e+03
......................................................AAAAUCACAUUGCCAGGGA........................  92        1.66e+03
......................................................AAAAUCACAUUGCCAGGGAUUA.....................  79        2.07e+03
......................................................AAAAUCACAUUGCCAGGG.........................  34        1.98e+03
......................................................AAAAUCACAUUGCCAGGGAUUAC....................  26        1.05e+03
......................................................AAAAUCACAUUGCCAGGGAUUACCA..................  20        1.73e+03
......................................................AAAAUCACAUUGCCAGG..........................  14        724
......................................................AAAAUCACAUUGCCAGGGAUU......................  11        405
......................................................AAAAUCACAUUGCCAGGGAUUACCACG................  9         171
......................................................AAAAUCACAUUGCCA............................  3         423
......................................................AAAAUCACAUUGCCAG...........................  3         127
.......................................................AAAUCACAUUGCCAGGGAUUACCA..................  167       2.83e+03
.......................................................AAAUCACAUUGCCAGGGAUUACCAC.................  127       1.45e+03
.......................................................AAAUCACAUUGCCAGGGAUUAC....................  90        1.76e+03
.......................................................AAAUCACAUUGCCAGGGAUUACC...................  86        978
.......................................................AAAUCACAUUGCCAGGGAUUA.....................  33        598
.......................................................AAAUCACAUUGCCAGGGAUU......................  23        451
.......................................................AAAUCACAUUGCCAGGGAUUACCACG................  10        213
.......................................................AAAUCACAUUGCCAGGGAU.......................  9         172
.......................................................AAAUCACAUUGCCAGGGA........................  3         137
.......................................................AAAUCACAUUGCCAGGG.........................  2         517
```

Method 2: mirbase



miRBase Sequence Download

- Go to the FTP site
- Previous releases

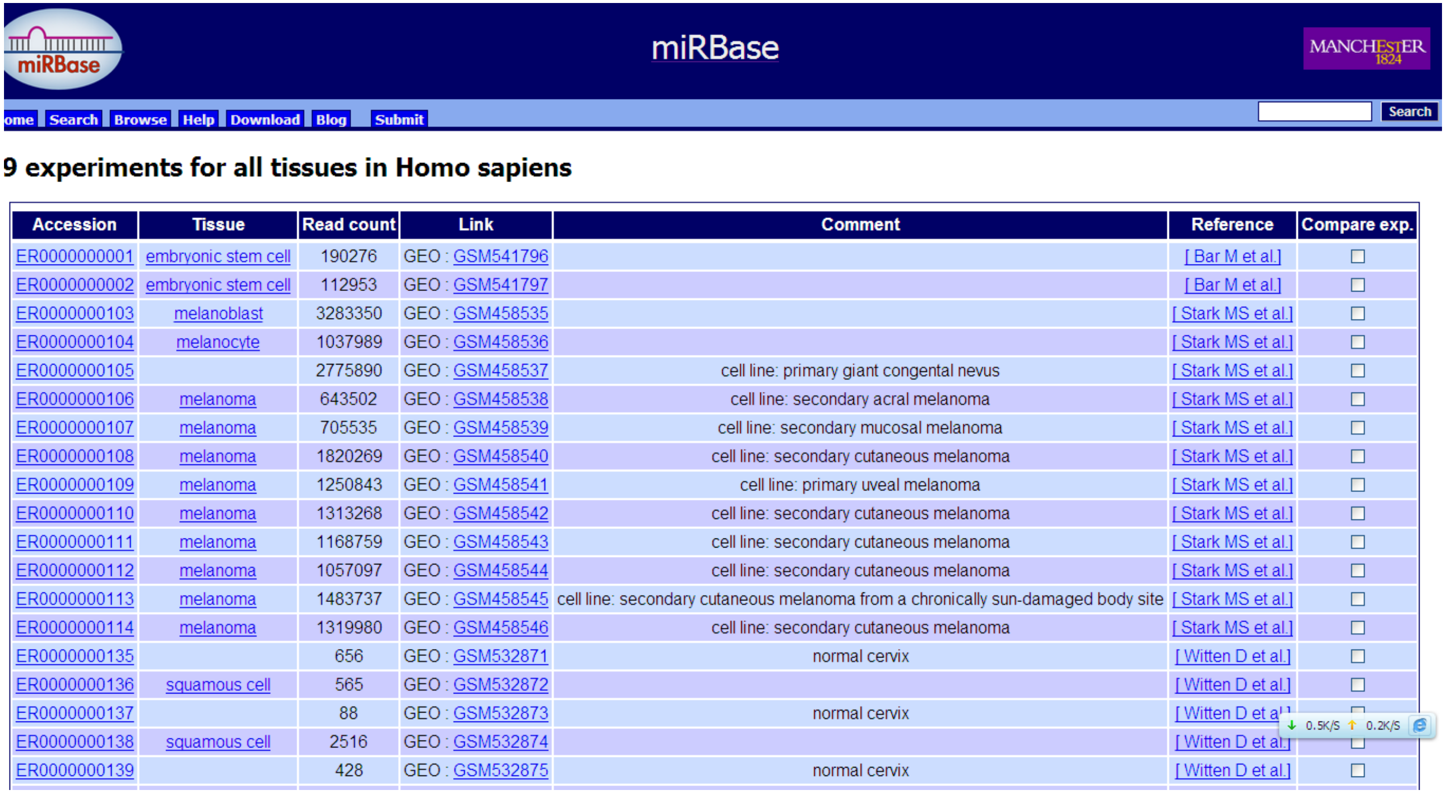
README	Release notes - read these first!
