

## Analysis of miRNAs with ClueGO and CluePedia

# Upload miRNAs in CluePedia

The screenshot displays the CluePedia software interface. The main window, titled "Results for Analysis4", shows a network diagram with three nodes labeled "hsa-miR-200a-3p", "hsa-miR-200c-3p", and "hsa-miR-200b-3p". The left sidebar contains the "Control Panel" with the following sections:

- Analysis Start Mode:** Radio buttons for "ClueGO: Function" and "CluePedia: Gene/miRNA" (selected).
- Load Gene Cluster List(s):** A list box containing "hsa-miR-200a", "hsa-miR-200b", and "hsa-miR-200c". A red arrow points to the list box, and another red arrow points to the "+" button below it.
- Add Genes/miRNAs:** An empty text input field and a "Start" button.
- Remaining Free Cytoscape Memory:** A progress bar showing 99%.

The bottom section of the interface is the "Table Panel", which includes:

- Buttons for "CluePedia Results (Cluster #1)", "ClueGO Log", and "CluePedia".
- A "Gene/Interaction Enrichment Options" panel with a list of "Edge Link Files". The file "CluePedia\_STRING-ACTIONS\_v9\_9606\_09.03.2012.txt.gz" is selected with a checkmark.
- Two empty panels for "Undirected Edges" and "Directed Edges".
- A list of interaction types: "activation", "binding", "expression" (checked), and "ptmod". Each has a corresponding score field set to "0.0000".
- Buttons for "Enrich", "Add", "Remove", and "Update".

At the bottom of the interface, there are tabs for "Node Table", "Edge Table", "Network Table", and "ClueGO+CluePedia".

miRNA format should be e.g. : "hsa-miR-200a"

# Enrich miRNAs with target genes

File Edit View Select Layout Apps Tools Help

Control Panel

Network Style Select ClueGO+CluePedia

ClueGO v2.1.5 + CluePedia v1.1.5

Analysis Start Mode

ClueGO: Function  CluePedia: Gene/miRNA

Load Gene Cluster List(s)

Homo Sapiens # Automatic #

File Network

hsa-miR-200a  
hsa-miR-200b  
hsa-miR-200c

Ellipse Cluster #1

Add Genes/miRNAs

Start

Remaining Free Cytoscape Memory

97%

Results for Analysis4

CTNND2 HGF  
TCEB1 CRKL  
TTLL7 hsa-miR-200c-3p  
hsa-miR-200b-3p  
hsa-miR-200a-3p TMEFF2  
MAGED4 RNF145 CITED2  
BPY2

Table Panel

Results for Analysis4

CluePedia Results (Cluster #1) ClueGO Log CluePedia

Gene/Interaction Enrichment Options

Edge Link Files

- CluePedia\_microRNA.org-human\_predictions\_S\_C\_aug2010.txt.gz
- Cytokine-cytokine receptor interaction\_TCGA\_eachEnr10mir5\_10.12.2013.txt.gz
- GSE29623-genes-mir\_MATRIX\_mirForm\_leucocyteChemotaxis\_19.09.2014.txt.gz
- GeneMRCancer\_leukocyte chemotaxis\_mir200fam\_selNodes\_19.09.2014.txt.gz
- HeadData\_BadResponders\_TTest\_min3bigger3\_entirefile\_08.07.2014\_BadResponders-ba
- Head\_Adherens junction vs whole input file\_31.01.2014.txt.gz
- Head\_EM\_T5genes vs whole input file\_31.01.2014.txt.gz
- Head\_EM\_TgeneList vs whole input file\_31.01.2014.txt.gz
- Head\_IL8Test\_Chemokine receptors bind chemokines vs whole input file\_31.01.2014.txt.g

Undirected Edges

<input type="checkbox"/> align_score/100_human_predictions_S_C_au...	0.6000
<input type="checkbox"/> conservation_human_predictions_S_C_aug2...	0.6000
<input checked="" type="checkbox"/> mirsvr_score*(-1)_human_predictions_S_C_...	0.1000

Directed Edges

Enrich Add Remove Update

Node Table Edge Table Network Table ClueGO+CluePedia

# Upload miRNAs in CluePedia

The screenshot displays the CluePedia software interface. The main window, titled "Results for Analysis4", shows a network diagram with three nodes labeled "hsa-miR-200a-3p", "hsa-miR-200c-3p", and "hsa-miR-200b-3p". The left sidebar contains the "Control Panel" with the following sections:

- Analysis Start Mode:** Radio buttons for "ClueGO: Function" and "CluePedia: Gene/miRNA" (selected).
- Load Gene Cluster List(s):** A dropdown menu set to "Homo Sapiens" and a list of miRNAs: "hsa-miR-200a", "hsa-miR-200b", and "hsa-miR-200c". A red arrow points to the list, and another red arrow points to a plus sign icon below it.
- Add Genes/miRNAs:** An empty text input field and a "Start" button.
- Remaining Free Cytoscape Memory:** A progress bar showing 99%.

