How To Find Your Way in a Metabolic Network

Some years ago, Boehringer distributed a map that shows a huge metabolic network, which every biochemist (and not only they) will certainly remember. This very impressive but complicated map helps the viewer to understand what happens inside a cell. However, one had to stand in a lab aisle for a very long time and hope not to be disturbed by the night-watch.

Nowadays, the internet allows people to make this kind of comprehensive information interactive and much more convenient to access. As an excellent example, the University of Minnesota Biocatalysis/Biodegradation Database (UM-BBD) is dedicated to microbial biocatalytic reactions and biodegradation pathways, primarily for xenobiotic compounds. It makes it easy to find out what happens to molecules during their enzymatic "digestion" by microbes. Although only smaller parts of the pathways are included, the database still contains a lot of information (currently: 108 pathways, 735 reactions, 658 compounds, 453 enzymes, 295 microorganisms, 49 organic functional groups, 73 reactions of naphthalene 1,2-dioxygenase, and 108 reactions of toluene dioxygenase). Many scientists focusing on the degradation of specific compounds by microorganisms contributed to the database,[1] which is maintained by University of Minnesota staff and supported by an International Scientific Advisory Board. This also ensures that updates and new pathways (suggestions and contributions are welcome!) are verified before they are included in the database. The goal of the UM-BBD is to provide information on microbial enzyme-catalyzed reactions that are important for biotechnology. At the University of Minnesota, it is also used in a graduate-level course offered over the internet.

Fortunately, the database does not only show a schematic drawing of a pathway (Figure 1). Each compound is "clickable" to provide specific and rapid access to all reactants involved as well as detailed information on the chemical properties of each metabolite (so as to satisfy the chemists). Maybe more exciting to biologists, enzymologists, and biochemists, access is provided to the respective enzymes, their sequence, availability, properties etc., related biocatalysts, and the producing microorganism.

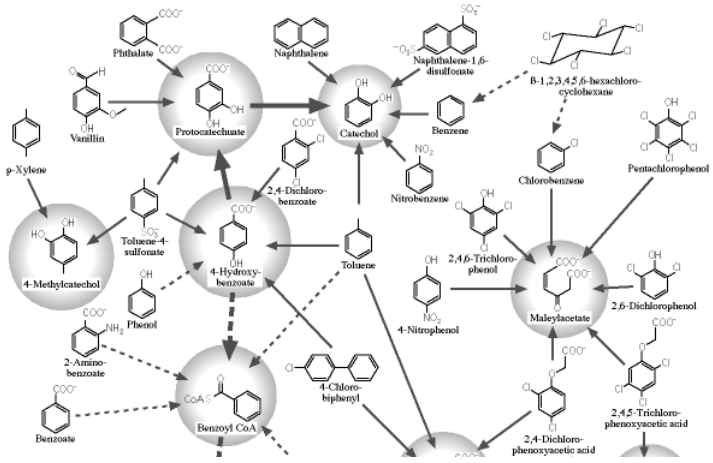

Fig. 1. Part of the metapathway map.

From p-Xylene to p-Methylbenzyl alcohol

Graphic (3k) of the reaction.

Medline reference
Shaw JP, Harayama S *Eur J Biochem* (1992) **209**(1): 51-61.

Search Medline titles for **xylene monooxygenase**.
6 citations on Feb. 27, 2001.

p-Xylene
|
| 1/2O_2
xylene | /
monooxygenase |/
1.14.13.- | Search GenBank, 8 hits on Nov. 03, 2000.
|
ExPASy |
|
v
p-Methylbenzyl alcohol

Generate a pathway starting from this reaction.

[p-Xylene] [BBD Main Menu]

Fig. 2. The degradation pathway of *p*-xylene.

The website is also a pleasure to work with, as the user can choose from several means to discover pathways for the degradation of specific molecules, for example in a pull-down menu or by clicking on the "metapathway map" (Figure 1). Whichever way you choose, you will find detailed background information (Figure 2). With links to Medline, GenBank, ExPASY, and others, rapid access to even more data, such as references, pdf files, or protein structures, is ensured.

As this website represents an extremely interactive and up-to-date source of information, I highly recommend it for fruitful discoveries. Moreover, I encourage all researchers who study biochemical pathways to contribute to this site or to develop new ones that use the same approach.

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Suggest a web site or submit a review:
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For further information visit:
http://umbbd.ahc.umn.edu/

[1] L. B. M. Ellis, C. D. Hershberger, E. M. Bryan, L. P. Wackett, *Nucl. Acids Res.* **2001**, *29*, 340 – 343.

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