miRNA.dat	all published miRNA data in EMBL format
hairpin.fa	Fasta format sequences of all miRNA hairpins
mature.fa	Fasta format sequences of all mature miRNA sequences
miRNA.diff	Changes between the last release and this
miRNA.dead	List of entries that have been removed from the database
miFam.dat	Family classification of miRNA hairpin sequences

Genome coordinates

aae.gff3
ame.gff3
ath.gff3
bmo.gff3
bta.gff3
cbr.gff3
cel.gff3
cfa.gff3
cre.gff3
dme.gff3
dps.gff3
dre.gff3
ebv.gff3
fru.gff3
gga.gff3
hcmv.gff3
hsa.gff3
kshv.gff3
mdo.gff3
mghv.gff3
mml.gff3
mmu.gff3
osa.gff3
ptc.gff3
ptr.gff3
rno.gff3
sme.gff3
tae.gff3
tni.gff3
vvi.gff3
xtr.gff3
zma.gff3

Comments, questions? Email mirbase@manchester.ac.uk

Method 2: mirbase



9 experiments for all tissues in Homo sapiens

Accession	Tissue	Read count	Link	Comment	Reference	Compare exp.
ER0000000001	embryonic stem cell	190276	GEO : GSM541796		[Bar M et al.]	☐
ER0000000002	embryonic stem cell	112953	GEO : GSM541797		[Bar M et al.]	☐
ER0000000103	melanoblast	3283350	GEO : GSM458535		[Stark MS et al.]	☐
ER0000000104	melanocyte	1037989	GEO : GSM458536		[Stark MS et al.]	☐
ER0000000105		2775890	GEO : GSM458537	cell line: primary giant congental nevus	[Stark MS et al.]	☐
ER0000000106	melanoma	643502	GEO : GSM458538	cell line: secondary acral melanoma	[Stark MS et al.]	☐
ER0000000107	melanoma	705535	GEO : GSM458539	cell line: secondary mucosal melanoma	[Stark MS et al.]	☐
ER0000000108	melanoma	1820269	GEO : GSM458540	cell line: secondary cutaneous melanoma	[Stark MS et al.]	☐
ER0000000109	melanoma	1250843	GEO : GSM458541	cell line: primary uveal melanoma	[Stark MS et al.]	☐
ER0000000110	melanoma	1313268	GEO : GSM458542	cell line: secondary cutaneous melanoma	[Stark MS et al.]	☐
