miRSystem

Tutorial

http://mirsystem.cgm.ntu.edu.tw

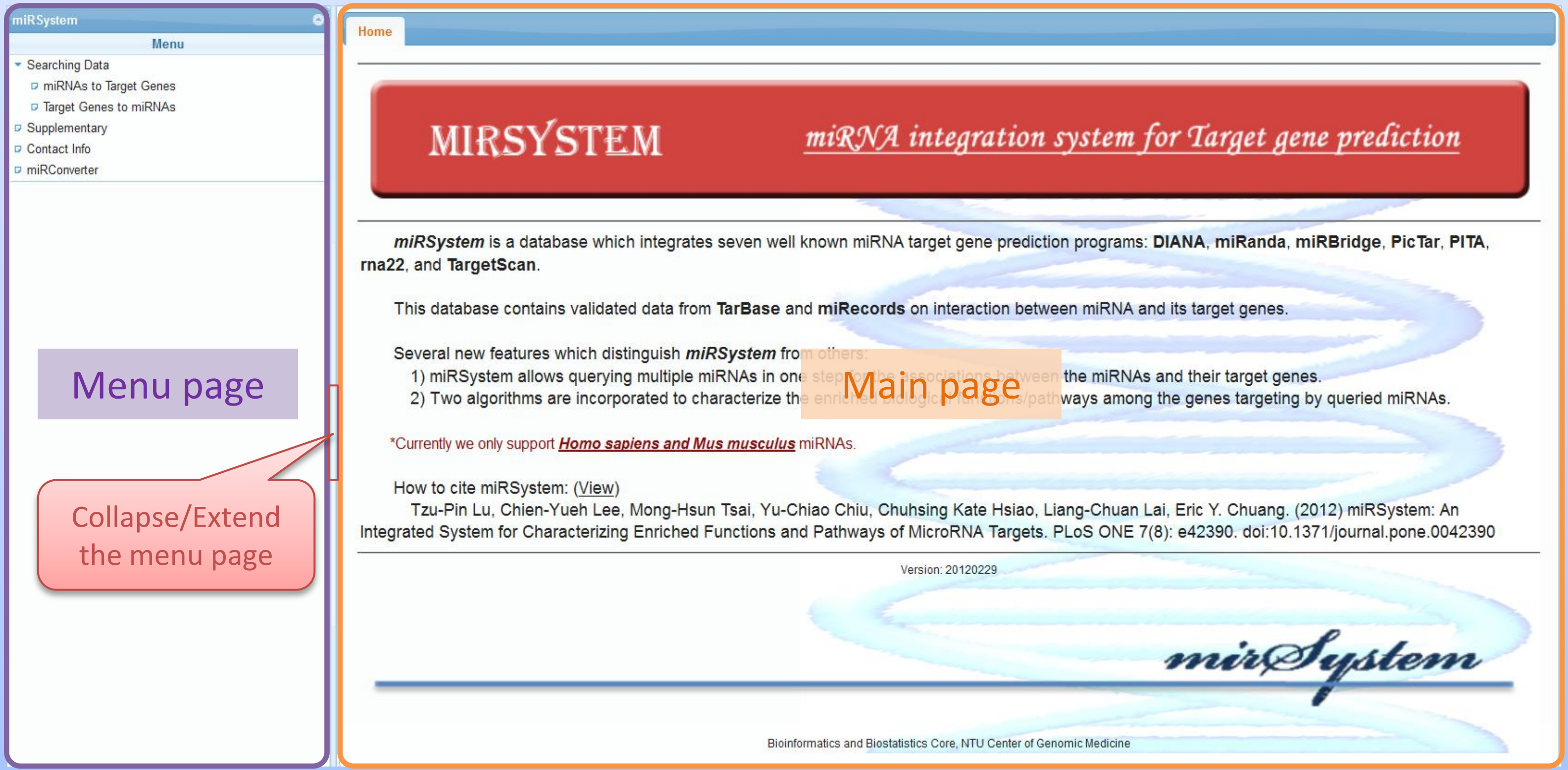
NTU CGM Bioinformatics & Biostatistics Core Lab.

Characteristics

- Feature
  - A web-based analysis platform, and friendly UI
  - Integration of 7 miRNA target gene prediction programs, and 2 experimental validation databases
  - Single or multiple miRNAs simultaneous analysis for biological pathways of KEGG, Biocarta, PID, Reactome, and Gene Ontology
  - Proposing 2 pathway analysis algorithm for multiple miRNAs
  - High efficiency
  - Tabular and graphical output

Link to miRSystem

- miRSystem homepage: http://mirsystem.cgm.ntu.edu.tw



miRSystem is a database which integrates seven well known miRNA target gene prediction programs: **DIANA**, **miRanda**, **miRBridge**, **PicTar**, **PITA**, **rna22**, and **TargetScan**.

This database contains validated data from **TarBase** and **miRecords** on interaction between miRNA and its target genes.

Several new features which distinguish ***miRSystem*** from others:
1) miRSystem allows querying multiple miRNAs in one step for the associations between the miRNAs and their target genes.
2) Two algorithms are incorporated to characterize the enriched biological functions/pathways among the genes targeting by queried miRNAs.

*Currently we only support ***Homo sapiens and Mus musculus*** miRNAs.

How to cite miRSystem: (View)
Tzu-Pin Lu, Chien-Yueh Lee, Mong-Hsun Tsai, Yu-Chiao Chiu, Chuhsing Kate Hsiao, Liang-Chuan Lai, Eric Y. Chuang. (2012) miRSystem: An Integrated System for Characterizing Enriched Functions and Pathways of MicroRNA Targets. PLoS ONE 7(8): e42390. doi:10.1371/journal.pone.0042390

Version: 20120229

Bioinformatics and Biostatistics Core, NTU Center of Genomic Medicine

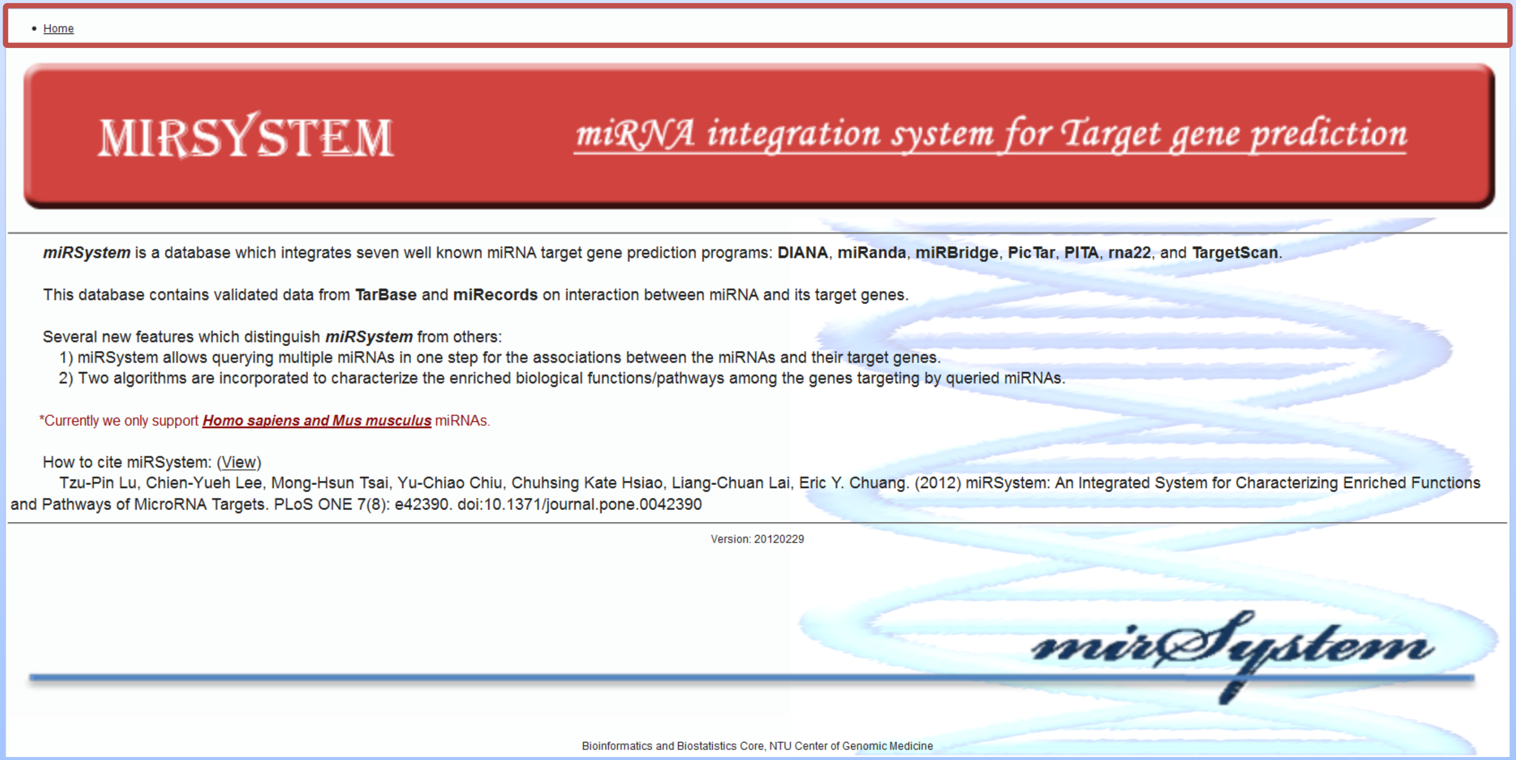
Menu page

Main page

Collapse/Extend the menu page

Link to miRSystem

- NOTICE: If you get the following page without the menu page, please ENABLE "JAVA Script" support on your browser and reload again.



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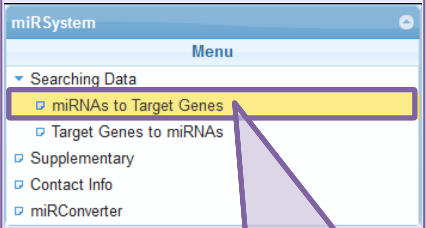
- miRNAs to Target Genes
- Target Genes to miRNAs
- miRConverter

Starting analysis

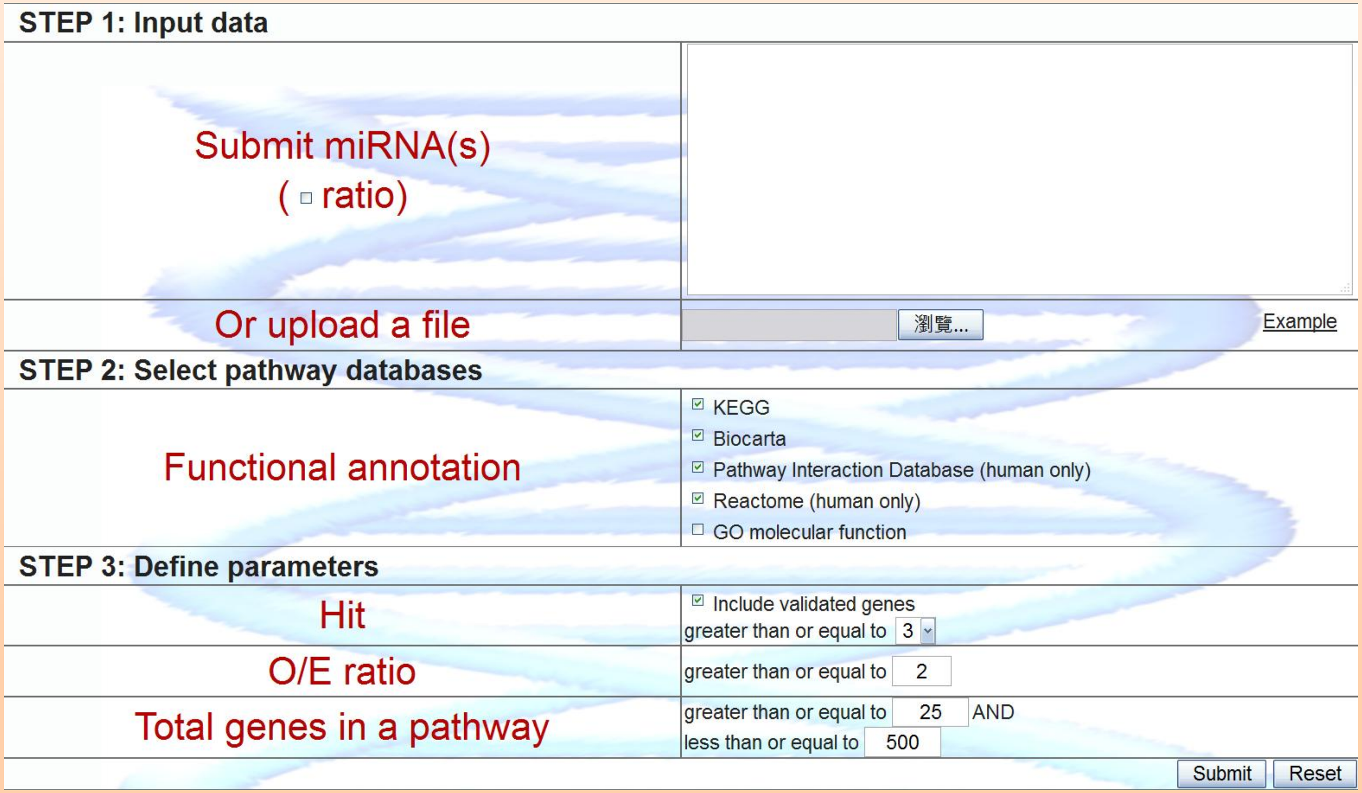
miRNAs to Target Genes

Menu page



Click "miRNAs to Target Genes" for analysis of biological functions and pathways

Main page



STEP 1: Input data

Submit miRNA(s) (☐ ratio)	
Or upload a file	瀏覽... Example

STEP 2: Select pathway databases

Functional annotation	☑ KEGG ☑ Biocarta ☑ Pathway Interaction Database (human only) ☑ Reactome (human only) ☐ GO molecular function

STEP 3: Define parameters

Hit	☑ Include validated genes greater than or equal to 3
O/E ratio	greater than or equal to 2
Total genes in a pathway	greater than or equal to 25 AND less than or equal to 500

STEP 1: Input data

Main page

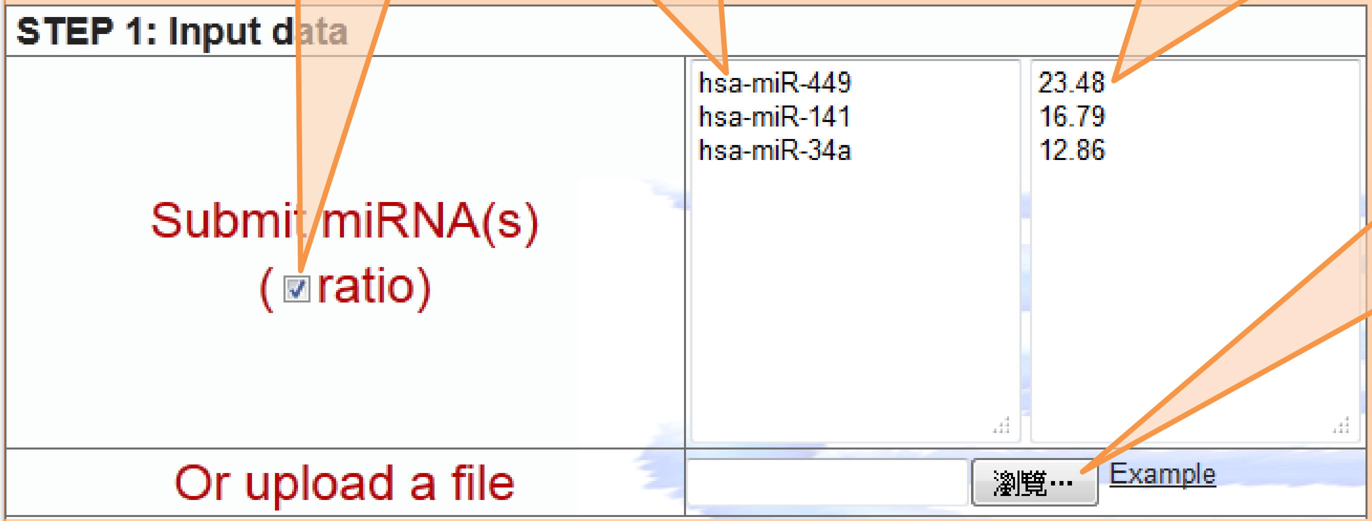
Check the “ratio” option to identify target genes by providing a list of miRNAs and optionally their expression values

Enter miRNA names with separators of carriage return

NOTICE: The prefix of “hsa-” or “mmu-” is necessary for identification of species in miRSystem

Enter the ratios of the miRNAs here. Positive and negative numbers indicate up-regulation and down-regulation respectively, however, they will not affect the analysis results

NOTICE: The number of rows MUST be consistent between miRNAs and ratios, missing values will be assigned 1.0 to corresponding miRNAs



STEP 1: Input data

Submit miRNA(s) (☑ ratio)

hsa-miR-449
hsa-miR-141
hsa-miR-34a

23.48
16.79
12.86

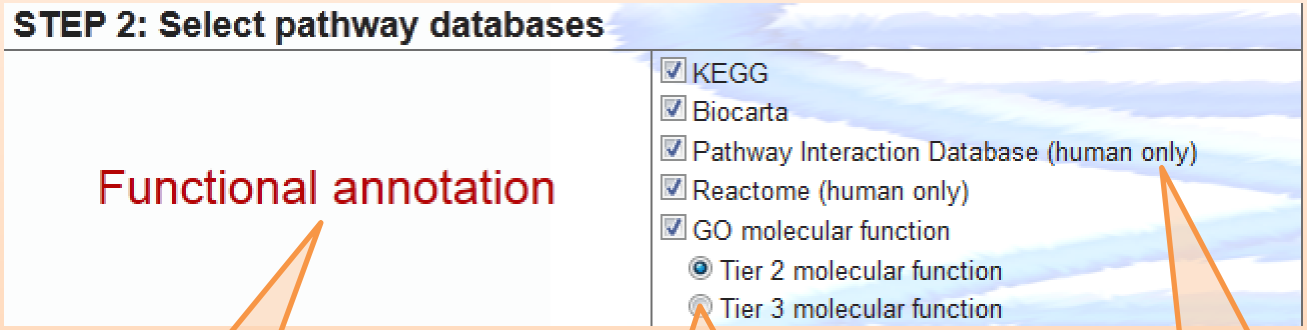
Or upload a file

Click “Browse” to upload a text file

NOTICE: The uploading function is higher priority than manually input data

STEP 2: Select pathway databases

Main page



STEP 2: Select pathway databases

Functional annotation

- ☑ KEGG
- ☑ Biocarta
- ☑ Pathway Interaction Database (human only)
- ☑ Reactome (human only)
- ☑ GO molecular function
  - ● Tier 2 molecular function
  - ○ Tier 3 molecular function

Choose biological functions/pathways for analysis of miRNA annotations

The tier 3 molecular function provides more detail categories than the tier 2 in GO molecular function

Pathway Interaction Database (IPA) and Reactome are supported by human miRNAs only

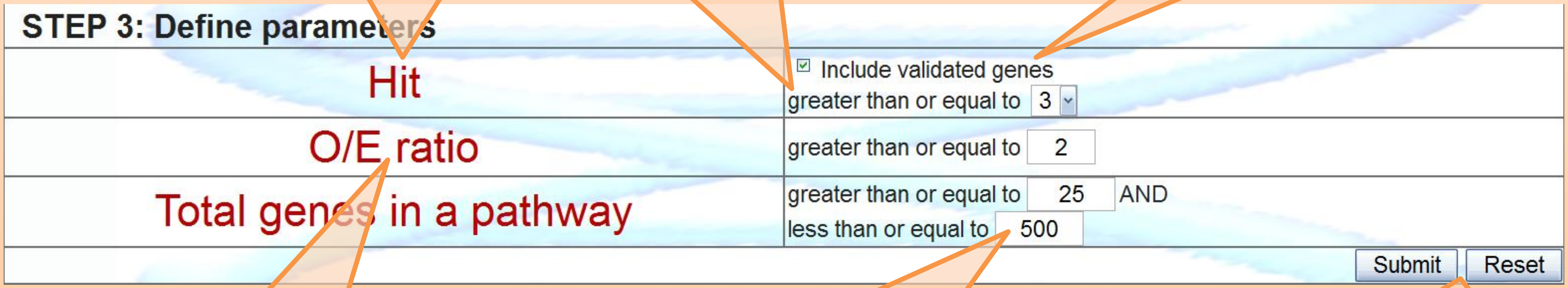
STEP 3: Define parameters

Main page

The “hit” represents the number of algorithms predicting the same miRNA-gene interaction pair

