

Introduction

Description

MIR155, located within the non-coding BIC transcript, is processed into mature forms hsa-miR-155-5p and -3p which exhibit coordinated, opposing regulation of IFNA, is involved in migration, adhesion, and proliferation, is downregulated in many diseases

Synonyms

MIR155; mir-155; MIRN155; miRNA155; miR-155-3p; miR-155-5p; hsa-miR-155; microRNA 155; hsa-miR-155*; hsa-miR-155-3p; hsa-miR-155-5p

Encoded products

Stem-loop : [hsa-mir-155](#)

Mature miRNA : [hsa-miR-155-5p](#), [hsa-miR-155-3p](#)

hsa-miR-155-5p, a mature miRNA which negatively regulates plasmacytoid dendritic cell activation through coordinated, opposing regulation of interferon alpha (IFNA) with co-expressed hsa-miR-155-3p, expression is altered in breast and other cancers

hsa-miR-155-3p, a mature miRNA which targets IRAKM and positively regulates plasmacytoid dendritic cell activation in response to TLR7/JNK signaling through coordinated, opposing regulation of interferon alpha (IFNA) with co-expressed hsa-miR-155-5p

Gene Ontology [what is this?](#)

Molecular function

Term	Mature form undetermined	hsa-miR-155-5p	hsa-miR-155-3p
mRNA 3'-UTR binding, [E]			✓

Showing 1 to 1 of 1 entries First Previous 1 Next Last

Biological process

Term	Mature form undetermined	hsa-miR-155-5p	hsa-miR-155-3p
gene silencing by miRNA, [E]			✓
miRNA mediated inhibition of translation, [E]	✓		✓
mRNA cleavage involved in gene silencing by miRNA, [E]	✓		
negative regulation of interferon-alpha production, [E]	✓		
negative regulation of interferon-beta production, [E]	✓		

Showing 1 to 5 of 42 entries First Previous 1 2 3 4 5 Next Last

Functional Attributes [what is this?](#)

Add a subscription to HumanPSD™ and this report will display detailed information about:

97 disease(s) and **329 biomarker annotation(s)** associated with MIR155

[Learn more...](#)

Orthologs & Molecular Hierarchy [what is this?](#)

Hierarchy of orthologous relationships for this locus

[+](#) View orthologous relationships

Detailed view of associated diseases



Expression [what is this?](#)

Tissue expression

high medium low

brain		breast	✓	colon		heart		intestine		kidney		liver		lung	
muscle		ovary		pancreas		placenta		spleen		stomach		testis		thymus	

[+](#) View organ or tissue, cell type, and tumor type entries in detail

Transcriptional Regulation [what is this?](#)

Regulation of MIR155 gene expression

Predicted promoter sequences : [Match →](#)

Best supported : [PM000829233](#)

All promoters for the gene : [PM000829233](#)



Viewing nucleotides -803 to -685

* Note: Only binding sites whose location is relative to the TSS are graphically displayed. Binding sites with an asterisk (*) are not included in the graphical display.

Transcription factor binding sites within the MIR155 gene (2 entries)

Show [5](#) entries Search:

Identifier	Relative Location	Genomic Location	Binding Factor(s)	DNA Binding Reaction	Effect
HS\$MIR155_02	-1108 to -1099		RelA-p65(h)	RelA-p65(h) --> MIR155(h)	DNA binding
HS\$MIR155_01	-716 to -692	Chr21 25573264 25573288 +	STAT3(h)	STAT3(h) --> MIR155(h)	DNA binding

Showing 1 to 2 of 2 entries [First](#) [Previous](#) [1](#) [Next](#) [Last](#)

Regions of the MIR155 gene with characterized functionality (1 entry)

[5](#) Search:

Identifier	Location	Name	Element
FE00690	-1108 to -1099	NFkappaB b.s.	promoter

Showing 1 to 1 of 1 entries [First](#) [Previous](#) [1](#) [Next](#) [Last](#)

RNA Features [what is this?](#)

Stem-loop hsa-mir-155

Synonyms : mir-155, MIR155, miR-155

CUGUAAUGCUAAUCGUGAUAGGGGUUUUUGCCUCCAACUGACUCCUACAUAUUAGCAUUAACAG

[FASTA ↓](#) [MI0000681 ↗](#)

Genomic coordinates : chr21 : 25573980-25574044 (+) [View in UCSC genome browser ↗](#)

Host gene : none

miR cluster : none

miR family : mir-155 [Find all family members →](#)

Mature miRNA hsa-miR-155-5p

Synonyms : miR-155-5p, hsa-miR-155-5p, hsa-miR-155

UAAUGCUAAUCGUGAUAGGGGUU

[FASTA ↓](#) [MIMAT0000646 ↗](#)

TargetScan seed family : miR-155-5p (UAAUGCU) [Find all family members →](#)

Species conservation, determined by TargetScan seed family membership :



