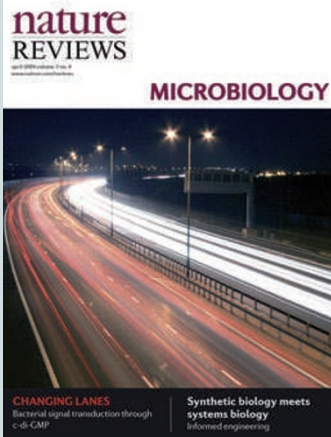




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► **COVER:** 'Changing lanes' by George Marshall, inspired by the Review on p263.



CHRISTIAAN VAN OOIJ



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Pathogenic neisseriae have striking similarities and differences, making them both challenging and intriguing organisms for the development of vaccines. *Neisseria meningitidis*, for example, can live as a commensal organism in the human nasopharynx and can cause fatal cases of meningitis, whereas *Neisseria gonorrhoeae* is sexually transmitted and causes gonorrhoea. Despite their different niche preferences, however, these organisms share a staggering ability to modulate their surface structures with remarkable speed. On page 274, Mumtaz Virji examines our current understanding of the pathogenic tactics of *Neisseria* spp., such as cellular adhesion and invasion mechanisms, with an eye towards future possibilities in vaccine development.

On page 263, Regine Hengge describes one of the recently arisen Sleeping Beauties of the bacterial world — bis-(3'-5')-cyclic dimeric guanosine monophosphate (c-di-GMP) signalling. c-di-GMP was first discovered in 1987, but it has only recently emerged that the enzymes that 'make and break' it are ubiquitous in bacteria. Moreover, these enzymes are key determinants for bacterial lifestyle: they are key players in the decision of whether a bacterium adopts a motile planktonic or a sedentary biofilm-associated lifestyle. By reviewing c-di-GMP signalling in various bacteria, Hengge sheds light on the general principles of why, when, where and how these systems operate.

Finally, Tie Koide, Wyming Lee Pang and Nitin Baliga delve into the role of predictive modelling in rational re-engineering of biological systems on page 297. In an Opinion article, the authors examine recent advances in the design of synthetic circuits and in predictive modelling of prokaryotes. They argue that to achieve effective large-scale and complex re-engineering, the fields of synthetic and systems level biology must converge.

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