The bottom section of the interface is the "Table Panel", which includes:

- Buttons for "CluePedia Results (Cluster #1)", "ClueGO Log", and "CluePedia".
- A "Gene/Interaction Enrichment Options" panel with a list of "Edge Link Files". The file "CluePedia\_STRING-ACTIONS\_v9\_9606\_09.03.2012.txt.gz" is selected with a checkmark.
- Options for "Undirected Edges" and "Directed Edges" with various icons.
- A table for interaction types: "activation" (0.0000), "binding" (0.0000), "expression" (checked, 0.0000), and "ptmod" (0.0000).
- Buttons for "Enrich", "Add", "Remove", and "Update".

At the bottom of the interface, there are tabs for "Node Table", "Edge Table", "Network Table", and "ClueGO+CluePedia".

miRNA format should be e.g. : "hsa-miR-200a"

# ClueGO functional analysis of target genes

File Edit View Select Layout Apps Tools Help

Control Panel

Network Style Select ClueGO+CluePedia

ClueGO v2.1.5 + CluePedia v1.1.5

**Analysis Start Mode**

ClueGO: Function  CluePedia: Gene/miRNA

**Gene Cluster List(s)**

Homo Sapiens # Automatic #

UNIQUE\_ID Load Attribu...

MIMAT0000617  
MIMAT0000682

File Network

Ellipse Cluster #1

**View Style Settings**

Groups  Significance

**ClueGO Settings**

Ontologies/Pathways Evidence

...	Name	Date	Shape	Code
<input checked="" type="checkbox"/>	GO Biologic...	29.06.2...	E...	<input checked="" type="checkbox"/> All
<input checked="" type="checkbox"/>	GO Cellular...	01.02.2...	E...	<input type="checkbox"/> All Ex...
<input checked="" type="checkbox"/>	GO Cellular...	02.09.2...	E...	<input type="checkbox"/> All wit...
<input type="checkbox"/>	GO Cellular...	11.11.2...	E...	<input type="checkbox"/> EXP (I...

Update Ontologies  
 Download New Organisms or Data

Network Specificity

Global Medium Detailed

Use GO Term Fusion

Show only Pathways with pV ≤ 0.05000

Advanced Term/Pathway Selection Options

GO Tree Interval

3 Min Level 8 Max Level

GO Term/Pathway Selection (#% Genes)

Cluster #1: 2 Min #Genes: 1 %Genes

GO Term/Pathway Network Connectivity (Kappa Score)

Low Medium High Score: 0.4

Statistical Options  
 Grouping Options  
 CluePedia Options

CluePedia: Show all genes (genes per term) Threshold

**Results for Analysis7 (Kappa:0.4)**

regulation of DNA-templated transcription in response to stress  
cellular response to decreased oxygen levels  
cellular response to hypoxia  
regulation of transcription from RNA polymerase II promoter in response to stress  
cellular response to oxygen levels

regulation of organ morphogenesis  
liver development  
mesenchymal cell differentiation  
mesenchymal cell development  
hepaticobiliary system development

