

Amino acid synthesis pathways in *Desulfovibrio vulgaris*

Morgan N. Price^{1,2}, Swapnil R. Chhabra^{1,2,3}, Yinjie J. Tang^{1,2}, Peter I. Benke^{1,2,3}, Edward E. Baidoo^{1,2,3}, on-Yi Fook^{1,2,3}, Samuel Myers¹, Paramvir S. Dehal^{1,2}, Aindrila Mukhopadhyay^{1,2,3}, Jennifer V. Kuehl^{1,2}, Thomas R. Juba¹, Grant M. Zane^{1,2,4}, Judy. D. Wall^{1,2,4}, Jay D. Keasling^{1,2,3,5}, Adam P. Arkin^{1,2,3,5}

¹Virtual Institute for Microbial Stress and Survival, <http://vimss.lbl.gov/>; ²Lawrence Berkeley National Laboratory, Berkeley, CA; ³DOE Joint BioEnergy Institute, Emeryville, CA; ⁴University of Missouri, Columbia, MO; and ⁵Department of Bioengineering, University of California, Berkeley, CA

Acknowledgements

This work was part of the Virtual Institute for Microbial Stress and Survival (<http://VIMSS.lbl.gov>) supported by the U. S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomics:GTL program through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U. S. Department of Energy

Several steps in amino acid synthesis pathways are not annotated in the *Desulfovibrio vulgaris* genome. We computationally predicted several new reactions, including isoleucine synthesis via citramalate synthase (DVU1914), methionine synthesis via a potential bifunctional cystathionine gamma-synthase and beta-lyase (DVU0171), synthesis of alpha-ketoglutarate and glutamate via an Re-citrate synthase (DVU0398), and synthesis of chorismate and aromatic amino acids via an archaeal-like transaldolase and 3-dehydroquinate cyclase/deaminase (DVU0460, DVU0461). We are using genetic knockouts and complementation assays to test these predictions.

≠