

Edinburgh Pathway Editor

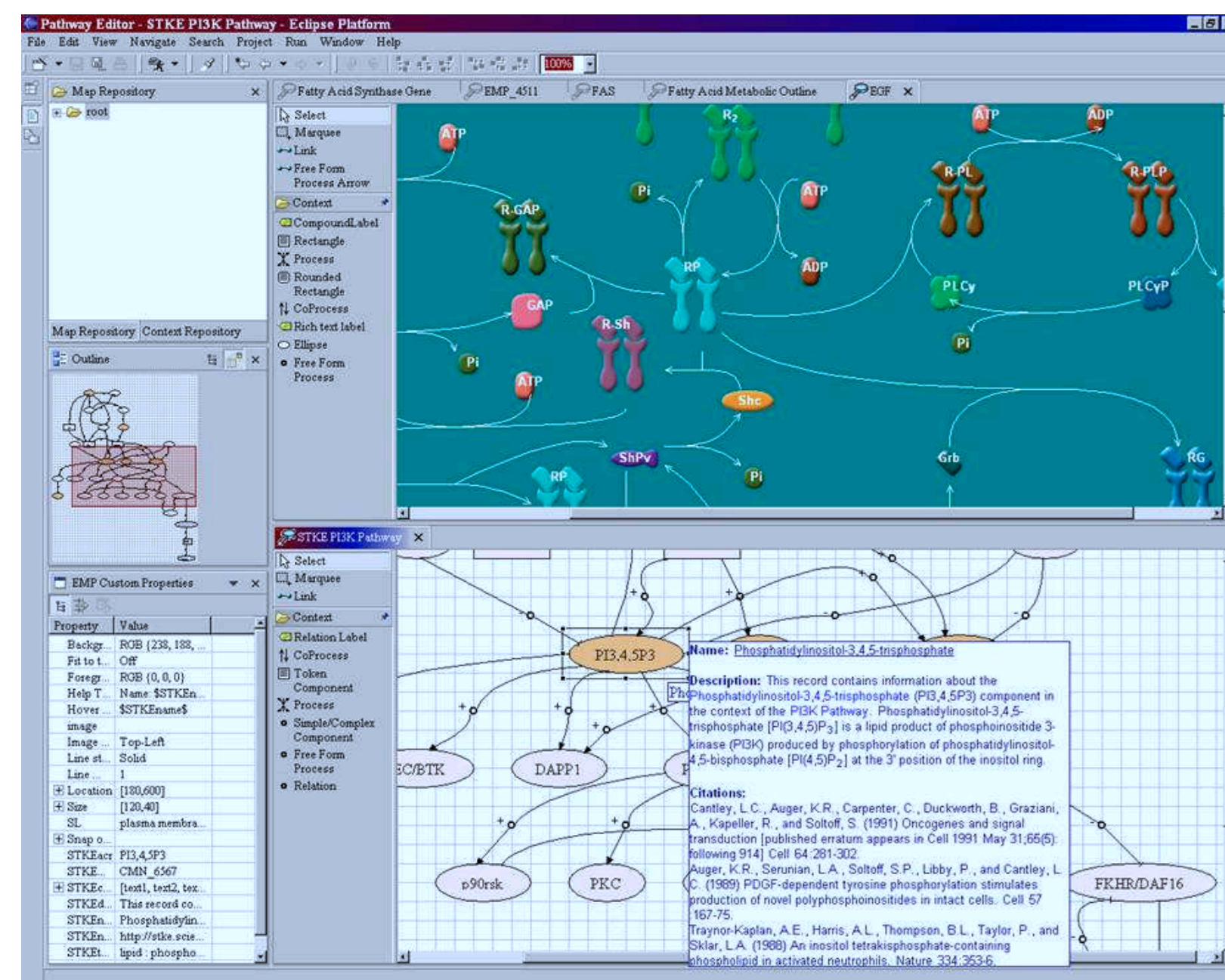
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<http://www.bioinformatics.ed.ac.uk/epe/>



EPE main screen



EPE is a visual editor designed for annotation, visualization and presentation of wide variety of biological networks, including metabolic, genetic and signal transduction pathways. It based on a metadata driven architecture, which makes it very flexible in drawing, storing, presenting and exporting information related to the network of interest.

