# IN BRIEF

## BACTERIAL PATHOGENESIS

### Invasive and adherent bacterial pathogens co-opt host clathrin for infection

Veiga, E. *et al. Cell Host & Microbe* **2**, 340–351 (2007)

Although many viruses enter host cells by clathrin-mediated endocytosis, it was thought that clathrin-coated vesicles were too small to internalize bacteria. So, it was a surprise when *Listeria monocytogenes* was shown to enter host cells by a clathrin-dependent mechanism. Building on this previously published finding, Veiga *et al.* investigated whether clathrin is required for the entry of other pathogens. They found that bacteria that enter cells after interactions with specific receptors, such as *Staphylococcus aureus*, require clathrin for entry, whereas those that inject effectors into host cells to facilitate their own entry by altering the host cytoskeleton, such as *Shigella flexneri*, do not. Clathrin was also required to assemble pedestals beneath adherent enteropathogenic *Escherichia coli*, which remain extracellular.

## MOLECULAR ECOLOGY

### Mutational activation of niche-specific genes provides insight into regulatory networks and bacterial function in a complex environment

Giddens, S. R. *et al. Proc. Natl Acad. Sci. USA* **104**, 18247–18252 (2007)

The identification of environment-induced loci (EIL) is hampered by a lack of discernable phenotypes in the laboratory when EIL are mutated. Giddens *et al.* describe a new, broadly applicable method — SpyVet (suppressor analysis with *in vivo* expression technology) — to identify regulatory loci that control EIL in the rhizosphere bacterium *Pseudomonas fluorescens*. Promoters of EIL are fused to *dapB* (required for lysine biosynthesis), rendering strains prototrophic in the rhizosphere, where EIL are expressed, but auxotrophic in minimal growth media, where EIL are not expressed. Transposon mutagenesis, coupled with a simple screen for prototrophy in the laboratory, can quickly identify genes that regulate EIL–*dapB* fusions. A secondary screen for other members of the regulatory hierarchy was also feasible, which enabled these researchers to identify a regulatory network of seven regulators.

## BACTERIAL SECRETION

### A minimal Tat system from a Gram-positive organism: a bifunctional TatA subunit participates in discrete TatAC and TatA complexes

Barnett, J. P. *et al. J. Biol. Chem.* 26 Nov 2007 (doi 10.1074/jbc.M708134200)

The Tat (twin-arginine) secretion system transports fully folded proteins across bacterial membranes. Gram-negative bacteria encode three subunits (TatABC) that are essential for secretion. TatABC form a substrate-binding complex that is thought to recruit a separate and heterogeneous TatA complex, which can form a translocation pore. *Bacillus subtilis* has three TatA and two TatC variants. However, it lacks *tatB*, as do all Gram-positive bacteria. The *B. subtilis tatAd* gene complemented a *tatB* mutant of *Escherichia coli*, indicating that *tatAd* can replace TatA and TatB. Importantly, a *B. subtilis* TatAdCd system secreted a Tat substrate upon expression in *E. coli*, even though the TatAd complex is discrete, in contrast to the heterogeneous *E. coli* TatA complex. Direct experiments in *B. subtilis* are now needed to resolve the current controversy over how Tat secretes proteins.