Target genes are shown if they fit greater than or equal to the number of criteria (8 in total) as chosen on the drop-down list: the criteria include literature validation plus 7 prediction algorithms

Target genes will be shown if they are validated, regardless of criteria below



STEP 3: Define parameters

Hit	☑ Include validated genes greater than or equal to 3
O/E ratio	greater than or equal to 2
Total genes in a pathway	greater than or equal to 25 AND less than or equal to 500

Target genes are shown if they the fit greater than or equal to the number of designated O/E ratio

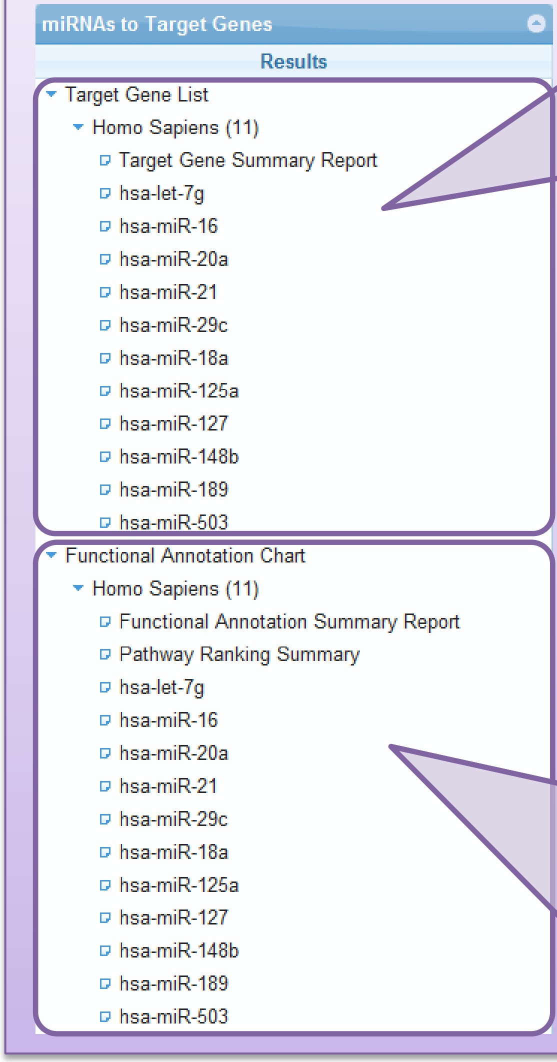
Biological functions/pathways with a minimum of 25 genes and a maximum of 500 genes are considered

Submit data and start to analyze

Click “Reset” button for initialization as the default values

Introduction to the result menu

Menu page



miRNAs to Target Genes

Results

- Target Gene List
  - Homo Sapiens (11)
    - Target Gene Summary Report
    - hsa-let-7g
    - hsa-miR-16
    - hsa-miR-20a
    - hsa-miR-21
    - hsa-miR-29c
    - hsa-miR-18a
    - hsa-miR-125a
    - hsa-miR-127
    - hsa-miR-148b
    - hsa-miR-189
    - hsa-miR-503
- Functional Annotation Chart
  - Homo Sapiens (11)
    - Functional Annotation Summary Report
    - Pathway Ranking Summary
    - hsa-let-7g
    - hsa-miR-16
    - hsa-miR-20a
    - hsa-miR-21
    - hsa-miR-29c
    - hsa-miR-18a
    - hsa-miR-125a
    - hsa-miR-127
    - hsa-miR-148b
    - hsa-miR-189
    - hsa-miR-503

The “Target Gene List” shows the union targets in the grouping miRNAs from the “Target Gene Summary Report” item.

The single miRNA targets in each submitted miRNA are listed by clicking miRNA name items.

For selecting target genes for pathway analysis, an observed to expected (O/E) ratio was calculated in the “Functional Annotation Summary Report” item.

Furthermore, another weighted pathway-ranking method calculated by the provided expression ratios was provided in the “Pathway Ranking Summary” item.

The single miRNA pathways in each submitted miRNA are shown by clicking miRNA name items.

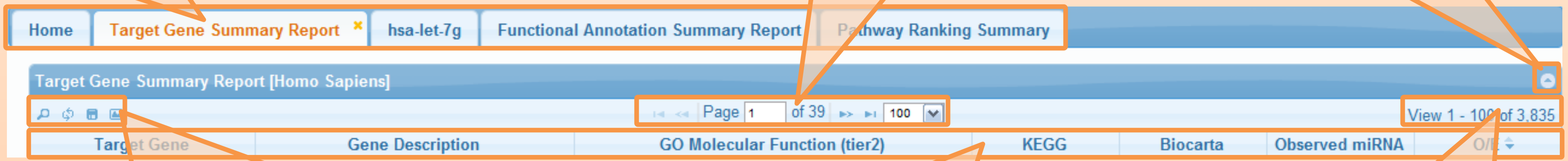
Introduction to general functions of the grid

Main page

Click the tabs to swap the different tabbed sections, or click the “x” icon to close the active tab

The page controller

Collapse/Extend the grid



Search on multiple fields at the same time with different conditions

Reload this grid and erase all searching conditions

Export records in a csv-format file

Plot records as a graphical output

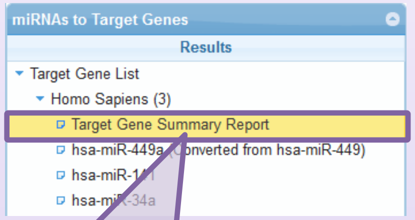
Click the header to sort in ascending or descending order on the designated field

The number of current records and the total records

Target Gene List

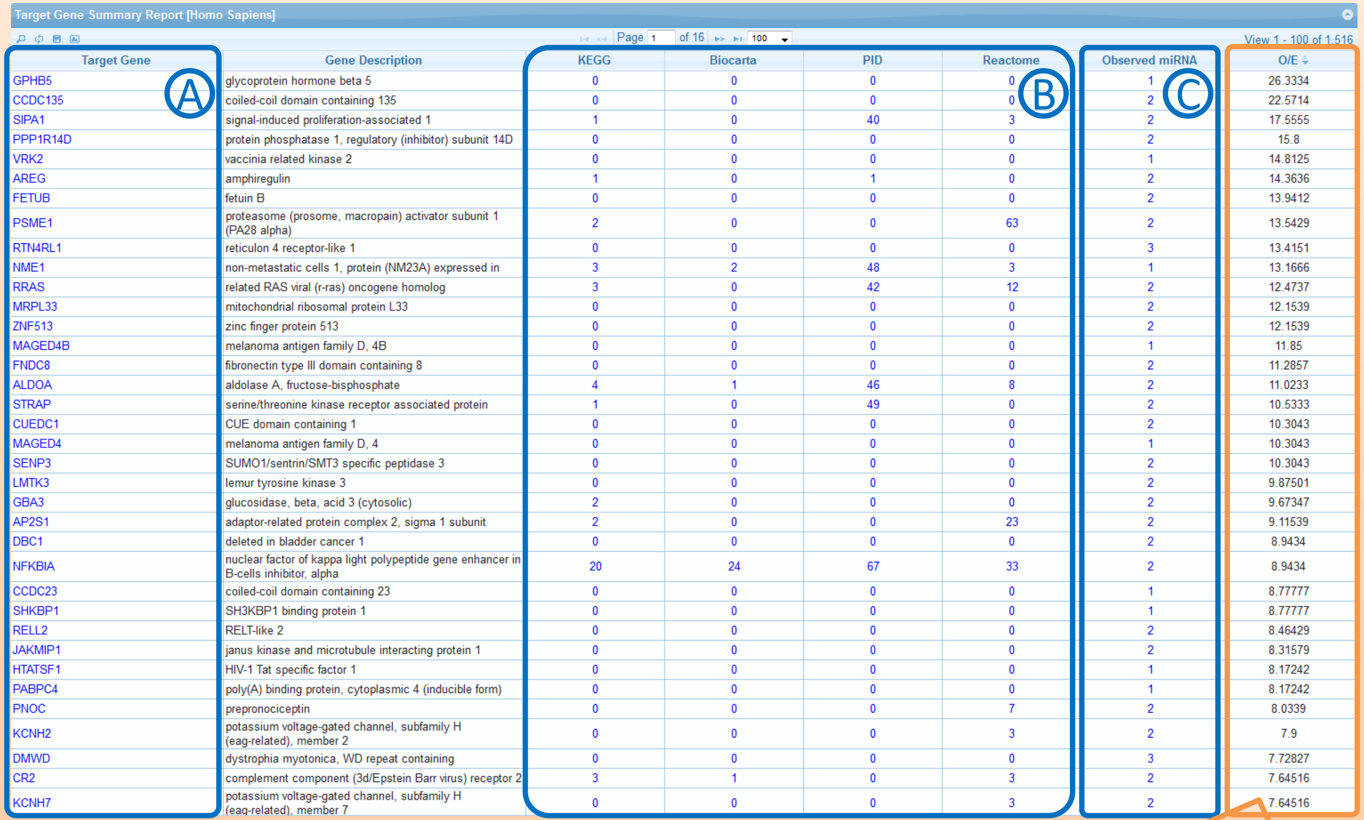
Target gene summary in multiple miRNAs

Menu page



Click to show the total gene list in grouping miRNAs

Main page



Target Gene	Gene Description	KEGG	Biocarta	PID	Reactome	Observed miRNA	O/E
GPHB5	glycoprotein hormone beta 5	0	0	0	0	1	26.3334
CCDC135	coiled-coil domain containing 135	0	0	0	0	2	22.5714
SIPA1	signal-induced proliferation-associated 1	1	0	40	3	2	17.5555
PPP1R14D	protein phosphatase 1, regulatory (inhibitor) subunit 14D	0	0	0	0	2	15.8
VRK2	vaccinia related kinase 2	0	0	0	0	1	14.8125
AREG	amphiregulin	1	0	1	0	2	14.3636
FETUB	fetuin B	0	0	0	0	2	13.9412
PSME1	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	2	0	0	63	2	13.5429
RTN4RL1	reticulon 4 receptor-like 1	0	0	0	0	3	13.4151
NME1	non-metastatic cells 1, protein (NM23A) expressed in	3	2	48	3	1	13.1666
RRAS	related RAS viral (r-ras) oncogene homolog	3	0	42	12	2	12.4737
MRPL33	mitochondrial ribosomal protein L33	0	0	0	0	2	12.1539
ZNF513	zinc finger protein 513	0	0	0	0	2	12.1539
MAGED4B	melanoma antigen family D, 4B	0	0	0	0	1	11.85
FNDC8	fibronectin type III domain containing 8	0	0	0	0	2	11.2857
ALDOA	aldolase A, fructose-bisphosphate	4	1	46	8	2	11.0233
STRAP	serine/threonine kinase receptor associated protein	1	0	49	0	2	10.5333
CUEDC1	CUE domain containing 1	0	0	0	0	2	10.3043
MAGED4	melanoma antigen family D, 4	0	0	0	0	1	10.3043
SENP3	SUMO1/sentrin/SMT3 specific peptidase 3	0	0	0	0	2	10.3043
LMTK3	lemur tyrosine kinase 3	0	0	0	0	2	9.87501
GBA3	glucosidase, beta, acid 3 (cytosolic)	2	0	0	0	2	9.67347
AP2S1	adaptor-related protein complex 2, sigma 1 subunit	2	0	0	23	2	9.11539
DBC1	deleted in bladder cancer 1	0	0	0	0	2	8.9434
NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	20	24	67	33	2	8.9434
CCDC23	coiled-coil domain containing 23	0	0	0	0	1	8.77777
SHKBP1	SH3KBP1 binding protein 1	0	0	0	0	1	8.77777
RELL2	RELT-like 2	0	0	0	0	2	8.46429
JAKMIP1	janus kinase and microtubule interacting protein 1	0	0	0	0	2	8.31579
HTATSF1	HIV-1 Tat specific factor 1	0	0	0	0	1	8.17242
PABPC4	poly(A) binding protein, cytoplasmic 4 (inducible form)	0	0	0	0	1	8.17242
PNOC	prepronociceptin	0	0	0	7	2	8.0339
KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	0	0	0	3	2	7.9
DMWD	dystrophia myotonica, WD repeat containing	0	0	0	0	3	7.72827
CR2	complement component (3d/Epstein Barr virus) receptor 2	3	1	0	3	2	7.64516
KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member 7	0	0	0	3	2	7.64516

Sorting by O/E ratio default

Target Gene Summary Report

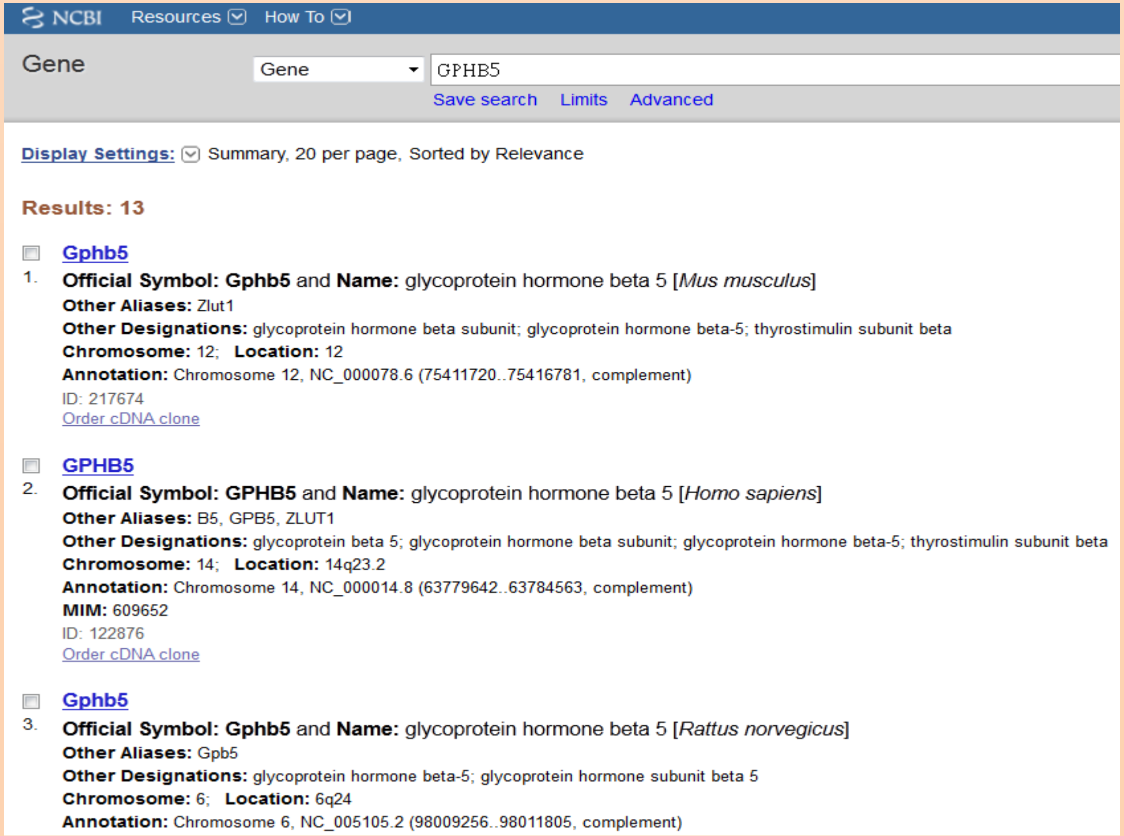
Hyperlink to NCBI Gene

Main page

Target Gene
GPHB5
CCDC135
SIPA1
PPP1R14D
VRK2
AREG
FETUB
PSME1
RTN4RL1
NME1
RRAS
MRPL33
ZNF513
MAGED4B
FNDC8
ALDOA
STRAP
CUEDC1
MAGED4
SENP3
LMTK3
GBA3
AP2S1
DBC1
NFKBIA
CCDC23
SHKBP1
RELL2
JAKMIP1
HTATSF1
PABPC4
PNOC
KCNH2
DMWD
CR2
KCNH7

Ⓐ

Link the designated gene to NCBI and get the annotation



Gene: GPHB5

Display Settings: Summary, 20 per page, Sorted by Relevance

Results: 13

☐ Gphb5

1. **Official Symbol: Gphb5** and **Name:** glycoprotein hormone beta 5 [*Mus musculus*]
Other Aliases: Zlut1
Other Designations: glycoprotein hormone beta subunit; glycoprotein hormone beta-5; thyrostimulin subunit beta
Chromosome: 12; **Location:** 12
Annotation: Chromosome 12, NC_000078.6 (75411720..75416781, complement)
ID: 217674
Order cDNA clone

☐ GPHB5

2. **Official Symbol: GPHB5** and **Name:** glycoprotein hormone beta 5 [*Homo sapiens*]
Other Aliases: B5, GPB5, ZLUT1
Other Designations: glycoprotein beta 5; glycoprotein hormone beta subunit; glycoprotein hormone beta-5; thyrostimulin subunit beta
Chromosome: 14; **Location:** 14q23.2
Annotation: Chromosome 14, NC_000014.8 (63779642..63784563, complement)
MIM: 609652
ID: 122876
Order cDNA clone

☐ Gphb5

3. **Official Symbol: Gphb5** and **Name:** glycoprotein hormone beta 5 [*Rattus norvegicus*]
Other Aliases: Gpb5
Other Designations: glycoprotein hormone beta-5; glycoprotein hormone subunit beta 5
Chromosome: 6; **Location:** 6q24
Annotation: Chromosome 6, NC_005105.2 (98009256..98011805, complement)

Target Gene Summary Report

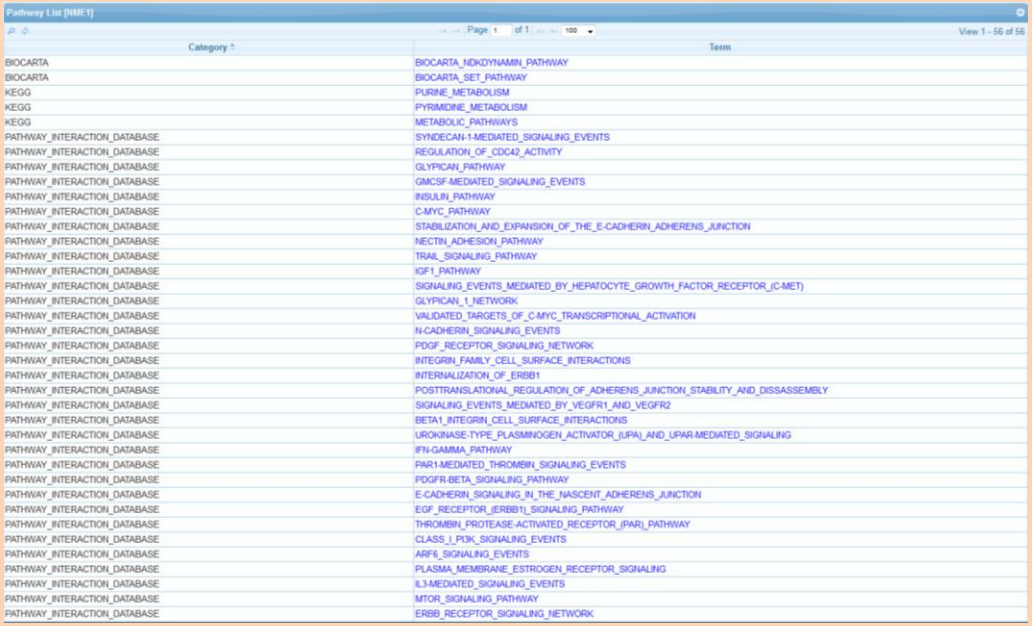
Hyperlink to function/pathway information

