

COXPRESdb: Home

COXPRESdb
version 3.3

Quick Search

☐ symbol search (e.g. DHCR)
☐ case sensitive

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Recent update

[2009.07.25] The search box next to the title logo has been renewed.
[2009.07.25] CoexViewer was renewed. [Tool > CoexViewer]
[2009.06.1] Technology terms was made available.
[2009.05.20] A tool to obtain tissue-specific expression data for human was made available. [Tool > TissueDataExtractor] [more]

data.

- To prevent confusions between the two types of versions, we added extra "c" for coexpression version.

COXPRESdb

gene coexpression database for human, mouse and rat

Takeshi Obayashi (Tokyo Univ.)

2009 / 7 / 29 Tutorial in IUPS36:

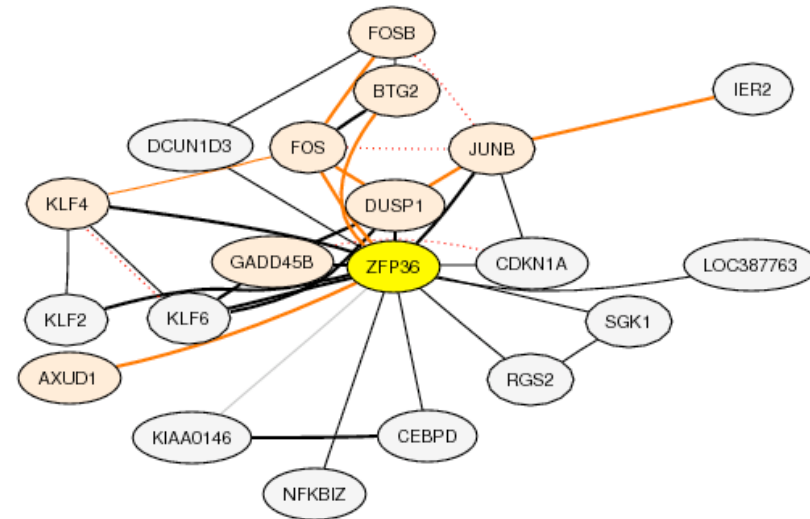
“Bioinformatics for physiology”

Contents of COXPRESdb

- Gene list

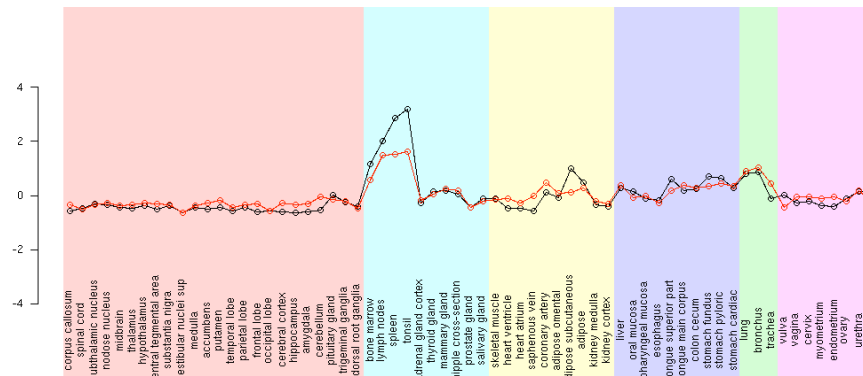
		MR*	COR*	symbol	function	coexpression detail	Entrez Gene ID
0	☒			ZFP36	zinc finger protein 36, C3H type, homolog (mouse)		7538
1	☐	1.0	0.77	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	[detail]	2353
2	☐	1.4	0.76	JUNB	jun B proto-oncogene	[detail]	3726
3	☐	1.7	0.76	DUSP1	dual specificity phosphatase 1	[detail]	1843
4	☐	3.2	0.62	KLF6	Kruppel-like factor 6	[detail]	1316
5	☐	3.3	0.61	GADD45B	growth arrest and DNA-damage-inducible, beta	[detail]	4616
6	☐	3.5	0.73	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	[detail]	2354
7	☐	3.7	0.60	PBEF1	pre-B-cell colony enhancing factor 1	[detail]	10135
8	☐	3.7	0.66	AXUD1	AXIN1 up-regulated 1	[detail]	64651
9	☐	3.9	0.59	KLF2	Kruppel-like factor 2 (lung)	[detail]	10365
10	☐	3.9	0.68	NR4A1	nuclear receptor subfamily 4, group A, member 1	[detail]	3164
11	☐	4.0	0.65	ATF3	activating transcription factor 3	[detail]	467
12	☐	4.0	0.59	BTG2	BTG family, member 2	[detail]	7832
				KLF4	Kruppel-like factor 4		

- Gene network



Contents of COXPRESdb

★ Gene expression pattern



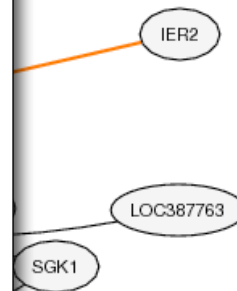
★ Predicted protein subcellular localization

subcellular localization ★	nucl 8, cyto_nucl 5	(prediction for NP_001071168.1)
	nucl 6, cyto_nucl 5, cyto 2	(prediction for NP_001071169.1)
	extr 6	(prediction for NP_001071170.1)
	nucl 8, cyto_nucl 5	(prediction for NP_001071171.1)
	nucl 6, cyto_nucl 4, cyto 2	(prediction for NP_001071172.1)
	extr 4, E.R. 2, E.R._golgi 2	(prediction for NP_065999.1)

★ Publicly available annotations

KEGG, Gene Ontology, PPI data

0	☒	
1	☐	
2	☐	
3	☐	
4	☐	
5	☐	
6	☐	
7	☐	
8	☐	
9	☐	
10	☐	
11	☐	
12	☐	

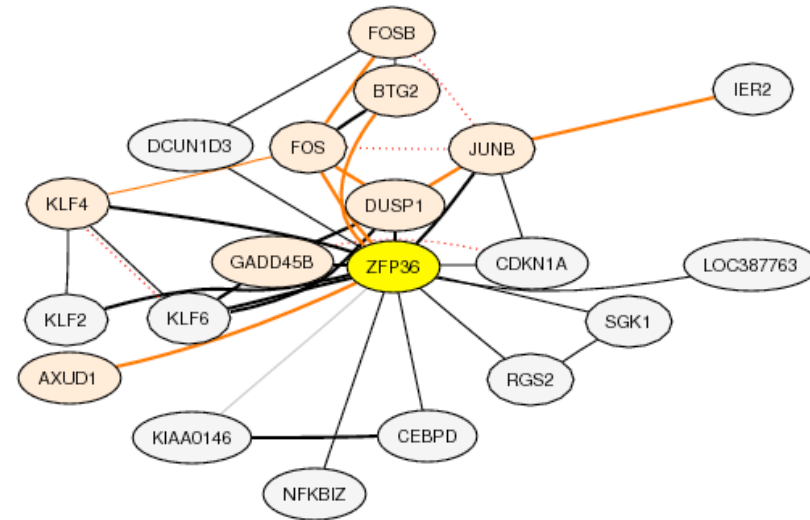


Contents of COXPRESdb

- Gene list

		MR*	COR*	symbol	function	coexpression detail	Entrez Gene ID
0	☒			ZFP36	zinc finger protein 36, C3H type, homolog (mouse)		7538
1	☐	1.0	0.77	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	[detail]	2353
2	☐	1.4	0.76	JUNB	jun B proto-oncogene	[detail]	3726
3	☐	1.7	0.76	DUSP1	dual specificity phosphatase 1	[detail]	1843
4	☐	3.2	0.62	KLF6	Kruppel-like factor 6	[detail]	1316
5	☐	3.3	0.61	GADD45B	growth arrest and DNA-damage-inducible, beta	[detail]	4616
6	☐	3.5	0.73	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	[detail]	2354
7	☐	3.7	0.60	PBEF1	pre-B-cell colony enhancing factor 1	[detail]	10135
8	☐	3.7	0.66	AXUD1	AXIN1 up-regulated 1	[detail]	64651
9	☐	3.9	0.59	KLF2	Kruppel-like factor 2 (lung)	[detail]	10365
10	☐	3.9	0.68	NR4A1	nuclear receptor subfamily 4, group A, member 1	[detail]	3164
11	☐	4.0	0.65	ATF3	activating transcription factor 3	[detail]	467
12	☐	4.0	0.59	BTG2	BTG family, member 2	[detail]	7832
				KLF4	Kruppel-like factor 4		

- Gene network



- ☐ For a locus
- ☐ For a set of genes
- ☐ For huge network

http://coxpresdb.jp

COXPRESdb
version 3.3

COXPRESdb; co-expressed gene database

(last update) 2009.07.25

Quick Search

☐ symbol search (e.g. DHCR)
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Home:

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Gene Symbol	Keyword	Entrez Gene ID
• DHCR7	• cholesterol	• 526
• DHCR		

[2009.07.25] The search box next to the database name was renewed. [Tool > CoexViewer]
[2009.07.25] CoexViewer was renewed. [Tool > CoexViewer]
[2009.06.17] A tool to draw hierarchical structures of Gene Ontology terms was made available. [Tool > GOPathDrawer]
[2009.05.20] A tool to obtain tissue-specific expression data for human was made available. [Tool > TissueDataExtractor]
[more]

- Version numbering (2008.10.31)

COXPRESdb has two types of versions: version for COXPRESdb and version for coexpression

Keyword search result (DHCR)

Search result by DHCR

Your request is "DHCR". (6 hits)

- Human gene search (2 hit)
- Mouse gene search (2 hit)
- Rat gene search (2 hit)

Human gene search

2 loci are found.

Shaded loci do not have affy data.

Locus*	Symbol	Function *	Entrez Gene ID	coexpressed gene list
Hsa	DHCR7	7-dehydrocholesterol reductase	1717	[list]
Hsa	DHCR24	24-dehydrocholesterol reductase	1718	[list]

Mouse gene search

2 loci are found.

Shaded loci do not have affy data.