**mesenchyme development**

endocrine system development  
**thymus development**

**regulation of transcription from RNA polymerase II promoter in response to hypoxia**

Table Panel

Results for Analysis4 Results for Analysis5 Results for Analysis7

ClueGO Results (Cluster #1) Cluster #1 ClueGO Log CluePedia

Gene/Interaction Enrichment Options

Edge Link Files

Undirected Edges: + -

Directed Edges: → ← ⇄ ⇆

Enrich Add Remove Update

CluePedia\_STRING-COOCURENCE-SCORE\_v9\_9606\_09.03.2012.txt.gz  
CluePedia\_STRING-DATABASE-SCORE\_v9\_9606\_09.03.2012.txt.gz  
CluePedia\_STRING-EXPERIMENTAL-SCORE\_v9\_9606\_09.03.2012.txt.gz  
CluePedia\_STRING-FUSION-SCORE\_v9\_9606\_09.03.2012.txt.gz  
CluePedia\_STRING-NEIGHBORHOOD-SCORE\_v9\_9606\_09.03.2012.txt.gz  
CluePedia\_STRING-TEXTMINING-SCORE\_v9\_9606\_09.03.2012.txt.gz  
CluePedia\_microRNA.org-human\_predictions\_0\_0\_aug2010.txt.gz  
CluePedia\_microRNA.org-human\_predictions\_0\_C\_aug2010.txt.gz  
CluePedia\_microRNA.org-human\_predictions\_S\_0\_aug2010.txt.gz

Node Table Edge Table Network Table ClueGO+CluePedia

In "CluePedia Options" Select 0 to see just the genes from the initial list or 1000 to see all genes from the terms  
To add the mirnas & not found genes (under current selection parameters) in the network select: "Include not found markers"

# ClueGO CluePedia network with pathways, genes and miRNAs

File Edit View Select Layout Apps Tools Help

Control Panel

Network Style Select ClueGO+CluePedia

Analysis Start Mode

ClueGO: Function CluePedia: Gene/miRNA

Load Gene Cluster List(s)

Homo Sapiens # Automatic #

UNIQUE\_ID Load Attribute...

MIMAT0000617  
MIMAT0000682

File Network

Ellipse Cluster #1

View Style Settings

Groups Significance

ClueGO Settings

Ontologies/Pathways Evidence

...	Name	Date	Shape	Code
<input checked="" type="checkbox"/>	GO Biologic...	29.06.2...	E...	All
<input type="checkbox"/>	GO Cellular...	01.02.2...	E...	All_Ext...
<input type="checkbox"/>	GO Cellular...	02.09.2...	E...	All_wit...
<input type="checkbox"/>	GO Cellular...	11.11.2...	E...	EXP (I...

Update Ontologies  
 Download New Organisms or Data

Network Specificity

Global Medium Detailed

Use GO Term Fusion

Show only Pathways with pV ≤ 0.05000

Advanced Term/Pathway Selection Options

GO Tree Interval

3 Min Level 8 Max Level

GO Term/Pathway Selection (#/% Genes)

Cluster #1

2 Min #Genes 1 %Genes

GO Term/Pathway Network Connectivity (Kappa Score)

Low Medium High Score: 0.4

Statistical Options  
 Grouping Options  
 CluePedia Options

CluePedia 'Show all genes' (genes per term) Threshold

Number of Gene Visualization Threshold

Results for Analysis7 (Kappa:0.4)

regulation of transcription from RNA polymerase II promoter in response to hypoxia

mesenchyme development

thymus development

regulation of DNA-templated transcription in response to stress

cellular response to hypoxia

cellular response to decreased oxygen levels

cellular response to oxygen levels

mesenchymal cell differentiation

mesenchymal cell development

hepaticobiliary system development

liver development

regulation of organ morphogenesis

endocrine system development

CITED2

HGF

TCEB1

CRKL

CTNND2

hsa-miR-200b-3p

hsa-miR-200c-3p

hsa-miR-200a-3p

RNF145

TMEFF2

TTLL7

BPY2

MAGED4

Table Panel

Results for Analysis4 Results for Analysis5 Results for Analysis7

ClueGO Results (Cluster #1) Cluster #1 ClueGO Log CluePedia

Gene/Interaction Enrichment Options

Edge Link Files

- CluePedia\_microRNA.org-human\_predictions\_S\_CO\_aug2010.txt.gz
- CluePedia\_microRNA.org-human\_predictions\_S\_C\_aug2010.txt.gz
- Cytokine-cytokine receptor interaction\_TCGA\_eachEnr10mir5\_10.12.2013.txt.gz
- GSE29623-genes-mir\_MATRIX\_mirForm\_leucocyteChemotaxis\_19.09.2014.txt.gz
- GeneMIRCancer\_leukocyte chemotaxis\_mir200fam\_selNodes\_19.09.2014.txt.gz
- HeadData\_BadResponders\_TTest\_min3bigger3\_entirefile\_08.07.2014\_BadResponders-ba
- Head\_Adherens junction vs whole input file\_31.01.2014.txt.gz
- Head\_EMT\_5genes vs whole input file\_31.01.2014.txt.gz
- Head\_EMTgeneList vs whole input file\_31.01.2014.txt.gz