ER0000000111	melanoma	1168759	GEO : GSM458543	cell line: secondary cutaneous melanoma	[Stark MS et al.]	☐
ER0000000112	melanoma	1057097	GEO : GSM458544	cell line: secondary cutaneous melanoma	[Stark MS et al.]	☐
ER0000000113	melanoma	1483737	GEO : GSM458545	cell line: secondary cutaneous melanoma from a chronically sun-damaged body site	[Stark MS et al.]	☐
ER0000000114	melanoma	1319980	GEO : GSM458546	cell line: secondary cutaneous melanoma	[Stark MS et al.]	☐
ER0000000135		656	GEO : GSM532871	normal cervix	[Witten D et al.]	☐
ER0000000136	squamous cell	565	GEO : GSM532872		[Witten D et al.]	☐
ER0000000137		88	GEO : GSM532873	normal cervix	[Witten D et a	☐
ER0000000138	squamous cell	2516	GEO : GSM532874		[Witten D et al.]	☐
ER0000000139		428	GEO : GSM532875	normal cervix	[Witten D et al.]	☐

Method 2: mirbase

targets	TARGETMINER: hsa-miR-23b-5p PICTAR-VERT: hsa-miR-23b

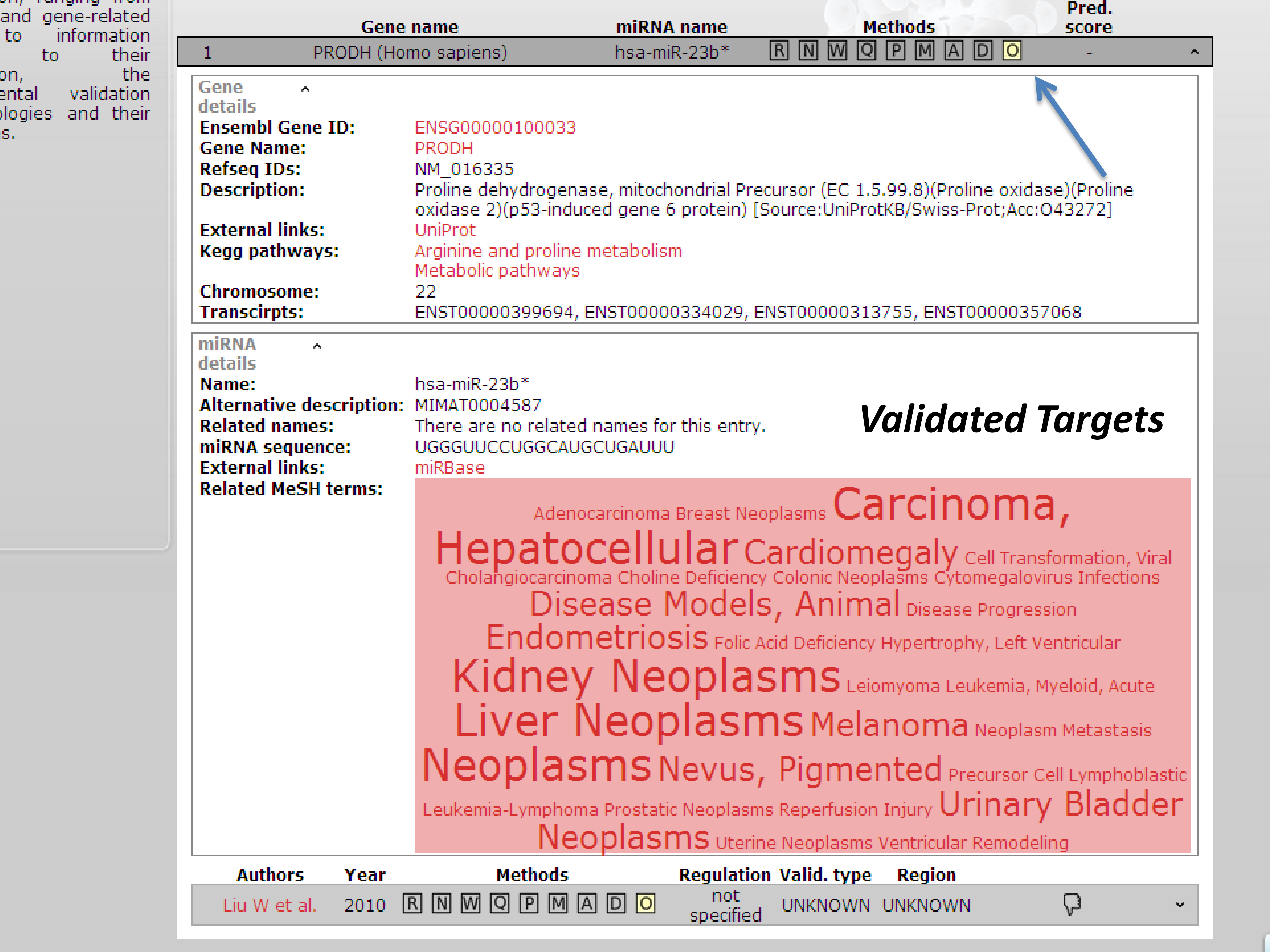
Mature sequence hsa-miR-23b-3p

Accession	MIMAT0000418
Previous IDs	hsa-miR-23b
Sequence	58 - aucacauugccagggauuacc - 78 Get sequence
Deep sequencing	109794 reads, 47 experiments
Evidence	experimental; cloned [2-3]
Validated targets	TARBASE: hsa-miR-23b-3p
Predicted targets	DIANA-MICROT: hsa-miR-23b-3p MICRORNA.ORG: hsa-miR-23b-3p MIRDB: hsa-miR-23b-3p TARGETMINER: hsa-miR-23b-3p TARGETSCAN-VERT: hsa-miR-23b PICTAR-VERT: hsa-miR-23b

References

1 PMID:12007417
"Identification of tissue-specific microRNAs from mouse"
Lagos-Quintana M, Rauhut R, Yalcin A, Meyer J, Lendeckel W, Tuschl T
Curr Biol. 12:735-739(2002).

PMID:17604727
"A mammalian microRNA expression atlas based on small RNA library sequencing"



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	Gene name	miRNA name	Methods	Pred. score
1	PRODH (Homo sapiens)	hsa-miR-23b*	R N W Q P M A D O	-

Gene details

Ensembl Gene ID:	ENSG00000100033