Locus*	Symbol	Function *	Entrez Gene ID	coexpressed gene list
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Coexpressed gene list (DHCR7)

co-expressed genes; DHCR7 (Hsa) -- COXPRESdb

Top 300 co-expressed genes to DHCR7 (Hsa)

search coexpressed genes from selected genes

		MR*	COR*	symbol	function	coexpression detail	Entrez Gene ID
0	☒			DHCR7	7-dehydrocholesterol reductase		1717
1	☐	2.5	0.55	SC4MOL	sterol-C4-methyl oxidase-like	[detail]	6307
2	☐	2.5	0.53	SQLE	squalene epoxidase	[detail]	6713
3	☐	3.9	0.51	FDFT1	farnesyl-diphosphate farnesyltransferase 1	[detail]	2222
4	☐	4.5	0.51	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	[detail]	1595
5	☐	4.7	0.48	DHCR24	24-dehydrocholesterol reductase	[detail]	1718
6	☐	5.3	0.49	INSIG1	insulin induced gene 1	[detail]	3638
7	☐	6.0	0.47	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	[detail]	6319
8	☐	6.3	0.51	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	[detail]	3157
9	☐	9.5	0.50	NSDHL	NAD(P) dependent steroid dehydrogenase-like	[detail]	50814
10	☐	9.5	0.43	SREBF2	sterol regulatory element binding transcription factor 2	[detail]	6721
11	☐	9.8	0.44	FASN	fatty acid synthase	[detail]	2194
12	☐	10.4	0.39	FADS1	fatty acid desaturase 1	[detail]	3992

Coexpressed gene list (DHCR7)

co-expressed genes; DHCR7 (Hsa) -- COXPRESdb

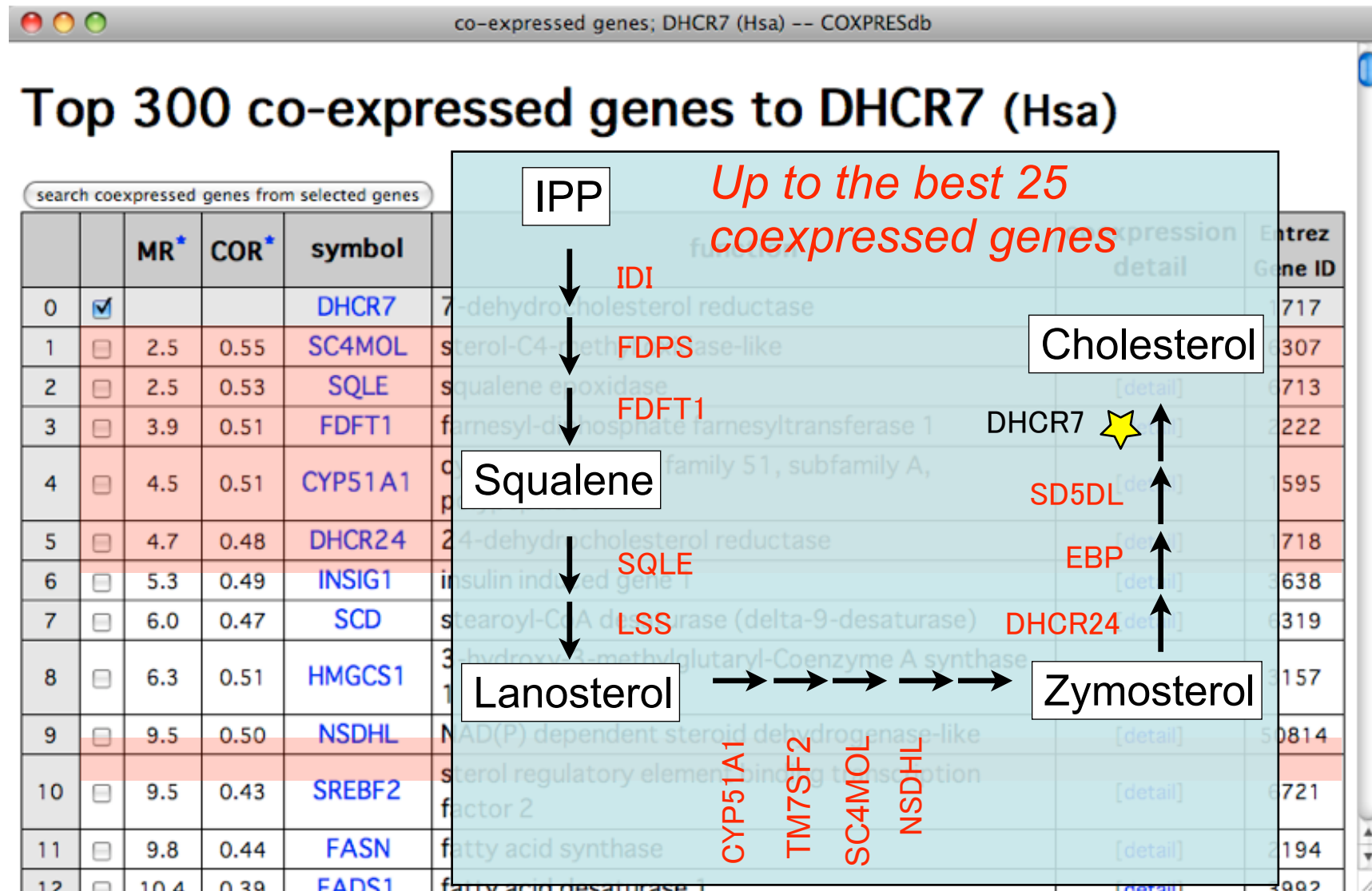
Top 300 co-expressed genes to DHCR7 (Hsa)

search coexpressed genes from selected genes

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0	☒			DHCR7	7-dehydrocholesterol reductase		6717
1	☐	2.5	0.55	SC4MOL	sterol-C4-methyl oxidase-like		6307
2	☐	2.5	0.53	SQLE	squalene epoxidase	[detail]	6713
3	☐	3.9	0.51	FDFT1	farnesyl-diphosphate farnesyltransferase 1		2222
4	☐	4.5	0.51	CYP51A1	cytochrome P-450 family 51, subfamily A, polypeptide 1	[detail]	595
5	☐	4.7	0.48	DHCR24	24-dehydrocholesterol reductase	[detail]	6718
6	☐	5.3	0.49	INSIG1	insulin induced gene 1	[detail]	3638
7	☐	6.0	0.47	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	[detail]	6319
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12	☐	10.4	0.39	FADS1	fatty acid desaturase 1	[detail]	3992

The diagram illustrates the cholesterol biosynthesis pathway. It starts with IPP (Isopentenyl pyrophosphate) at the top, which is converted to Squalene via a series of downward arrows. Squalene is then converted to Lanosterol, also indicated by a downward arrow. From Lanosterol, the pathway branches: one branch continues with downward arrows to Zymosterol, and another branch goes rightward with a series of arrows to Zymosterol. Finally, Zymosterol is converted to Cholesterol via a series of upward arrows. A yellow star highlights the DHCR7 gene in the table, which is associated with the conversion of 7-dehydrocholesterol to cholesterol.

Coexpressed gene list (DHCR7)



Coexpressed gene list (DHCR7)

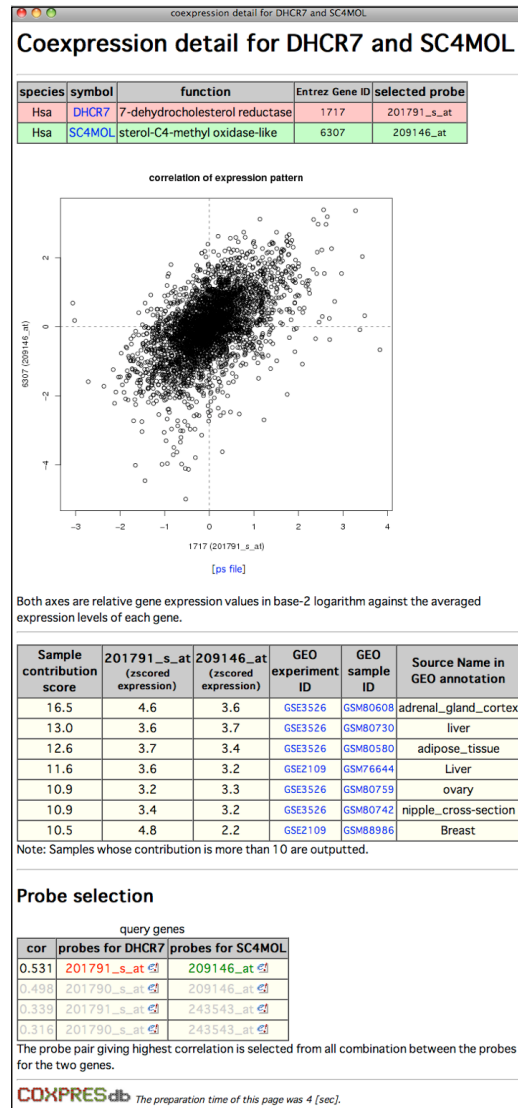
co-expressed genes; DHCR7 (Hsa) -- COXPRESdb

Top 300 co-expressed genes to DHCR7 (Hsa)

search coexpressed genes from selected genes

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Coexpression detail (DHCR7, SC4MOL)

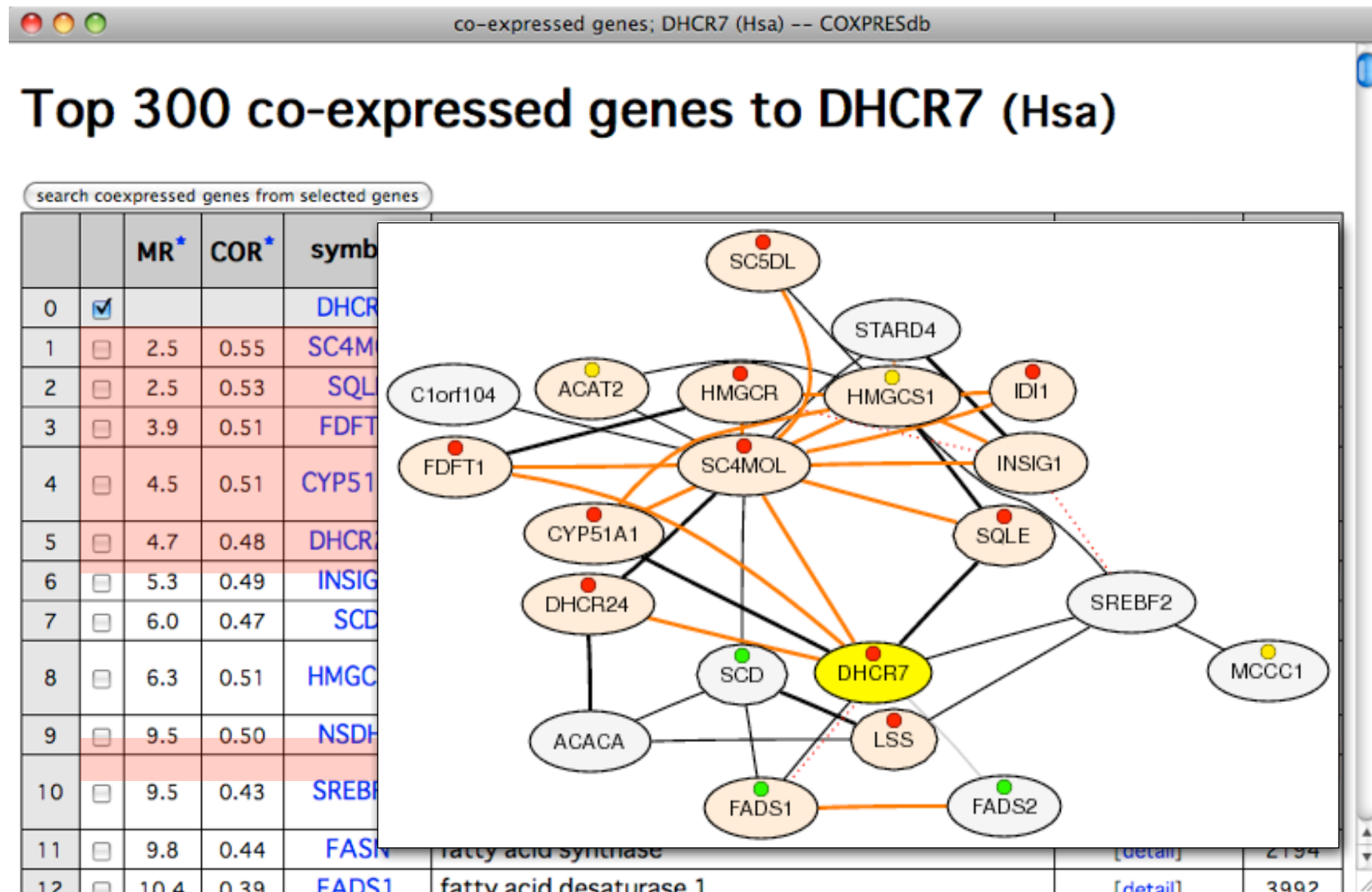


- Scatter plot of the selected two genes
- x-axis: relative expression of DHCR7
 - y-axis: relative expression of SC4MOL
 - plotted: microarray samples

Table of the most important samples.