Main page

Ⓑ

KEGG	Biocarta	PID	Reactome
0	0	0	0
0	0	0	0
1	0	40	3
0	0	0	0
0	0	0	0
1	0	1	0
0	0	0	0
2	0	0	63
0	0	0	0
3	2	48	3
3	0	42	12
0	0	0	0
0	0	0	0
0	0	0	0
0	0	0	0
4	1	46	8
1	0	49	0
0	0	0	0
0	0	0	0
0	0	0	0
0	0	0	0
2	0	0	0
2	0	0	23
0	0	0	0
20	24	67	33
0	0	0	0
0	0	0	0
0	0	0	0
0	0	0	0
0	0	0	0
0	0	0	0
0	0	0	7
0	0	0	3
0	0	0	0
3	1	0	3
0	0	0	3

Show the corresponding functions/pathways information of the designated gene



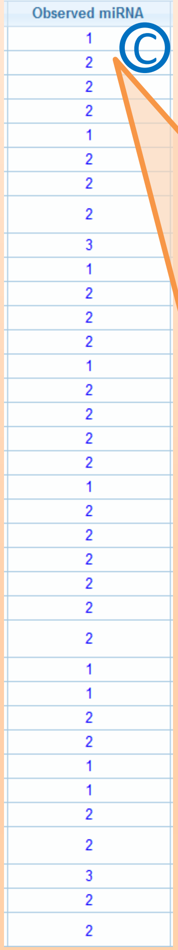
Pathway List [NME1]

Category	Term
BIOCARTA	BIOCARTA_NDKDYNAMIN_PATHWAY
BIOCARTA	BIOCARTA_SET_PATHWAY
KEGG	PURINE_METABOLISM
KEGG	PYRIMIDINE_METABOLISM
KEGG	METABOLIC_PATHWAYS
PATHWAY_INTERACTION_DATABASE	SYNDECAN-1-MEDIATED_SIGNALING_EVENTS
PATHWAY_INTERACTION_DATABASE	REGULATION_OF_CDC42_ACTIVITY
PATHWAY_INTERACTION_DATABASE	GLYPICAN_PATHWAY
PATHWAY_INTERACTION_DATABASE	GMCSF-MEDIATED_SIGNALING_EVENTS
PATHWAY_INTERACTION_DATABASE	INSULIN_PATHWAY
PATHWAY_INTERACTION_DATABASE	C-MYC_PATHWAY
PATHWAY_INTERACTION_DATABASE	STABILIZATION_AND_EXPANSION_OF_THE_E-CADHERIN_ADHERENS_JUNCTION
PATHWAY_INTERACTION_DATABASE	NECTIN_ADHESION_PATHWAY
PATHWAY_INTERACTION_DATABASE	TRAIL_SIGNALING_PATHWAY
PATHWAY_INTERACTION_DATABASE	IGF1_PATHWAY
PATHWAY_INTERACTION_DATABASE	SIGNALING_EVENTS_MEDIATED_BY_HEPATOCYTE_GROWTH_FACTOR_RECEPTOR_(C-MET)
PATHWAY_INTERACTION_DATABASE	GLYPICAN_1_NETWORK
PATHWAY_INTERACTION_DATABASE	VALIDATED_TARGETS_OF_C-MYC_TRANSCRIPTIONAL_ACTIVATION
PATHWAY_INTERACTION_DATABASE	N-CADHERIN_SIGNALING_EVENTS
PATHWAY_INTERACTION_DATABASE	PDGF_RECEPTOR_SIGNALING_NETWORK
PATHWAY_INTERACTION_DATABASE	INTEGRIN_FAMILY_CELL_SURFACE_INTERACTIONS
PATHWAY_INTERACTION_DATABASE	INTERNALIZATION_OF_ERBB1
PATHWAY_INTERACTION_DATABASE	POSTTRANSLATIONAL_REGULATION_OF_ADHERENS_JUNCTION_STABILITY_AND_DISSASSEMBLY
PATHWAY_INTERACTION_DATABASE	SIGNALING_EVENTS_MEDIATED_BY_VEGFR1_AND_VEGFR2
PATHWAY_INTERACTION_DATABASE	BETA1_INTEGRIN_CELL_SURFACE_INTERACTIONS
PATHWAY_INTERACTION_DATABASE	UROKINASE-TYPE_PLASMINOGEN_ACTIVATOR_(UPA)_AND_UPAR-MEDIATED_SIGNALING
PATHWAY_INTERACTION_DATABASE	IFN-GAMMA_PATHWAY
PATHWAY_INTERACTION_DATABASE	PAR1-MEDIATED_THROMBIN_SIGNALING_EVENTS
PATHWAY_INTERACTION_DATABASE	PDGFR-BETA_SIGNALING_PATHWAY
PATHWAY_INTERACTION_DATABASE	E-CADHERIN_SIGNALING_IN_THE_NASCENT_ADHERENS_JUNCTION
PATHWAY_INTERACTION_DATABASE	EGF_RECEPTOR_(ERBB1)_SIGNALING_PATHWAY
PATHWAY_INTERACTION_DATABASE	THROMBIN_PROTEASE-ACTIVATED_RECEPTOR_(PAR)_PATHWAY
PATHWAY_INTERACTION_DATABASE	CLASS_I_PI3K_SIGNALING_EVENTS
PATHWAY_INTERACTION_DATABASE	ARF6_SIGNALING_EVENTS
PATHWAY_INTERACTION_DATABASE	PLASMA_MEMBRANE_ESTROGEN_RECEPTOR_SIGNALING
PATHWAY_INTERACTION_DATABASE	IL3-MEDIATED_SIGNALING_EVENTS
PATHWAY_INTERACTION_DATABASE	MTOR_SIGNALING_PATHWAY
PATHWAY_INTERACTION_DATABASE	ERBB_RECEPTOR_SIGNALING_NETWORK

Target Gene Summary Report

Hyperlink to the observed miRNA list

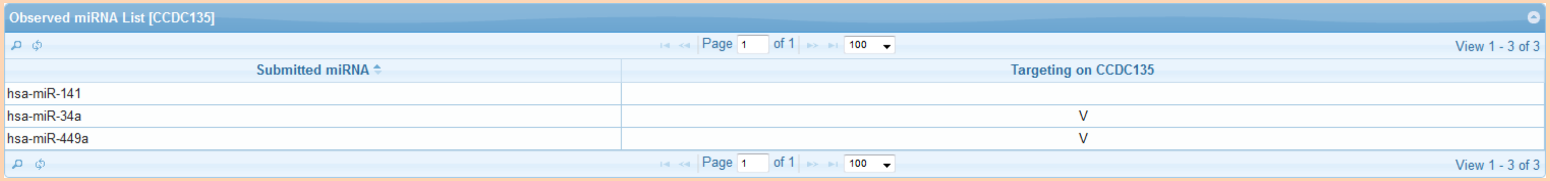
Main page



Observed miRNA
1
2
2
2
1
2
2
2
3
1
2
2
2
1
2
2
2
2
1
2
2
2
2
2
2
1
1
2
2
1
1
2
2
3
2
2

Ⓒ

Show the observed miRNA list of the designated gene



Observed miRNA List [CCDC135]

Page 1 of 1 | 100 | View 1 - 3 of 3

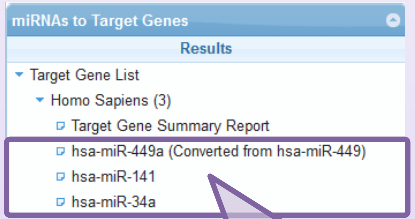
Submitted miRNA	Targeting on CCDC135
hsa-miR-141	
hsa-miR-34a	V
hsa-miR-449a	V

Page 1 of 1 | 100 | View 1 - 3 of 3

Target Gene List

Target gene list in the queried miRNA

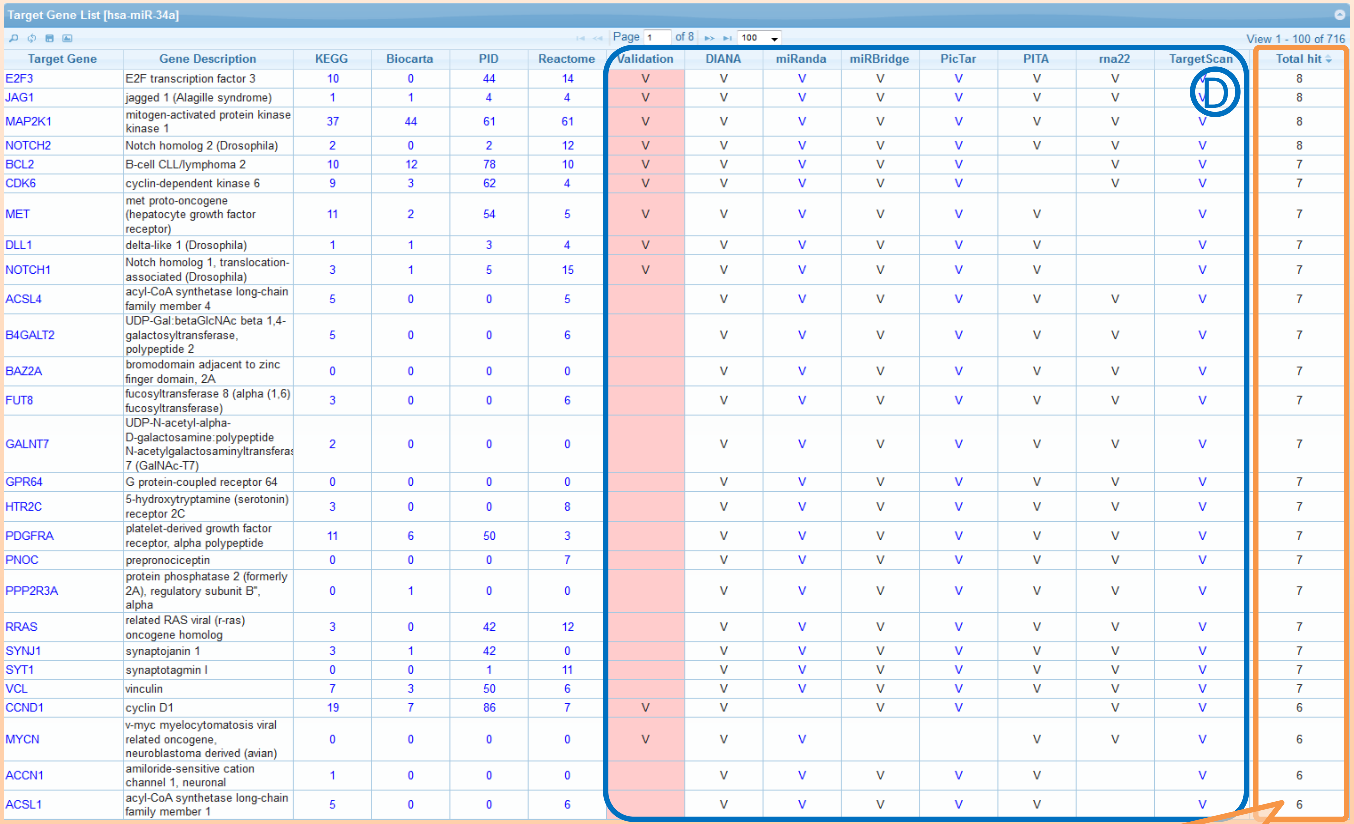
Menu page



- Target Gene List
  - Homo Sapiens (3)
    - Target Gene Summary Report
    - hsa-miR-449a (Converted from hsa-miR-449)
    - hsa-miR-141
    - hsa-miR-34a

Click one of the miRNA names for showing the corresponding target genes

Main page



Target Gene List [hsa-miR-34a]

View 1 - 100 of 716

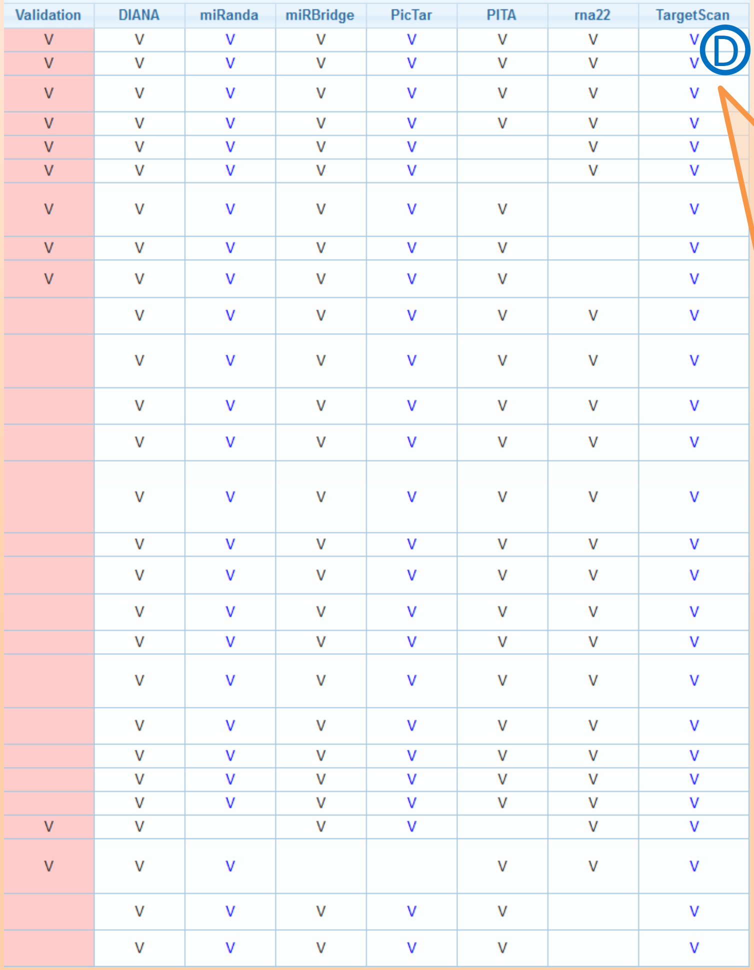
Target Gene	Gene Description	KEGG	Biocarta	PID	Reactome	Validation	DIANA	miRanda	miRBridge	PicTar	PITA	rna22	TargetScan	Total hit
E2F3	E2F transcription factor 3	10	0	44	14	V	V	V	V	V	V	V	V	8
JAG1	jagged 1 (Alagille syndrome)	1	1	4	4	V	V	V	V	V	V	V	V	8
MAP2K1	mitogen-activated protein kinase kinase 1	37	44	61	61	V	V	V	V	V	V	V	V	8
NOTCH2	Notch homolog 2 (Drosophila)	2	0	2	12	V	V	V	V	V	V	V	V	8
BCL2	B-cell CLL/lymphoma 2	10	12	78	10	V	V	V	V	V		V	V	7
CDK6	cyclin-dependent kinase 6	9	3	62	4	V	V	V	V	V		V	V	7
MET	met proto-oncogene (hepatocyte growth factor receptor)	11	2	54	5	V	V	V	V	V	V		V	7
DLL1	delta-like 1 (Drosophila)	1	1	3	4	V	V	V	V	V	V		V	7
NOTCH1	Notch homolog 1, translocation-associated (Drosophila)	3	1	5	15	V	V	V	V	V	V		V	7
ACSL4	acyl-CoA synthetase long-chain family member 4	5	0	0	5		V	V	V	V	V	V	V	7
B4GALT2	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	5	0	0	6		V	V	V	V	V	V	V	7
BAZ2A	bromodomain adjacent to zinc finger domain, 2A	0	0	0	0		V	V	V	V	V	V	V	7
FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	3	0	0	6		V	V	V	V	V	V	V	7
GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferas 7 (GalNAc-T7)	2	0	0	0		V	V	V	V	V	V	V	7
GPR64	G protein-coupled receptor 64	0	0	0	0		V	V	V	V	V	V	V	7
HTR2C	5-hydroxytryptamine (serotonin) receptor 2C	3	0	0	8		V	V	V	V	V	V	V	7
PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	11	6	50	3		V	V	V	V	V	V	V	7
PNOC	prepronociceptin	0	0	0	7		V	V	V	V	V	V	V	7
PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	0	1	0	0		V	V	V	V	V	V	V	7
RRAS	related RAS viral (r-ras) oncogene homolog	3	0	42	12		V	V	V	V	V	V	V	7
SYNJ1	synaptojanin 1	3	1	42	0		V	V	V	V	V	V	V	7
SYT1	synaptotagmin I	0	0	1	11		V	V	V	V	V	V	V	7
VCL	vinculin	7	3	50	6		V	V	V	V	V	V	V	7
CCND1	cyclin D1	19	7	86	7	V	V		V	V		V	V	6
MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	0	0	0	0	V	V	V			V	V	V	6
ACCN1	amiloride-sensitive cation channel 1, neuronal	1	0	0	0		V	V	V	V	V		V	6
ACSL1	acyl-CoA synthetase long-chain family member 1	5	0	0	6		V	V	V	V	V		V	6

Sorting by total hit counts default

Target Gene List in the Queried miRNA

Hyperlink to the original websites of prediction algorithms

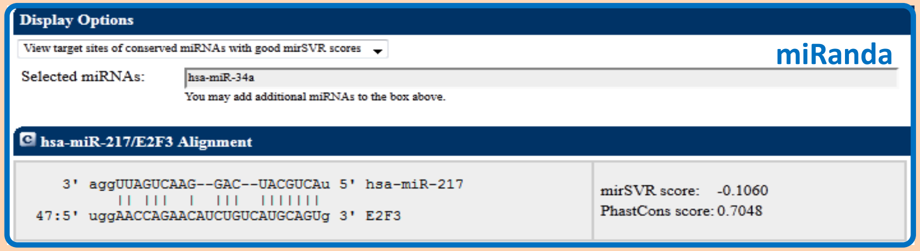
Main page



Validation	DIANA	miRanda	miRBridge	PicTar	PITA	rna22	TargetScan
V	V	V	V	V	V	V	V
V	V	V	V	V	V	V	V
V	V	V	V	V	V	V	V
V	V	V	V	V	V	V	V
V	V	V	V	V		V	V
V	V	V	V	V		V	V
V	V	V	V	V	V		V
V	V	V	V	V	V		V
V	V	V	V	V	V		V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
	V	V	V	V	V	V	V
V	V		V	V		V	V
V	V	V			V	V	V
	V	V	V	V	V		V
	V	V	V	V	V		V

The validation column indicates the gene was verified by an experimental validation

miRSystem provides to hyperlink the original websites for more detailed prediction information in miRanda, PicTar, and TargetScan



View target sites of conserved miRNAs with good mirSVR scores

miRanda

Selected miRNAs: hsa-miR-34a

You may add additional miRNAs to the box above.

