METHODS IN BRIEF

MASS SPECTROMETRY

A method for glycan sequencing

Though protein glycosylation is known to play an important role in many biological processes, glycan and glycopeptide structures remain very challenging to characterize owing to their diverse and heterogeneous nature. Although mass spectrometry has been a considerably useful technology for obtaining structural information about complex mixtures of glycoconjugates, a remaining challenge has been the inability to distinguish epimers (stereoisomers that differ only by a single chiral center). Both *et al.* now report a method using ion-mobility mass spectrometry (IM-MS) that is able to distinguish epimers on the basis of the unique ion-mobility drift times of the monomers generated by collision-induced dissociation. They further showed that a series of epimeric disaccharides could be successfully analyzed by the IM-MS technique, which suggests that the approach could be used generally for glycan sequencing.

Both, P. *et al. Nat. Chem.* **6**, 65–74 (2014).

NEUROSCIENCE

A scar with potential

A common hallmark of injured brain areas is the appearance of a 'gliotic scar'. Gliosis involves the activation of glial cells such that they proliferate and secrete factors that can prevent neuronal growth and recovery. Reactive glial cells—including astrocytes, oligodendrocyte precursors (NG2 cells) and microglia—can be detected in brains from patients that have suffered from stroke, glioma or neurodegeneration. Guo *et al.* devised a strategy to reprogram activated glial cells into functional neurons in adult mouse brains, possibly providing new ways of promoting recovery of injured or diseased brains. They did this by using retroviruses, which selectively target dividing cells in the brain (such as reactive glial cells or progenitor cells), and overexpressing in these cells the transcription factor NeuroD1. This single transcription factor was able to reprogram astrocytes into glutamatergic neurons and NG2 cells into both glutamatergic and GABAergic neurons.

Guo Z. *et al. Cell Stem Cell* doi:10.1016/j.stem.2013.12.001 (19 December 2013).

GENOMICS

Profiling of RNA editing

According to the central dogma of molecular biology, information flows from DNA to RNA to protein; but in some instances, such as RNA editing, genomically encoded information can be altered. During A-to-I editing, adenosine deaminases convert adenosine to inosine in double-stranded RNA, which is subsequently read as a guanosine. A-to-I editing in primates occurs mostly in Alu sequences, which make up about 10% of the human genome and are frequent in gene-rich regions. A comprehensive profiling approach of A-to-I sites by Bazak *et al.* showed that all adenosines in Alu repeats that form double-stranded RNA are edited at low levels per site. The next step will be to explore the function of these variations in the human transcriptome.

Bazak, L. *et al. Genome Res.* doi:10.1101/gr.164749.113 (17 December 2013).

STRUCTURAL BIOLOGY

Using idle computers to stretch simulations

G protein–coupled receptors (GPCRs) control important signaling pathways in the body and are the targets of over one-third of medical drugs. Predicting how GPCRs convert between active and inactive forms can provide insights into ligand binding and suggest new modes of activation, but detailed molecular dynamics simulations require modeling thousands of atoms and are feasible only on supercomputers. Kohlhoff *et al.* now take advantage of excess cloud computing power at Google to carry out an atomic-scale simulation of the GPCR β_2-adrenergic receptor, which is involved in obesity, diabetes and asthma. They use idle time on servers with Google Exacycle and then use Markov state modeling to compile shorter simulations into a two-millisecond-long model, revealing a number of parallel conformational pathways and breaking the previous simulation length record by an order of magnitude.

Kohlhoff, K.J. *et al. Nat. Chem.* **6**, 15–21 (2014).