Gene Name:	PRODH
Refseq IDs:	NM_016335
Description:	Proline dehydrogenase, mitochondrial Precursor (EC 1.5.99.8)(Proline oxidase)(Proline oxidase 2)(p53-induced gene 6 protein) [Source:UniProtKB/Swiss-Prot;Acc:O43272]
External links:	UniProt
Kegg pathways:	Arginine and proline metabolism Metabolic pathways
Chromosome:	22
Transcirpts:	ENST00000399694, ENST00000334029, ENST00000313755, ENST00000357068

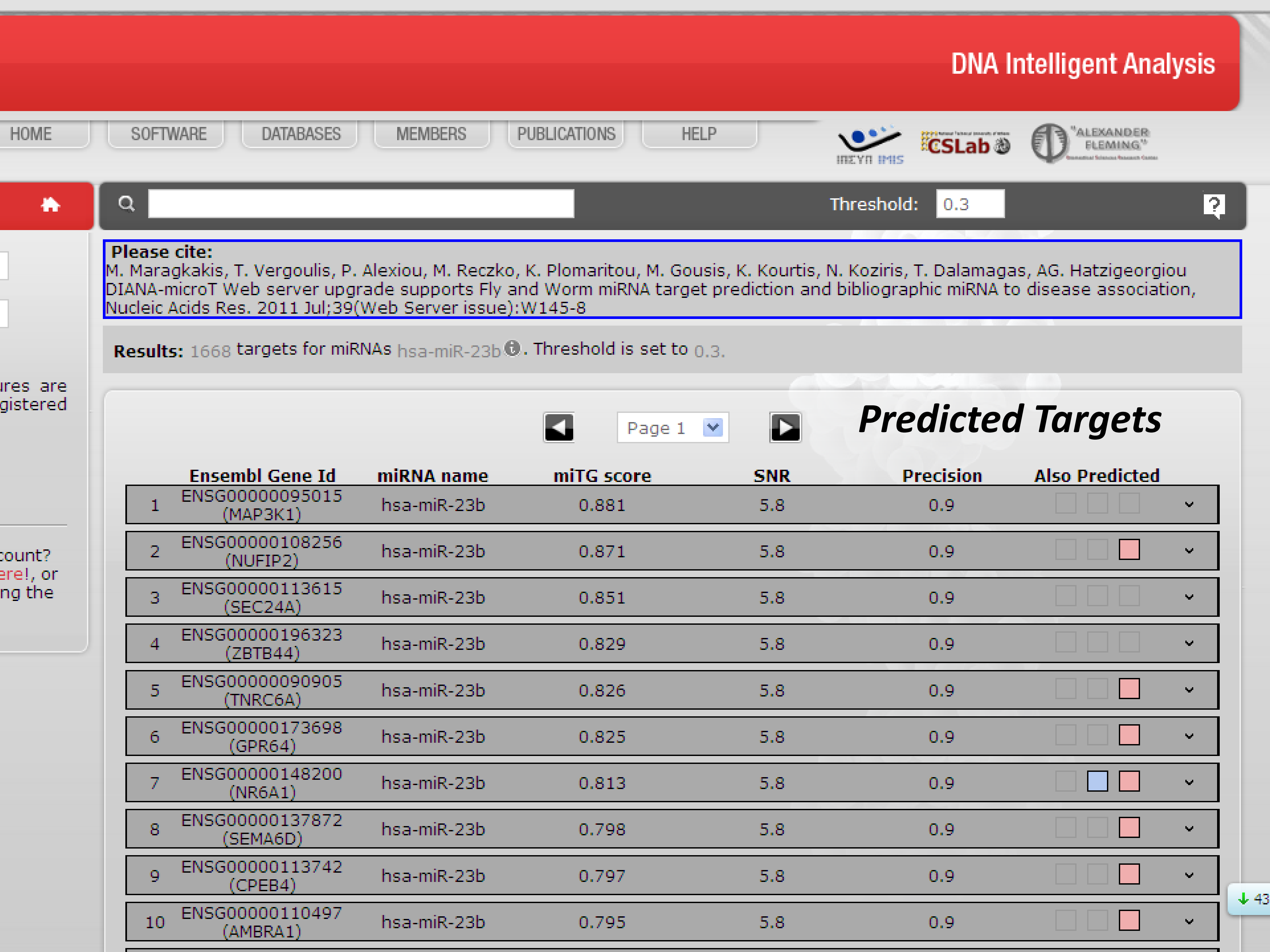
miRNA details

Name:	hsa-miR-23b*
Alternative description:	MIMAT0004587
Related names:	There are no related names for this entry.
miRNA sequence:	UGGGUUCCUGGCAUGCUGAUUU
External links:	miRBase
Related MeSH terms:	Adenocarcinoma Breast Neoplasms Carcinoma, Hepatocellular Cardiomegaly Cell Transformation, Viral Cholangiocarcinoma Choline Deficiency Colonic Neoplasms Cytomegalovirus Infections Disease Models, Animal Disease Progression Endometriosis Folic Acid Deficiency Hypertrophy, Left Ventricular Kidney Neoplasms Leiomyoma Leukemia, Myeloid, Acute Liver Neoplasms Melanoma Neoplasm Metastasis Neoplasms Nevus, Pigmented Precursor Cell Lymphoblastic Leukemia-Lymphoma Prostatic Neoplasms Reperfusion Injury Urinary Bladder Neoplasms Uterine Neoplasms Ventricular Remodeling

Validated Targets

Authors	Year	Methods	Regulation	Valid. type	Region
Liu W et al.	2010	R N W Q P M A D O	not specified	UNKNOWN	UNKNOWN

Predicted Targets



Please cite:
M. Maragkakis, T. Vergoulis, P. Alexiou, M. Reczko, K. Plomaritou, M. Gousis, K. Kourtis, N. Koziris, T. Dalamagas, AG. Hatzigeorgiou DIANA-microT Web server upgrade supports Fly and Worm miRNA target prediction and bibliographic miRNA to disease association, Nucleic Acids Res. 2011 Jul;39(Web Server issue):W145-8

Results: 1668 targets for miRNAs hsa-miR-23b. Threshold is set to 0.3.