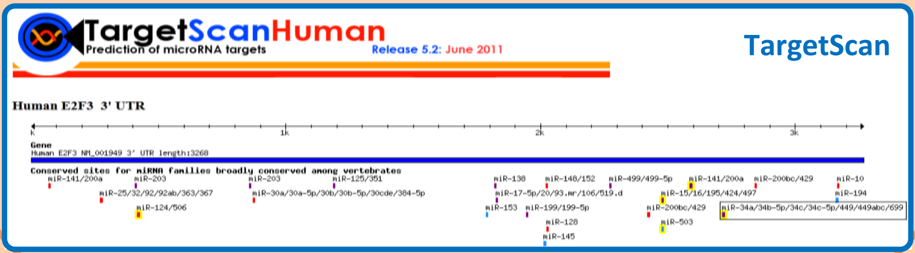
hsa-miR-217/E2F3 Alignment

```
   3' aggUUAGUCAAG--GAC--UACGUCAu 5' hsa-miR-217
         || |||   |  |||  |||||||
47:5' uggAACCAGAACAUCUGUCAUGCAGUg 3' E2F3
```

mirSVR score: -0.1060
PhastCons score: 0.7048

PicTar

Rank Click here for detailed 3'utr alignments and location of predicted site	human RefSeq Id	All miRNAs predicted to target the gene	PicTar score	microRNA	Genome Browser	N-Browse	annotation
64	NM_001949	All miRNA predictions	22.4083	hsa-miR-34a	Genome browser	N-Browse	Homo sapiens E2F transcription factor 3 (E2F3), mRNA



TargetScan

Human E2F3 3' UTR

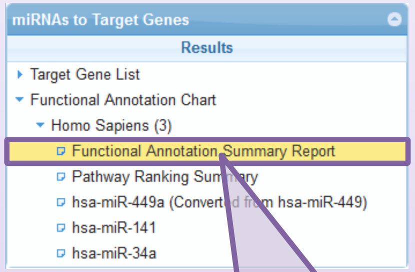
Gene
Human E2F3 NM_001949 3' UTR length:3268

Conserved sites for miRNA families broadly conserved among vertebrates

Functional Annotation Chart

Functional annotation summary report in multiple miRNAs

Menu page



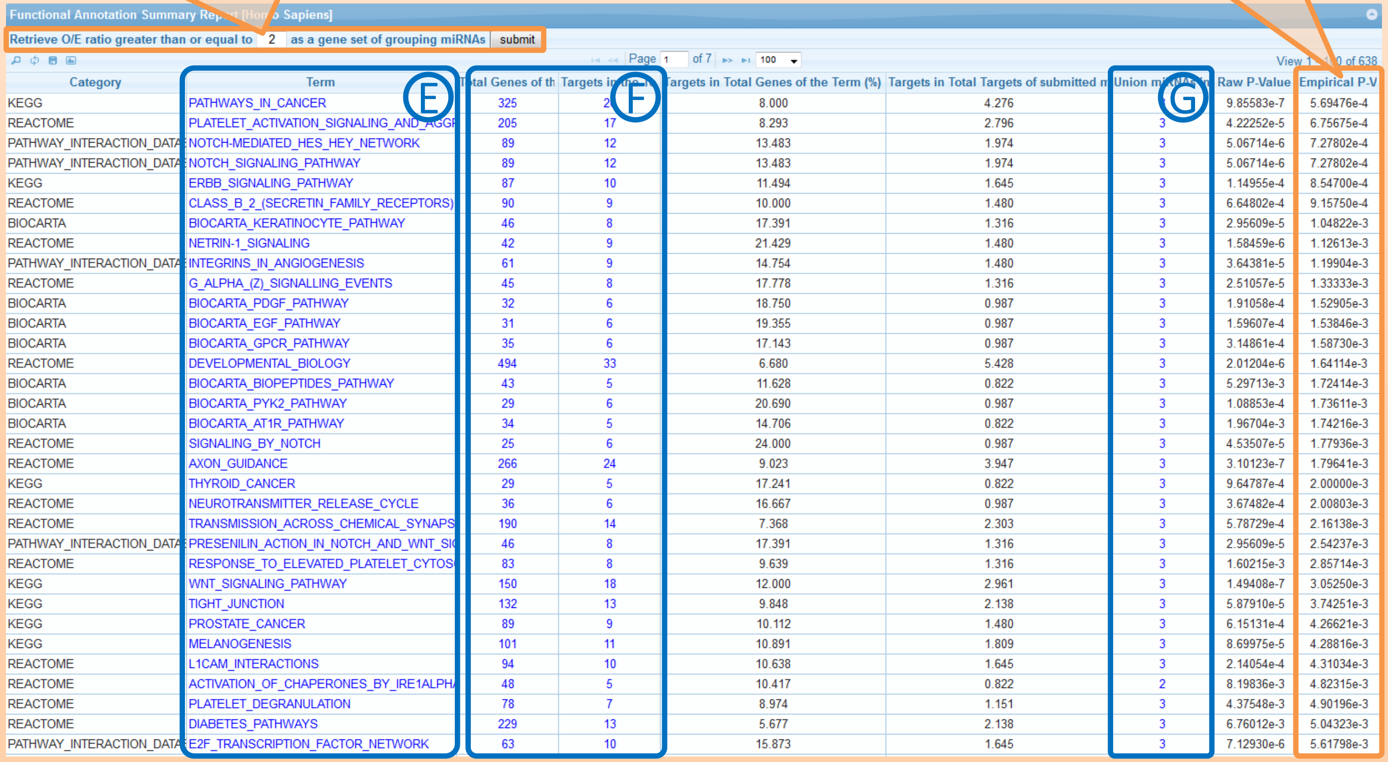
- Target Gene List
- Functional Annotation Chart
  - Homo Sapiens (3)
    - Functional Annotation Summary Report
    - Pathway Ranking Summary
    - hsa-miR-449a (Converted from hsa-miR-449)
    - hsa-miR-141
    - hsa-miR-34a

The function analyzes pathways with a gene set under selected O/E ratio

Main page

Adjust a new O/E ratio for retrieving another gene set and re-analyzing functions and pathways

Sorting by empirical p-value default



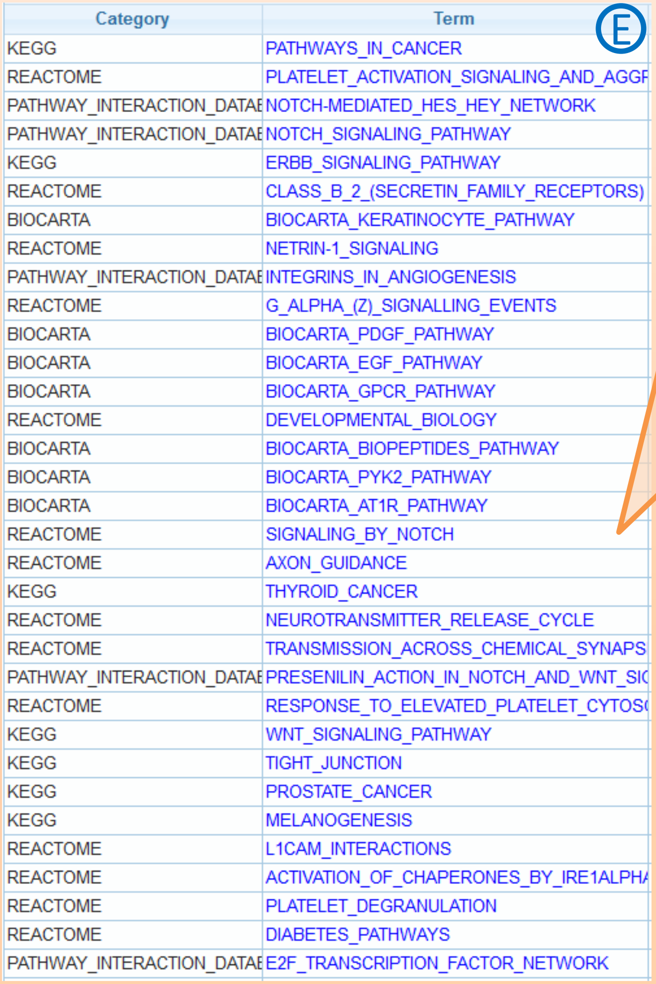
Retrieve O/E ratio greater than or equal to 2 as a gene set of grouping miRNAs

Category	Term	Total Genes of th	Targets in the	Targets in Total Genes of the Term (%)	Targets in Total Targets of submitted m	Union miRNAs in	Raw P-Value	Empirical P-V
KEGG	PATHWAYS_IN_CANCER	325	2	8.000	4.276	3	9.85583e-7	5.69476e-4
REACTOME	PLATELET_ACTIVATION_SIGNALING_AND_AGGF	205	17	8.293	2.796	3	4.22252e-5	6.75675e-4
PATHWAY_INTERACTION_DATA	NOTCH-MEDIATED_HES_HEY_NETWORK	89	12	13.483	1.974	3	5.06714e-6	7.27802e-4
PATHWAY_INTERACTION_DATA	NOTCH_SIGNALING_PATHWAY	89	12	13.483	1.974	3	5.06714e-6	7.27802e-4
KEGG	ERBB_SIGNALING_PATHWAY	87	10	11.494	1.645	3	1.14955e-4	8.54700e-4
REACTOME	CLASS_B_2_(SECRETIN_FAMILY_RECEPTORS)	90	9	10.000	1.480	3	6.64802e-4	9.15750e-4
BIOCARTA	BIOCARTA_KERATINOCYTE_PATHWAY	46	8	17.391	1.316	3	2.95609e-5	1.04822e-3
REACTOME	NETRIN-1_SIGNALING	42	9	21.429	1.480	3	1.58459e-6	1.12613e-3
PATHWAY_INTERACTION_DATA	INTEGRINS_IN_ANGIOGENESIS	61	9	14.754	1.480	3	3.64381e-5	1.19904e-3
REACTOME	G_ALPHA_(Z)_SIGNALLING_EVENTS	45	8	17.778	1.316	3	2.51057e-5	1.33333e-3
BIOCARTA	BIOCARTA_PDGF_PATHWAY	32	6	18.750	0.987	3	1.91058e-4	1.52905e-3
BIOCARTA	BIOCARTA_EGF_PATHWAY	31	6	19.355	0.987	3	1.59607e-4	1.53846e-3
BIOCARTA	BIOCARTA_GPCR_PATHWAY	35	6	17.143	0.987	3	3.14861e-4	1.58730e-3
REACTOME	DEVELOPMENTAL_BIOLOGY	494	33	6.680	5.428	3	2.01204e-6	1.64114e-3
BIOCARTA	BIOCARTA_BIOPEPTIDES_PATHWAY	43	5	11.628	0.822	3	5.29713e-3	1.72414e-3
BIOCARTA	BIOCARTA_PYK2_PATHWAY	29	6	20.690	0.987	3	1.08853e-4	1.73611e-3
BIOCARTA	BIOCARTA_AT1R_PATHWAY	34	5	14.706	0.822	3	1.96704e-3	1.74216e-3
REACTOME	SIGNALING_BY_NOTCH	25	6	24.000	0.987	3	4.53507e-5	1.77936e-3
REACTOME	AXON_GUIDANCE	266	24	9.023	3.947	3	3.10123e-7	1.79641e-3
KEGG	THYROID_CANCER	29	5	17.241	0.822	3	9.64787e-4	2.00000e-3
REACTOME	NEUROTRANSMITTER_RELEASE_CYCLE	36	6	16.667	0.987	3	3.67482e-4	2.00803e-3
REACTOME	TRANSMISSION_ACROSS_CHEMICAL_SYNAPS	190	14	7.368	2.303	3	5.78729e-4	2.16138e-3
PATHWAY_INTERACTION_DATA	PRESENILIN_ACTION_IN_NOTCH_AND_WNT_SI	46	8	17.391	1.316	3	2.95609e-5	2.54237e-3
REACTOME	RESPONSE_TO_ELEVATED_PLATELET_CYTOS	83	8	9.639	1.316	3	1.60215e-3	2.85714e-3
KEGG	WNT_SIGNALING_PATHWAY	150	18	12.000	2.961	3	1.49408e-7	3.05250e-3
KEGG	TIGHT_JUNCTION	132	13	9.848	2.138	3	5.87910e-5	3.74251e-3
KEGG	PROSTATE_CANCER	89	9	10.112	1.480	3	6.15131e-4	4.26621e-3
KEGG	MELANOGENESIS	101	11	10.891	1.809	3	8.69975e-5	4.28816e-3
REACTOME	L1CAM_INTERACTIONS	94	10	10.638	1.645	3	2.14054e-4	4.31034e-3
REACTOME	ACTIVATION_OF_CHAPERONES_BY_IRE1ALPH	48	5	10.417	0.822	2	8.19836e-3	4.82315e-3
REACTOME	PLATELET_DEGRANULATION	78	7	8.974	1.151	3	4.37548e-3	4.90196e-3
REACTOME	DIABETES_PATHWAYS	229	13	5.677	2.138	3	6.76012e-3	5.04323e-3
PATHWAY_INTERACTION_DATA	E2F_TRANSCRIPTION_FACTOR_NETWORK	63	10	15.873	1.645	3	7.12930e-6	5.61798e-3

Functional Annotation Summary Report

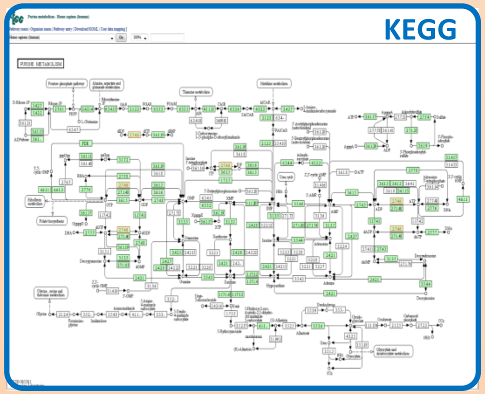
Hyperlink to original pathway databases

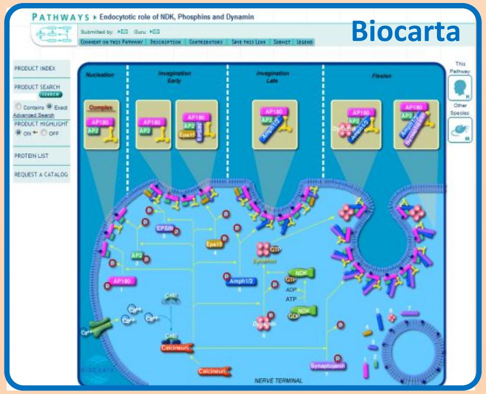
Main page

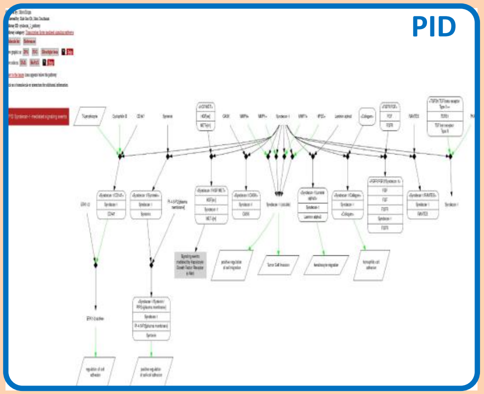


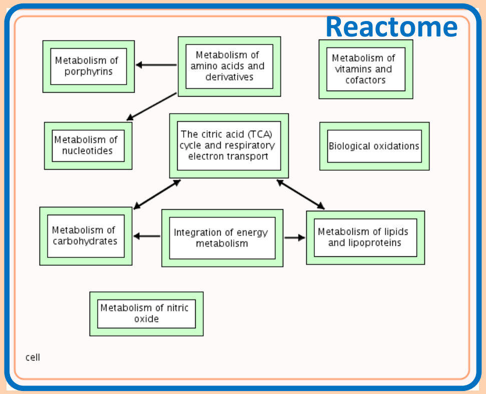
Category	Term
KEGG	PATHWAYS_IN_CANCER
REACTOME	PLATELET_ACTIVATION_SIGNALING_AND_AGG
PATHWAY_INTERACTION_DATA	NOTCH-MEDIATED_HES_HEY_NETWORK
PATHWAY_INTERACTION_DATA	NOTCH_SIGNALING_PATHWAY
KEGG	ERBB_SIGNALING_PATHWAY
REACTOME	CLASS_B_2_(SECRETIN_FAMILY_RECEPTORS)
BIOCARTA	BIOCARTA_KERATINOCYTE_PATHWAY
REACTOME	NETRIN-1_SIGNALING
PATHWAY_INTERACTION_DATA	INTEGRINS_IN_ANGIOGENESIS
REACTOME	G_ALPHA_(Z)_SIGNALLING_EVENTS
BIOCARTA	BIOCARTA_PDGF_PATHWAY
BIOCARTA	BIOCARTA_EGF_PATHWAY
BIOCARTA	BIOCARTA_GPCR_PATHWAY
REACTOME	DEVELOPMENTAL_BIOLOGY
BIOCARTA	BIOCARTA_BIOPEPTIDES_PATHWAY
BIOCARTA	BIOCARTA_PYK2_PATHWAY
BIOCARTA	BIOCARTA_AT1R_PATHWAY
REACTOME	SIGNALING_BY_NOTCH
REACTOME	AXON_GUIDANCE
KEGG	THYROID_CANCER
REACTOME	NEUROTRANSMITTER_RELEASE_CYCLE
REACTOME	TRANSMISSION_ACROSS_CHEMICAL_SYNAPS
PATHWAY_INTERACTION_DATA	PRESENILIN_ACTION_IN_NOTCH_AND_WNT_SI
REACTOME	RESPONSE_TO_ELEVATED_PLATELET_CYTOS
KEGG	WNT_SIGNALING_PATHWAY
KEGG	TIGHT_JUNCTION
KEGG	PROSTATE_CANCER
KEGG	MELANOGENESIS
REACTOME	L1CAM_INTERACTIONS
REACTOME	ACTIVATION_OF_CHAPERONES_BY_IRE1ALPH
REACTOME	PLATELET_DEGRANULATION
REACTOME	DIABETES_PATHWAYS
PATHWAY_INTERACTION_DATA	E2F_TRANSCRIPTION_FACTOR_NETWORK

Show the graphical annotation of the designated term





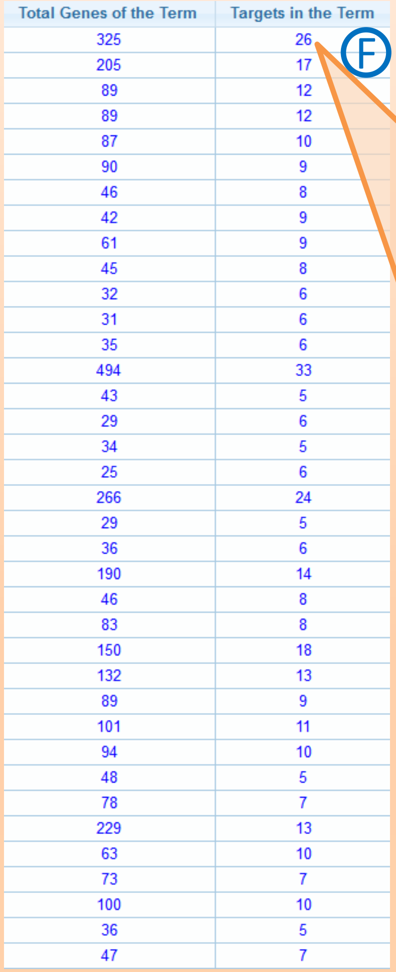




Functional Annotation Summary Report

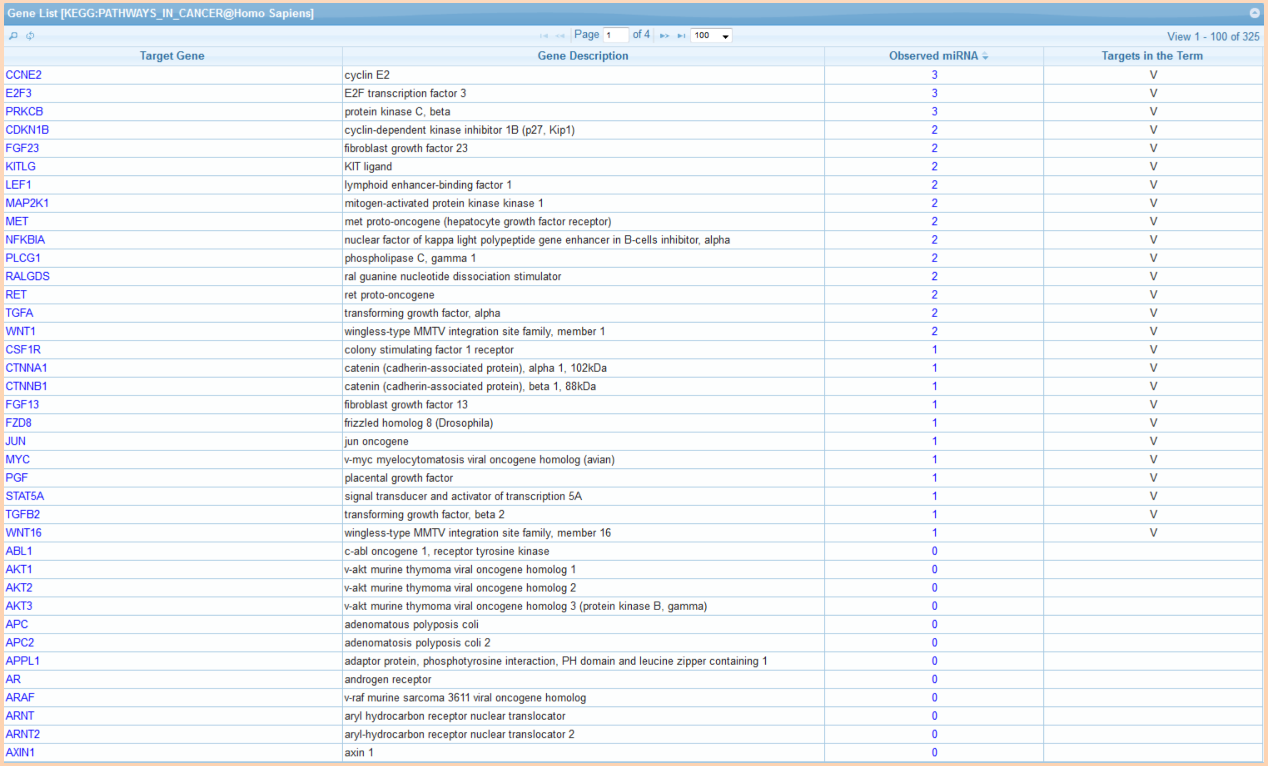
Hyperlink to gene list of a specific pathway