Probe selection

Coexpressed gene list (DHCR7)

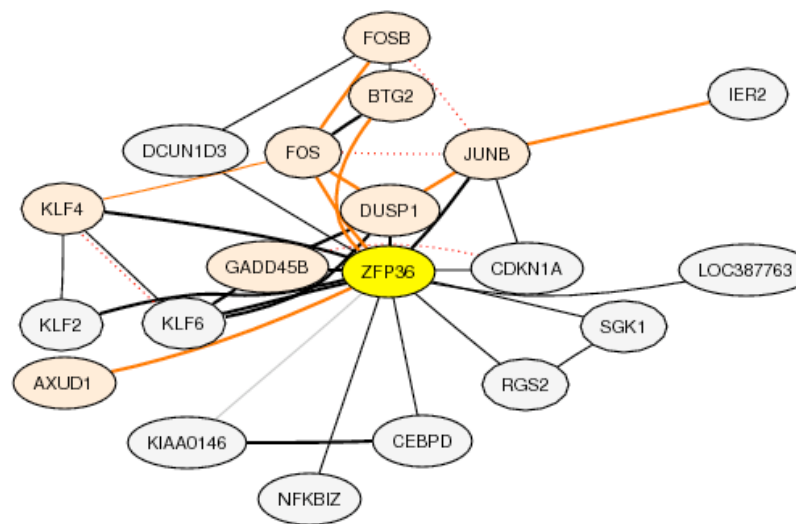


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7	☐	3.7	0.60	PBEF1	pre-B-cell colony enhancing factor 1	[detail]	10135
8	☐	3.7	0.66	AXUD1	AXIN1 up-regulated 1	[detail]	64651
9	☐	3.9	0.59	KLF2	Kruppel-like factor 2 (lung)	[detail]	10365
10	☐	3.9	0.68	NR4A1	nuclear receptor subfamily 4, group A, member 1	[detail]	3164
11	☐	4.0	0.65	ATF3	activating transcription factor 3	[detail]	467
12	☐	4.0	0.59	BTG2	BTG family, member 2	[detail]	7832
					Kruppel-like factor 4		

- Gene network



- ☐ For a locus
- ☐ For a set of genes
- ☐ For huge network

http://coxpresdb.jp

COXPRESdb
version 3.3

COXPRESdb; co-expressed gene database

(last update) 2009.07.25

Quick Search

☐ symbol search (e.g. DHCR)
☐ case sensitive

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- **Recent update**

Gene Symbol	Keyword	Entrez Gene ID
• CD3D	• CD3	• 915

[2009.07.25] The search box next to the fish logo has been renewed.
[2009.07.25] CoexViewer was renewed. [Tool > CoexViewer]
[2009.06.14] A tool to draw hierarchical structures of Gene Ontology terms was made available.
[Tool > GOPathDrawer]
[2009.05.20] A tool to obtain tissue-specific expression data for human was made available.
[Tool > TissueDataExtractor]
[more]
- **Version numbering** (2008.10.31)

COXPERSdb has two types of versions: version for COXPRESdb and version for coexpression

Keyword search result (CD3D)



Search result by CD3D

Your request is "CD3D". (3 hits)

- [Human gene search](#) (1 hit)
- [Mouse gene search](#) (1 hit)
- [Rat gene search](#) (1 hit)

Human gene search

One locus is found.

Shaded loci do not have affy data.

Locus*	Symbol	Function*	Entrez Gene ID	coexpressed gene list
Hsa	CD3D	CD3d molecule, delta (CD3-TCR complex)	915	[list]

Mouse gene search

One locus is found.

Gene page (CD3D)

Color of pages

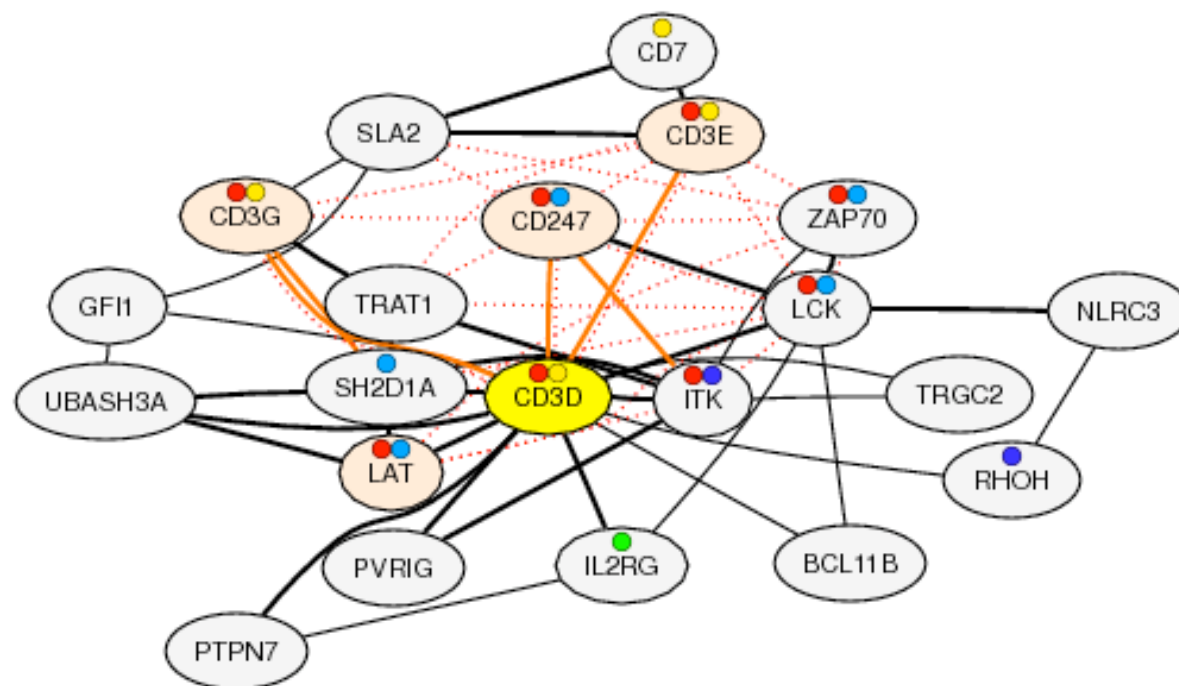
- Ref; Human
- Green; Mouse
- Purple; Rat

Public annotation

Coexpression

Expression

Gene page (CD3D)



KEGG ID	Title	#genes	Link to the KEGG map (multiple genes)
hsa04660	T cell receptor signaling pathway	8	
hsa04640	Hematopoietic cell lineage	4	
hsa04060	Cytokine-cytokine receptor interaction	1	
hsa04650	Natural killer cell mediated cytotoxicity	5	
hsa04670	Leukocyte transendothelial migration	2	

Construction of gene network

Network drawing rule:

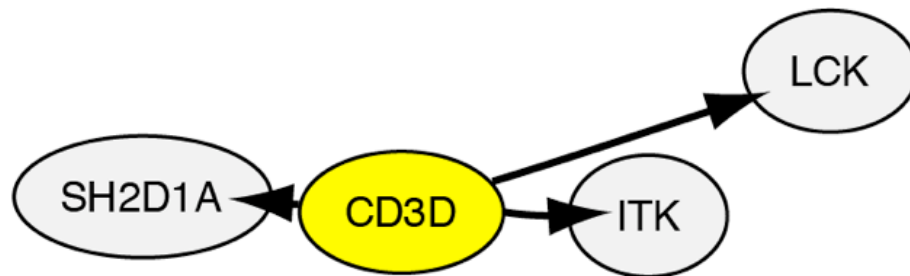
Connecting the best 3 coexpressed genes for each gene



Construction of gene network

Network drawing rule:

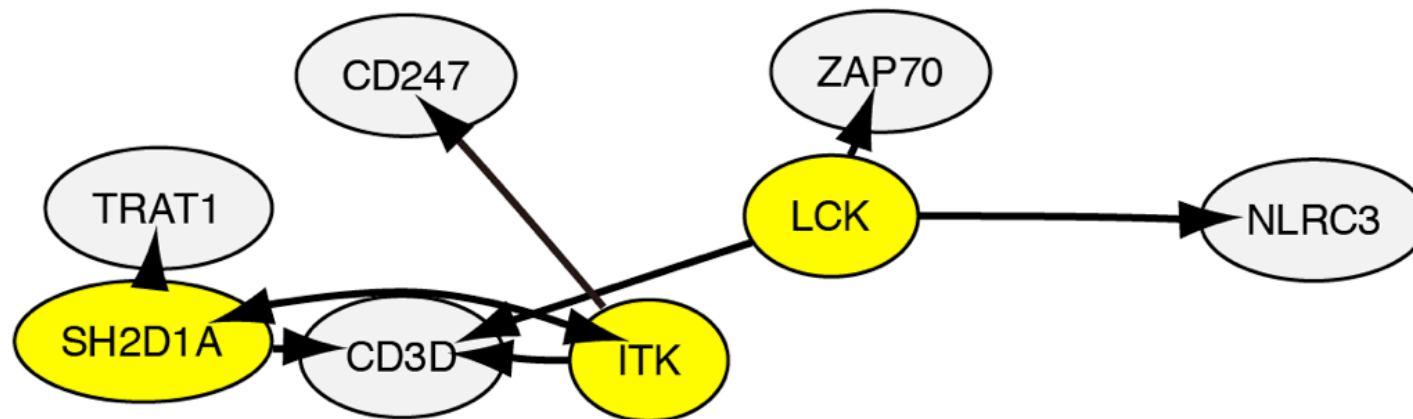
Connecting the best 3 coexpressed genes for each gene