	Ensembl Gene Id	miRNA name	miTG score	SNR	Precision	Also Predicted
1	ENSG00000095015 (MAP3K1)	hsa-miR-23b	0.881	5.8	0.9	☐ ☐ ☐
2	ENSG00000108256 (NUFIP2)	hsa-miR-23b	0.871	5.8	0.9	☐ ☐ 🟥
3	ENSG00000113615 (SEC24A)	hsa-miR-23b	0.851	5.8	0.9	☐ ☐ ☐
4	ENSG00000196323 (ZBTB44)	hsa-miR-23b	0.829	5.8	0.9	☐ ☐ ☐
5	ENSG00000090905 (TNRC6A)	hsa-miR-23b	0.826	5.8	0.9	☐ ☐ 🟥
6	ENSG00000173698 (GPR64)	hsa-miR-23b	0.825	5.8	0.9	☐ ☐ 🟥
7	ENSG00000148200 (NR6A1)	hsa-miR-23b	0.813	5.8	0.9	☐ 🟦 🟥
8	ENSG00000137872 (SEMA6D)	hsa-miR-23b	0.798	5.8	0.9	☐ ☐ 🟥
9	ENSG00000113742 (CPEB4)	hsa-miR-23b	0.797	5.8	0.9	☐ ☐ 🟥
10	ENSG00000110497 (AMBRA1)	hsa-miR-23b	0.795	5.8	0.9	☐ ☐ 🟥

Guidance for Further Research

DIANA mirPath

DIANA - mirPath

Single microRNA Analysis (Precompiled results)

Select Species

● **Human**
○ **Mouse**

Select Prediction Software

● DIANA-microT-3.0 Strict
○ DIANA-microT-3.0 Loose
○ DIANA-microT-4.0 (beta version)
○ PicTar
○ TargetScan 5

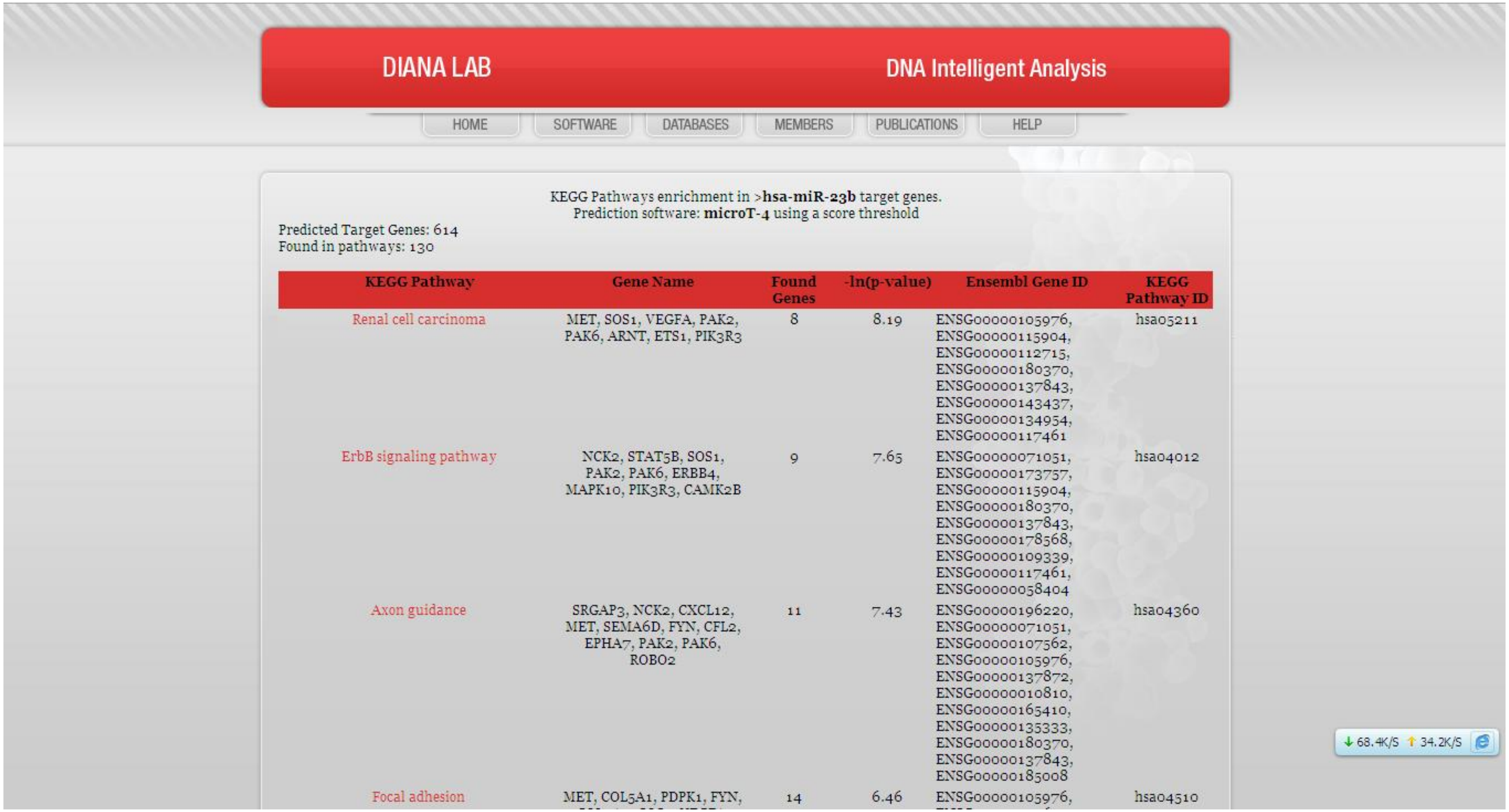
Select miRNA

let-7a
let-7b
let-7c
let-7d
let-7e
let-7f
let-7g
let-7i
miR-1
miR-100
miR-101

For analysis of MULTIPLE microRNAs (online) CLICK HERE

If used, please cite: DIANA-mirPath: Integrating human and mouse microRNAs in pathways GL Papadopoulos; P Alexiou; M Maragkakis; M Reczko; AG Hatzigeorgiou Bioinformatics 2009; doi: 10.1093/bioinformatics/btp299

DIANA mirPath

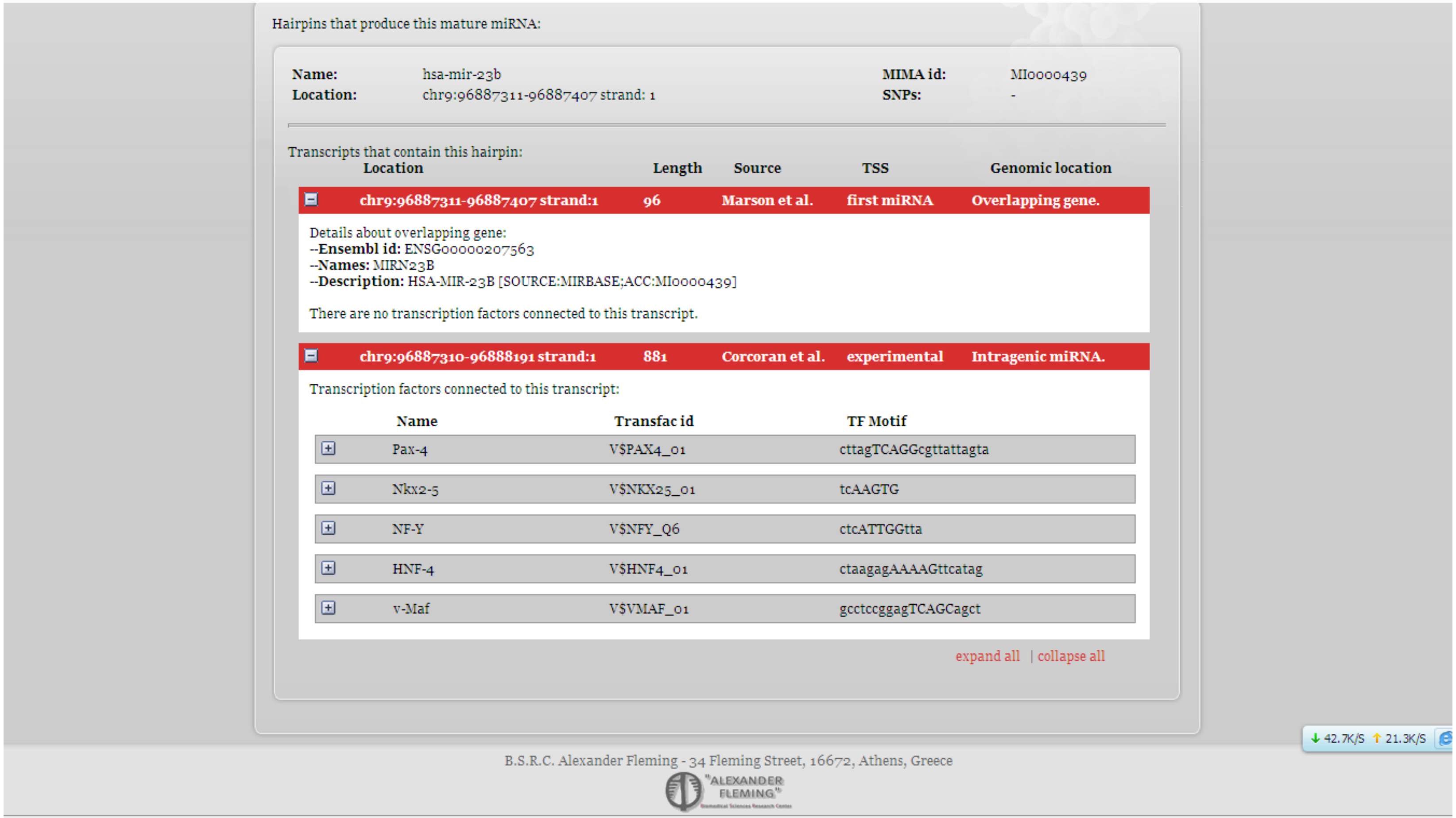


KEGG Pathways enrichment in >**hsa-miR-23b** target genes.
Prediction software: **microT-4** using a score threshold

