

Abstract Submitted
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Genome-scale reconstruction of the metabolic network in *Yersinia pestis* CO92¹ ALI NAVID, EIVIND ALMAAS, Lawrence Livermore National Laboratory — The gram-negative bacterium *Yersinia pestis* is the causative agent of bubonic plague. Using publicly available genomic, biochemical and physiological data, we have developed a constraint-based flux balance model of metabolism in the CO92 strain (biovar *Orientalis*) of this organism. The metabolic reactions were appropriately compartmentalized, and the model accounts for the exchange of metabolites, as well as the import of nutrients and export of waste products. We have characterized the metabolic capabilities and phenotypes of this organism, after comparing the model predictions with available experimental observations to evaluate accuracy and completeness. We have also begun preliminary studies into how cellular metabolism affects virulence.

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Ali Navid
Lawrence Livermore National Laboratory

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