Network Objects

Click on any object in the network to obtain class info

Enzymes

	Generic enzyme

KINASE		PHOSPHATASE	
	Generic kinase		Generic phosphatase
	Protein kinase		Protein phosphatase
	Lipid kinase		Lipid phosphatase

PHOSPHOLIPASE	
	Generic phospholipase

PROTEASE		GTPase	
	Generic protease		G-alpha
	Metalloprotease		RAS - superfamily

Generic classes

	Receptor ligand
	Transcription factor
	Protein
	Cell membrane glycoprotein
	Compound
	Predicted metabolite or user's structure
	Inorganic ion
	Reaction
	DNA
	RNA
	Generic binding protein

Channels / Transporters	
	Generic channel
	Ligand-gated ion channel
	Voltage-gated ion channel
	Transporter

Receptors	
	Generic receptor
	GPCR
	Receptors with enzyme activity

G protein adaptor / regulators	
	G beta/gamma
	Regulators (GDI, GAP, GEF etc.)

Groups of objects	
	A complex or a group Proteins or compounds physically connected into a complex or related as a group
	Logical association Related proteins or compounds are connected into groups. To see the relations (logical associations) within a group, use «Expand group» function in the scroll-down right-button menu. Use «Collapse logical relations» function to close the group.
	Custom association Group of collapsed objects chosen by user

Object highlighting

Nodes and root nodes

Found object

Object selected on the search pane

Manually selected node(s)

Object(s) selected by ctrl + click on it or by click + drag rectangle around it

Highlight by mouse over

Highlight downstream objects

When the mouse is over an object (node on a network), the closest interacting nodes are highlighted in CYAN if the direction of interaction is **from** the initial object

Highlight upstream objects

When the mouse is over an object (node on a network), the closest interacting nodes are highlighted in yellow if the direction of interaction is **towards** the initial object

Root nodes

Root node(s) for network expansion (building)

Object(s) from a user-specified uploaded list or from experiments

Initial object(s)

Object(s) chosen to build the pathways **from**

Intermediate object(s)

Object(s) situated along the pathway

Terminal object(s)

Object(s) the pathways terminate **on**

Possible combinations of three above marks (except the first one)

Expression data	
	Overexpressed gene(s) Genes with higher conditional expression level compared to the experimental "control"
	Underexpressed gene(s) Genes with lower conditional expression level compare to the experimental "control"
	Mixed-expressed gene(s) Genes with conditional expression level statistically different from the experimental "control", with the "sign" of expression varying in different experiments

Interactions between objects

Click on any hexagon in the networks for interaction annotation

Link legend

	Positive effect
	Negative effect
	Unspecified effect
	Technical link

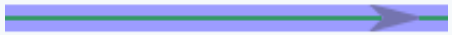
Mechanisms

Physical interactions

B	**Binding** Protein or compound binds other protein or compound
C	**Cleavage** Cleavage of a protein at a specific site yielding distinctive peptide fragments. Proteolytic cleavage can be carried out by both enzymes and compounds
CM	**Covalent modifications** (neddylation/deneddylation, sumoylation/desumoylation, ubiquitination/deubiquitination and etc.) Protein activity regulation by covalent binding of a small chemical group to the aminoacids of an active site.
+P	**Phosphorylation** Protein activity regulation by an addition of a phosphate group
-P	**Dephosphorylation** Protein activity regulation by a removal of a phosphate group
T	**Transformation** Protein activity regulation by binding & hydrolysis of GTP
Tn	**Transport** Transport of a protein or a compound between organelles

Z	**Catalysis** Catalysis of an enzymatic reaction
Tr	**Transcription regulation** Physical binding of a transcription factor to target gene's promoter
M	**MicroRNA binding** Regulation of gene expression by binding of microRNA to target mRNA
Functional interactions	
IE	**Influence on expression** Protein's or compound's action results in changing the expression level of target gene(s)
Cn	**Competition** Protein activity regulation by competition at the substrate binding site
?	**Unspecified interactions** Mechanism is unknown or/and effect is indirect
PE	**Drug-Drug interactions. Pharmacological effect** Drugs change pharmacological effects of other drugs, for instance by competing for drug metabolism enzymes or organic transporters
TE	**Drug-Drug interactions. Toxic effect** Drugs change toxic effects of other drugs, for instance by competing for drug metabolism enzymes or organic transporters
Logical relations	
GR	**Group relation** Object belongs to a generic group of related objects
CS	**Complex subunit** Protein is a subunit of a protein complex
SR	**Similarity relation** Chemically similar compounds with chosen Tanimoto similarity score

Connectors

Connectors	
	**Incoming interaction** When the mouse is over an object, yellow link indicates direction **to** the object
	**Outgoing interaction** Cyan link indicates direction **from** the object
	**Bidirectional interaction** Blue link indicates **BI-DIRECTIONAL** interaction
	**Non-directional link** Blue link also indicates an interaction for which the direction is not specified
	**Traced link** The link is always highlighted in blue if both linked objects are selected in "Trace" mode
Interactions from custom list	
	**Interaction is in the network** Interaction is represented by a thin solid line and is highlighted in blue
	**Interaction is in the base, but not in network** Interaction is highlighted in yellow
	**Interaction is not present in the base** Interaction is highlighted in magenta
Canonical pathways	
	**Canonical pathways** The link is highlighted in thick cyan line
Custom marked links (user's choice)