Mouse : [mmu-miR-155-5p](#)

Rat : [rno-miR-155-5p](#)

Mature miRNA hsa-miR-155-3p

Synonyms : miR-155-3p, hsa-miR-155-3p, hsa-miR-155*

CUCCUACAUAUUAGCAUUAACA

[FASTA](#) ↓

[MIMAT0004658](#) ↗

TargetScan seed family : miR-155-3p (UCCUACA) [Find all family members](#) →

Species conservation, determined by TargetScan seed family membership :

Mouse : [mmu-miR-155-3p](#)

Rat : [rno-miR-155-3p](#)

mRNA Targets [what is this?](#)

mRNAs targeted by hsa-miR-155-5p (147 entries)

Show **5** entries Search:

mRNA	Region	Location within mRNA	Binding site details	Experimental details	Effect
AGTR1(h)	3' UTR	70 to 90, from stop codon	HS\$AGTR1_01	AL DM FA HC MR NO RT WE OT	increase of mRNA decay
AICDA(h)	3' UTR		HS\$AICDA_04	AL DM FA HC MR NO RT WE OT	translational repression
APC(h)	3' UTR		HS\$APC_07	AL DM FA HC MR NO RT WE OT	increase of mRNA decay
APC(h)			HS\$APC_12	AL DM FA HC MR NO RT WE OT	undefined
ARID2(h)	3' UTR		HS\$ARID2_01	AL DM FA HC MR NO RT WE OT	decrease of protein abundance

Showing 1 to 5 of 147 entries First Previous 1 2 3 4 5 Next Last

mRNAs targeted by hsa-miR-155-3p (4 entries)

Show **5** entries Search:

mRNA	Region	Location within mRNA	Binding site details	Experimental details	Effect
CREBRF(h)			HS\$CREBRF_01	AL DM FA MR NO RT WE OT	undefined
FBXW7(h)			HS\$FBXW7_22	AL DM FA MR NO RT WE OT	undefined
PTEN(h)			HS\$PTEN_127	AL DM FA MR NO RT WE OT	undefined
SIRT1(h)			HS\$SIRT1_44	AL DM FA MR NO RT WE OT	undefined

Showing 1 to 4 of 4 entries Previous 1 Next Last

Pathways & Interactions [what is this?](#)

Pathways from WikiPathways (6 entries)

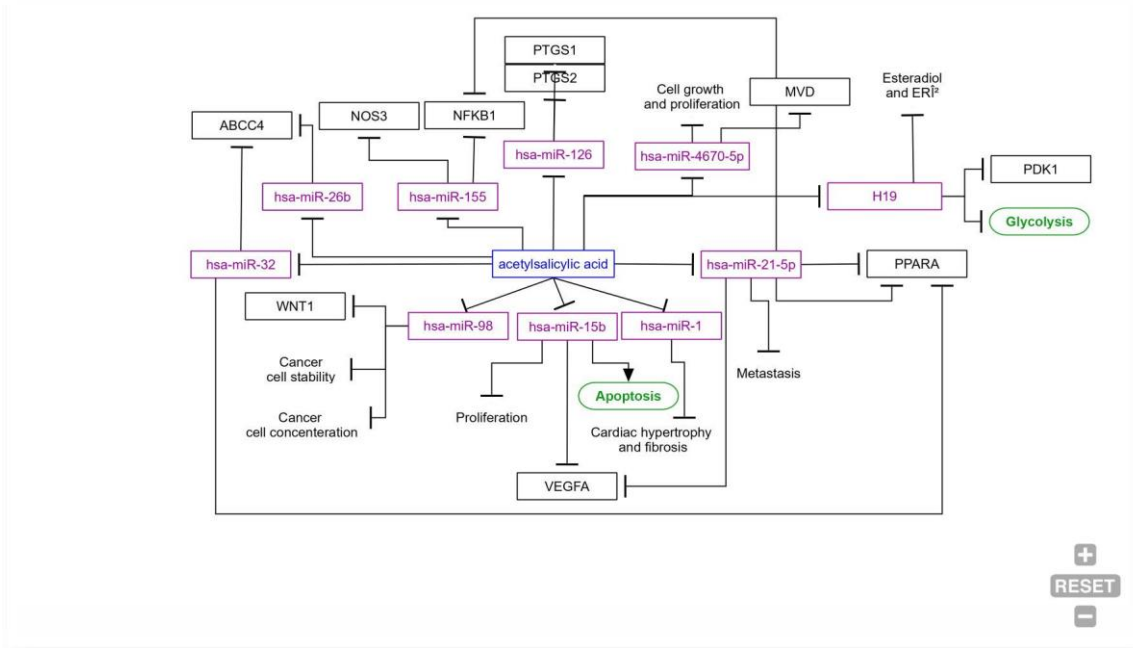
Provided by the [WikiPathways](#) database.

