Supporting Information

Iminoguanidines as Allosteric Inhibitors of the Iron-Regulated Heme Oxygenase (HemO) of *Pseudomonas aeruginosa*

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Figure S1. HXMS peptide coverage map for HemO following pepsin digestion. Protease treatment following hydrogen exchange and peptide analysis as described in "Experimental Section".

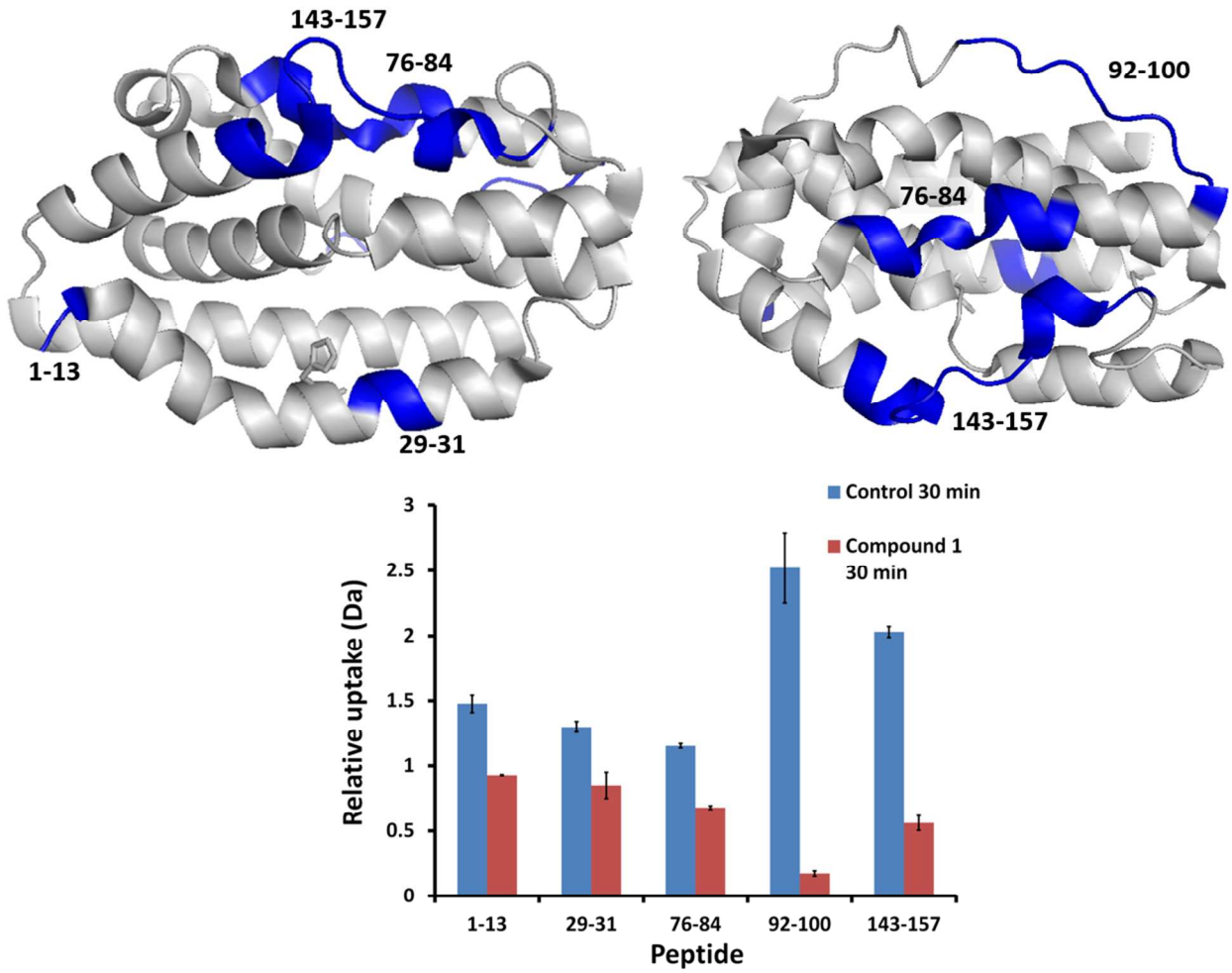

Figure S2. Color coded protein structure of apo-HemO representing deuterium uptake change upon binding of compound 1. Deuterium incorporation was mapped onto the HemO crystal structure (PDB 1SK7) as viewed from front (heme-binding pocket, upper left) and from above (upper right). Peptide regions of apo-HemO which were more protected from deuterium exchange in the presence of **1** are colored in blue, whereas regions which became more prone to deuterium exchange are colored in red. Relative deuterium uptake of peptides showed differences between apo-HemO and apo-HemO in the presence of **1** at 30 min (bottom). All five peptides were significantly more protected from deuterium exchange upon binding of **1** (Student's *t*-test, $p < 0.05$, n=2). Error bar, standard deviation.

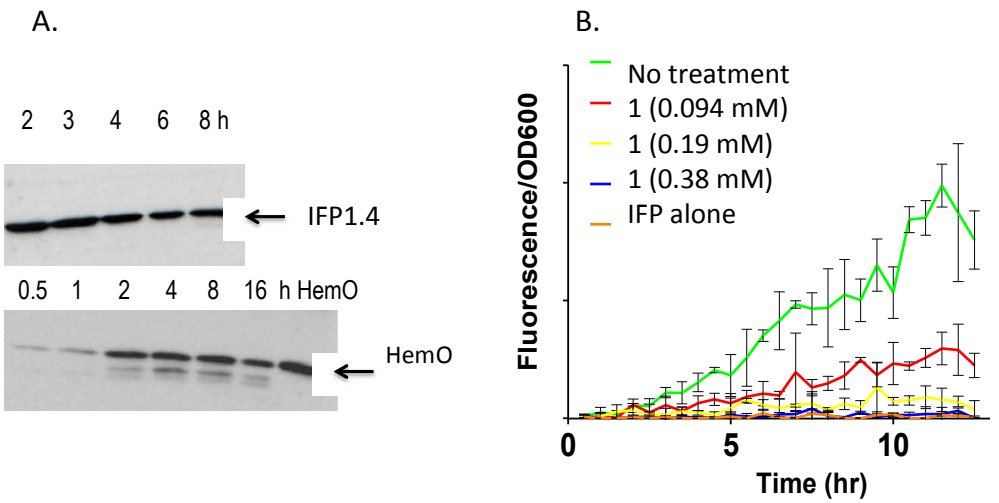

Figure S3. Fluorescence quenching as a function of HemO inhibition. A. Western blot over the time course of the experiment following induction of HemO with 0.02% arabinose. All experiments were performed in triplicate and averaged. IFP1.4 is induced at time 0 with 1 mM IPTG. B. Fluorescence as a function of growth corrected for OD_{600} and concentration dependent quenching with compound **1**. Experiments were performed as described in "Experimental Section".