







METACORE QUICK REFERENCE GUIDE

USER DATA

<p>NETWORKS</p>  <p>Up-regulated (+) Object has user data with positive value</p>  <p>Down-regulated (-) Object has user data with negative value</p>  <p>Mixed-signal (+/-) Object has user data with both positive and negative values</p>	<p>MAPS</p>   
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NETWORK OBJECTS

<p>ENZYMES</p> <p>Generic enzyme</p> <p>KINASEP</p> <p>Generic kinase</p> <p>Protein kinase</p> <p>Lipid kinase</p> <p>HOSPHATASE</p> <p>Generic phosphatase</p> <p>Protein phosphatase</p> <p>Lipid phosphatase</p> <p>PHOSPHOLIPASE</p> <p>Generic phospholipase</p> <p>PROTEASE</p> <p>Generic protease</p> <p>Metalloprotease</p> <p>GTPASE</p> <p>G-alpha</p> <p>RAS - superfamily</p>	<p>GENERIC CLASSES</p> <p>Receptor ligand</p> <p>Transcription factor</p> <p>Protein</p> <p>Compound</p> <p>Predicted metabolite or user's structure</p> <p>Inorganic ion</p> <p>Reaction</p> <p>DNA</p> <p>RNA</p> <p>Generic binding protein</p>
<p>CHANNELS/TRANSPORTERS</p> <p>Generic channel</p> <p>Ligand-gated ion channel</p> <p>Voltage-gated ion channel</p> <p>Transporter</p>	<p>RECEPTORS</p> <p>Generic</p> <p>GPCR</p> <p>Receptors with kinase activity</p>
<p>G PROTEIN ADAPTOR/REGULATORS</p> <p>G beta/gamma</p> <p>Regulators (GDI, GAP, GEF, etc.)</p>	
<p>GROUPS OF OBJECTS</p> <p>A complex or a group Proteins physically connected into a complex or related as a family</p> <p>Logical association Proteins linked by logical relations or physical interactions</p> <p>Custom association Group of collapsed objects chosen by user</p>	

INTERACTIONS BETWEEN OBJECTS

<p>EFFECTS</p>  <p>Positive / activation</p>  <p>Negative / inhibition</p>  <p>Unspecified</p>	<p>MECHANISMS</p> <p>PHYSICAL INTERACTIONS</p> <p>B Binding Compound binds the enzyme or receptor</p> <p>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</p> <p>CM Covalent modifications Protein activity regulation by covalent binding of a small chemical group to the aminoacids of an active site</p> <p>+P Phosphorylation Protein activity is altered via addition of a phosphate group</p> <p>-P Dephosphorylation Protein activity is altered via removal of a phosphate group</p> <p>T Transformation Protein activity regulation by binding & hydrolysis of GTP</p> <p>Tn Transport Transport of a protein or a compound between organelles</p> <p>Z Catalysis Catalysis of an enzymatic reaction</p> <p>Tr Transcription regulation Physical binding of a transcription factor to target gene's promoter</p> <p>M MicroRNA binding Regulation of gene expression by binding of microRNA to target mRNA</p>
<p>FUNCTIONAL INTERACTIONS</p> <p>IE Influence on expression Compounds change the expression level of target genes indirectly, for instance by binding to upstream receptors</p> <p>Cn Competition Protein activity regulation by competition at the substrate binding site</p> <p>? Unspecified interactions Mechanism is unknown or/and effect is indirect</p> <p>PE Drug-Drug interactions. Pharmacological effect Drugs change pharmacological effects of other drugs, for instance by competing for drug metabolism enzymes or organic transporters</p> <p>TE Drug-Drug interactions. Toxic effect Drugs change toxic effects of other drugs, for instance by competing for drug metabolism enzymes or organic transporters</p>	
<p>LOGICAL RELATIONS</p> <p>GR Group relation Object belongs to a generic group of related objects</p> <p>CS Complex subunit Protein is a subunit of a protein complex</p> <p>SR Similarity relation Chemically similar compounds with chosen Tanimoto similarity score</p>	

LINKS ON NETWORKS

Incoming interaction
When the mouse is over object, yellow link indicates direction to object

Outgoing interaction
Cyan link indicates direction FROM the object

INTERACTIONS FROM CUSTOM LIST (MetaLink™)

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 in the network
Interaction is highlighted in magenta

CANONICAL PATHWAYS

Canonical pathway
The link is highlighted in a thick cyan or magenta line

LINKS ON MAPS

Disrupts in disease

Weakens in disease

Emerges in disease

Enhances in disease

Species specific interactions

OBJECTS ON MAPS

<p>LOCALIZATION</p> <p>Mitochondria</p> <p>EPR</p> <p>Golgi</p> <p>Nucleus</p> <p>Lysosome</p> <p>Peroxisome</p> <p>Cytoplasm</p> <p>Extracellular</p>	<p>OTHER MAP OBJECTS</p> <p>Note</p> <p>Normal process</p> <p>Pathological process</p> <p>Normal map</p> <p>Disease map</p> <p>Species specific object</p> <p>Path start</p>
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