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Cover photograph (Copyright © 2008, American Society for Microbiology. All Rights Reserved.): Depiction of the reconstructed genome-scale metabolic network of *Pseudomonas aeruginosa*, accounting for the function of 1,056 genes and with validated predictive ability for gene lethality (with approximately 85% accuracy) and other cellular phenotypes. This reconstruction facilitated the refinement of gene annotations, and its analysis also provided evidence to resolve the effects of transposon insertion mutations on neighboring genes. (See related article on page 2790.)