Predicted Target Genes: 614
Found in pathways: 130

KEGG Pathway	Gene Name	Found Genes	-ln(p-value)	Ensembl Gene ID	KEGG Pathway ID
Renal cell carcinoma	MET, SOS1, VEGFA, PAK2, PAK6, ARNT, ETS1, PIK3R3	8	8.19	ENSG00000105976, ENSG00000115904, ENSG00000112715, ENSG00000180370, ENSG00000137843, ENSG00000143437, ENSG00000134954, ENSG00000117461	hsa05211
ErbB signaling pathway	NCK2, STAT5B, SOS1, PAK2, PAK6, ERBB4, MAPK10, PIK3R3, CAMK2B	9	7.65	ENSG00000071051, ENSG00000173757, ENSG00000115904, ENSG00000180370, ENSG00000137843, ENSG00000178568, ENSG00000109339, ENSG00000117461, ENSG00000058404	hsa04012
Axon guidance	SRGAP3, NCK2, CXCL12, MET, SEMA6D, FYN, CFL2, EPHA7, PAK2, PAK6, ROBO2	11	7.43	ENSG00000196220, ENSG00000071051, ENSG00000107562, ENSG00000105976, ENSG00000137872, ENSG00000010810, ENSG00000165410, ENSG00000135333, ENSG00000180370, ENSG00000137843, ENSG00000185008	hsa04360
Focal adhesion	MET, COL5A1, PDPK1, FYN,	14	6.46	ENSG00000105976,	hsa04510

DIANA mirGen



Hairpins that produce this mature miRNA:

Name: hsa-mir-23b
Location: chr9:96887311-96887407 strand: 1
MIMA id: MI0000439
SNPs: -

Transcripts that contain this hairpin:

	Location	Length	Source	TSS	Genomic location
⊟	**chr9:96887311-96887407 strand:1**	**96**	**Marson et al.**	**first miRNA**	**Overlapping gene.**

Details about overlapping gene:
--**Ensembl id:** ENSG00000207563
--**Names:** MIRN23B
--**Description:** HSA-MIR-23B [SOURCE:MIRBASE;ACC:MI0000439]

There are no transcription factors connected to this transcript.