EPE uses a small number of basic objects to represent main concepts of the biological network. "Shape" represents the biological object or subsystem, treated as "a black box" with number of Ports interfacing with it. Process visualizes sequences of events e.g. a biochemical reaction or protein interaction. Link is used to represent any pair-wise relation between objects including "identity" or "act on" relations. Label is a visual object to represent textual information and to allow links to other maps and resources. The EPE concept of "context" separates metadata and visual standards from pathway maps and pathway data. It allows one to tune the "drawing palette" for selected type of map. With the context one could create a new object with special customized properties. The context is a collection of objects, their properties and their default values. The context allows the user to create new objects on the basis of existent ones. The context property editor provides a great flexibility in the description of storage standards and the visual presentation.

EPE allows the user to customize the list of object properties, to store these data within object, and to visualize it via linked pages or pop-up windows.

There is a further type of information that usually is not shown in visual representations of the pathway map. It captures toe provenance of the relations including literature annotation and links to databases corroborating the relationships depicted in the map. This information is normally stored in the database or as annotation comments to the map.

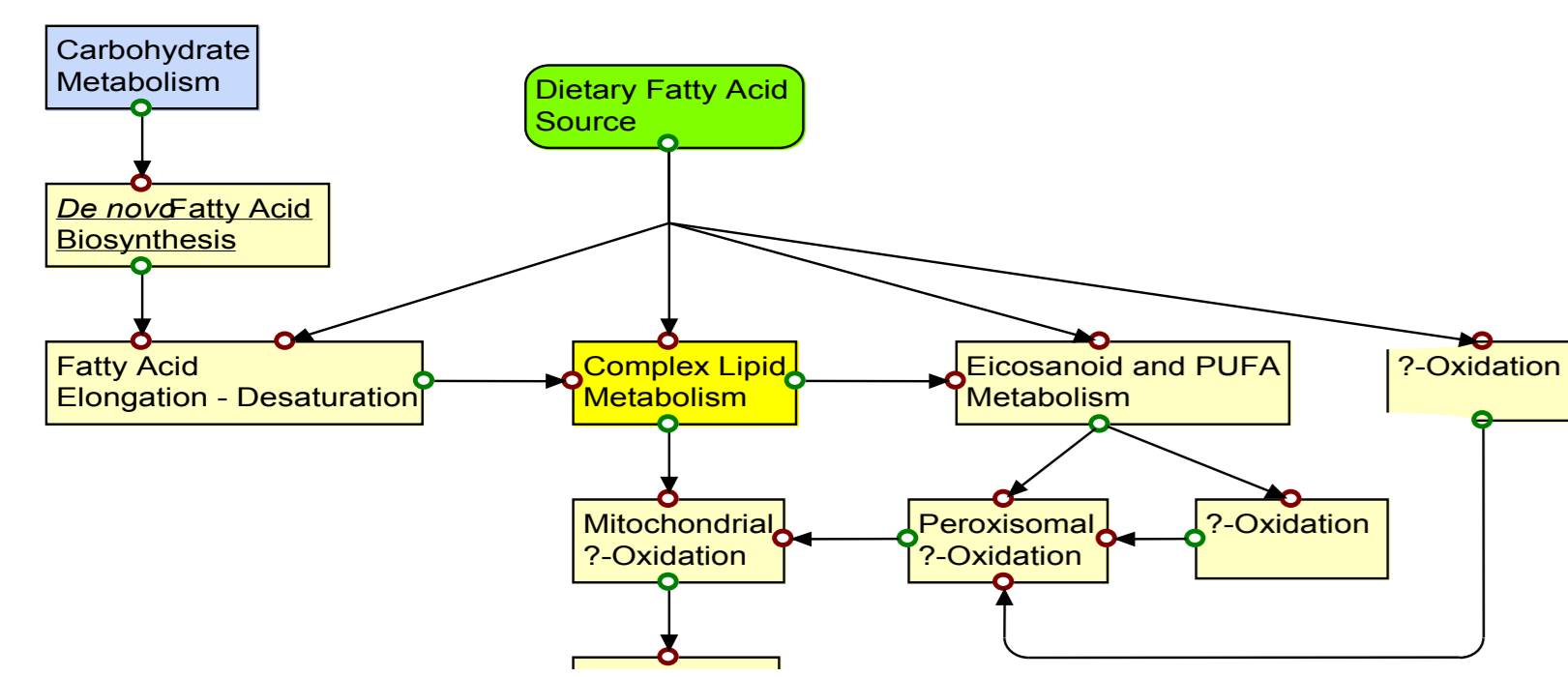
EPE was created as an Eclipse stand-alone application, with Eclipse open framework architecture. This enables the development of extensions to enhance the existing capabilities. Specific plug-ins, to perform scientific computing and other tasks can be easily incorporated.