Construction of gene network

Network drawing rule:

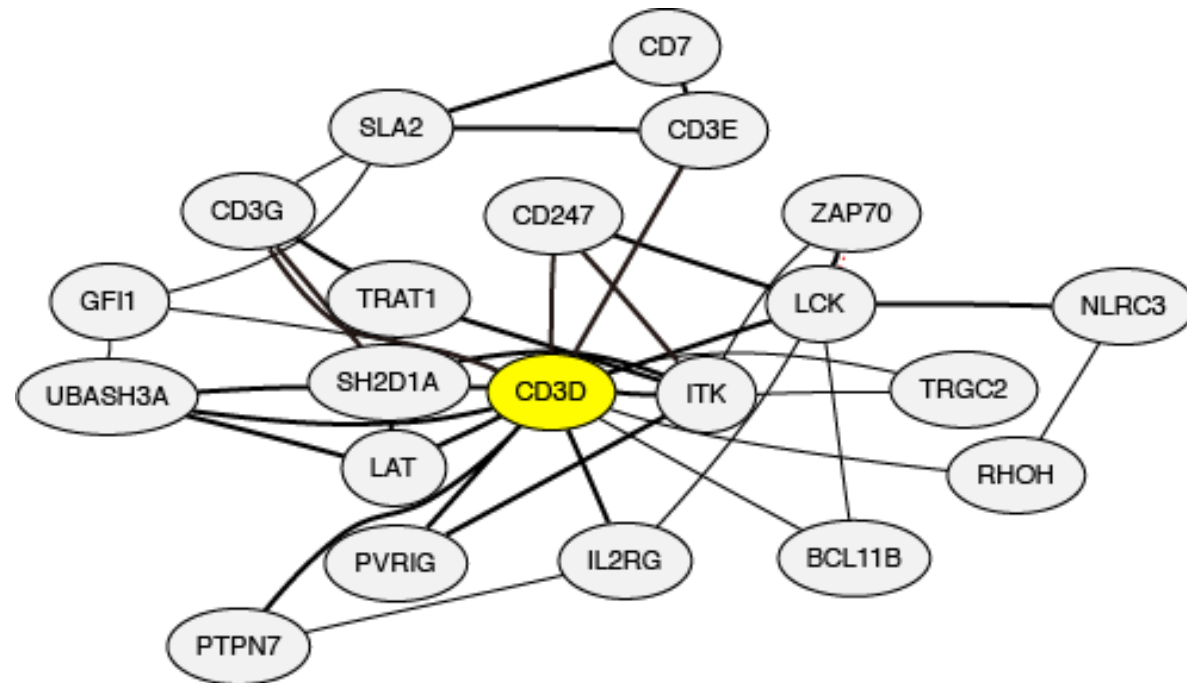
Connecting the best 3 coexpressed genes for each gene



Construction of gene network

Network drawing rule:

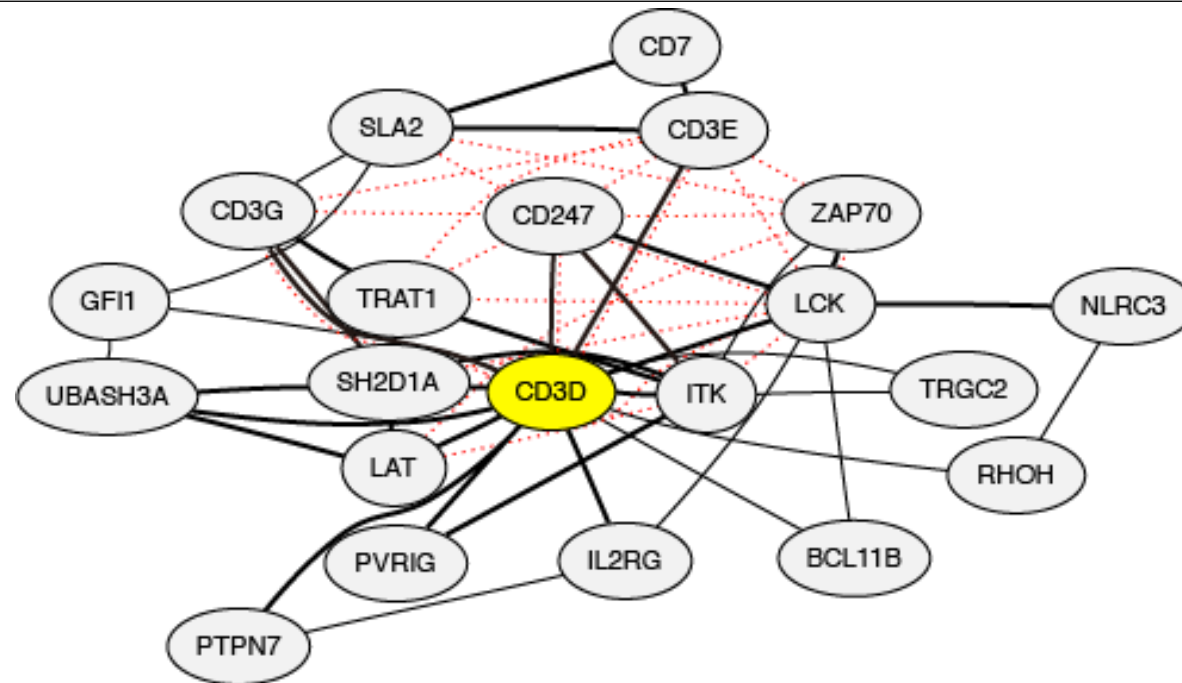
Connecting the best 3 coexpressed genes for each gene



Edge thickness: Strength of coexpression

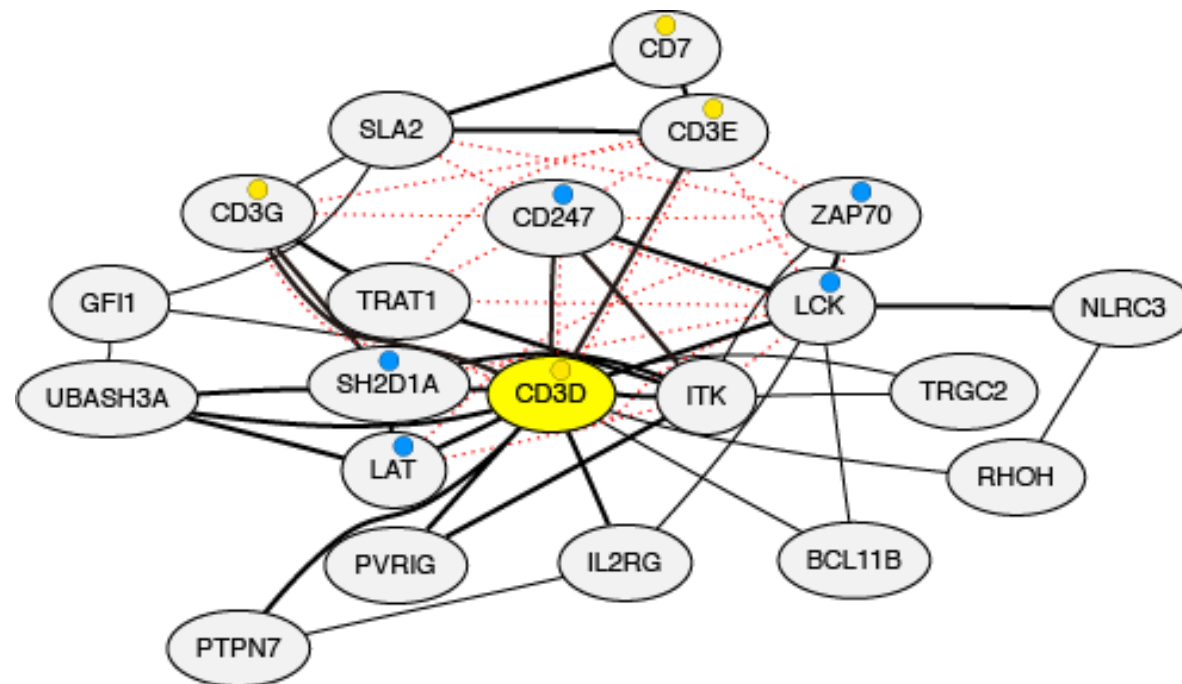
Additional information on network

Reported PPI is represented by red dotted line.



Additional information on network

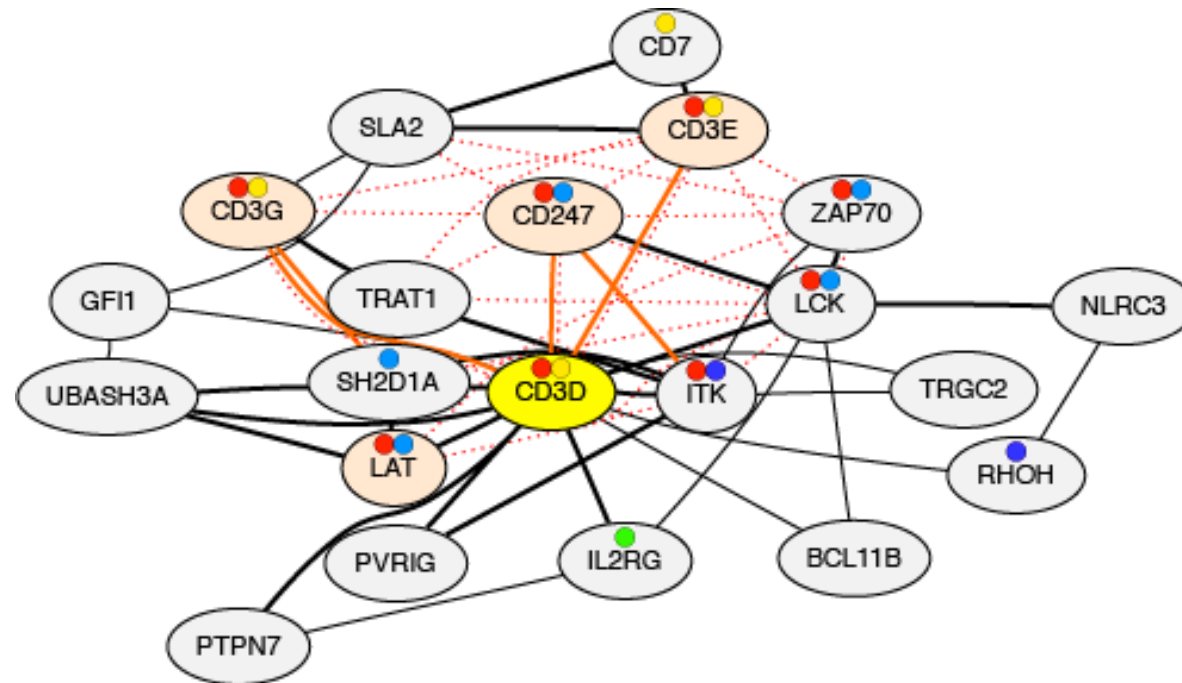
Marking up genes with same KEGG annotation