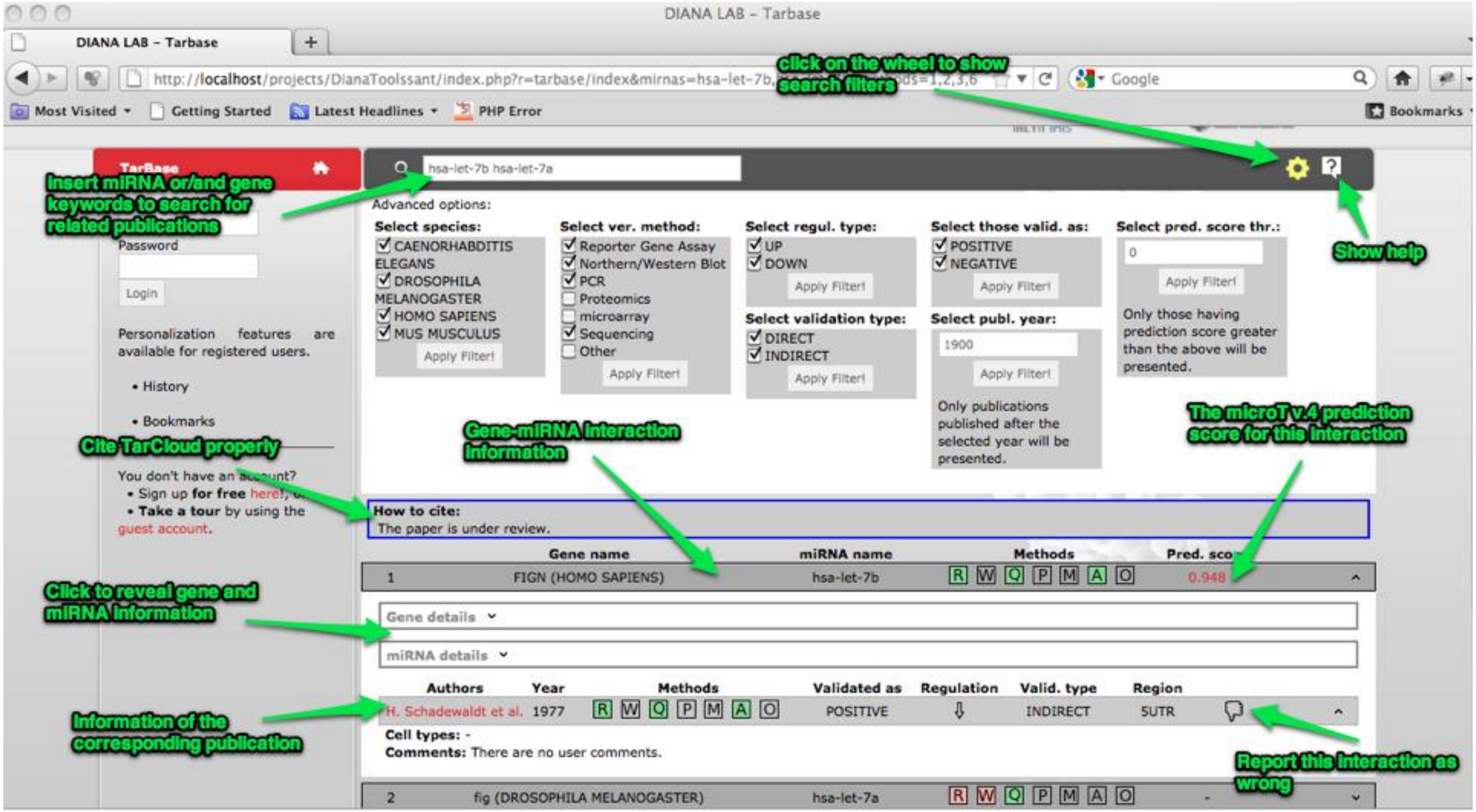
⊟	**chr9:96887310-96888191 strand:1**	**881**	**Corcoran et al.**	**experimental**	**Intragenic miRNA.**

Transcription factors connected to this transcript:

	Name	Transfac id	TF Motif
⊞	Pax-4	V$PAX4_01	cttagTCAGGcgttattagta
⊞	Nkx2-5	V$NKX25_01	tcAAGTG
⊞	NF-Y	V$NFY_Q6	ctcATTGGtta
⊞	HNF-4	V$HNF4_01	ctaagagAAAAGttcatag
⊞	v-Maf	V$VMAF_01	gcctccggagTCAGCagct

B.S.R.C. Alexander Fleming - 34 Fleming Street, 16672, Athens, Greece

DIANA Tarbase



click on the wheel to show search filters

Insert miRNA or/and gene keywords to search for related publications

Show help

hsa-let-7b hsa-let-7a

Password

Personalization features are available for registered users.

- History
- Bookmarks

Cite TarCloud properly

You don't have an account?

- Sign up **for free** here!,
- **Take a tour** by using the guest account.