Show **5** entries Search:

Name	Display below	WikiPathways external link
aspirin and miRNAs	View ↗	WikiPathways ↗
Cell Differentiation - Index	View ↗	WikiPathways ↗
Hepatitis C and Hepatocellular Carcinoma	View ↗	WikiPathways ↗
Interactions between immune cells and microRNAs in tumor microenvironment	View ↗	WikiPathways ↗
miRNAs involvement in the immune response in sepsis	View ↗	WikiPathways ↗

Showing 1 to 5 of 6 entries First Previous 1 2 Next Last





Annotations [what is this?](#)

[Display all annotations](#)

Description

- Hsa-miR-155-3p, a mature miRNA which targets [IRAKM](#) and positively regulates plasmacytoid dendritic cell activation in response to [TLR7 / JNK](#) signaling through coordinated, opposing regulation of interferon alpha ([IFNA](#)) with co-expressed hsa-miR-155-5p [20852130](#)
- Hsa-miR-155-5p, a mature miRNA which negatively regulates plasmacytoid dendritic cell activation through coordinated, opposing regulation of interferon alpha ([IFNA](#)) with co-expressed hsa-miR-155-3p, expression is altered in breast and other cancers [21355095](#) [21690378](#)
- [MIR155](#) , located within the non-coding [BIC](#) transcript, is processed into mature forms hsa-miR-155-5p and -3p which exhibit coordinated, opposing regulation of [IFNA](#) , is involved in migration, adhesion, and proliferation, is downregulated in many diseases [21355095](#) [21385848](#)

Function

- Overexpression decrease the *H. pylori* inflammation by downregulating the [MyD88](#) protein [20219467](#)

Identifiers [what is this?](#)

Accessions mapped to this record

BIOBASE gene accession : GN000229388, G057294

BIOBASE RNA accession : RI000007079, RI000000950, RI000000949

Gene

Affymetrix	16921827, 229437_at, 3916514, 3916515, 3916516, 3916517, 57761_at, 8068022, 89695_at, Hs.89104.0.A1_3p_at,
Ensembl	ENSG00000283904
EntrezGene	406947
Illumina	0101990300, ILMN_3248910
OMIM	609337
RefSeq	NR_030784.1
WikiPathways	WP1449 WP2029 WP3646 WP4329 WP4559 WP4707

mRNA

Agilent	A_25_P00012270
---------	----------------



Exiqon 10964, 42949
TaqMan 000479, 002287, 002623
miRBase MI0000681 , MIMAT0000646 , MIMAT0004658

References (296 entries)

Show 5 entries Search:

Sl.No	PMID	Citation
1	31775754	Moldovan, LI, Hansen, TB, Ven?, MT, Okholm, TLH, Andersen, TL, Hager, H, Iversen, L, Kjems, J, Johansen, C, Kristensen, LS, High-throughput RNA sequencing from paired lesional- and non-lesional skin reveals major alterations in the psoriasis circRNAome. <i>BMC medical genomics</i> 12 (1) 174-174 (2019) Show abstract
2	31773868	Palmieri, O, Mazza, T, Bassotti, G, Merla, A, Tolone, S, Biagini, T, Cuttitta, A, Bossa, F, Martino, G, Latiano, T, Corritore, G, Gioffreda, D, Palumbo, O, Carella, M, Panza, A, Andriulli, A, Latiano, A, microRNA-mRNA network model in patients with achalasia. <i>Neurogastroenterol Motil</i> e13764-e13764 (2019) Show abstract
3	29327732	Ricciardiello, F, Capasso, R, Kawasaki, H, Abate, T, Oliva, F, Lombardi, A, Misso, G, Ingrosso, D, Leone, CA, Iengo, M, Caraglia, M, A miRNA signature suggestive of nodal metastases from laryngeal carcinoma. <i>Acta Otorhinolaryngol Ital</i> 37 (6) 467-474 (2017) Show abstract
4	28850112	Bam, M, Yang, X, Zumbrun, EE, Ginsberg, JP, Leyden, Q, Zhang, J, Nagarkatti, PS, Nagarkatti, M, Decreased AGO2 and DCR1 in PBMCs from War Veterans with PTSD leads to diminished miRNA resulting in elevated inflammation. <i>Transl Psychiatry</i> 7 (8) e1222-e1222 (2017) Show abstract
5	28339495	Chen, JQ, Papp, G, Poliska, S, Szabo, K, Tarr, T, Balint, BL, Szodoray, P, Zeher, M, MicroRNA expression profiles identify disease-specific alterations in systemic lupus erythematosus and primary Sjogren's syndrome. <i>PLoS ONE</i> 12 (3) e0174585-e017458 (2017) Show abstract

Showing 1 to 5 of 296 entries
[First](#) [Previous](#) [1](#) [2](#) [3](#) [4](#) [5](#) [Next](#) [Last](#)

Copyright QIAGEN
All rights reserved. Not for distribution.