Main page



Total Genes of the Term	Targets in the Term
325	26
205	17
89	12
89	12
87	10
90	9
46	8
42	9
61	9
45	8
32	6
31	6
35	6
494	33
43	5
29	6
34	5
25	6
266	24
29	5
36	6
190	14
46	8
83	8
150	18
132	13
89	9
101	11
94	10
48	5
78	7
229	13
63	10
73	7
100	10
36	5
47	7

Show the detail gene list of the designated term



Gene List [KEGG:PATHWAYS_IN_CANCER@Homo Sapiens]

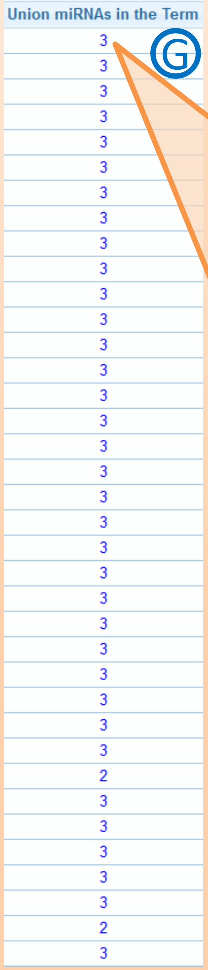
View 1 - 100 of 325

Target Gene	Gene Description	Observed miRNA	Targets in the Term
CCNE2	cyclin E2	3	V
E2F3	E2F transcription factor 3	3	V
PRKCB	protein kinase C, beta	3	V
CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	2	V
FGF23	fibroblast growth factor 23	2	V
KITLG	KIT ligand	2	V
LEF1	lymphoid enhancer-binding factor 1	2	V
MAP2K1	mitogen-activated protein kinase kinase 1	2	V
MET	met proto-oncogene (hepatocyte growth factor receptor)	2	V
NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	2	V
PLCG1	phospholipase C, gamma 1	2	V
RALGDS	ral guanine nucleotide dissociation stimulator	2	V
RET	ret proto-oncogene	2	V
TGFA	transforming growth factor, alpha	2	V
WNT1	wingless-type MMTV integration site family, member 1	2	V
CSF1R	colony stimulating factor 1 receptor	1	V
CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	1	V
CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	1	V
FGF13	fibroblast growth factor 13	1	V
FZD8	frizzled homolog 8 (Drosophila)	1	V
JUN	jun oncogene	1	V
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	1	V
PGF	placental growth factor	1	V
STAT5A	signal transducer and activator of transcription 5A	1	V
TGFB2	transforming growth factor, beta 2	1	V
WNT16	wingless-type MMTV integration site family, member 16	1	V
ABL1	c-abl oncogene 1, receptor tyrosine kinase	0	
AKT1	v-akt murine thymoma viral oncogene homolog 1	0	
AKT2	v-akt murine thymoma viral oncogene homolog 2	0	
AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	0	
APC	adenomatous polyposis coli	0	
APC2	adenomatosis polyposis coli 2	0	
APPL1	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	0	
AR	androgen receptor	0	
ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	0	
ARNT	aryl hydrocarbon receptor nuclear translocator	0	
ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	0	
AXIN1	axin 1	0	

Functional Annotation Summary Report

Hyperlink to the observed miRNA list

Main page



Union miRNAs in the Term
3
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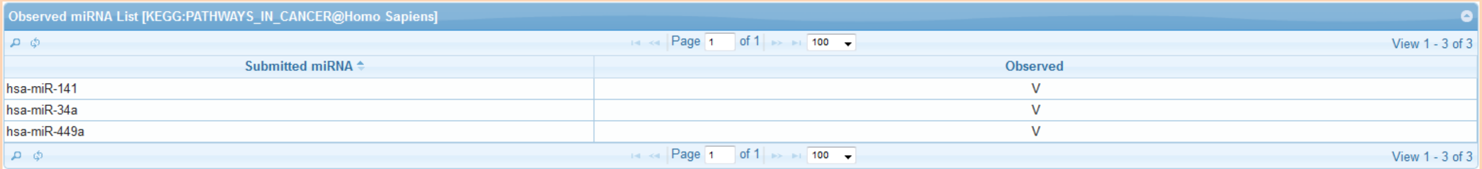
Show the observed miRNA list of the designated term



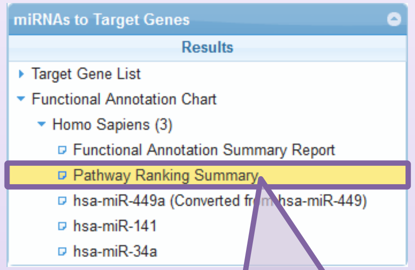
Observed miRNA List [KEGG:PATHWAYS_IN_CANCER@Homo Sapiens]

Submitted miRNA	Observed
hsa-miR-141	V
hsa-miR-34a	V
hsa-miR-449a	V

Functional Annotation Chart

Pathway ranking summary in multiple miRNAs

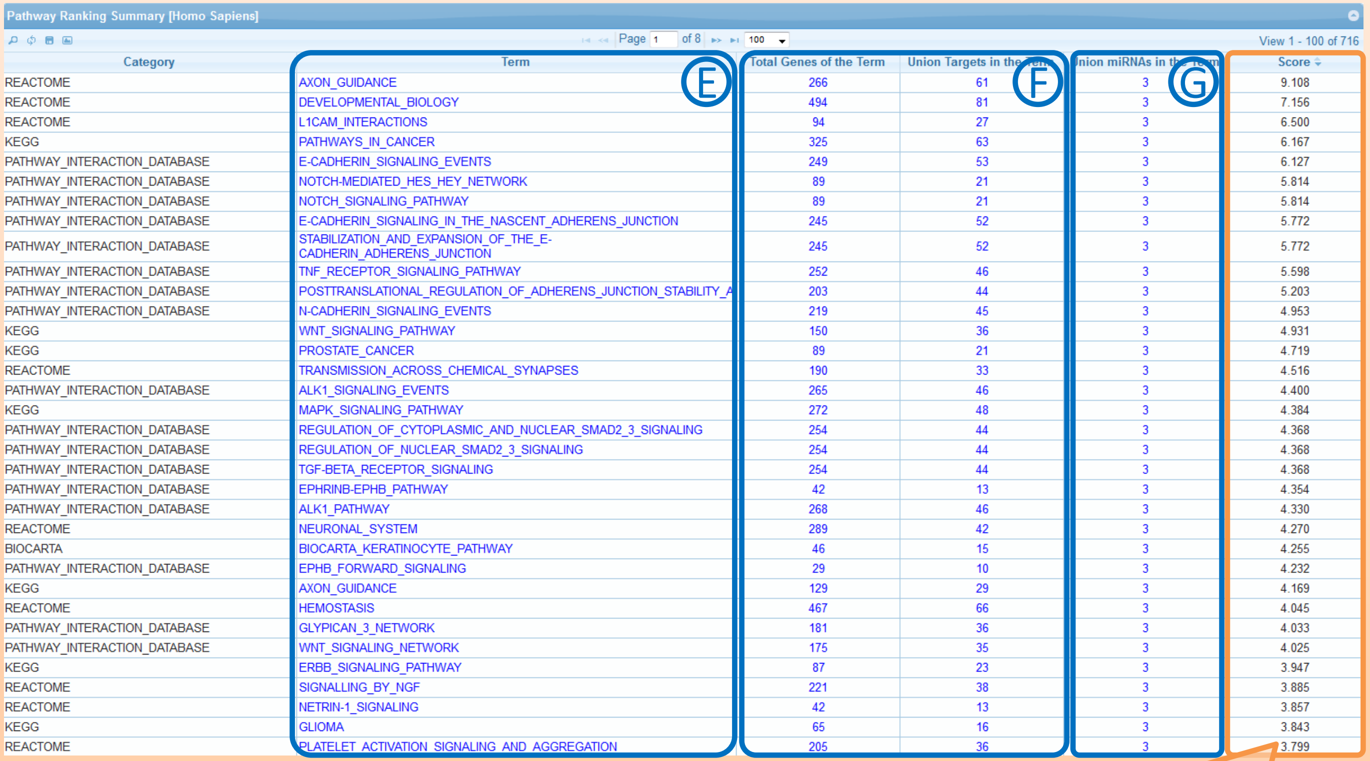
Menu page



- Target Gene List
- Functional Annotation Chart
  - Homo Sapiens (3)
    - Functional Annotation Summary Report
    - Pathway Ranking Summary
    - hsa-miR-449a (Converted from hsa-miR-449)
    - hsa-miR-141
    - hsa-miR-34a

Click to identify pathways based on provided expression ratios

Main page



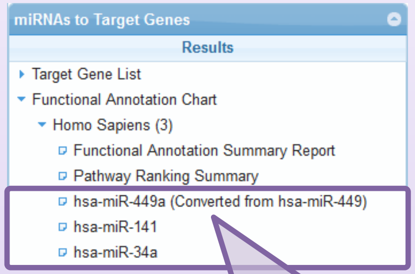
Category	Term	Total Genes of the Term	Union Targets in the Term	nion miRNAs in the Term	Score
REACTOME	AXON_GUIDANCE	266	61	3	9.108
REACTOME	DEVELOPMENTAL_BIOLOGY	494	81	3	7.156
REACTOME	L1CAM_INTERACTIONS	94	27	3	6.500
KEGG	PATHWAYS_IN_CANCER	325	63	3	6.167
PATHWAY_INTERACTION_DATABASE	E-CADHERIN_SIGNALING_EVENTS	249	53	3	6.127
PATHWAY_INTERACTION_DATABASE	NOTCH-MEDIATED_HES_HEY_NETWORK	89	21	3	5.814
PATHWAY_INTERACTION_DATABASE	NOTCH_SIGNALING_PATHWAY	89	21	3	5.814
PATHWAY_INTERACTION_DATABASE	E-CADHERIN_SIGNALING_IN_THE_NASCENT_ADHERENS_JUNCTION	245	52	3	5.772
PATHWAY_INTERACTION_DATABASE	STABILIZATION_AND_EXPANSION_OF_THE_E-CADHERIN_ADHERENS_JUNCTION	245	52	3	5.772
PATHWAY_INTERACTION_DATABASE	TNF_RECEPTOR_SIGNALING_PATHWAY	252	46	3	5.598
PATHWAY_INTERACTION_DATABASE	POSTTRANSLATIONAL_REGULATION_OF_ADHERENS_JUNCTION_STABILITY_A	203	44	3	5.203
PATHWAY_INTERACTION_DATABASE	N-CADHERIN_SIGNALING_EVENTS	219	45	3	4.953
KEGG	WNT_SIGNALING_PATHWAY	150	36	3	4.931
KEGG	PROSTATE_CANCER	89	21	3	4.719
REACTOME	TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	190	33	3	4.516
PATHWAY_INTERACTION_DATABASE	ALK1_SIGNALING_EVENTS	265	46	3	4.400
KEGG	MAPK_SIGNALING_PATHWAY	272	48	3	4.384
PATHWAY_INTERACTION_DATABASE	REGULATION_OF_CYTOPLASMIC_AND_NUCLEAR_SMAD2_3_SIGNALING	254	44	3	4.368
PATHWAY_INTERACTION_DATABASE	REGULATION_OF_NUCLEAR_SMAD2_3_SIGNALING	254	44	3	4.368
PATHWAY_INTERACTION_DATABASE	TGF-BETA_RECEPTOR_SIGNALING	254	44	3	4.368
PATHWAY_INTERACTION_DATABASE	EPHRINB-EPHB_PATHWAY	42	13	3	4.354
PATHWAY_INTERACTION_DATABASE	ALK1_PATHWAY	268	46	3	4.330
REACTOME	NEURONAL_SYSTEM	289	42	3	4.270
BIOCARTA	BIOCARTA_KERATINOCYTE_PATHWAY	46	15	3	4.255
PATHWAY_INTERACTION_DATABASE	EPHB_FORWARD_SIGNALING	29	10	3	4.232
KEGG	AXON_GUIDANCE	129	29	3	4.169
REACTOME	HEMOSTASIS	467	66	3	4.045
PATHWAY_INTERACTION_DATABASE	GLYPICAN_3_NETWORK	181	36	3	4.033
PATHWAY_INTERACTION_DATABASE	WNT_SIGNALING_NETWORK	175	35	3	4.025
KEGG	ERBB_SIGNALING_PATHWAY	87	23	3	3.947
REACTOME	SIGNALLING_BY_NGF	221	38	3	3.885
REACTOME	NETRIN-1_SIGNALING	42	13	3	3.857
KEGG	GLIOMA	65	16	3	3.843
REACTOME	PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	205	36	3	3.799

Sorting by ranking scores default

Functional Annotation Chart

Functions/pathways of the queried miRNA

Menu page



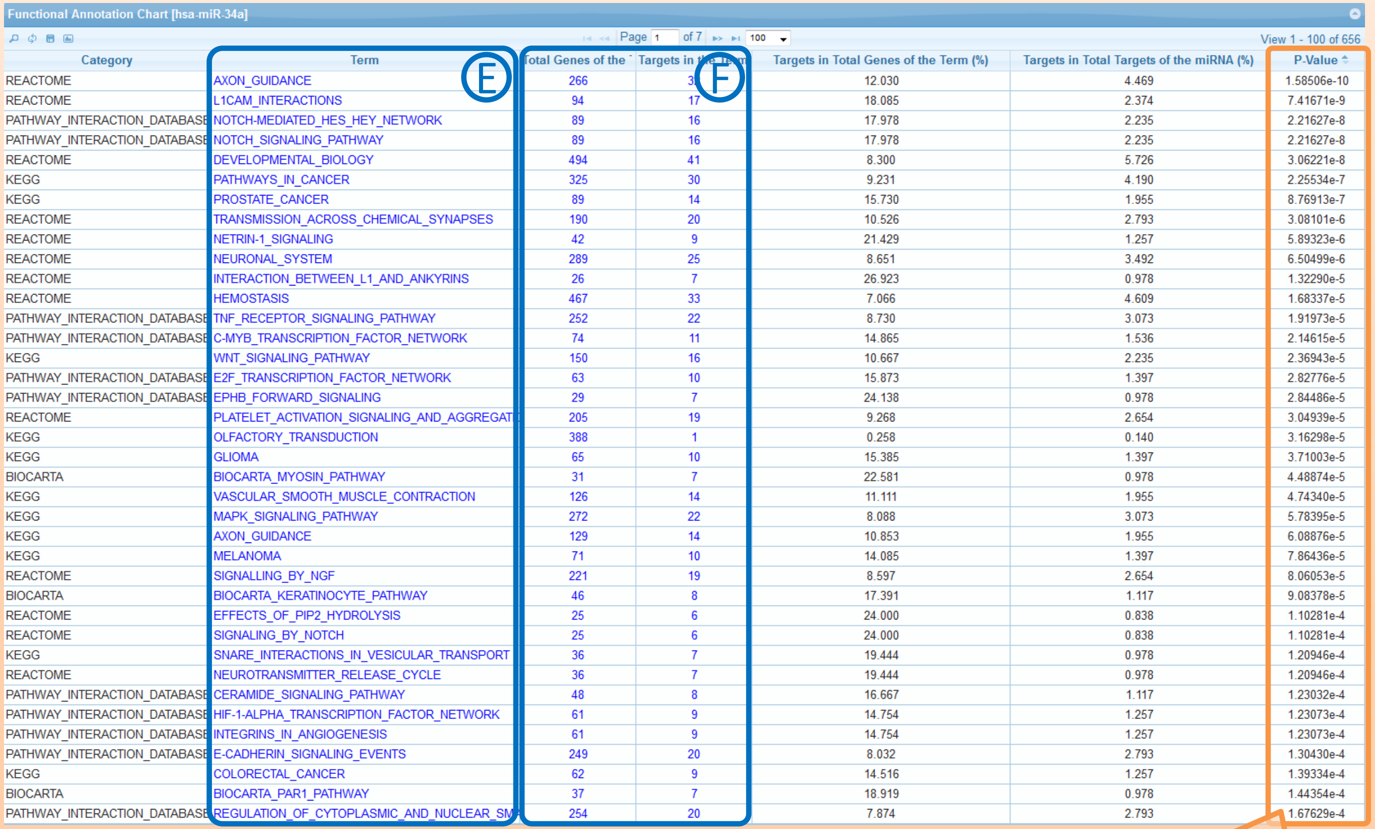
miRNAs to Target Genes

Results

- Target Gene List
- Functional Annotation Chart
  - Homo Sapiens (3)
    - Functional Annotation Summary Report
    - Pathway Ranking Summary
    - hsa-miR-449a (Converted from hsa-miR-449)
    - hsa-miR-141
    - hsa-miR-34a

Click one of the miRNA names for showing the corresponding biological functions/pathways

Main page



Functional Annotation Chart [hsa-miR-34a]

