Articles of Significant Interest Selected from This Issue by the Editors

Separating the Activities of a Stress Response Enzyme Suggests the Mechanisms of Stress-Mediated Damage

The DNA-binding protein from starved cells (Dps) is a highly conserved, potent bacterial stress response protein that can increase survival rates during exposure to a great number of different stressors. Karas et al. (p. 3206–3215) have identified the critical residues for both of the biochemical activities of *Escherichia coli* Dps: DNA binding and iron oxidation. Each activity when tested individually was seen to be required for protection of DNA from oxidative damage *in vitro* as well as enhanced survival of environmental stresses. These results suggest that many different types of stress may cause both oxidative/metal stress and physical damage to the chromosome.

Characterization of the *Escherichia coli flhDC* Regulatory Region through Activating Mutations

The *flhDC* operon encodes transcription factors that initiate flagellar synthesis. Studies of “wild-type” motility and taxis in *Escherichia coli* K-12 have often used strains with activating insertion elements in the *flhDC* regulatory region. However, strains with the native AT-rich regulatory region tend to have low *flhDC* expression and are marginally motile above room temperature. Fahrner and Berg (p. 3087–3096) describe a new set of activating mutations, including single nucleotide substitutions in the promoter spacer region. Genes inserted far upstream of the promoter also activated expression, suggesting that their higher GC content perturbs a regulating architecture for this operon.

The NirS-DnaK-FliC Triple Complex Is the First Part of Periplasmic Protein Network To Come

A combination of interactomics and electron microscopy was used by Borrero-de Acuña et al. (p. 3066–3075) to discover a nitrate reductase NirS-chaperone DnaK-flagellar protein FliC triple complex in the periplasm of the opportunistic pathogen *Pseudomonas aeruginosa*. NirS and DnaK serve as essential structural components for flagellar formation and motility. Interestingly, DnaK was considered to be cytoplasmic, while FliC was part of the extracellular flagellum. This study points toward a strictly organized protein network in the periplasmic compartment of Gram-negative bacteria.