IN BRIEF

CELL CYCLE

A Nup133-dependent NPC-anchored network tethers centrosomes to the nuclear envelope in prophase

Bolhy, S. *et al. J. Cell Biol.* **192**, 855–871 (2011)

During the G2–M transition, microtubules exert pulling forces on the nuclear envelope, leading to nuclear envelope breakdown. The motor protein dynein and its activator, dynactin, were known to have a role in this process, but how they bind to the nuclear envelope was unclear. This study shows that binding to the nuclear envelope is mediated by the nuclear pore complex protein NUP133. The amino-terminal domain of NUP133 (which is dispensable for nuclear pore complex assembly) binds centromere protein F (CENP-F) and recruits it to the nuclear envelope during the G2–M transition. CENP-F can then anchor dynein–dynactin to the nuclear envelope in prophase, and this interaction is mediated by the dynein-interacting proteins NuDE and NuDEL. NUP133-mediated recruitment of dynein–dynactin to the nuclear envelope is necessary to tether centrosomes to the nuclear envelope during the G2–M transition.

SMALL RNAS

Argonaute2 complexes carry a population of circulating microRNAs independent of vesicles in human plasma

Arroyo, J. D. *et al. Proc. Natl Acad. Sci. USA* 7 Mar 2011 (doi:10.1073/pnas.1019055108)

MicroRNAs (miRNAs) were thought to remain stable outside of cells in blood plasma by being encapsulated in vesicles, but this study shows that most are protected by associating with a ribonucleoprotein complex. First, the authors confirmed that circulating miRNAs are sensitive to degradation by RNases. Of the three miRNAs tested, two were not found in vesicles and instead were protected by associating with protein complexes. Further analysis of 88 plasma miRNAs revealed that there are three classes of circulating miRNAs: vesicle-associated miRNAs, non-vesicle-associated miRNAs and miRNAs that can be stabilized by both mechanisms. The non-vesicle-associated miRNAs associated with Argonaute 2, which suggests that this is the mechanism by which they remain stable in plasma. Whether other Argonaute proteins or other ribonucleoproteins can act as carriers of circulating miRNAs remains to be determined.

DNA REPAIR

HDACs link the DNA damage response, processing of double-strand breaks and autophagy

Robert, T. *et al. Nature* **471**, 74–79 (2011)

The DNA damage response is sensitive to the dynamics of protein acetylation. Foiani and colleagues find that this is partly because acetylation of the Sae2 repair protein targets it for degradation through autophagy. They observed that inhibition of histone deacetylases (HDACs) by valproic acid (VPA) impaired processing and resection of double-strand breaks and that this correlated with reduced levels of Sae2. Acetylation can affect protein turnover by inducing autophagy. Indeed, Sae2 was found to be acetylated, and its loss owing to VPA inhibition was rescued when autophagy was blocked. Similar effects on Sae2 levels were observed in mutants for two HDAC enzymes, Rpd3 and Hda1. These mutants were sensitive to the DNA-damaging agent camptothecin, and this sensitivity was relieved by inhibition of autophagy. Thus, the levels of key repair proteins such as Sae2 are controlled by acetylation, which drives their selective turnover through autophagy.