Page 1 of 7 100

View 1 - 100 of 656

Category	Term	Total Genes of the	Targets in the Term	Targets in Total Genes of the Term (%)	Targets in Total Targets of the miRNA (%)	P-Value
REACTOME	AXON_GUIDANCE	266	3	12.030	4.469	1.58506e-10
REACTOME	L1CAM_INTERACTIONS	94	17	18.085	2.374	7.41671e-9
PATHWAY_INTERACTION_DATABASE	NOTCH-MEDIATED_HES_HEY_NETWORK	89	16	17.978	2.235	2.21627e-8
PATHWAY_INTERACTION_DATABASE	NOTCH_SIGNALING_PATHWAY	89	16	17.978	2.235	2.21627e-8
REACTOME	DEVELOPMENTAL_BIOLOGY	494	41	8.300	5.726	3.06221e-8
KEGG	PATHWAYS_IN_CANCER	325	30	9.231	4.190	2.25534e-7
KEGG	PROSTATE_CANCER	89	14	15.730	1.955	8.76913e-7
REACTOME	TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	190	20	10.526	2.793	3.08101e-6
REACTOME	NETRIN-1_SIGNALING	42	9	21.429	1.257	5.89323e-6
REACTOME	NEURONAL_SYSTEM	289	25	8.651	3.492	6.50499e-6
REACTOME	INTERACTION_BETWEEN_L1_AND_ANKYRINS	26	7	26.923	0.978	1.32290e-5
REACTOME	HEMOSTASIS	467	33	7.066	4.609	1.68337e-5
PATHWAY_INTERACTION_DATABASE	TNF_RECEPTOR_SIGNALING_PATHWAY	252	22	8.730	3.073	1.91973e-5
PATHWAY_INTERACTION_DATABASE	C-MYB_TRANSCRIPTION_FACTOR_NETWORK	74	11	14.865	1.536	2.14615e-5
KEGG	WNT_SIGNALING_PATHWAY	150	16	10.667	2.235	2.36943e-5
PATHWAY_INTERACTION_DATABASE	E2F_TRANSCRIPTION_FACTOR_NETWORK	63	10	15.873	1.397	2.82776e-5
PATHWAY_INTERACTION_DATABASE	EPHB_FORWARD_SIGNALING	29	7	24.138	0.978	2.84486e-5
REACTOME	PLATELET_ACTIVATION_SIGNALING_AND_AGGREGAT	205	19	9.268	2.654	3.04939e-5
KEGG	OLFACTORY_TRANSDUCTION	388	1	0.258	0.140	3.16298e-5
KEGG	GLIOMA	65	10	15.385	1.397	3.71003e-5
BIOCARTA	BIOCARTA_MYOSIN_PATHWAY	31	7	22.581	0.978	4.48874e-5
KEGG	VASCULAR_SMOOTH_MUSCLE_CONTRACTION	126	14	11.111	1.955	4.74340e-5
KEGG	MAPK_SIGNALING_PATHWAY	272	22	8.088	3.073	5.78395e-5
KEGG	AXON_GUIDANCE	129	14	10.853	1.955	6.08876e-5
KEGG	MELANOMA	71	10	14.085	1.397	7.86436e-5
REACTOME	SIGNALLING_BY_NGF	221	19	8.597	2.654	8.06053e-5
BIOCARTA	BIOCARTA_KERATINOCYTE_PATHWAY	46	8	17.391	1.117	9.08378e-5
REACTOME	EFFECTS_OF_PIP2_HYDROLYSIS	25	6	24.000	0.838	1.10281e-4
REACTOME	SIGNALING_BY_NOTCH	25	6	24.000	0.838	1.10281e-4
KEGG	SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	36	7	19.444	0.978	1.20946e-4
REACTOME	NEUROTRANSMITTER_RELEASE_CYCLE	36	7	19.444	0.978	1.20946e-4
PATHWAY_INTERACTION_DATABASE	CERAMIDE_SIGNALING_PATHWAY	48	8	16.667	1.117	1.23032e-4
PATHWAY_INTERACTION_DATABASE	HIF-1-ALPHA_TRANSCRIPTION_FACTOR_NETWORK	61	9	14.754	1.257	1.23073e-4
PATHWAY_INTERACTION_DATABASE	INTEGRINS_IN_ANGIOGENESIS	61	9	14.754	1.257	1.23073e-4
PATHWAY_INTERACTION_DATABASE	E-CADHERIN_SIGNALING_EVENTS	249	20	8.032	2.793	1.30430e-4
KEGG	COLORECTAL_CANCER	62	9	14.516	1.257	1.39334e-4
BIOCARTA	BIOCARTA_PAR1_PATHWAY	37	7	18.919	0.978	1.44354e-4
PATHWAY_INTERACTION_DATABASE	REGULATION_OF_CYTOPLASMIC_AND_NUCLEAR_SM	254	20	7.874	2.793	1.67629e-4

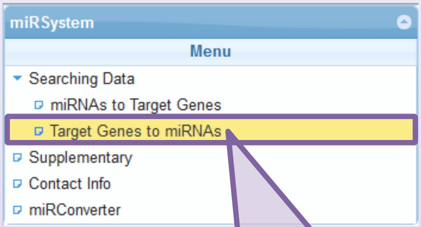
Sorting by p-value default

- miRNAs to Target Genes
- Target Genes to miRNAs
- miRConverter

Starting analysis

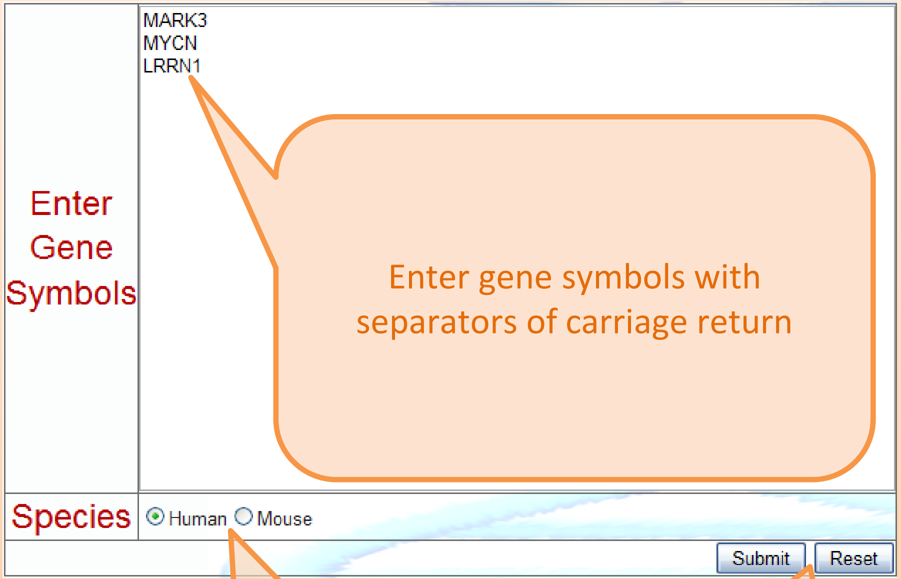
Target Genes to miRNAs

Menu page



Click “Target Genes to miRNAs” for searching the interactions of predicted targets and miRNAs

Main page


Enter Gene Symbols

MARK3
MYCN
LRRN1

Species ● Human ○ Mouse

Enter gene symbols with separators of carriage return

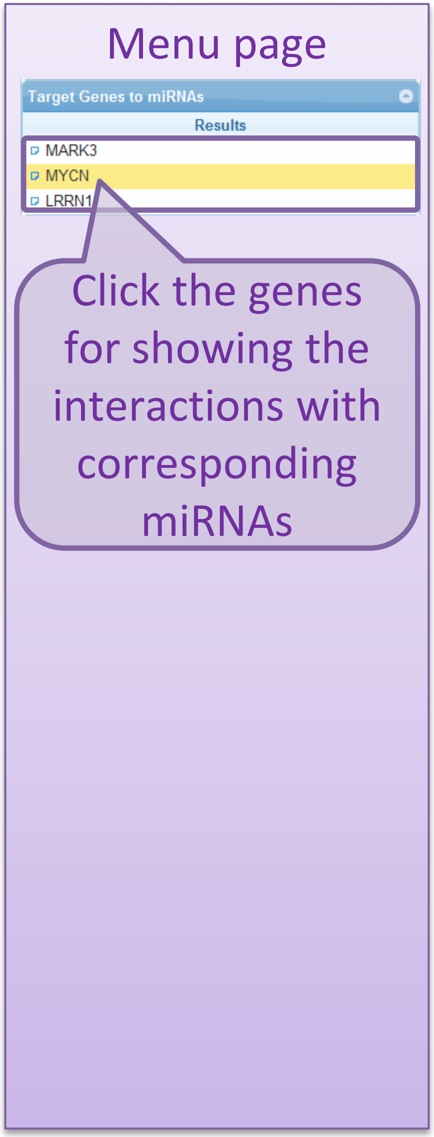
Choose the species of target genes

Submit data and start to search

Click “Reset” button for initialization as the default values

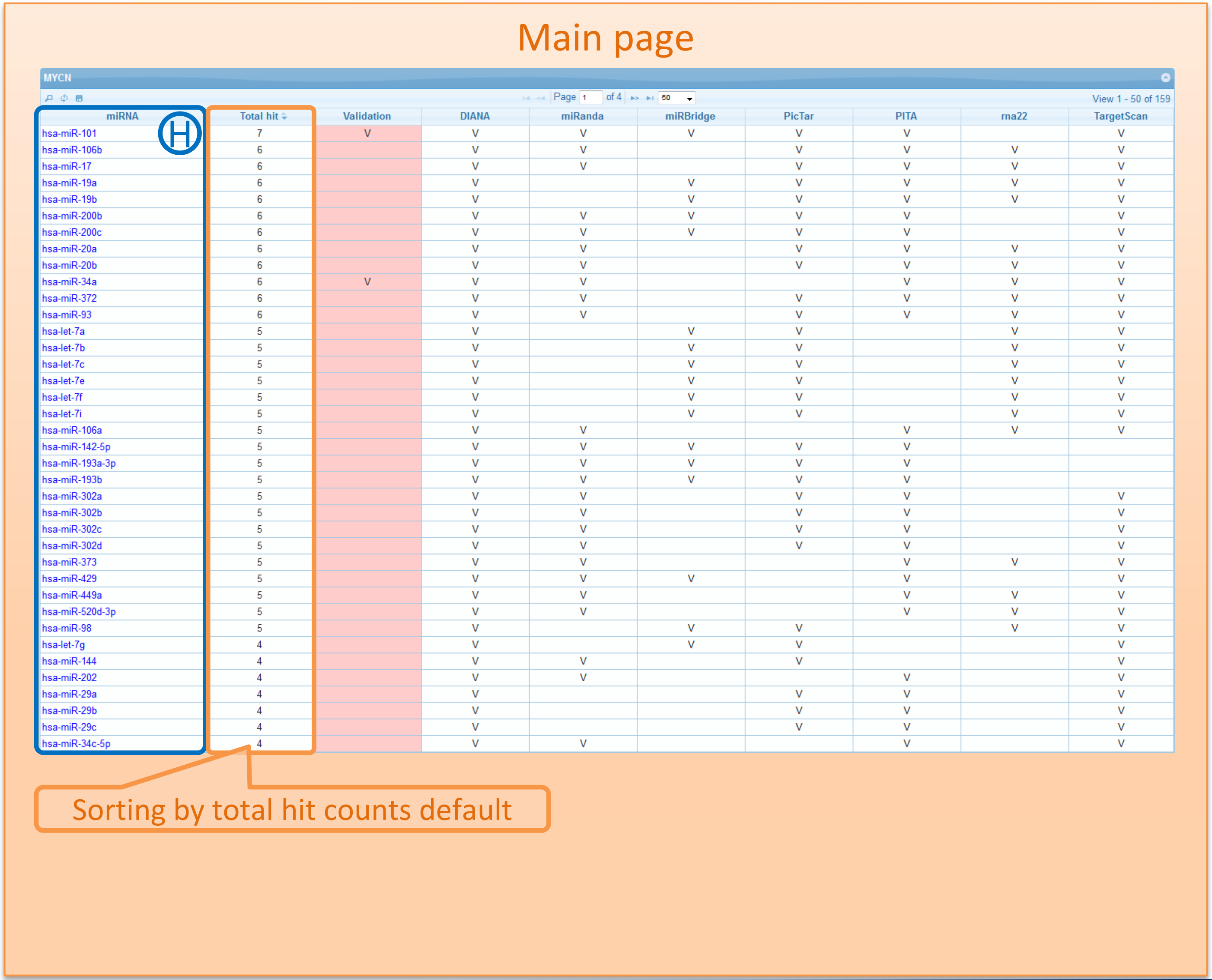
Target Genes to miRNA

miRNAs of the queried target gene



Menu page

Click the genes for showing the interactions with corresponding miRNAs



Main page

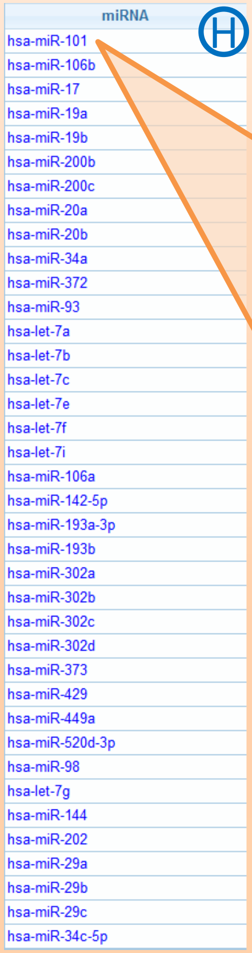
miRNA	Total hit	Validation	DIANA	miRanda	miRBridge	PicTar	PITA	rna22	TargetScan
hsa-miR-101	7	V	V	V	V	V	V		V
hsa-miR-106b	6		V	V		V	V	V	V
hsa-miR-17	6		V	V		V	V	V	V
hsa-miR-19a	6		V		V	V	V	V	V
hsa-miR-19b	6		V		V	V	V	V	V
hsa-miR-200b	6		V	V	V	V	V		V
hsa-miR-200c	6		V	V	V	V	V		V
hsa-miR-20a	6		V	V		V	V	V	V
hsa-miR-20b	6		V	V		V	V	V	V
hsa-miR-34a	6	V	V	V			V	V	V
hsa-miR-372	6		V	V		V	V	V	V
hsa-miR-93	6		V	V		V	V	V	V
hsa-let-7a	5		V		V	V		V	V
hsa-let-7b	5		V		V	V		V	V
hsa-let-7c	5		V		V	V		V	V
hsa-let-7e	5		V		V	V		V	V
hsa-let-7f	5		V		V	V		V	V
hsa-let-7i	5		V		V	V		V	V
hsa-miR-106a	5		V	V			V	V	V
hsa-miR-142-5p	5		V	V	V	V	V		
hsa-miR-193a-3p	5		V	V	V	V	V		
hsa-miR-193b	5		V	V	V	V	V		
hsa-miR-302a	5		V	V		V	V		V
hsa-miR-302b	5		V	V		V	V		V
hsa-miR-302c	5		V	V		V	V		V
hsa-miR-302d	5		V	V		V	V		V
hsa-miR-373	5		V	V			V	V	V
hsa-miR-429	5		V	V	V		V		V
hsa-miR-449a	5		V	V			V	V	V
hsa-miR-520d-3p	5		V	V			V	V	V
hsa-miR-98	5		V		V	V		V	V
hsa-let-7g	4		V		V	V			V
hsa-miR-144	4		V	V		V			V
hsa-miR-202	4		V	V			V		V
hsa-miR-29a	4		V			V	V		V
hsa-miR-29b	4		V			V	V		V
hsa-miR-29c	4		V			V	V		V
hsa-miR-34c-5p	4		V	V			V		V

Sorting by total hit counts default

miRNAs of the Queried Target Gene

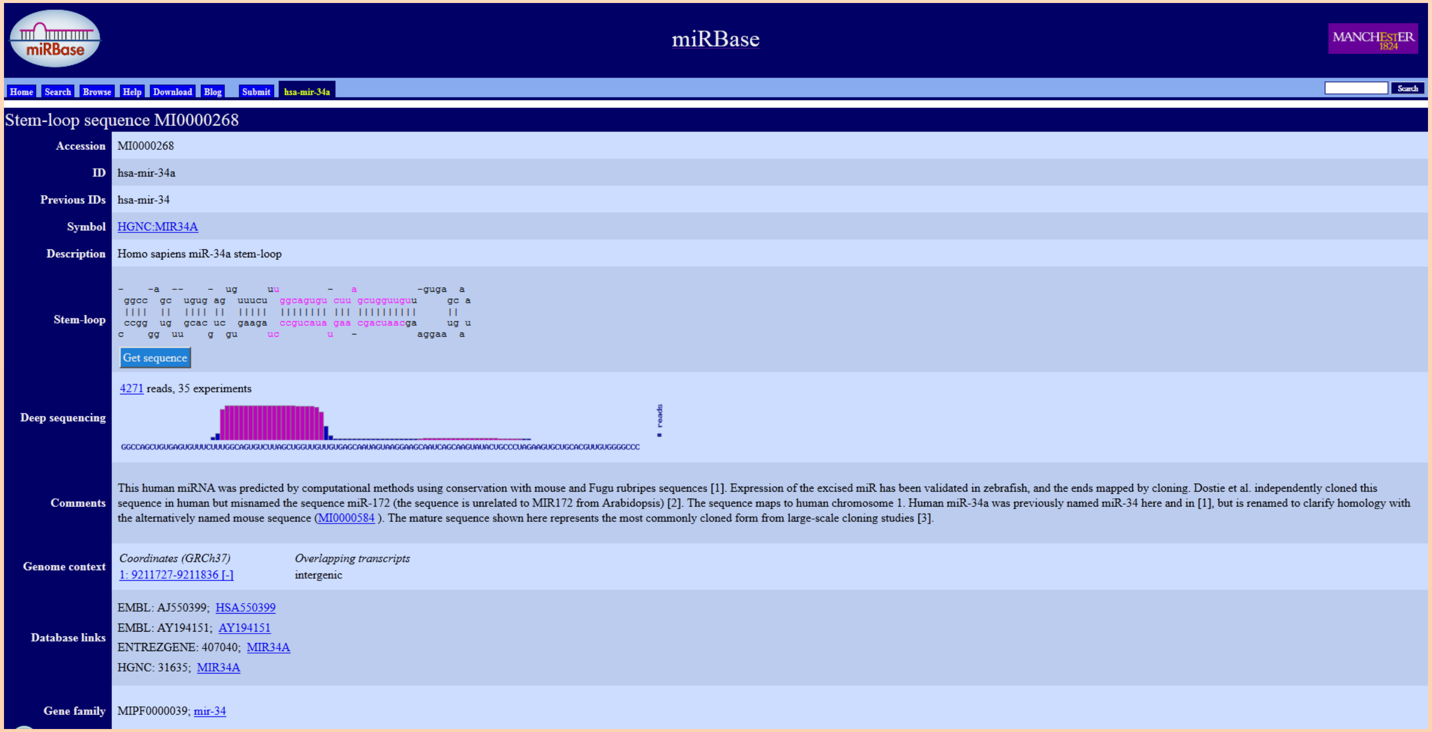
Hyperlink to miRBase

Main page



miRNA
hsa-miR-101
hsa-miR-106b
hsa-miR-17
hsa-miR-19a
hsa-miR-19b
hsa-miR-200b
hsa-miR-200c
hsa-miR-20a
hsa-miR-20b
hsa-miR-34a
hsa-miR-372
hsa-miR-93
hsa-let-7a
hsa-let-7b
hsa-let-7c
hsa-let-7e
hsa-let-7f
hsa-let-7i
hsa-miR-106a
hsa-miR-142-5p
hsa-miR-193a-3p
hsa-miR-193b
hsa-miR-302a
hsa-miR-302b
hsa-miR-302c
hsa-miR-302d
hsa-miR-373
hsa-miR-429
hsa-miR-449a
hsa-miR-520d-3p
hsa-miR-98
hsa-let-7g
hsa-miR-144
hsa-miR-202
hsa-miR-29a
hsa-miR-29b
hsa-miR-29c
hsa-miR-34c-5p

Click one of the miRNAs to link to miRBase for more its annotation



Stem-loop sequence MI0000268

Accession	MI0000268
ID	hsa-mir-34a
Previous IDs	hsa-mir-34
Symbol	HGNC:MIR34A
Description	Homo sapiens miR-34a stem-loop

Stem-loop

```
-     -a   --     -  ug      uu         -    a            -guga   a
 ggcc   gc   ugug ag   uucucu  ggcagugu cuu gcugguuguu       gc a
 ||||   ||   |||| ||   |||||  |||||||| ||| ||||||||||       ||
 ccgg   ug   gcac uc   gaaga  ccgucaua gaa cgacuaacga       ug u
c     gg   uu     g  gu      uc         u    -            aggaa   a
```

Deep sequencing

4271 reads, 35 experiments

GGCCAGCUGUGAGUGUUUCUUUGGCAGUGUCUUAGCUGGUUGUUGUGAGCAAUAGUAAGGAAGCAAUCAGCAAGUAUACUGCCCUAGAAGUGCUGCACGUUGUGGGGCCC

Comments

This human miRNA was predicted by computational methods using conservation with mouse and Fugu rubripes sequences [1]. Expression of the excised miR has been validated in zebrafish, and the ends mapped by cloning. Dostie et al. independently cloned this sequence in human but misnamed the sequence miR-172 (the sequence is unrelated to MIR172 from Arabidopsis) [2]. The sequence maps to human chromosome 1. Human miR-34a was previously named miR-34 here and in [1], but is renamed to clarify homology with the alternatively named mouse sequence (MI0000584). The mature sequence shown here represents the most commonly cloned form from large-scale cloning studies [3].

