# IN BRIEF

## BACTERIAL GENOMICS

### The Bronze Age: a time before bubonic plague

*Yersinia pestis*, the causative agent of plague, is thought to have arisen from the less virulent enteric bacterium *Yersinia pseudotuberculosis* between 2,600 and 28,000 years ago. Until now, *Y. pestis* had not been recovered from human remains older than 1,500 years. Now, a report identifies *Y. pestis* in the teeth of 7 (out of 101) Eurasian individuals dating from 2,800 to 5,000 years ago. Notably, the *Y. pestis* genomes from these Bronze Age individuals all lacked *ymt*, the gene encoding a phospholipase that is essential for bacterial survival in the flea vector, which is responsible for transmission of bubonic plague. Furthermore, the ancient *Y. pestis* genomes encoded the Pla protein, which is essential for deep tissue invasion, but they lacked an isoleucine-to-threonine mutation that is essential for developing bubonic plague. These data suggest that a less pathogenic *Y. pestis* was already endemic in humans before it acquired genetic changes that enabled bacterial survival in the flea vector and deep tissue invasion, which gave rise to more virulent strains responsible for pandemic bubonic plague.

**ORIGINAL RESEARCH PAPER** Rasmussen, S. *et al.* Early divergent strains of *Yersinia pestis* in Eurasia 5,000 years ago. *Cell* **163**, 571–582 (2015)

## VIRAL INFECTION

### Highly flexible influenza polymerase

Influenza viruses rely on an RNA-dependent RNA polymerase, sometimes known as FluPol (comprising PB1, PB2 and P3 subunits), that both transcribes and replicates the viral RNA genome. Transcription initiation occurs by cap-snatching and depends on a viral RNA (vRNA) promoter; all currently available FluPol structures reflect this transcription pre-initiation state, with vRNA bound to FluPol. Now, Hengrung *et al.* report a new FluPol structure without vRNA. This structure reveals a novel 'closed' conformation in which the central PB1 subunit (which houses the polymerase active site) is capped on one end by PB2 and clamped between the two globular domains of P3. Notably, the cap-binding domain of PB2 is occluded in this closed state, suggesting that binding of the vRNA is responsible for substantial conformational changes that induce the transition of FluPol to the 'opened' transcription pre-initiation state.

**ORIGINAL RESEARCH PAPER** Hengrung, N. *et al.* Crystal structure of the RNA-dependent RNA polymerase from influenza C virus. *Nature* http://dx.doi.org/10.1038/nature15525 (2015)

## MICROBIOME

### Commensal bacterium prevents wasting

One common consequence of infection and inflammation is wasting of skeletal muscle and fat tissue. Now, a new study shows that gut colonization with the O21:H$^+$ commensal strain of *Escherichia coli* can prevent wasting in a mouse model of intestinal inflammation or in mice infected with *Salmonella enterica* subsp. *enterica* serovar Typhimurium or *Burkholderia thailandensis*. Protection mediated by *E. coli* O21:H$^+$ required bacterial translocation to the white adipose tissue (WAT) following infection or intestinal inflammation. In the WAT, *E. coli* O21:H$^+$ induced high levels of insulin-like growth factor 1 (IGF1), in a process that was dependent on activation of the NLRC4 inflammasome. The high levels of IGF1 then stimulated the IGF1–phosphatidylinositol 3-kinase (PI3K)–AKT pathway in skeletal muscle, preventing muscle loss.

**ORIGINAL RESEARCH PAPER** Palaferri Schieber, A. M. *et al.* Disease tolerance mediated by microbiome *E. coli* involves inflammasome and IGF-1 signaling. *Science* **350**, 558–563 (2015)