EPE allows users to create hyperlinks between maps, which makes it possible to organize information as a hierarchy of maps. It makes easy the process of analysis and verification, by allowing people to focus on small subset of data, covered by the whole model. A Java-based architecture makes it possible to run **EPE** on different platforms from Mac to Unix workstations. XML-based export allow easily exchange with diagrams and support for Oracle-based RDBMS storage system allows team development of large scale models.

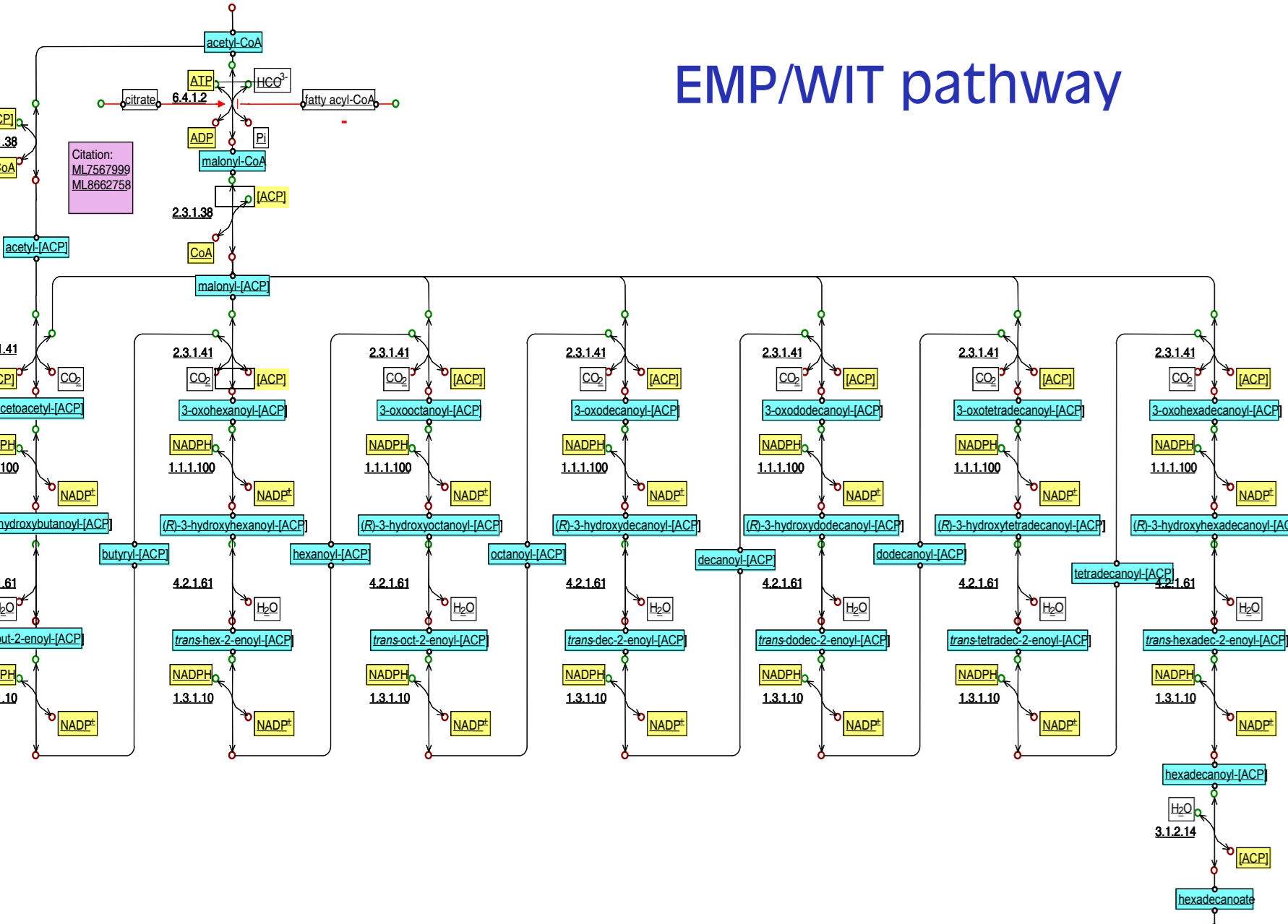
EPE Export formats

- Built-in SBML-1 export of metabolic networks
- Extended SBML-2 export of predefined contexts
- Internal XML representation for backup and data exchange
- Export map as list of chemical reactions
- Export of whole folder tree to the HTML
- Save diagrams in standard graphic formats (JPG,PNG,GIF,EMF,SWF)