Genome context

Coordinates (GRCh37)	*Overlapping transcripts*
1: 9211727-9211836 [-]	intergenic

Database links

EMBL: AJ550399; HSA550399
EMBL: AY194151; AY194151
ENTREZGENE: 407040; MIR34A
HGNC: 31635; MIR34A

Gene family

MIPF0000039; mir-34

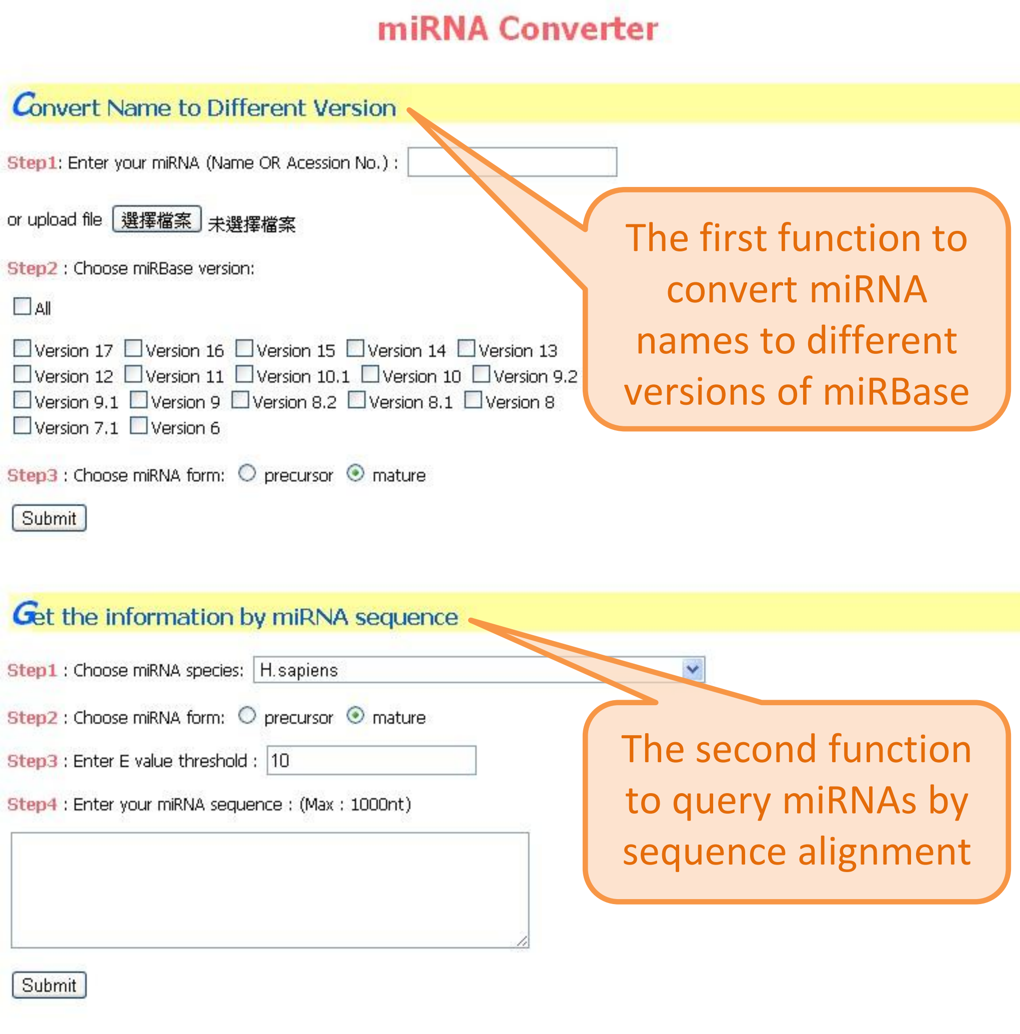
- miRNAs to Target Genes
- Target Genes to miRNAs
- miRConverter

miRConverter

Menu page

Click to show miRConverter

Main page



miRNA Converter

Convert Name to Different Version

Step1: Enter your miRNA (Name OR Acession No.) :

or upload file 選擇檔案 未選擇檔案

Step2 : Choose miRBase version:

☐ All

☐ Version 17 ☐ Version 16 ☐ Version 15 ☐ Version 14 ☐ Version 13
☐ Version 12 ☐ Version 11 ☐ Version 10.1 ☐ Version 10 ☐ Version 9.2
☐ Version 9.1 ☐ Version 9 ☐ Version 8.2 ☐ Version 8.1 ☐ Version 8
☐ Version 7.1 ☐ Version 6

Step3 : Choose miRNA form: ○ precursor ● mature

Submit

Get the information by miRNA sequence

Step1 : Choose miRNA species: H.sapiens

Step2 : Choose miRNA form: ○ precursor ● mature

Step3 : Enter E value threshold : 10

Step4 : Enter your miRNA sequence : (Max : 1000nt)

Submit

The first function to convert miRNA names to different versions of miRBase

The second function to query miRNAs by sequence alignment

1st function : Name conversion

By a name of miRNA

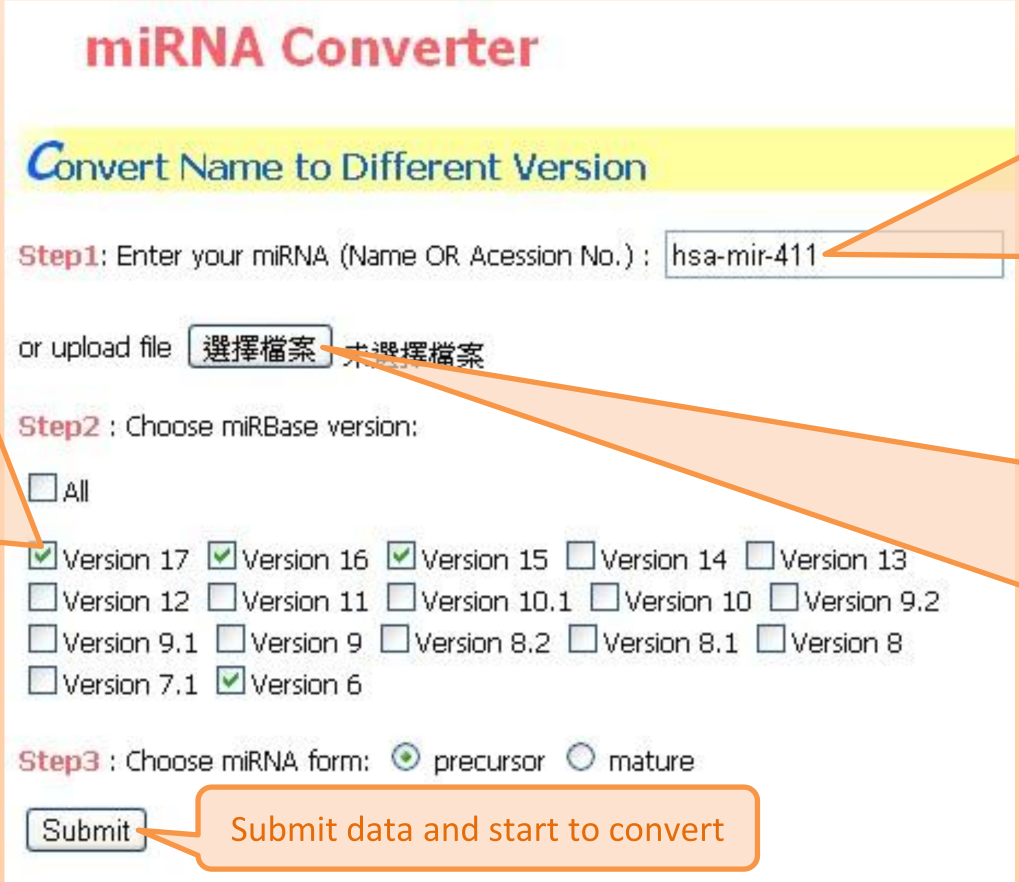
Main page

Enter a miRNA name or accession number for querying

NOTICE: The name should be a full complete format of the official name in miRBase

Check the “Version” option to select target version of name conversion

NOTICE: the latest miRBase version provided in miRConverter is 17 and the oldest is 6



miRNA Converter

Convert Name to Different Version

Step1: Enter your miRNA (Name OR Acession No.) : hsa-mir-411

or upload file 未選擇檔案

Step2 : Choose miRBase version:

☐ All

☑ Version 17 ☑ Version 16 ☑ Version 15 ☐ Version 14 ☐ Version 13
☐ Version 12 ☐ Version 11 ☐ Version 10.1 ☐ Version 10 ☐ Version 9.2
☐ Version 9.1 ☐ Version 9 ☐ Version 8.2 ☐ Version 8.1 ☐ Version 8
☐ Version 7.1 ☑ Version 6

Step3 : Choose miRNA form: ● precursor ○ mature

Submit data and start to convert

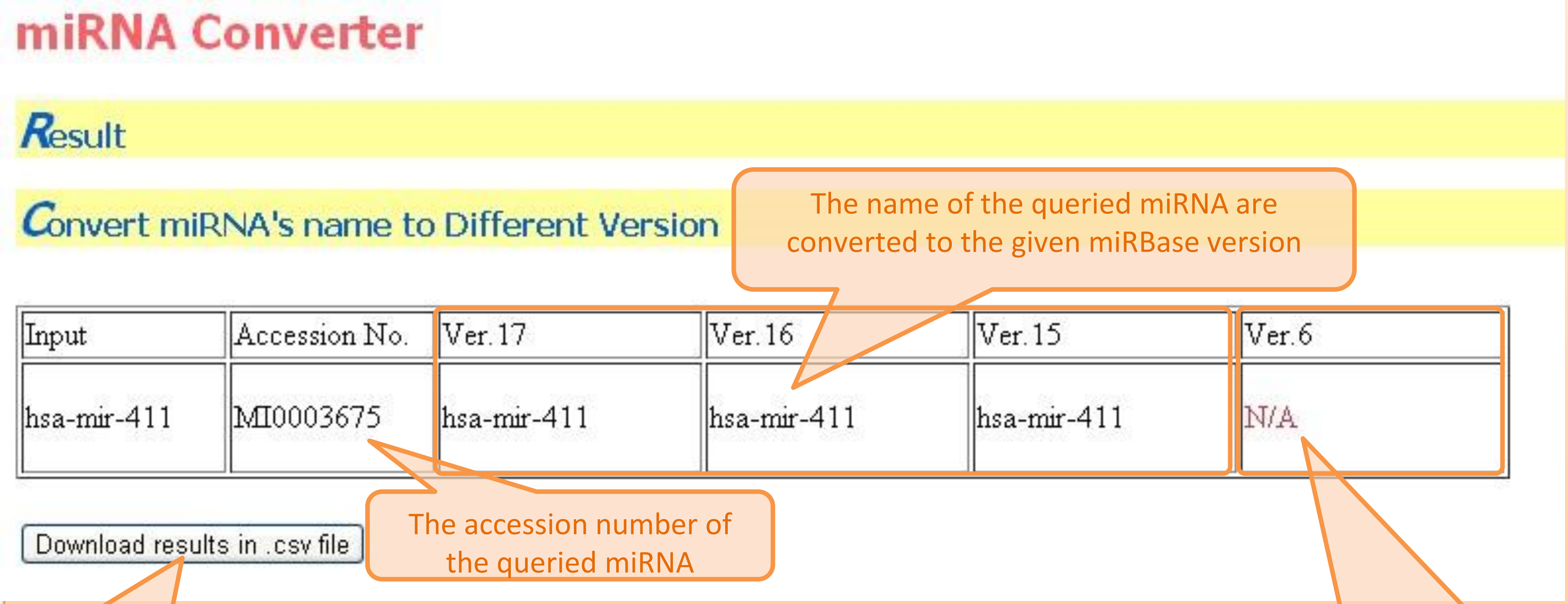
Click “Browse” to upload a text file containing miRNA names or accession for a multiple query

NOTICE: The uploading function has a higher priority than manually input

1st function : Name conversion

By a name of miRNA

Main page



miRNA Converter

Result

Convert miRNA's name to Different Version

Input	Accession No.	Ver.17	Ver.16	Ver.15	Ver.6
hsa-mir-411	MI0003675	hsa-mir-411	hsa-mir-411	hsa-mir-411	N/A

The name of the queried miRNA are converted to the given miRBase version

The accession number of the queried miRNA

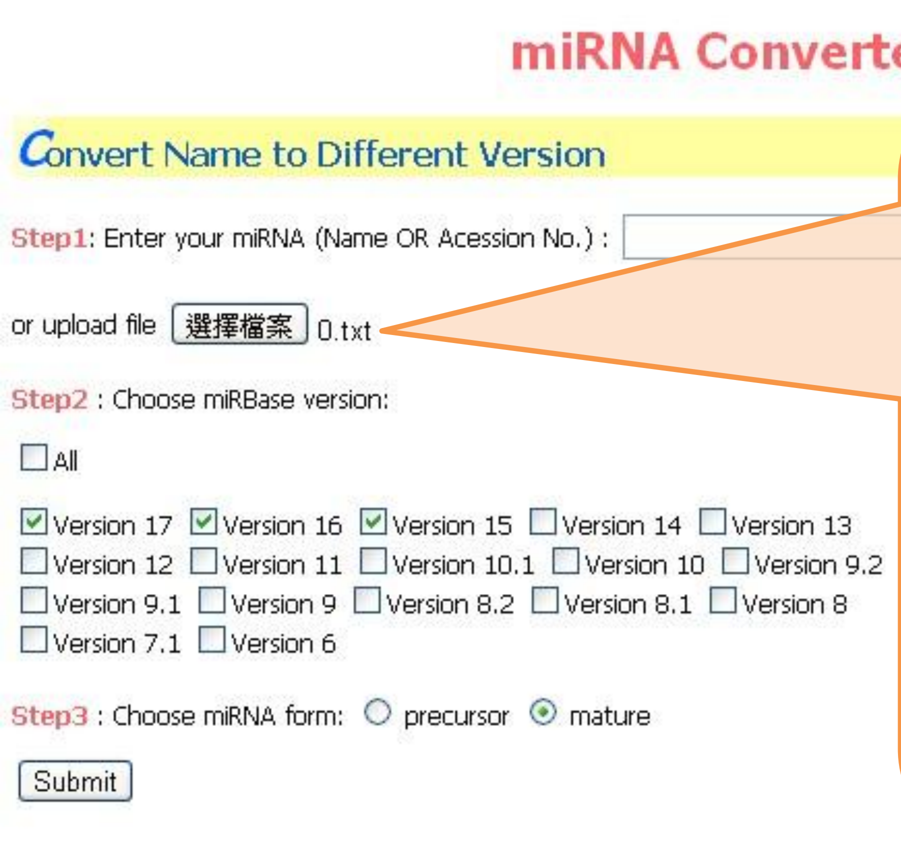
Click “Download results in .csv file” to download the result

The “N/A” represented no record of the name or accession number in this version of miRBase

1st function : Name conversion

By accession numbers of miRNA

Main page



miRNA Converter

Convert Name to Different Version

Step1: Enter your miRNA (Name OR Acession No.) :

or upload file 選擇檔案 0.txt

Step2 : Choose miRBase version:

☐ All

☑ Version 17 ☑ Version 16 ☑ Version 15 ☐ Version 14 ☐ Version 13
☐ Version 12 ☐ Version 11 ☐ Version 10.1 ☐ Version 10 ☐ Version 9.2
☐ Version 9.1 ☐ Version 9 ☐ Version 8.2 ☐ Version 8.1 ☐ Version 8
☐ Version 7.1 ☐ Version 6

Step3 : Choose miRNA form: ○ precursor ● mature

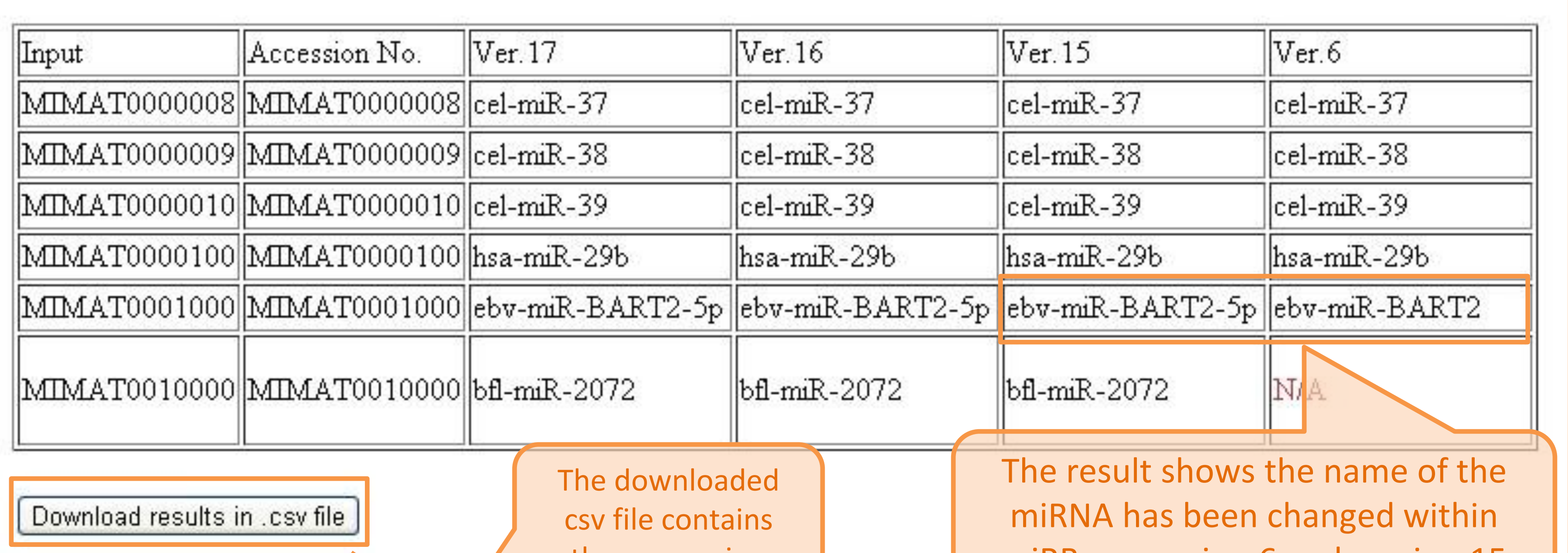
Upload a text file containing miRNA names or accession numbers separated by a carriage return or space

```
MIMAT0000008
MIMAT0000009
MIMAT0000010
MIMAT0000100
MIMAT0001000
MIMAT0010000
```

1st function : Name conversion

By accession numbers of miRNA

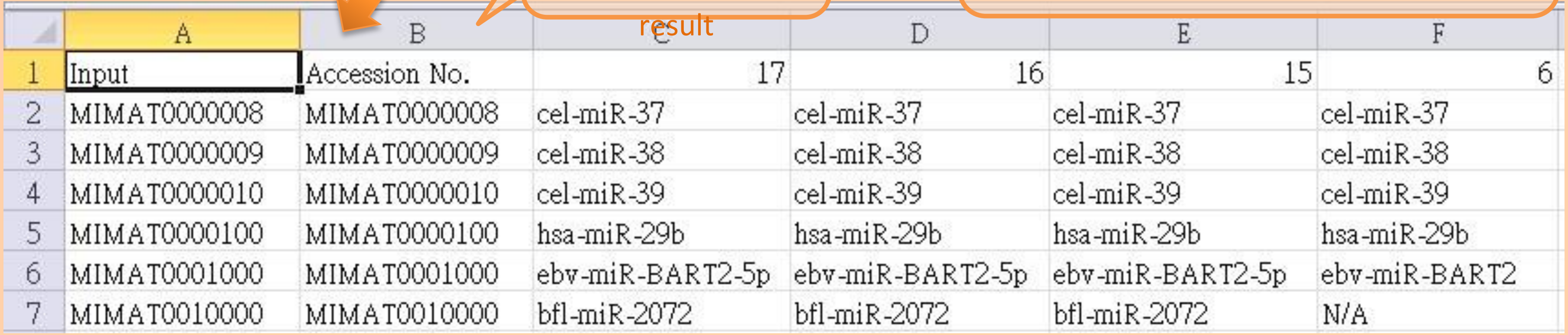
Main page



Input	Accession No.	Ver. 17	Ver. 16	Ver. 15	Ver. 6
MIMAT0000008	MIMAT0000008	cel-miR-37	cel-miR-37	cel-miR-37	cel-miR-37
MIMAT0000009	MIMAT0000009	cel-miR-38	cel-miR-38	cel-miR-38	cel-miR-38
MIMAT0000010	MIMAT0000010	cel-miR-39	cel-miR-39	cel-miR-39	cel-miR-39
MIMAT0000100	MIMAT0000100	hsa-miR-29b	hsa-miR-29b	hsa-miR-29b	hsa-miR-29b
MIMAT0001000	MIMAT0001000	ebv-miR-BART2-5p	ebv-miR-BART2-5p	ebv-miR-BART2-5p	ebv-miR-BART2
MIMAT0010000	MIMAT0010000	bfl-miR-2072	bfl-miR-2072	bfl-miR-2072	N/A

