

METACORE QUICK REFERENCE GUIDE

USER DATA

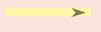
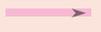
<p>NETWORKS</p>  <p>Up-regulated (+) Object has user data with positive value</p>  <p>Down-regulated (-) Object has user data with negative value</p>  <p>Mixed-signal (+/-) Object has user data with both positive and negative values</p>	<p>MAPS</p>   
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NETWORK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

<p>LINKS ON NETWORKS</p>  <p>Incoming interaction When the mouse is over object, yellow link indicates direction to object</p>  <p>Outgoing interaction Cyan link indicates direction FROM the object</p>	<p>INTERACTIONS FROM CUSTOM LIST (MetaLink™)</p>  <p>Interaction is in the network Interaction is represented by a thin solid line and is highlighted in blue</p>  <p>Interaction is in the base, but not in network Interaction is highlighted in yellow</p>  <p>Interaction is in the network Interaction is highlighted in magenta</p>
<p>CANONICAL PATHWAYS</p>  <p>Canonical pathway The link is highlighted in a thick cyan or magenta line</p>	
<p>LINKS ON MAPS</p>  <p>Disrupts in disease</p>  <p>Weakens in disease</p>  <p>Emerges in disease</p>  <p>Enhances in disease</p>  <p>Species specific interactions</p>	

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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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