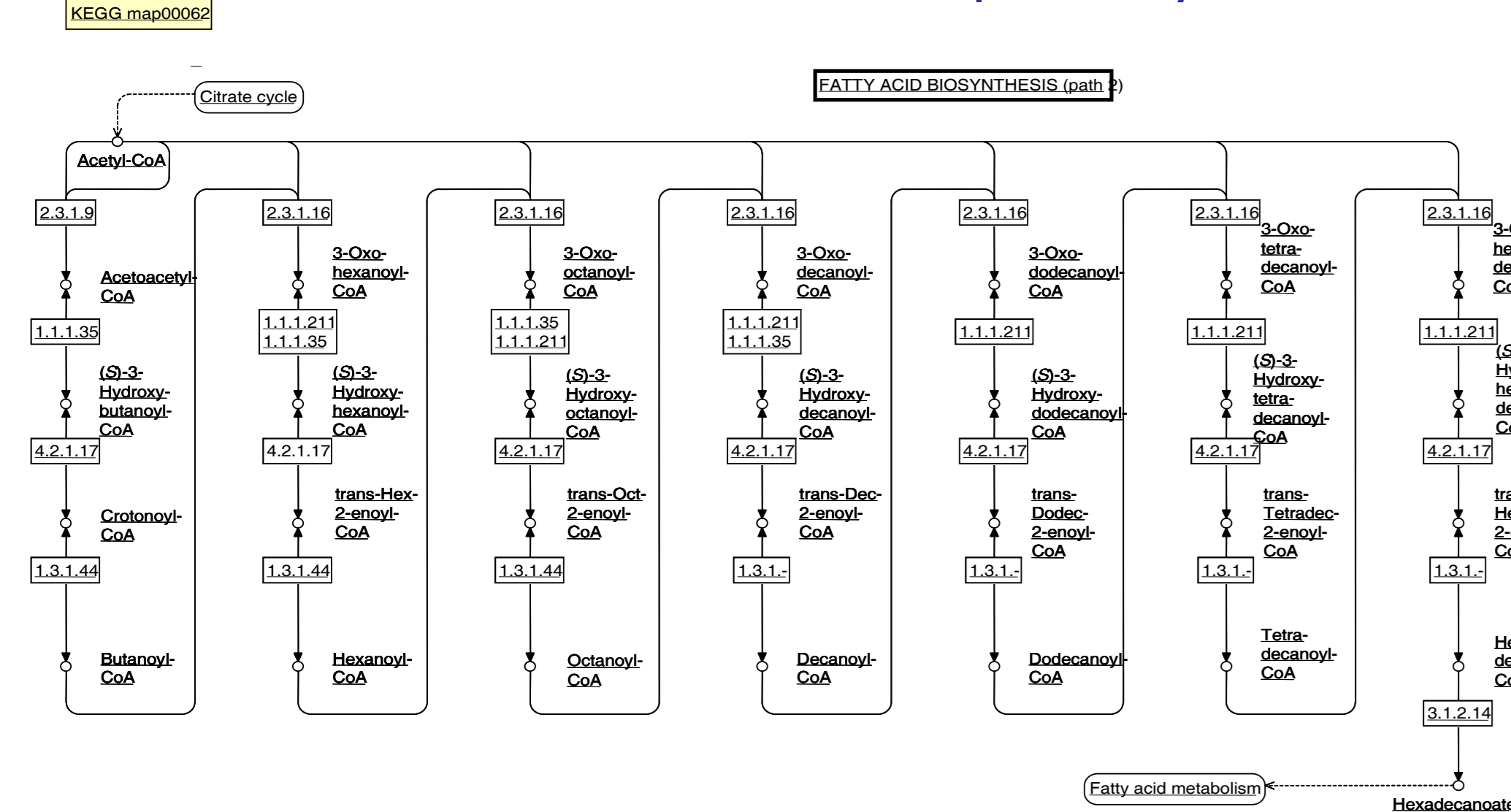
EMP/WIT outline



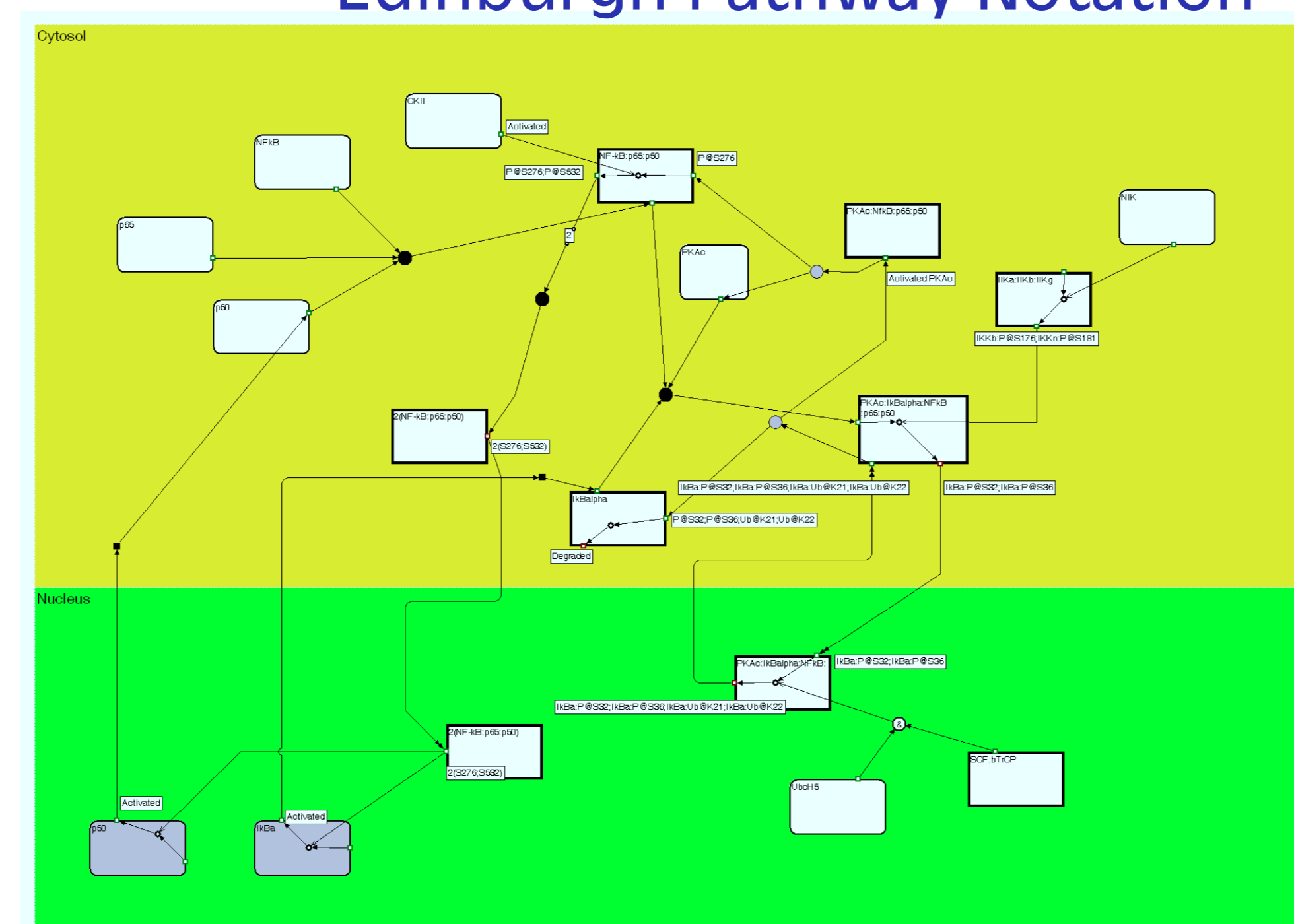
EMP/WIT pathway



KEGG pathway



