

IN BRIEF

ENVIRONMENTAL MICROBIOLOGY**Is evidence for ancient microbial life set in stone?**

Ancient oceanic hydrothermal vents may have been one of the earliest habitable environments on Earth. Dodd *et al.* examined ferruginous sedimentary rock from the Nuvvuagittuq supracrustal belt (NSB) in Quebec, Canada, for the presence of microfossils that are suggestive of early microbial life. The NSB is a fragment of primitive oceanic crust with evidence of hydrothermal vent activity that is between 3,774 and 3,751 million years (possibly up to 4,280 million years) old. Remarkably, the authors observed distinctive filament and tube microstructures in NSB rock samples. These structures were similar in morphology to filamentous iron-oxidizing bacteria that are found in modern hydrothermal vents. The samples also contained preserved minerals and carbonaceous material in rosettes and granules, which may have been formed by the oxidation of biomass. This is suggestive of metabolic processes that are inherent in life. These microfossils are thus far the oldest evidence of life on Earth.

ORIGINAL ARTICLE Dodd, M. S. *et al.* Evidence for early life in Earth's oldest hydrothermal vent precipitates. *Nature* **543**, 60–64 (2017)

VIRAL EVOLUTION**On the origin of capsids**

The origin and evolution of viruses is a topic of debate; in particular, the timing and relationship of cellular and viral evolution are controversial. To identify cellular homologues of viral proteins, Krupovic and Koonin performed an analysis of sequences and structures of capsid and nucleocapsid proteins from representative members of 135 virus taxa. The authors identified 20 architectural classes of viral capsid and nucleocapsid proteins, which were hypothesized to have evolved independently. A systematic comparison of viral proteins with a database of protein sequences and structures from cellular organisms identified substantial similarities between viral and cellular proteins. Virus genomes were also found to contain distinct structural modules that have different evolutionary paths. The authors argue that these observations support a view that viruses evolved on several, independent occasions by co-opting host cellular proteins to become part of virions.

ORIGINAL ARTICLE Krupovic, M. & Koonin, E. V. Multiple origins of viral capsid proteins from cellular ancestors. *Proc. Natl Acad. Sci. USA* <http://dx.doi.org/10.1073/pnas.1621061114> (2017)

STRUCTURAL BIOLOGY***In situ* architecture of the type III secretion system**

Type III secretion systems (T3SSs) are multi-protein assemblies that traverse the inner and outer membranes of Gram-negative bacteria and deliver effectors into host cells. They comprise an outer membrane needle complex, an inner membrane export apparatus and a cytoplasmic sorting platform. High-resolution structures of the needle complex have been obtained by cryo-electron microscopy; however, little is known about the structure of the T3SS machinery *in situ*. Now, Hu *et al.* report the high-resolution structure of the *Salmonella* Typhimurium T3SS *in situ*. Using molecular modelling and comparative analysis of deletion mutants, or T3SSs that were assembled with tagged subunits, the authors localized the major structural components of the injectisome. They also show that assembly of the sorting platform triggers conformational changes in the needle complex. This work provides fresh insight into a conserved bacterial secretion system.

ORIGINAL ARTICLE Hu, B. *et al.* *In situ* molecular architecture of the *Salmonella* type III secretion machine. *Cell* **168**, 1065–1074 (2017)