**No.604**

## Reprogramming the Genetic Code

In terrestrial life, DNA is copied to messenger RNA, and the 64 triplet codons in messenger RNAs are decoded – in the process of translation – to synthesize proteins. Cellular protein translation provides the ultimate paradigm for the synthesis of long polymers of defined sequence and composition, but is commonly limited to polymerizing the 20 canonical amino acids. Professor Chin will describe their progress towards the encoded synthesis of non-canonical biopolymers. These advances may form a basis for new classes of genetically encoded polymeric materials and medicines. Professor Chin group are re-imagining some of the most conserved features of the cell to realize their goals; They have created new ribosomes, new aminoacyl-tRNA synthetase/tRNA pairs, and organisms with entirely synthetic genomes in which they have rewritten the genetic code.

**Jason W. Chin** is currently a programme leader at the Medical Research Council Laboratory of Molecular Biology (MRC-LMB), where he is also head of the Centre for Chemical & Synthetic Biology (CCSB). He is professor of Chemistry & Chemical Biology at the University of Cambridge, and holds a joint appointment at the University of Cambridge Department of Chemistry. He is also a fellow in Natural Sciences at Trinity College, Cambridge.

His research interests focus on: genetic code expansion in model organisms, photochemical genetics, protein labeling and imaging, post-translational modifications and reprogramming translation. His lab has pioneered both the development and application of methods for reprogramming the genetic code of living organisms and the use of pyrrolysyl-tRNA synthetase/tRNA pairs for genetic code expansion. Professor Chin's group have developed approaches to make proteins bearing post-translational modifications that were previously inaccessible and have developed approaches to rapidly control enzymatic activity and protein

transport in cells with a millisecond pulse of light. Professor Chin's group are developing approaches that allow any site in a protein of interest to be rapidly, specifically and efficiently labelled with a probe of interest in vivo.