

# Unravelling proteome response to deletion of genes related to mercury methylation and dissimilatory metal reduction in *G. sulfurreducens* PCA

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## Challenge

- *Geobacter sulfurreducens* PCA is able to methylate and reduce mercury (Hg). Deletion of *hgcAB* and *omcBESTZ* genes impairs its ability for methylation and dissimilatory reduction. However, the underlying biochemical mechanisms of these processes and the impact of the loss of these genes on interdependent metabolic pathways are unknown.

## Approach and Results

- Shotgun proteomics is used to delineate the global response of *G. sulfurreducens* PCA after deletion of *hgcAB* and *omcBESTZ* genes related to Hg methylation and dissimilatory metal reduction.
- Deletion of *hgcAB* genes results in increased relative abundances of proteins associated with the extracellular electron transfer in *G. sulfurreducens* PCA, including PilA-C, OmpB and many outer membrane cytochromes.
- Deletion of *omcBESTZ* genes leads to increased protein abundance in central metabolic processes, particularly an increased abundance of methyltransferases.
- The results supports the hypothesis that the function of HgcA and HgcB is linked to one carbon (C1) metabolism through the folate branch of the reductive acetyl-CoA pathway.

## Significance and Impact

- This is the first study comparing differences in the proteomes of  $\Delta hgcAB$ ,  $\Delta omcBESTZ$  and wild-type strains of *G. sulfurreducens* PCA. We provide insight into the impact of these gene deletions on key metabolic processes, the function of HgcA and HgcB, and their linkages to C1 metabolism.

**Reference:** Qian, C.; Johs, A.; Chen, H.; Mann, B. F.; Lu, X.; Abraham, P. E.; Hettich, R. L.; Gu, B., Global proteome response to deletion of genes related to mercury methylation and dissimilatory metal reduction reveals changes in respiratory metabolism in *Geobacter sulfurreducens* PCA. *J. Prot. Res.* 2016. DOI: 10.1021/acs.jproteome.6b00263.