Undirected Edges

<input type="checkbox"/> align_score/100_human_predictions_S_C_au...	0.6000
<input type="checkbox"/> conservation_human_predictions_S_C_aug2...	0.6000
<input checked="" type="checkbox"/> mirsvr_score(-1)_human_predictions_S_C...	0.1000

Directed Edges

Enrich Add Remove Update

Node Table Edge Table Network Table ClueGO+CluePedia

# ClueGO CluePedia network with major pathways, genes and miRNAs

File Edit View Select Layout Apps Tools Help

Control Panel

Network Style Select ClueGO+CluePedia

ClueGO v2.1.5 + CluePedia v1.1.5

Analysis Start Mode  
 ClueGO: Function  CluePedia: Gene/miRNA

Load Gene Cluster List(s)  
 Homo Sapiens # Automatic #  
 UNIQUE\_ID Load Attrib...  
 MIMAT0000617  
 MIMAT0000682  
 File  Network  
 Ellipse Cluster #1

View Style Settings  
 Groups  Significance

ClueGO Settings

Ontologies/Pathways

Name	Date	Shape	Code
<input checked="" type="checkbox"/> GO Biologic...	29.06.2...	E...	<input checked="" type="checkbox"/> All
<input type="checkbox"/> GO Cellular...	01.02.2...	E...	<input type="checkbox"/> All_Ex...
<input type="checkbox"/> GO Cellular...	02.09.2...	E...	<input type="checkbox"/> All_wit...
<input type="checkbox"/> GO Cellular...	11.11.2...	E...	<input type="checkbox"/> EXP (I...

Evidence

Update Ontologies  
 Download New Organisms or Data

Network Specificity

Global  Use GO Term Fusion  Medium  Detailed

Show only Pathways with pV ≤ 0.05000

Advanced Term/Pathway Selection Options  
 GO Tree Interval  
 3 Min Level 8 Max Level

GO Term/Pathway Selection (#/% Genes)  
 Cluster #1  
 2 Min #Genes 1 %Genes

GO Term/Pathway Network Connectivity (Kappa Score)  
 Low Medium High Score: 0.4

Statistical Options  
 Grouping Options  
 CluePedia Options  
 CluePedia 'Show all genes' (genes per term) Threshold

Results for Analysis7 (Kappa:0.4)

regulation of transcription from RNA polymerase II promoter in response to hypoxia

