

ADVANCES IN MICROBIAL PHYSIOLOGY

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C O N T E N T S

Novel Bacterial MerR-Like Regulators: Their Role in the Response to Carbonyl and Nitrosative Stress

Alastair G. McEwan, Karrera Y. Djoko, Nathan H. Chen, Rafael L.M. Couñago, Stephen P. Kidd, Adam J. Potter and Michael P. Jennings

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Metal Sensing in *Salmonella*: Implications for Pathogenesis

Deenah Osman and Jennifer S. Cavet

Cover illustration. Homology model of NmlR from *N. gonorrhoeae*. Ribbon diagram showing the location of the four cysteine residues (indicated by red spheres) found on the NmlR molecule. The model suggests that the two cysteine residues absolutely conserved on the NmlR family of transcriptional regulators (Cys 54 and Cys-71, indicated) are solvent-exposed and located in the DNA-binding domain of the molecule. Based on the structural information from related transcriptional regulators, NmlR was modeled as a dimer (yellow and green cartoons). The gonococcal NmlR model was produced using the ModWeb Server at UCSF with default parameters and used as template PDB entry 3gp4 (30% sequence identity to gonococcal NmlR). The DNA molecule (shown as ribbons – phosphate backbone and rods – bases) was introduced to the model following a simple rigid body superposition of the gonococcal NmlR with the DNA-bound MerR-like transcriptional regulator from PDB entry 2vz4 (22% identity to gonococcal NmlR). (McEwan, Djoko, Chen, Couñago, Kidd, Potter, & Jennings.)



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