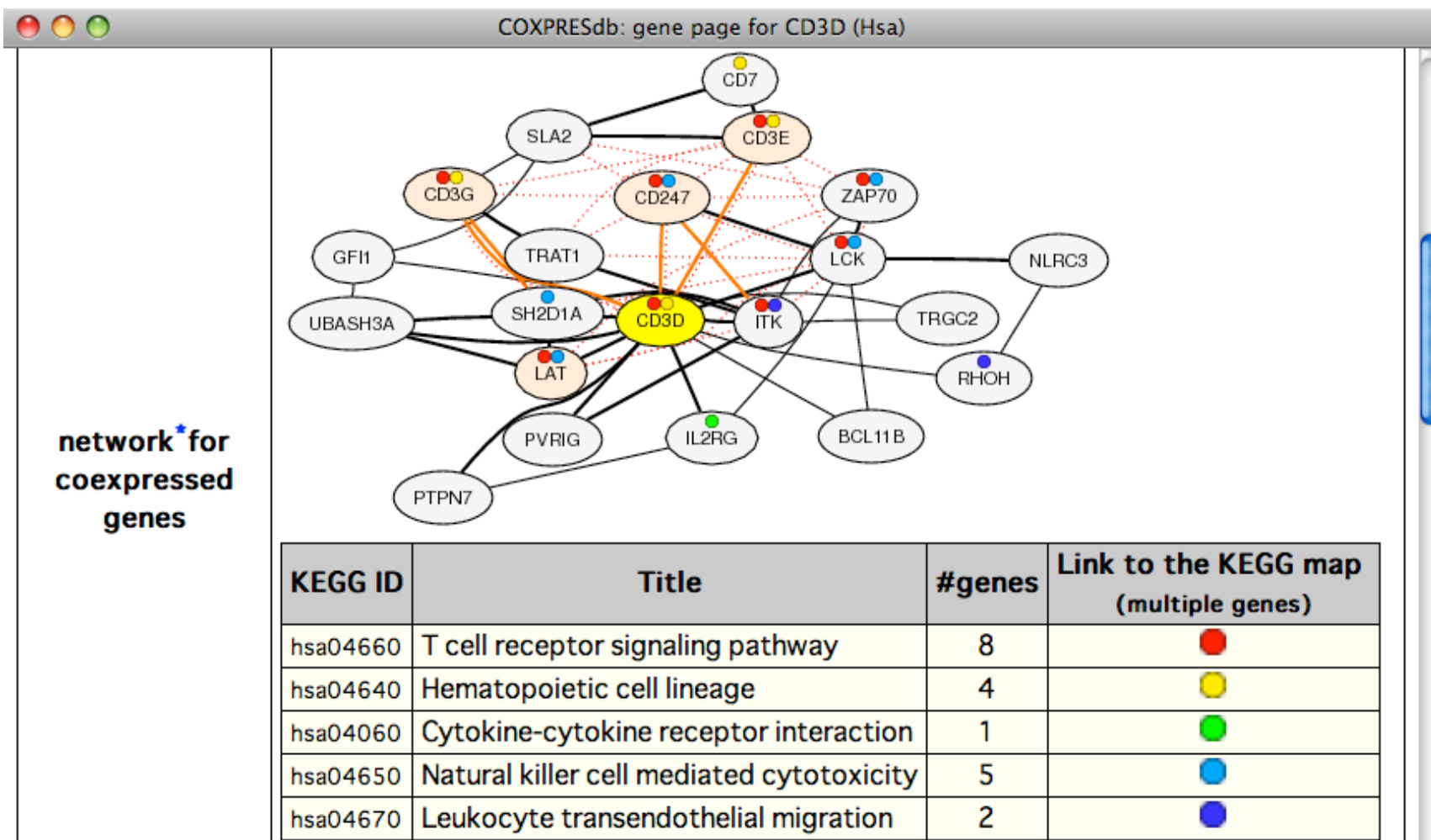
Up to 5 KEGG annotations are marked.

Additional information on network

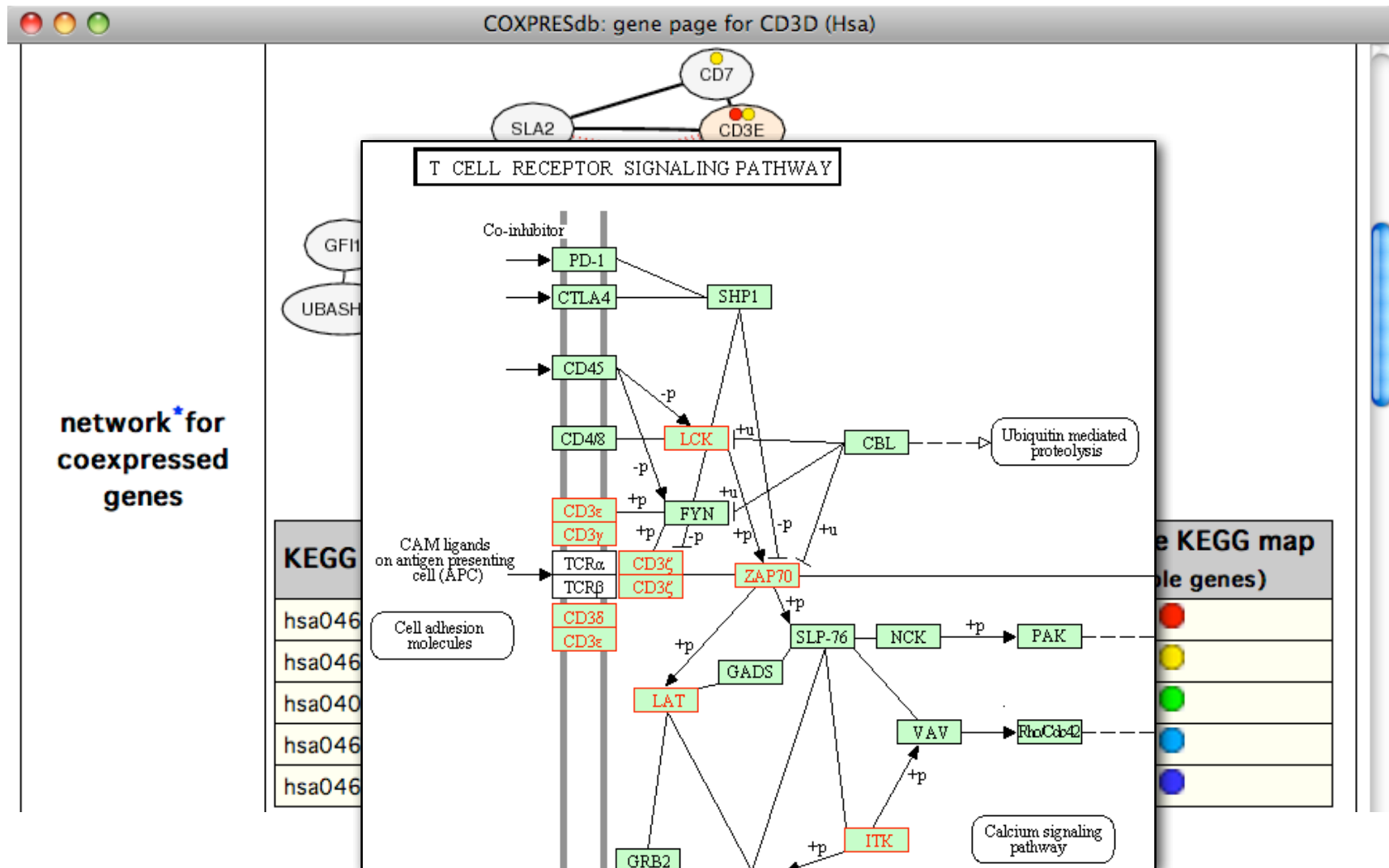
Conserved coexpression is represented as orange nodes and edges.



Gene page (CD3D)



Gene page (CD3D)



Gene page (CD3D)

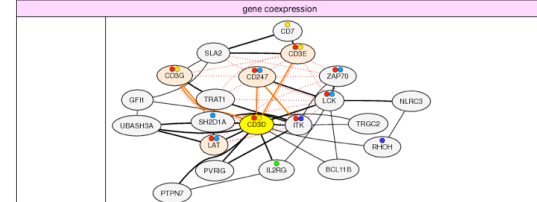
Color of pages

- Ref; Human
- Green; Mouse
- Purple; Rat

COXPRESdb: gene page for CD3D (Hsa)

Hsa CD3D Gene

function*	CD3d molecule, delta (CD3-TCR complex)
GO BP*	GO:0045059 [list] [network] positive thymic T cell selection (4 genes) ISS
GO CC*	GO:0042101 [list] [network] T cell receptor complex (12 genes) NAS GO:0005886 [list] [network] plasma membrane (3418 genes) EXP GO:0016021 [list] [network] integral to membrane (5266 genes) IEA GO:0005737 [list] [network] cytoplasm (7101 genes) NAS
GO MF*	GO:0046982 [list] [network] protein heterodimerization activity (129 genes) IPI GO:0005515 [list] [network] protein binding (7230 genes) ISS
KEGG*	hsa04640 Hematopoietic cell lineage hsa04660 T cell receptor signaling pathway hsa05340 Primary immunodeficiency
orthologous	[Ortholog page] Cd3d(Mmu) Cd3d(Rno)
subcellular	extr 8 (prediction for NP_000723.1)
localization*	extr 5, mito 2 (prediction for NP_001035741.1)



KEGG ID	Title	#genes	Link to the KEGG map (multiple genes)
hsa04660	T cell receptor signaling pathway	8	
hsa04640	Hematopoietic cell lineage	4	
hsa04060	Cytokine-cytokine receptor interaction	1	
hsa04650	Natural killer cell mediated cytotoxicity	5	
hsa04670	Leukocyte transendothelial migration	2	