The downloaded csv file contains the conversion result

The result shows the name of the miRNA has been changed within miRBase version 6 and version 15



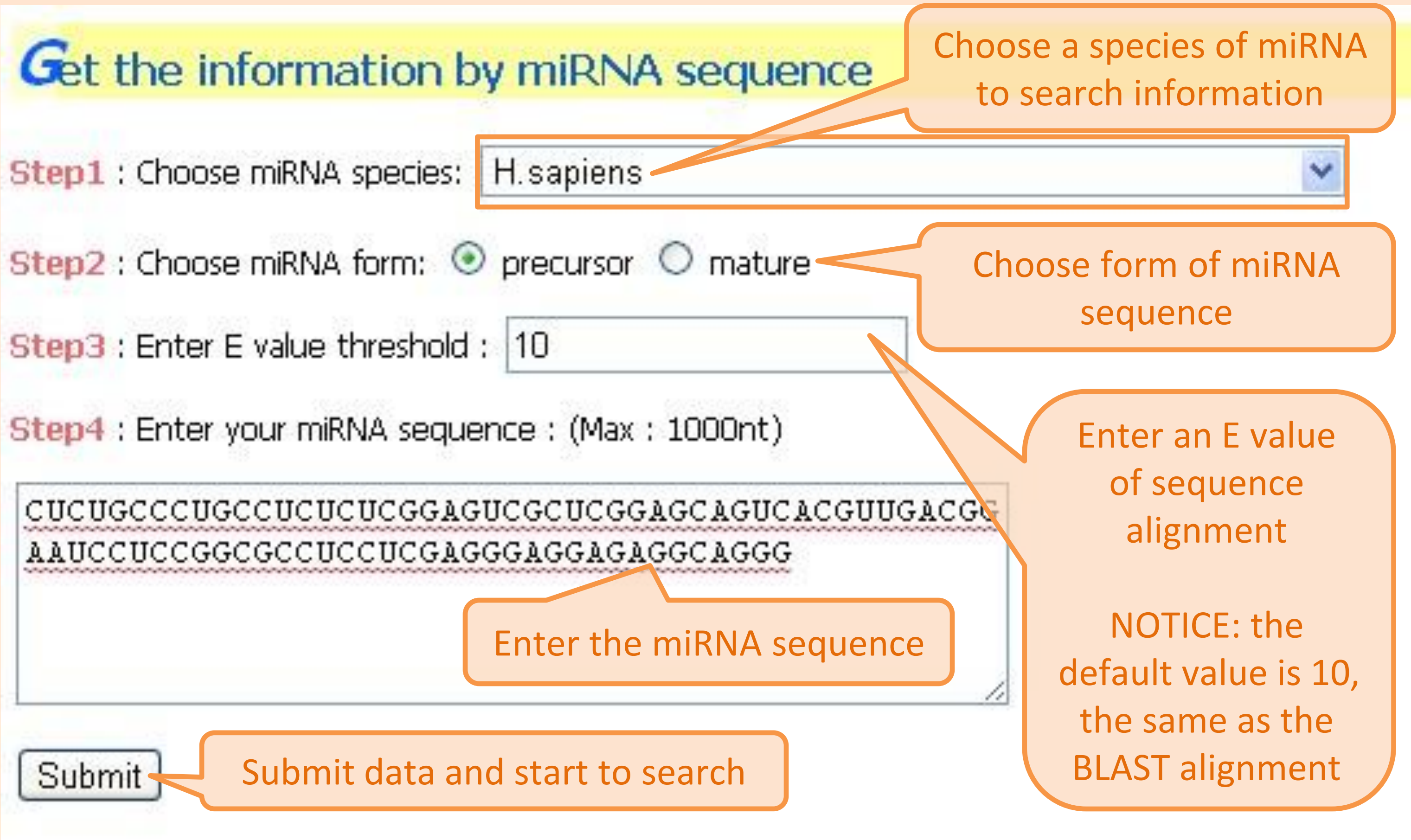
	A	B	C	D	E	F
1	Input	Accession No.	17	16	15	6
2	MIMAT0000008	MIMAT0000008	cel-miR-37	cel-miR-37	cel-miR-37	cel-miR-37
3	MIMAT0000009	MIMAT0000009	cel-miR-38	cel-miR-38	cel-miR-38	cel-miR-38
4	MIMAT0000010	MIMAT0000010	cel-miR-39	cel-miR-39	cel-miR-39	cel-miR-39
5	MIMAT0000100	MIMAT0000100	hsa-miR-29b	hsa-miR-29b	hsa-miR-29b	hsa-miR-29b
6	MIMAT0001000	MIMAT0001000	ebv-miR-BART2-5p	ebv-miR-BART2-5p	ebv-miR-BART2-5p	ebv-miR-BART2
7	MIMAT0010000	MIMAT0010000	bfl-miR-2072	bfl-miR-2072	bfl-miR-2072	N/A

2nd function : Sequence searching

Homo sapiens

Main page

Example: hsa-mir-3183 from *Homo sapiens*



Get the information by miRNA sequence

Step1 : Choose miRNA species: H.sapiens

Step2 : Choose miRNA form: ● precursor ○ mature

Step3 : Enter E value threshold : 10

Step4 : Enter your miRNA sequence : (Max : 1000nt)

```
CUCUGCCCUGCCUCUCUCGGAGUCGCUCGGAGCAGUCACGUUGACGG
AAUCCUCCGGCGCCUCCUCGAGGGAGGAGAGGCAGGG
```

Choose a species of miRNA to search information

Choose form of miRNA sequence

Enter an E value of sequence alignment

NOTICE: the default value is 10, the same as the BLAST alignment

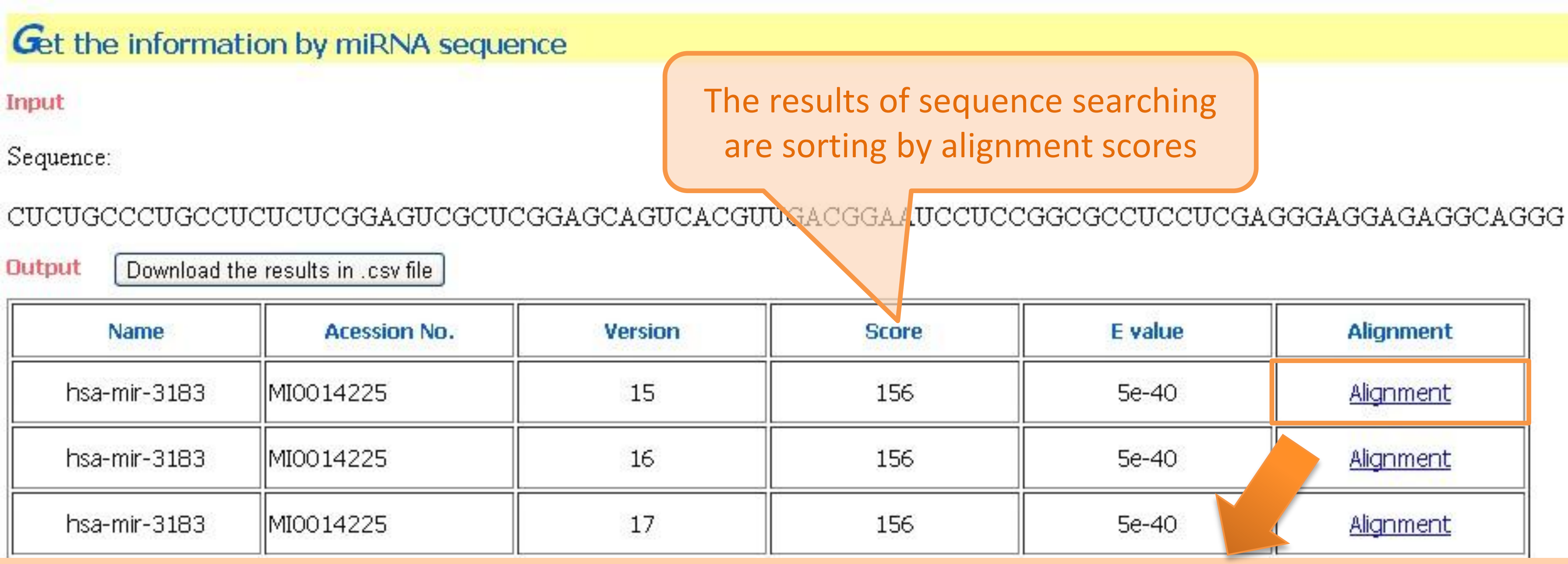
Enter the miRNA sequence

Submit data and start to search

2nd function : Sequence searching

Homo sapiens

Main page



Get the information by miRNA sequence

Input

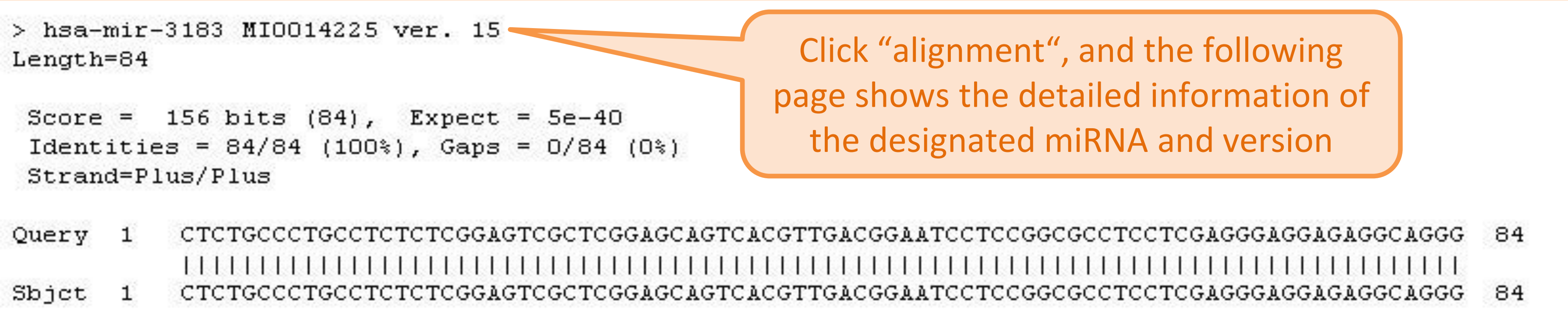
Sequence:

CUCUGCCCUGCCUCUCUCGGAGUCGCUCGGAGCAGUCACGUUGACGGAAUCCUCCGGCGCCUCCUCGAGGGAGGAGAGGCAGGG

Output

Name	Acession No.	Version	Score	E value	Alignment
hsa-mir-3183	MI0014225	15	156	5e-40	Alignment
hsa-mir-3183	MI0014225	16	156	5e-40	Alignment
hsa-mir-3183	MI0014225	17	156	5e-40	Alignment

The results of sequence searching are sorting by alignment scores



```
> hsa-mir-3183 MI0014225 ver. 15
Length=84

 Score =  156 bits (84),  Expect = 5e-40
 Identities = 84/84 (100%), Gaps = 0/84 (0%)
 Strand=Plus/Plus

Query  1    CTCTGCCCTGCCTCTCTCGGAGTCGCTCGGAGCAGTCACGTTGACGGAATCCTCCGGCGCCTCCTCGAGGGAGGAGAGGCAGGG  84
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCTGCCCTGCCTCTCTCGGAGTCGCTCGGAGCAGTCACGTTGACGGAATCCTCCGGCGCCTCCTCGAGGGAGGAGAGGCAGGG  84
```

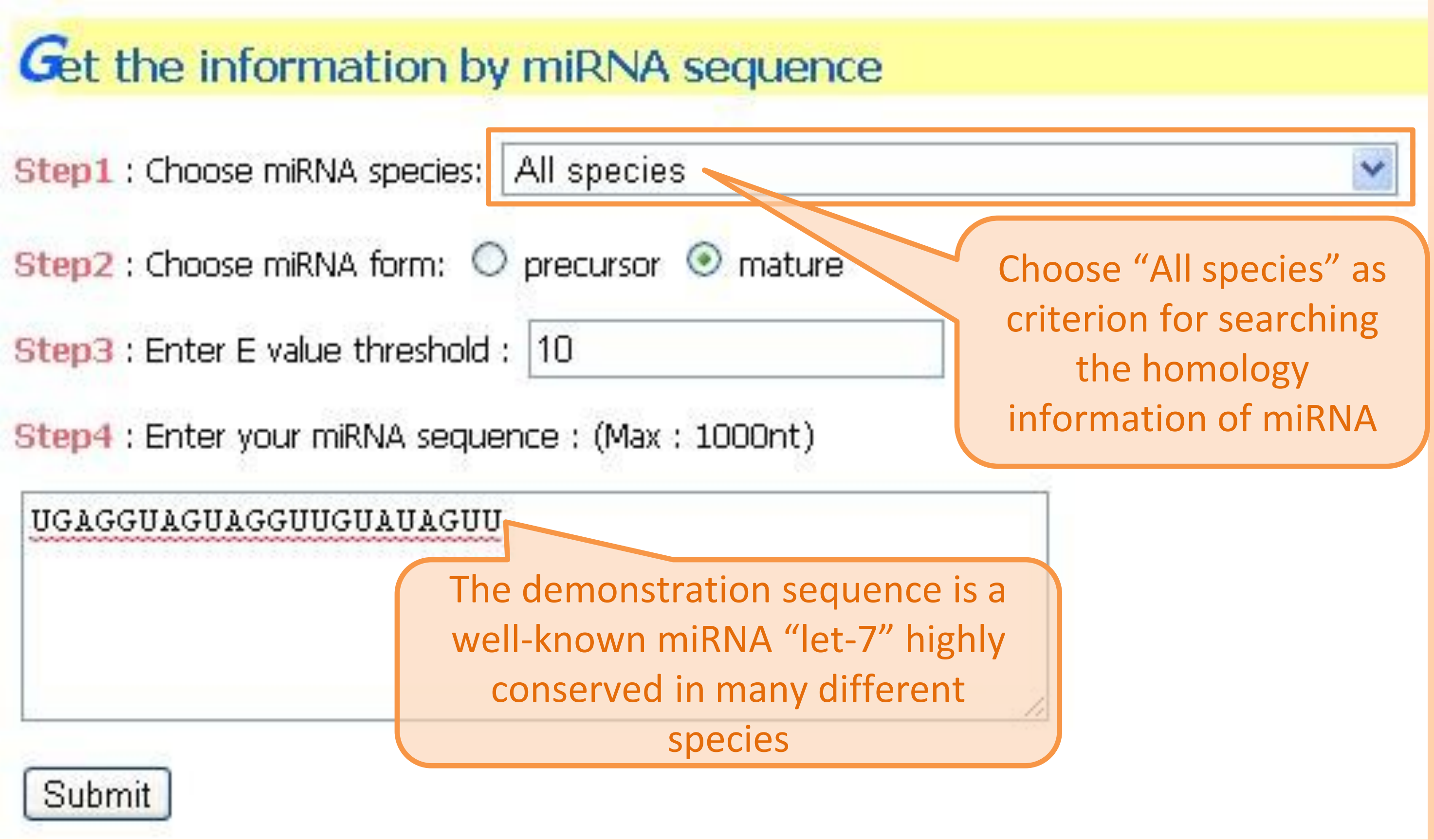
Click “alignment“, and the following page shows the detailed information of the designated miRNA and version

2nd function : Sequence searching

All species

Main page

Example: cel-let-7 from *Caenorhabditis elegans*



Get the information by miRNA sequence

Step1 : Choose miRNA species: All species

Step2 : Choose miRNA form: ○ precursor ● mature

Step3 : Enter E value threshold : 10

Step4 : Enter your miRNA sequence : (Max : 1000nt)

UGAGGUAGUAGGUUGUAUAGUU

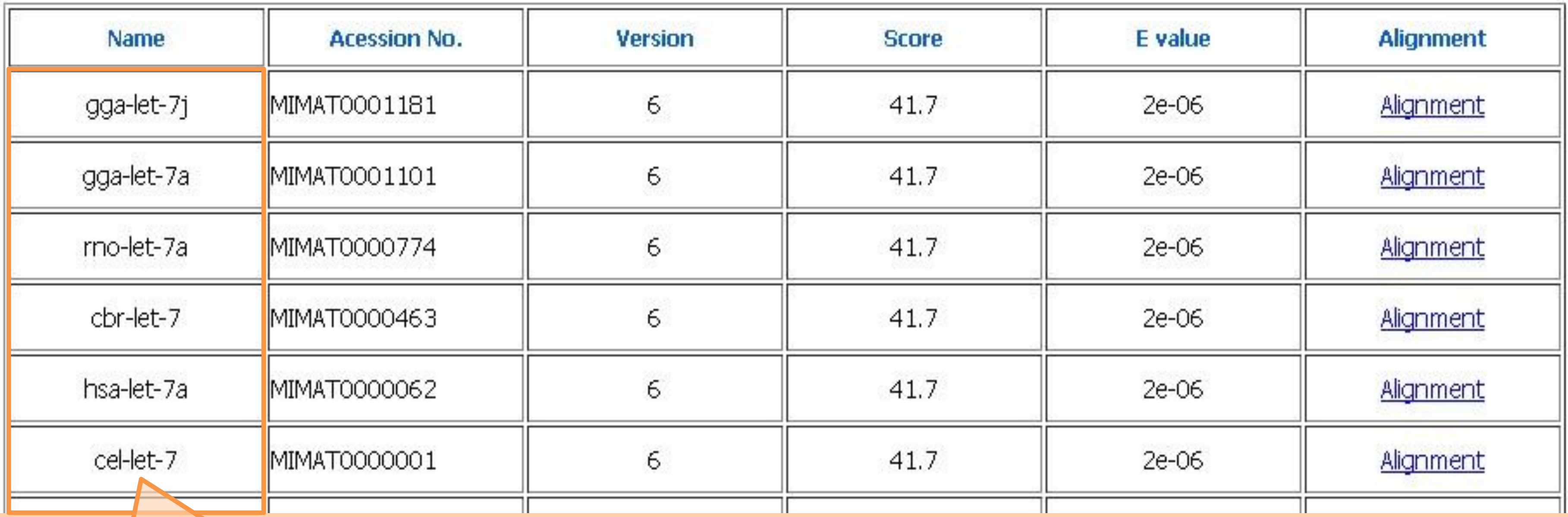
Choose "All species" as criterion for searching the homology information of miRNA

The demonstration sequence is a well-known miRNA "let-7" highly conserved in many different species

2nd function : Sequence searching

All species

Main page



Name	Acession No.	Version	Score	E value	Alignment
gga-let-7j	MIMAT0001181	6	41.7	2e-06	Alignment
gga-let-7a	MIMAT0001101	6	41.7	2e-06	Alignment
rno-let-7a	MIMAT0000774	6	41.7	2e-06	Alignment
cbr-let-7	MIMAT0000463	6	41.7	2e-06	Alignment
hsa-let-7a	MIMAT0000062	6	41.7	2e-06	Alignment
cel-let-7	MIMAT0000001	6	41.7	2e-06	Alignment

The result shows sequence conservation within different species: the scores and sequences of these miRNAs are the same