

## Understanding the Metabolic Capabilities of *Desulfovibrio vulgaris* Hildenborough

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*Desulfovibrio vulgaris* Hildenborough is one of the organisms focused on by the Department of Energy because it possesses the ability to reduce heavy metals such as uranium and chromium. To better understand the capabilities of this organism with respect to growth, reducing potential, and bioremediation, we have developed a flux balance model based on the most recent version of the genome annotation available from the Genomes to Life project. The model accounts for primary and secondary metabolism and takes into account the most current understanding of energy metabolism within the anaerobe *D. vulgaris*.

In addition to the most recent genome annotation, the flux balance model was augmented with experimental observations regarding required growth conditions, in vitro enzymatic assays, and suggested enzymatic species to complete missing pathway steps using the SRI Pathway Tools software. These analyses reveal several distinct pathway features in *D. vulgaris*.

The preliminary version of this flux balance model accounts for components of over 160 pathways from the METACYC database, 500 enzymes catalyzing over 850 reactions, and approximately 600 compounds. Using this model as a starting point, strategies for maximizing metal reduction, minimizing hydrogen sulfide production, and identifying alternative growth conditions have been explored. These correspond to exploring the objectives of minimizing corrosion due to *D. vulgaris* and maximizing bio-based metal recovery from contaminated water supplies.