MR*	Cor*	symbol	function	coexpression detail	Entrez Gene ID
1.0	0.84	LCK	lymphocyte-specific protein tyrosine kinase	[detail]	3932
1.4	0.82	SH2D1A	SH2 domain protein 1A	[detail]	4068
1.7	0.82	ITK	IL2-inducible T-cell kinase	[detail]	3702
2.0	0.80	CD3G	CD3g molecule, gamma (CD3-TCR complex)	[detail]	917
2.6	0.76	CD3E	CD3e molecule, epsilon (CD3-TCR complex)	[detail]	916
3.5	0.78	CD247	CD247 molecule	[detail]	919
3.7	0.70	PVRIG	poliovirus receptor related immunoglobulin domain containing	[detail]	79037
4.1	0.68	PTPN7	protein tyrosine phosphatase, non-receptor type 7	[detail]	5778

network* in tissue

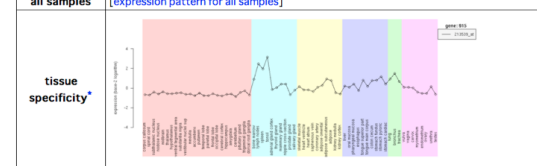
- Lymphocyte
- T_Cell

coexpressed gene list

[coexpressed gene list for CD3D]

gene expression

[expression pattern for all samples]



Public annotation

Ortholog page

Coexpression

Expression

Ortholog page (CD3D)

COXPRESdb: ortholog page for hid:585

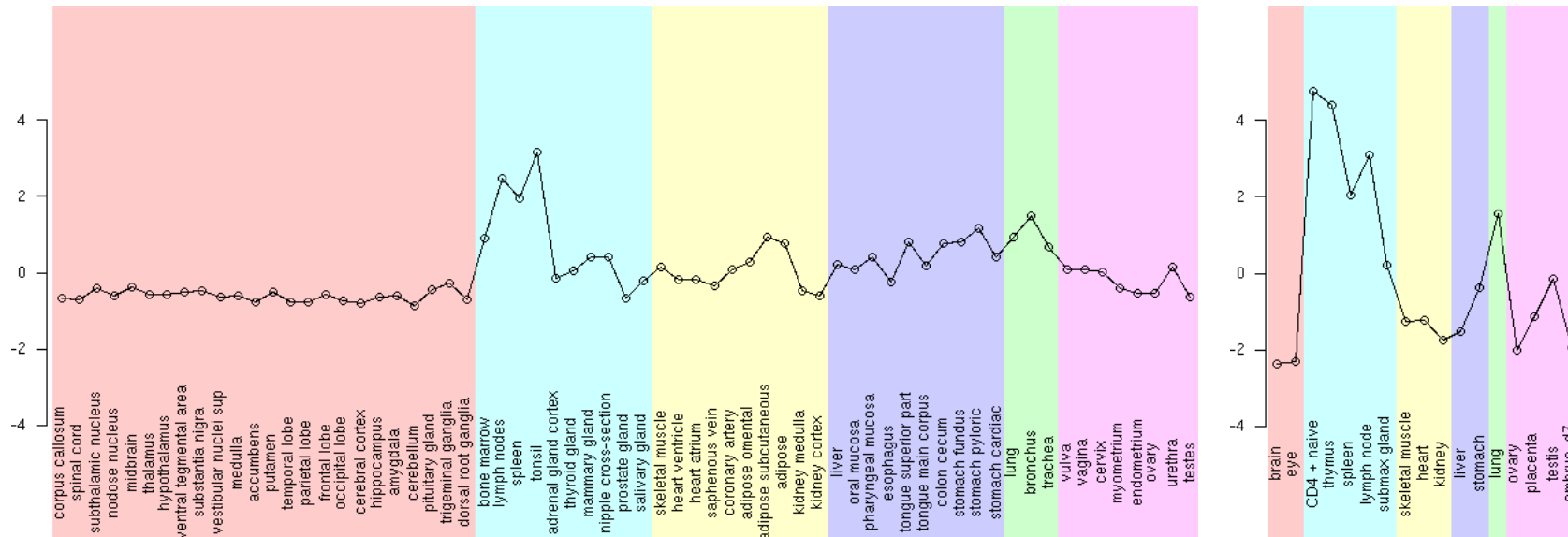
Ortholog ID: 585

species	Hsa	Mmu	Rno																																																																				
symbol	CD3D	Cd3d	Cd3d																																																																				
function	CD3d molecule, delta (CD3-TCR complex)	CD3 antigen, delta polypeptide	CD3 molecule delta polypeptide																																																																				
expression																																																																							
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GO CC	GO:0042101 [L] [N] T cell receptor complex (12 genes) GO:0005886 [L] [N] plasma membrane (3418 genes)	GO:0042105 [L] [N] alpha-beta T cell receptor complex (7 genes) GO:0042101 [L] [N] T cell receptor complex (10 genes)	GO:0042105 [L] [N] alpha-beta T cell receptor complex (6 genes) GO:0005886 [L] [N] plasma membrane (2059 genes)																																																																				

Ortholog page (CD3D)

65 human organs

17 mouse organs



Brain Immune Digestive Reproductive
Locomotory Respiratory

CD3D expresses in immune system

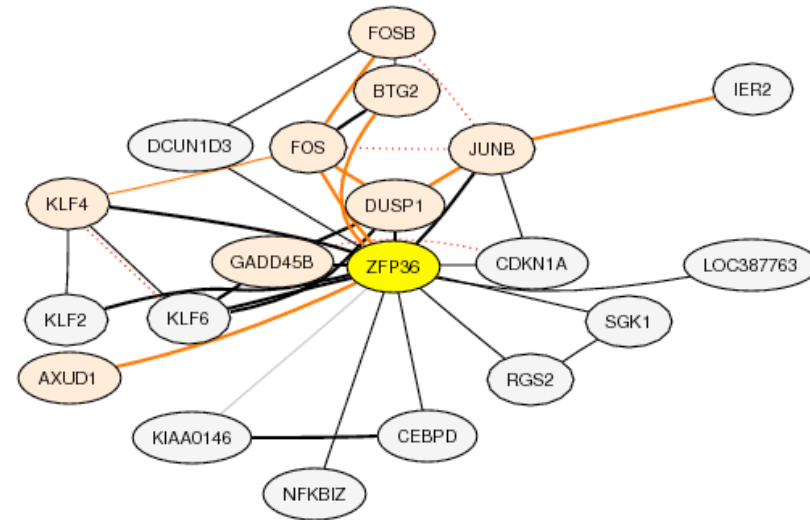
<http://coxpresdb.hgc.jp/data/ortholog/839.shtml>

Contents of COXPRESdb

- Gene list

		MR*	COR*	symbol	function	coexpression detail	Entrez Gene ID
0	☒			ZFP36	zinc finger protein 36, C3H type, homolog (mouse)		7538
1	☐	1.0	0.77	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	[detail]	2353
2	☐	1.4	0.76	JUNB	jun B proto-oncogene	[detail]	3726
3	☐	1.7	0.76	DUSP1	dual specificity phosphatase 1	[detail]	1843
4	☐	3.2	0.62	KLF6	Kruppel-like factor 6	[detail]	1316
5	☐	3.3	0.61	GADD45B	growth arrest and DNA-damage-inducible, beta	[detail]	4616
6	☐	3.5	0.73	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	[detail]	2354
7	☐	3.7	0.60	PBEF1	pre-B-cell colony enhancing factor 1	[detail]	10135
8	☐	3.7	0.66	AXUD1	AXIN1 up-regulated 1	[detail]	64651
9	☐	3.9	0.59	KLF2	Kruppel-like factor 2 (lung)	[detail]	10365
10	☐	3.9	0.68	NR4A1	nuclear receptor subfamily 4, group A, member 1	[detail]	3164
11	☐	4.0	0.65	ATF3	activating transcription factor 3	[detail]	467
12	☐	4.0	0.59	BTG2	BTG family, member 2	[detail]	7832
				KLF4	Kruppel-like factor 4		

- Gene network



☐ For a locus

☐ **For a set of genes**

☐ For huge network

http://coxpresdb.jp

COXPRESdb: Home



version 3.3

COXPRESdb; co-expressed gene database

(last update) 2009.07.25

Quick Search

☐ symbol search (e.g. DHCR)
☐ case sensitive

Home	Home:
Search	
Tool	NetworkDrawer
Browse	HCluster
Help	CoexViewer
Publication	ExViewer
Download	GOPathDrawer
Statistics	
Log	

The search box next to the title logo has been renewed.

CoexViewer was renewed. [Tool > CoexViewer]

A tool to draw hierarchical structures of Gene Ontology terms was made available.
[Tool > GOPathDrawer]

[2009.05.20] A tool to obtain tissue-specific expression data for human was made available.
[Tool > TissueDataExtractor]
[more]

- **Version numbering** (2008.10.31)

COXPRESdb has two types of versions: version for COXPRESdb and version for coexpression

"NetworkDrawer" in Tool tab

The screenshot shows the COXPRESdb website interface. At the top, the title "COXPRESdb" is displayed in a large, stylized font made of red and green dots, with "version 3.3" below it. The subtitle "COXPRESdb; co-expressed gene database" is centered. On the right, there is a "Quick Search" section with a text input field and two checkboxes: "symbol search (e.g. DHCR)" and "case sensitive". The date "(last update) 2009.07.25" is shown in the bottom right corner of the header area.

On the left side, there is a vertical navigation menu with the following items: Home, Search, Tool, Browse, Help, Publication, Download, Statistics, and Log. The "Tool" item is highlighted.

The main content area is titled "Tool:" and contains a list of tools. The first tool listed is "<NetworkDrawer>" with the description "Drawing coexpressed gene network in query genes." Below this, there are two buttons: "submit" and "example". To the right of these buttons is a list of gene IDs: 1586, 1589, 1717, 1718, 1727, 3284, 4047, 5563, and 6307. To the right of the list is a vertical scrollbar.

Below the gene list, there is a section titled "Functions" which contains three steps: (1) Preparing information files for network, (2) Drawing coexpressed gene network, and (3) Making coexpressed gene list.