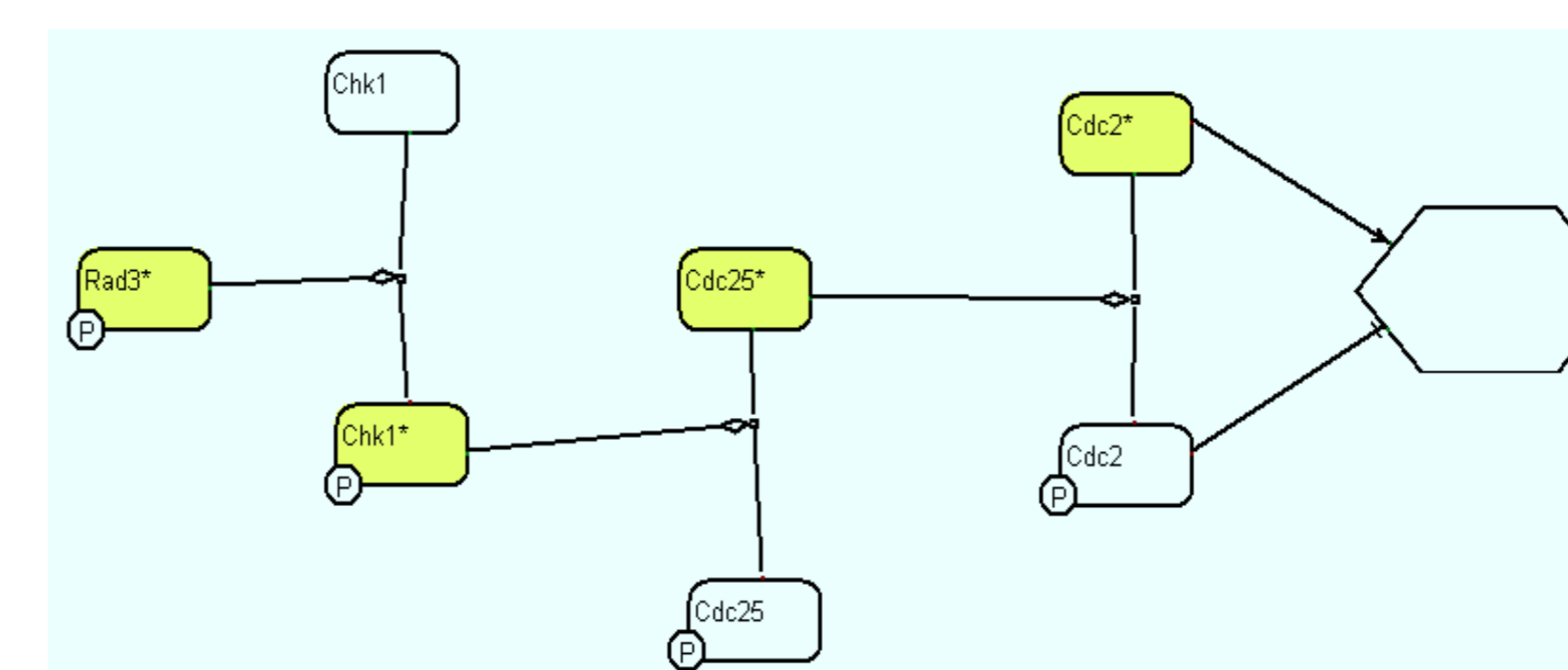
Edinburgh Pathway Notation



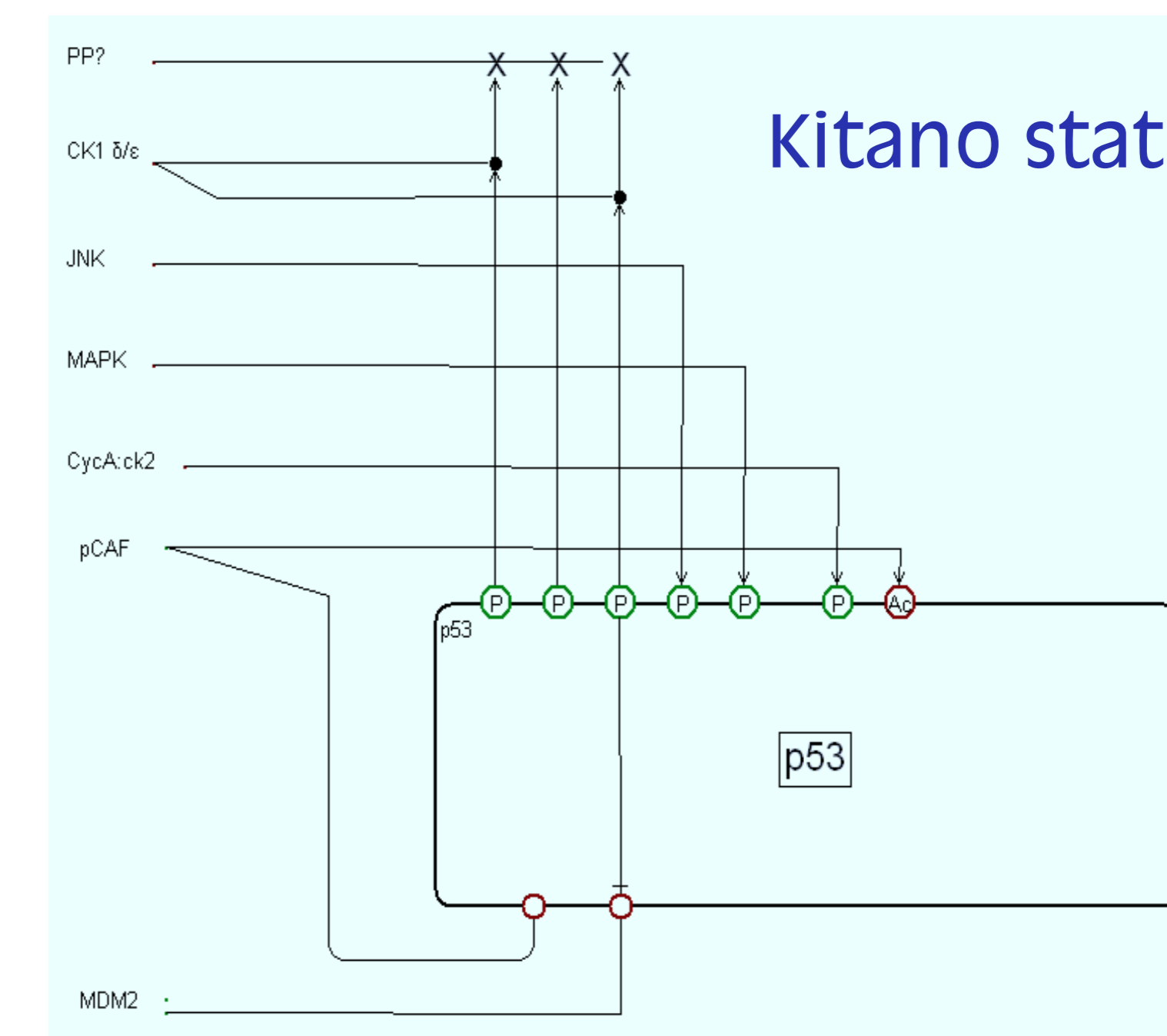
Implemented Notations

- EMP/WIT metabolic pathway
- KEGG-like metabolic pathway description
- Edinburgh process notation
- STKE
- Kitano process notation
- Kitano state notation
- Biocarta-like artistic notation

Kitano process notation



Kitano state notation



STKE pathway

