

IN BRIEF

 VIRAL PATHOGENESIS**Five is the magic number**

Previous studies have shown that the highly pathogenic avian influenza A virus H5N1 can transmit between ferrets via the airborne route following the acquisition of several mutations. Fouchier and colleagues now show that a minimal set of five mutations is sufficient for this phenotype. Two of the mutations altered the preference of viral haemagglutinin (HA) from avian to mammalian receptors, another substitution increased HA thermostability and the final two mutations (which occurred in the RNA polymerase proteins PB1 and PB2) together increased viral transcription and replication. These adaptive mutations emerged rapidly during viral passage in ferrets and became dominant. As airborne transmissibility is a major contributing factor to the pandemic potential of pathogens, these data should aid surveillance programmes that assess the public health risks of H5N1.

ORIGINAL RESEARCH PAPER Linster, M. *et al.* Identification, characterization and natural selection of mutations driving airborne transmission of A/H5N1 virus. *Cell* **157**, 329–339 (2014)

 STRUCTURAL BIOLOGY**First model of the entire AcrAB–TolC efflux pump**

The AcrAB–TolC efflux pump is widespread in Gram-negative bacteria and confers resistance to multiple antibiotics, as it can extrude a large repertoire of chemically diverse compounds. Du *et al.* now present the first three-dimensional crystal structure of the entire pump from *Escherichia coli*, in complex with its partner protein AcrZ. The pump consists of an AcrB trimer in the inner membrane and a TolC trimer in the outer membrane, which are linked by a periplasmic AcrA hexamer. The authors observed a continuous channel that extends from AcrB through AcrA and into TolC, which is probably the exit conduit for substrates. As TolC is closed in the resting state, the authors propose that it adopts an open conformation owing to direct interactions with AcrA and allosteric cooperativity within TolC. The structure also suggests that the modulatory effects of AcrZ on substrate preference are probably mediated by allosteric interactions with AcrB.

ORIGINAL RESEARCH PAPER Du, D. *et al.* Structure of the AcrAB–TolC multidrug efflux pump. *Nature* <http://dx.doi.org/10.1038/nature13205> (2014)

 MICROBIOME**Introducing the ‘community type’ concept**

In a re-analysis of the 16S rRNA sequences from the Human Microbiome Project, Ding and Schloss show that the bacterial communities from the 18 sampled body sites can be partitioned into distinct ‘community types’. The authors identified between two and seven community types per body site, which, when combined with demographic and life history data, were strongly associated with several factors, including gender and level of education. Interestingly, although the compositions of the oral and gut microbiomes are different, the community types at these sites were predictive of each other. Furthermore, community types from the oral cavity were the least stable, whereas those in the gut and vagina were the most stable. Similar to the enterotype concept for the gut microbiome, the authors argue that the considerable intrapersonal and interpersonal variation of the human microbiome can be interpreted in terms of community types, which should improve our understanding of the influence of the microbiome on human health.

ORIGINAL RESEARCH PAPER Ding, T. & Schloss P.D. Dynamics and associations of microbial community types across the human body. *Nature* <http://dx.doi.org/10.1038/nature13178> (2014)