Advanced options:

Select species:
- ☑ CAENORHABDITIS ELEGANS
- ☑ DROSOPHILA MELANOGASTER
- ☑ HOMO SAPIENS
- ☑ MUS MUSCULUS

Apply Filter!

Select ver. method:
- ☑ Reporter Gene Assay
- ☑ Northern/Western Blot
- ☑ PCR
- ☐ Proteomics
- ☐ microarray
- ☑ Sequencing
- ☐ Other

Apply Filter!

Select regul. type:
- ☑ UP
- ☑ DOWN

Apply Filter!

Select validation type:
- ☑ DIRECT
- ☑ INDIRECT

Apply Filter!

Select those valid. as:
- ☑ POSITIVE
- ☑ NEGATIVE

Apply Filter!

Select publ. year: 1900

Apply Filter!

Only publications published after the selected year will be presented.

Select pred. score thr.: 0

Apply Filter!

Only those having prediction score greater than the above will be presented.

Gene-miRNA Interaction information

The microT v.4 prediction score for this interaction

How to cite:
The paper is under review.

	Gene name	miRNA name	Methods	Pred. sco
1	FIGN (HOMO SAPIENS)	hsa-let-7b	R W Q P M A O	0.948

Click to reveal gene and miRNA information

Gene details ˅

miRNA details ˅

Authors	Year	Methods	Validated as	Regulation	Valid. type	Region
H. Schadewaldt et al.	1977	R W Q P M A O	POSITIVE	⇩	INDIRECT	5UTR

Information of the corresponding publication

Report this interaction as wrong

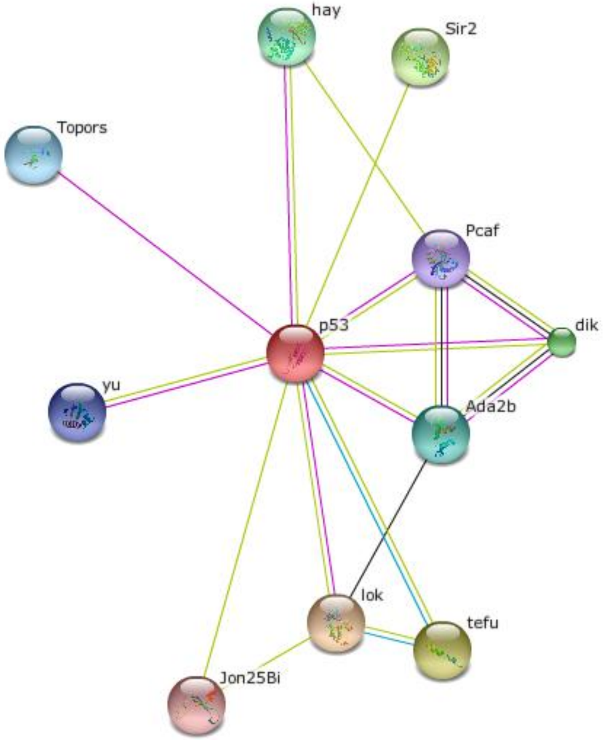
Cell types: -
Comments: There are no user comments.

	Gene name	miRNA name	Methods	Pred. sco
2	fig (DROSOPHILA MELANOGASTER)	hsa-let-7a	R W Q P M A O	-

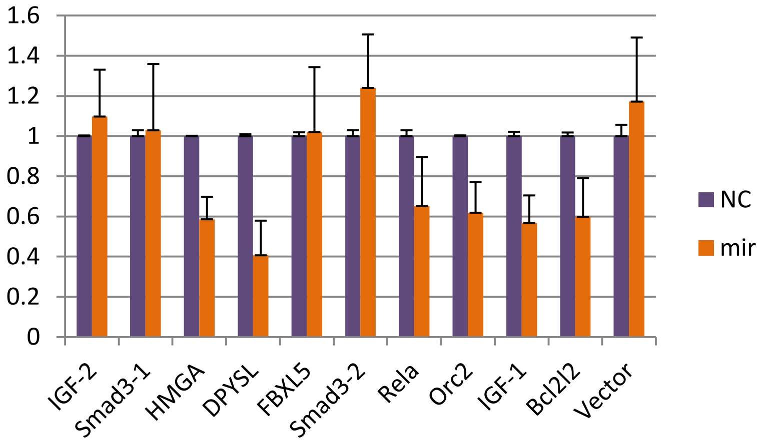
Selection of Candidates

- Genes related with p53
- Tools:
  - String
  - Google scholar

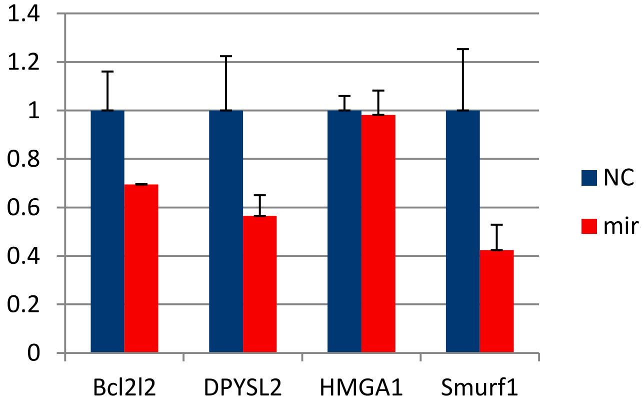
- Ten Genes are selected



Further Experiments Validation



Luciferase Experiment



Realtime Detection


Thank You!