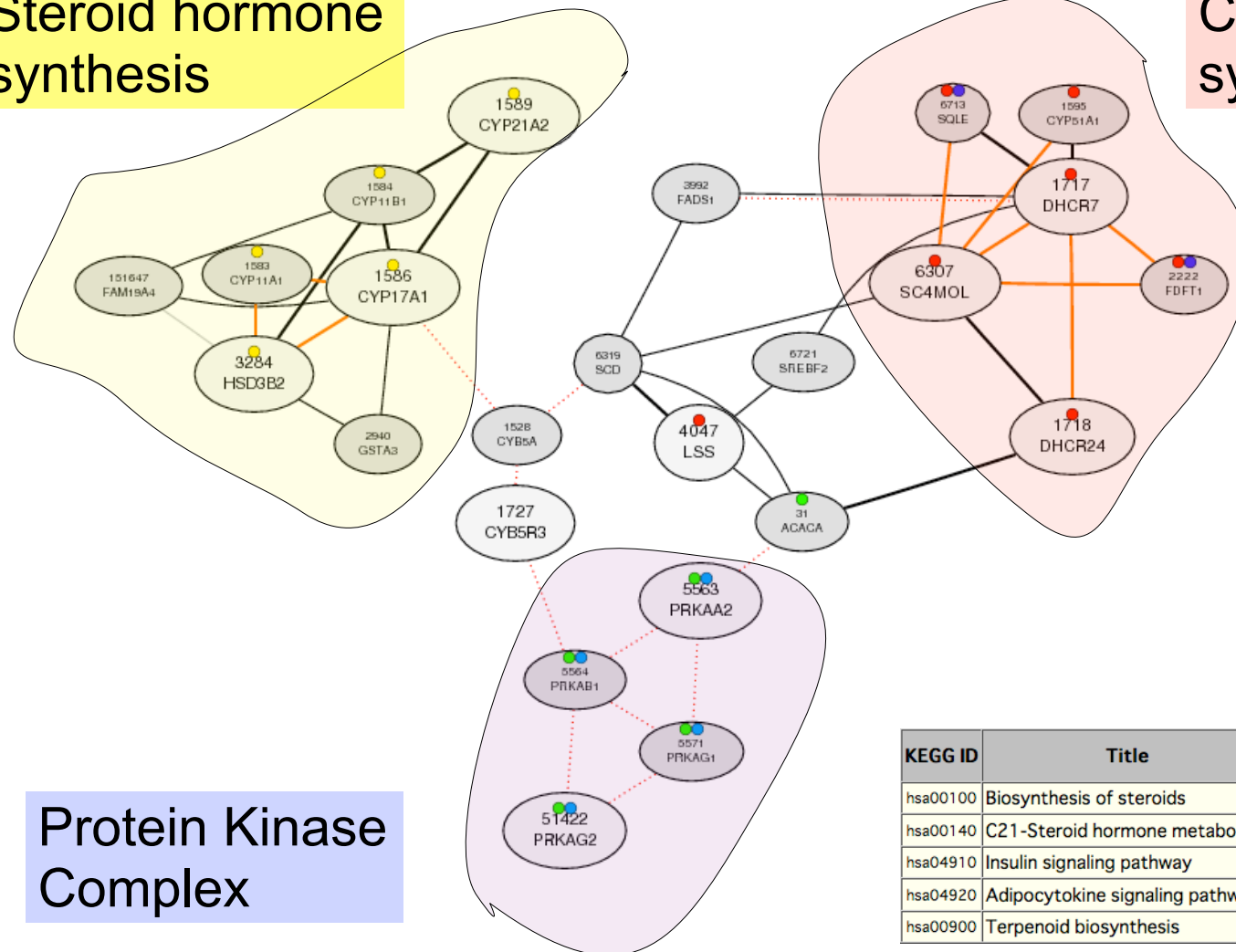
On the right side of the main content area, there is a list of bullet points describing the tool's functionality:

- This form draws coexpressed gene network in query genes.
- Input Entrez Gene IDs.
- The example is 10 genes related to steroid biosynthetic process ([GO:0006694](#))

NetworkDrawer

Steroid hormone synthesis

Cholesterol synthesis



KEGG ID	Title	#genes	KEGG map (multiple genes)
hsa00100	Biosynthesis of steroids	7	●
hsa00140	C21-Steroid hormone metabolism	5	●
hsa04910	Insulin signaling pathway	5	●
hsa04920	Adipocytokine signaling pathway	4	●
hsa00900	Terpenoid biosynthesis	2	●

"HCluster" in Tool tab

The screenshot shows the COXPRESdb Tool interface. The title bar reads "COXPRESdb: Tool". The main header features the COXPRESdb logo (version 3.3) and the text "COXPRESdb; co-expressed gene database". A "Quick Search" box is on the right with checkboxes for "symbol search (e.g. DHCR)" and "case sensitive". The date "(last update) 2009.07.25" is in the bottom right of the header.

A left sidebar contains a menu with the following items: Home, Search, Tool (highlighted with a red circle), Browse, Help, Publication, Download, Statistics, and Log. The "Tool" menu is expanded, showing a list of tools: NetworkDrawer, HCluster (highlighted with a red circle), CoexViewer, ExViewer, and GOPathDrawer.

The main content area is titled "Tool:" and displays the "HCluster" tool. The description reads: "Draw co-expressed gene network in query genes." Below this, a list of bullet points states: "This form draws coexpressed gene network in query genes.", "Input Entrez Gene IDs.", and "The example is 10 genes related to steroid biosynthetic process (GO:0006694)". To the left of the text is a vertical list of gene IDs: 1717, 1718, 1727, 3284, 4047, 5563, and 6307.

At the bottom, a section titled "Functions" contains a table with three columns:

(1) Preparing information files for network	(2) Drawing coexpressed gene network	(3) Making coexpressed gene list

"HCluster" in Tool tab

The screenshot shows a web browser window titled "COXPRESdb: Tool". On the left is a blue sidebar. The main content area has a light gray background. It features two tool sections. The first section, "<HCluster> Hierarchical clustering for query genes", includes a "submit" button, an "example" button, a list of gene IDs (1824, 3655, 1829, 3673, 3914, 3918, 7039, 374, 2071), and three radio button options: "Single linkage method" (selected), "Averaged linkage method", and "Ward method". To the right of this section are two bullet points: "This form performs hierarchical clustering for query genes." and "Input Entrez Gene IDs." The second section, "<CoexViewer> Coexpression viewer", includes a "submit" button, an "example" button, and two input fields labeled "gene1:" (containing "21454") and "gene2:" (containing "12461"). To the right of this section are two bullet points: "This form returns scatter plot of coexpression between two genes." and "Input two Entrez Gene IDs." The bottom of the page shows the start of a third section, "<ExViewers>".

COXPRESdb: Tool

- **<HCluster>**
Hierarchical clustering for query genes

submit example
1824
3655
1829
3673
3914
3918
7039
374
2071

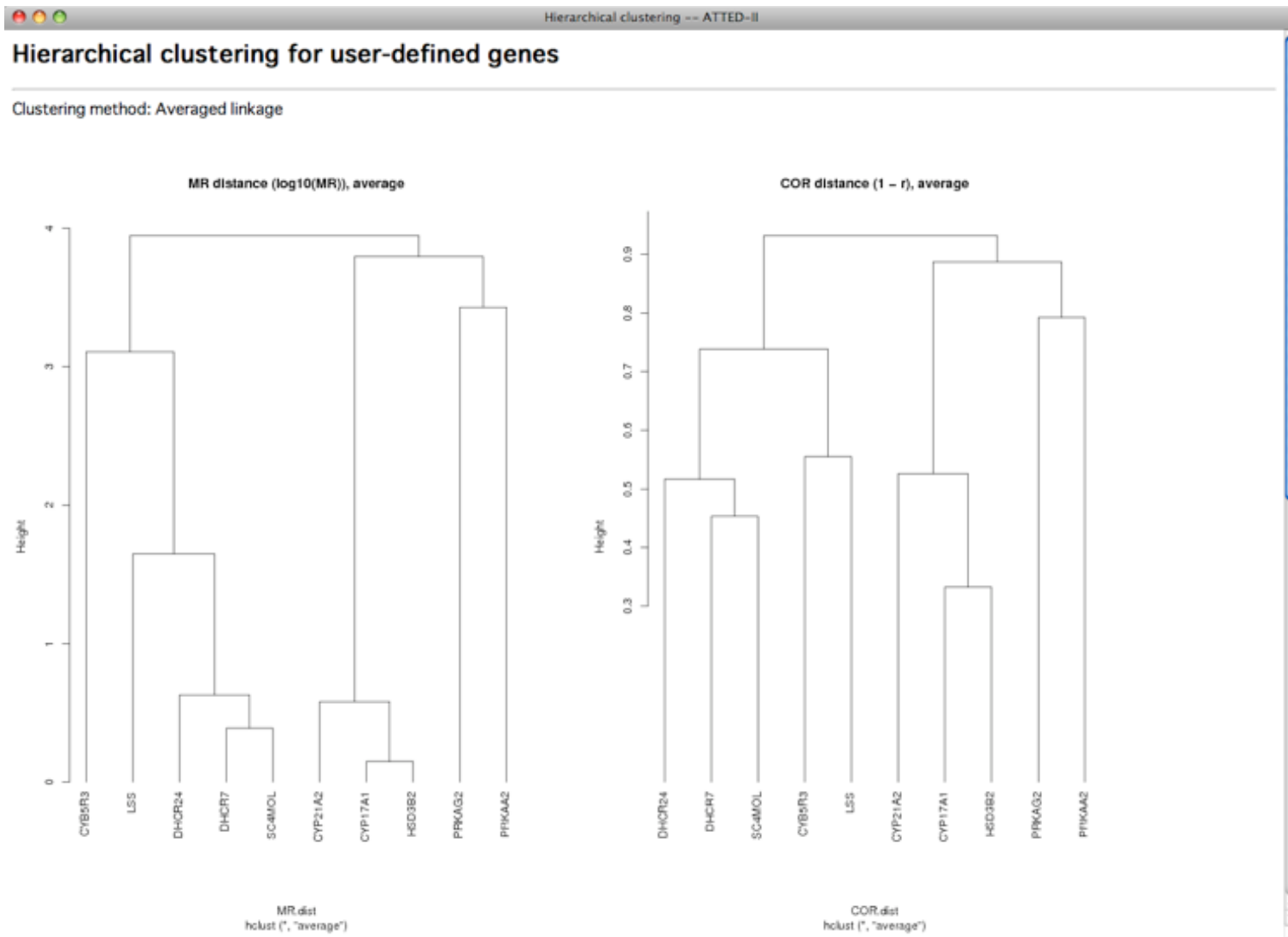
☒ Single linkage method
☐ Averaged linkage method
☐ Ward method

◦ This form performs hierarchical clustering for query genes.
◦ Input Entrez Gene IDs.
- **<CoexViewer>**
Coexpression viewer

submit example
gene1:
21454
gene2:
12461

◦ This form returns scatter plot of coexpression between two genes.
◦ Input two Entrez Gene IDs.
- **<ExViewers>**

"HCluster" in Tool tab



"EdgeAnnotation" in Search tab

COXPRESdb
version 3.3
COXPRESdb; co-expressed gene database
(last update) 2009.07

Quick Search

☐ symbol search (e.g. DHCR7)
☐ case sensitive

Home
Search
Tool
Browse
Help
Publication
Download
Statistics
Log

Search:
GeneTable
EdgeAnnotation
TissueDataExtractor
BLAST
PPIsearch

submit example

Entrez Gene IDs
Affy probe IDs

function table

- These forms simply add information about gene function and predicted subcellular localization for query genes.

