Fig. S1. Redox status of DsbA2. The redox state of DsbA2 in stationary phase *L. pneumophila* was interrogated by AMS-alkylation. Lane 1 corresponds to the fully reduced and alkylated migration of DsbA2. *L. pneumophila* whole cells were reduced in buffer containing 10mM DTT, TCA precipitated, and re-suspended in 20mM AMS. Lane 2 corresponds to the oxidized control, DsbA2 without AMS alkylation. Lane 3 shows that DsbA2 exists in both an oxidized and reduced form during stationary phase.

Fig. S2. DsbA2 disulfide bond oxidase mechanism. Diagram of DsbA2 interacting with substrates via S_N2 mechanism adapted from Kadokura, *et al*. shows active site cysteine residues donating their disulfide bond to substrates, producing an S_N2 intermediate of DsbA2-substrate before resolution of enzyme-substrate complex. Also depicted are cartoons of C89S and P198T mutant proteins displaying their predicted mutant structures.

Fig. S3. Expression of C89S or P198T mutant proteins does not affect *in vitro* growth (A) *L. pneumophila* strain AA100 containing: pMMB vector, pMMB:C89S, or pMMB:P198T were grown in BYE broth with or without induction (5 mM IPTG). (B) Immunoblot of IPTG induced (0, 0.5 and 5 mM IPTG) mutant proteins probed with DsbA2-specific antibody at 2, 4, 6 and 10 h of growth. DsbA2 P198T has a His_6 tag and runs at a slightly higher molecular mass than native DsbA2. The C89S protein is not his-tagged. All constructs show increased protein levels following induction.