

## Pathway Tools Tutorial

### Exercise 3: Superpathways

- **Please only modify the *H. pylori* database.**

For many reasons, both biological and logistical, we keep the pathways in MetaCyc small. However, it is often useful to present a larger portion of the metabolic network. This is achieved by construction of superpathways.

**In this exercise we will create a superpathway for the biosynthesis of biotin.**

1. Open the pathway “biotin biosynthesis from 8-amino-7-oxononanoate I” (**PWY0-1507**). The pathway starts with 8-amino-7-oxononanoate, which is produced in this organism by the pathway “8-amino-7-oxononanoate biosynthesis I” (**PWY-6519**). Click on this link, and you will see that this pathway is in turn linked to another pathway – “fatty acid biosynthesis initiation I” (**PWY-4381**).
2. Create a new pathway with the common name “**superpathway of biotin biosynthesis**”. Classify it in two classes: “Biosynthesis → Cofactors, Electron Carriers Biosynthesis → Vitamin Biosynthesis → Biotin Biosynthesis”, and “Superpathways”.
3. When the Pathway Editor opens, select Pathway -> Add Subpathway by Frame ID, and type the frame IDs, each on a different line (**PWY-4381, PWY-6519, PWY0-1507**). When you click OK, the pathways show up, but are not connected.
4. Click on “a malonyl-[acp]” in first subpathway, then on the first reaction of the second pathway (which lights up in green). The software will connect the two pathways. Now click on the last compound of the connected pathways and connect it to the last subpathway.
5. Exit the editor saving your changes.
6. What if you want to remove a subpathway from the superpathway? Open the pathway editor and select Pathway -> Delete Subpathway. From the list that

opens, select the “fatty acid biosynthesis initiation” subpathway and click “use these values”. The subpathway is gone.

The final superpathway should look like this:

