METHODS IN BRIEF

PROTEOMICS

The apoptotic phosphoproteome

During apoptosis, or programmed cell death, a substantial portion of the proteome is chewed up by caspases in a process regulated at least in part by phosphorylation. However, the global relationship between proteolysis and phosphorylation in apoptosis has not been well studied. Dix *et al.* applied a quantitative method called PROTOMAP (protein topography and migration analysis platform) to investigate the global apoptotic phosphoproteome of mammalian cells. PROTOMAP uses SDS-PAGE to determine the size and topography of SILAC-labeled proteins, followed by in-gel digestion, phosphopeptide enrichment, and peptide identification and quantification by mass spectrometry. The output is a quantitative 'peptograph' that highlights phosphorylation sites on the topographical map of cleaved proteins. Dix *et al.* discovered ~500 apoptosis-specific phosphorylation events that were enriched on cleaved proteins and at caspase cleavage sites.

Dix, M.M. *et al. Cell* **150**, 426–440 (2012).

GENE EXPRESSION

Single-cell transcriptome sequencing

Although the genome of all cells in a given organism is largely the same, the transcriptome varies even within cells of the same tissue. Understanding this heterogeneity in gene expression will shed light on many developmental and disease processes but is technically challenging, even in the age of high-throughput RNA sequencing (RNA-seq). With their 'Smart-seq' method, Ramsköld *et al.* improve on previous protocols for single-cell RNA-seq, achieving balanced coverage across full transcripts rather than just the 3′ ends of mRNAs. The researchers characterized the effect of low RNA input on the sensitivity of the method and its ability to detect differential expression. When applied to circulating tumor cells in a melanoma patient, Smart-seq yielded interesting leads for potential biomarkers.

Ramsköld, D. *et al. Nat. Biotechnol.* **30**, 777–782 (2012).

CHEMICAL BIOLOGY

Glycosyltransferase discovery

Glycans are biosynthesized by a very large class of enzymes called glycosyltransferases, which transfer a sugar from a nucleotide donor to an acceptor substrate, forming a glycosidic linkage in the process. However, only a handful of these enzymes have been characterized in terms of their specific functions. Ban *et al.* now describe a screening method to assign glycosyltransferase function. The approach uses a self-assembled monolayer on a gold surface to array a series of carbohydrate acceptor substrates. The researchers apply a solution containing a nucleotide donor and a glycosyltransferase of interest to the array, and then they use a surface-based mass spectrometry technique referred to as SAMDI to identify newly formed glycosidic linkages. Ban *et al.* used the approach to monitor ~60,000 reactions, allowing them to functionally characterize four new glycosyltransferases.

Ban, L. *et al. Nat. Chem. Biol.* **8**, 769–773 (2012).

EPIGENETICS

Profiling chromatin at specific loci

It's not just DNA that matters—it's what binds to it that exerts regulatory influence. Chromatin modification is an intricately orchestrated process that involves many players such as remodeling proteins and histones. Capturing this assembly in an unbiased fashion at a specific genomic locus is far from a trivial task because current methods such as chromatin immunoprecipitation only look at one player at a time. To achieve simultaneous profiling of multiple targets, Byrum *et al.* have developed chromatin affinity purification coupled with mass spectrometry (ChAP-MS). They isolated a 1,000-kb region around a transcriptionally active or inactive *GAL1* promoter in yeast and compared the associated proteins and histone modifications. This molecular snapshot at a specific locus will allow insights into epigenetic regulatory mechanisms.

Byrum, S.D. *et al. Cell Reports* **2**, 198–205 (2012).