Shaded loci do not have affy data.

species	symbol*	function*	Entrez Gene ID
Hsa	MED6	mediator complex subunit 6	10001
Mmu	Oog3	oogenesis 3	100012
Mmu	AA673240	expressed sequence AA673240	100014
Mmu	Ldlrap1	low density lipoprotein receptor adaptor protein 1	100017

"EdgeAnnotation" in Search tab

Query genes		
symbol	function	Entrez Gene ID
CYP17A1	cytochrome P450, family 17, subfamily A, polypeptide 1	1586
CYP21A2	cytochrome P450, family 21, subfamily A, polypeptide 2	1589
DHCR7	7-dehydrocholesterol reductase	1717
DHCR24	24-dehydrocholesterol reductase	1718
CYB5R3	cytochrome b5 reductase 3	1727
HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	3284
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	4047
PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	51422
PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	5563
SC4MOL	sterol-C4-methyl oxidase-like	6307

Summary of
query genes

Coexpression degree of all inter-connected query pairs								
gene1		gene2		MR	Cor	coexpression detail	Reported PPI	Conserved coexpression
symbol	Entrez Gene ID	symbol	Entrez Gene ID					
CYP17A1	1586	HSD3B2	3284	1.4	0.67	detail		Hsa,Mmu
DHCR7	1717	SC4MOL	6307	2.5	0.55	detail		Hsa,Mmu
CYP17A1	1586	CYP21A2	1589	3.2	0.48	detail		
DHCR24	1718	SC4MOL	6307	3.9	0.49	detail		
CYP21A2	1589	HSD3B2	3284	4.6	0.47	detail		
DHCR7	1717	DHCR24	1718	4.7	0.48	detail		Rno,Hsa
DHCR7	1717	LSS	4047	24.8	0.41	detail		
CYB5R3	1727	LSS	4047	46.2	0.44	detail		
LSS	4047	SC4MOL	6307	54.5	0.37	detail		
DHCR24	1718	LSS	4047	65.6	0.34	detail		
DHCR7	1717	CYB5R3	1727	1277.9	0.26	detail		
CYP17A1	1586	PRKAG2	51422	2100.9	0.22	detail		

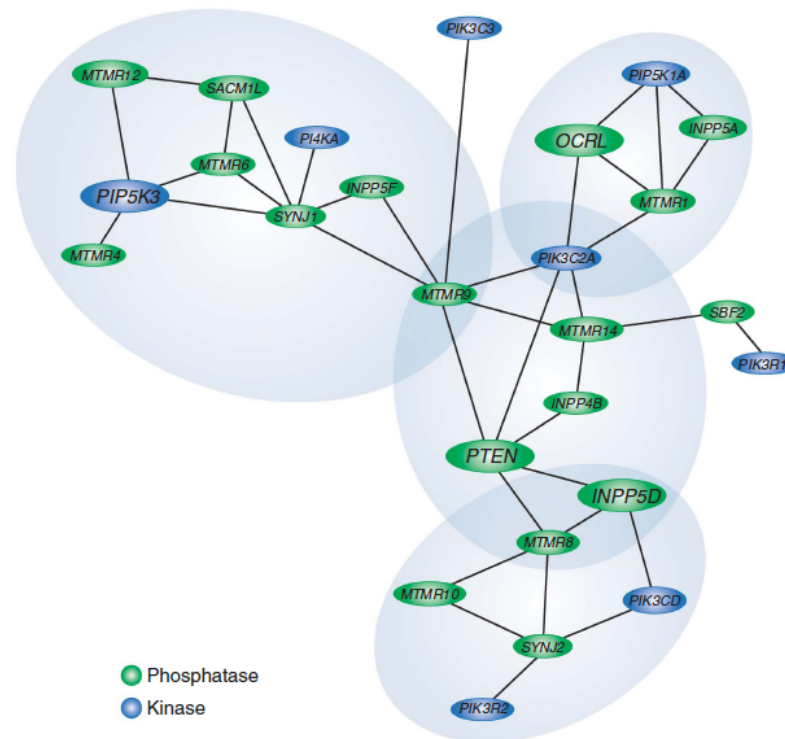
Coexpression
among all pairs
of query genes

Example to use "EdgeAnnotation"

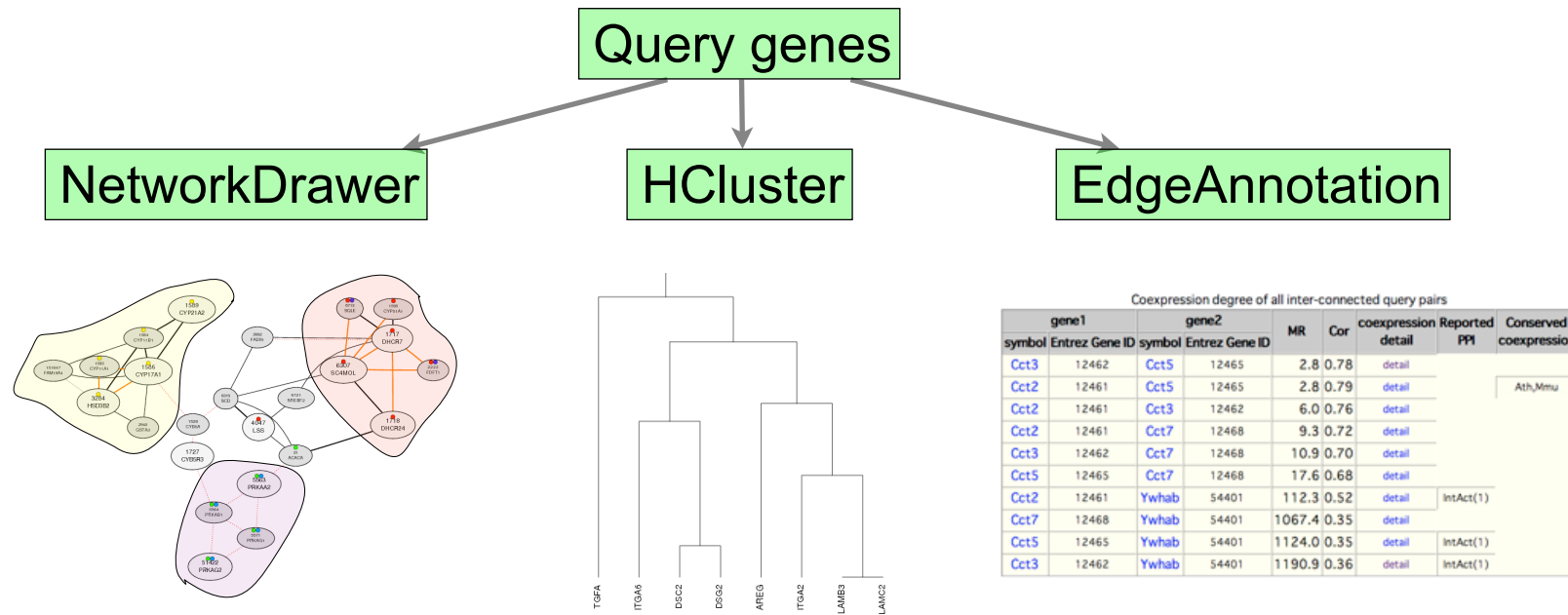
Grouping of enzymes

□ Vicinanza *et al.* (2008) *EMBO J*

- Phosphatases, Kinases to regulate PI system
- They used weaker threshold ($PCC > 0.4$).



COXPRESdb analyses for a set of genes



- (1) Searching new targets for a gene of interest
- (2) Inferring relationships among cellular processes.
- (3) Identifying biological function of paralogs.
- (4) Grouping of genes after large-scale experiments.

Summary of tools in COXPRESdb

 Top page → Search

- ◆ GeneTable
- ◆ EdgeAnnotation
- ◆ TissueDataExtractor
- ◆ BLAST
- ◆ PPIsearch

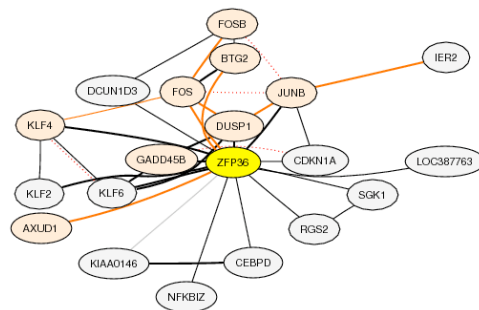
 Top page → Tool

- ◆ NetworkDrawer
- ◆ HCluster
- ◆ CoexViewer
- ◆ ExViewer
- ◆ GOPathDrawer

Summary of COXPRESdb

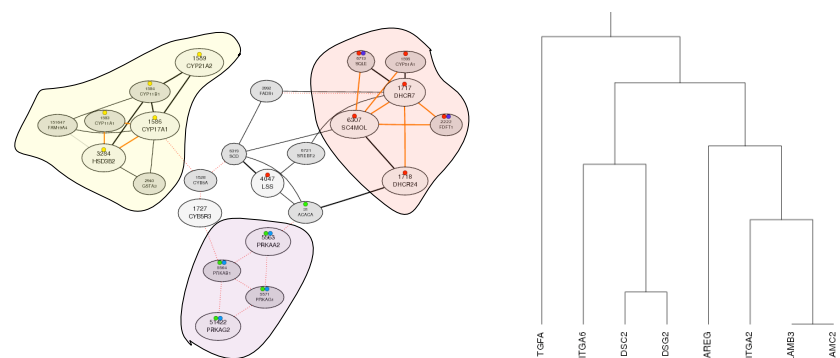
COXPRESdb provides gene coexpression as the main content.

Single query gene



	MR*	COR*	symbol	function	coexpression detail	Entrez Gene ID
0	☒		ZFP36	zinc finger protein 36, C3H type, homolog (mouse)		7538
1	☐	1.0	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	[detail]	2353
2	☐	1.4	JUNB	jun B proto-oncogene	[detail]	3726
3	☐	1.7	DUSP1	dual specificity phosphatase 1	[detail]	1843
4	☐	3.2	KLF6	Kruppel-like factor 6	[detail]	1316
5	☐	3.3	GADD45B	growth arrest and DNA-damage-inducible, beta	[detail]	4616
6	☐	3.5	FOSB	FBJ murine osteosarcoma	[detail]	2354

A set of query genes



Coexpression degree of all inter-connected query pairs

gene1	gene2	MR	Cor	coexpression detail	Reported PP1	Conserved coexpression
symbol	Entrez Gene ID	symbol	Entrez Gene ID			
Cct3	12462	Cct5	12465	2.8 0.78	detail	Ath,Mmu
Cct2	12461	Cct5	12465	2.8 0.79	detail	
Cct2	12461	Cct3	12462	6.0 0.76	detail	
Cct2	12461	Cct7	12468	9.3 0.72	detail	
Cct3	12462	Cct7	12468	10.9 0.70	detail	IntAct(1)
Cct5	12465	Cct7	12468	17.6 0.68	detail	
Cct2	12461	Ywhab	54401	112.3 0.52	detail	
Cct7	12468	Ywhab	54401	1067.4 0.35	detail	
Cct5	12465	Ywhab	54401	1124.0 0.35	detail	IntAct(1)
Cct3	12462	Ywhab	54401	1190.9 0.36	detail	IntAct(1)