mesenchyme development

thymus development

Table Panel

Results for Analysis4 Results for Analysis5 Results for Analysis7

ClueGO Results (Cluster #1) Cluster #1 ClueGO Log CluePedia

GOID	GO Term	Ontology Source	Term PValue	Term PValue Corr	Selection	GeneID	Symbol Name	Gene Aliases
<input type="checkbox"/> 71453	cellular response to oxygen levels	GO_BiologicalProces...	1.2 E-3	1.0 E-2	<input checked="" type="checkbox"/> Initial Cluster #1	10370	CITED2	[ASD8, MRG-1, MRG1, P...
<input type="checkbox"/> 36294	cellular response to decreased oxygen levels	GO_BiologicalProces...	1.1 E-3	9.9 E-3	<input checked="" type="checkbox"/> Initial Cluster #1	1399	CRKL	[ ]
<input type="checkbox"/> 71456	cellular response to hypoxia	GO_BiologicalProces...	1.0 E-3	1.0 E-2	<input checked="" type="checkbox"/> Initial	1501	CTNND2	[GT24, NPRAP]
<input type="checkbox"/> 43620	regulation of DNA-templated transcription in response to stress	GO_BiologicalProces...	2.2 E-4	2.4 E-3	<input checked="" type="checkbox"/> Initial	153830	RNF145	[DKFZp686M11215, FLJ...
<input type="checkbox"/> 43618	regulation of transcription from RNA polymerase II promoter in response to stress	GO_BiologicalProces...	1.7 E-4	2.1 E-3	<input checked="" type="checkbox"/> Initial	23671	TMEFF2	[CT120.2, HPP1, TENB2...
<input checked="" type="checkbox"/> 61418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	GO_BiologicalProces...	1.0 E-4	1.3 E-3	<input checked="" type="checkbox"/> Initial Cluster #1	3082	HGF	[DFNB39, F-TCF, HGFB,...
<input type="checkbox"/> 1889	liver development	GO_BiologicalProces...	1.3 E-3	9.2 E-3	<input checked="" type="checkbox"/> Initial Cluster #1	6921	TCEB1	[SIII, eloC]
<input type="checkbox"/> 61008	hepaticobiliary system development	GO_BiologicalProces...	1.3 E-3	8.2 E-3	<input checked="" type="checkbox"/> Initial	728239	MAGED4	[FLJ39060, KIAA1859, M...
<input checked="" type="checkbox"/> 60485	mesenchyme development	GO_BiologicalProces...	3.5 E-3	3.5 E-3	<input checked="" type="checkbox"/> Initial	79739	TTLL7	[FLJ23033, FLJ36855, RF...
<input type="checkbox"/> 200...	regulation of organ morphogenesis	GO_BiologicalProces...	2.8 E-3	5.7 E-3	<input checked="" type="checkbox"/> Initial	9083	BPY2	[BPY2A, VCY2, VCY2A]
<input type="checkbox"/> 48762	mesenchymal cell differentiation	GO_BiologicalProces...	2.6 E-3	7.8 E-3	<input checked="" type="checkbox"/> Initial	-1	hsa-miR-200...	[ ]
<input type="checkbox"/> 14031	mesenchymal cell development	GO_BiologicalProces...	2.1 E-3	8.7 E-3	<input checked="" type="checkbox"/> Initial	-1	hsa-miR-200...	[ ]
<input type="checkbox"/> 35270	endocrine system development	GO_BiologicalProces...	1.9 E-3	9.9 E-3	<input checked="" type="checkbox"/> Initial	-1	hsa-miR-200...	[ ]
<input checked="" type="checkbox"/> 48538	thymus development	GO_BiologicalProces...	1.7 E-4	2.1 E-3	<input checked="" type="checkbox"/> Initial			

Node Table Edge Table Network Table ClueGO+CluePedia

# ClueGO CluePedia network with pathways, genes and miRNAs

## Similar analysis, with fusion

File Edit View Select Layout Apps Tools Help

The screenshot displays the ClueGO CluePedia software interface. The main window shows a network diagram with nodes and edges. The nodes are color-coded: green for biological processes and red for miRNAs. The network is centered around the term "regulation of transcription from RNA polymerase II promoter in response to hypoxia". Other terms include "mesenchymal cell development" and "liver development".

The interface includes several control panels:

- Control Panel:** Contains tabs for "Network", "Style", and "Select". The "ClueGO+CluePedia" tab is active.
- Analysis Start Mode:** Includes radio buttons for "ClueGO: Function" (selected) and "CluePedia: Gene/miRNA".
- Load Gene Cluster List(s):** Features a dropdown for "Homo Sapiens", a "# Automatic #" field, and a "UNIQUE\_ID" dropdown. It also has "Load Attribu..." and "Load" buttons.
- View Style Settings:** Includes checkboxes for "Groups" and "Significance".
- ClueGO Settings:** Contains a table for "Ontologies/Pathways" and "Evidence".
 

...	Name	Date	Shape	Evidence
<input checked="" type="checkbox"/>	GO Biologic...	22.01.2...	E...	<input checked="" type="checkbox"/> All
<input type="checkbox"/>	GO Biologic...	23.05.2...	E...	<input type="checkbox"/> All_E...
<input type="checkbox"/>	GO Biologic...	24.02.2...	E...	<input type="checkbox"/> All_wit...
<input checked="" type="checkbox"/>	GO Biologic...	29.06.2...	E...	<input type="checkbox"/> EXP (L...
- Table Panel:** Shows "Results for Analysis4" and "Results for Analysis5". It includes tabs for "ClueGO Results (Cluster #1)", "Cluster #1", "ClueGO Log", and "CluePedia".
- Gene/Interaction Enrichment Options:** Includes a list of "Edge Link Files" and "Undirected Edges".
 

Edge Link File	Score
align_score/100_human_predictions_S_C_au...	0.6000
conservation_human_predictions_S_C_aug2...	0.6000
<input checked="" type="checkbox"/> mirsvr_score*(-1)_human_predictions_S_C_...	0.1000
Cytokine-cytokine receptor interaction_TCGA_eachEnr10mir5_10.12.2013.txt.gz	