Increased microtubule dynamics during mitosis allows for the construction of a spindle, but may make the cytoskeleton vulnerable to the type of defects noted by Rogers et al. on page 873. They find that depletion of a fly microtubule-associated protein (MAP) called EB1 leads to problems in spindle construction, positioning, and functioning, probably because of a failure to counteract microtubule-destabilizing factors.

The product of the budding yeast homologue of EB1, called Bim1p, has been identified as a plus-end microtubule-binding protein necessary for positioning the spindle and promoting microtubule dynamics. Rogers et al. looked first in fly tissue culture cells that were grown so they flattened to double their normal diameter. This allowed the authors to visualize individual microtubules in vivo and confirm that microtubule dynamics are suppressed upon loss of EB1. This probably reflects the presence of an endogenous factor (normally counteracted by EB1) that suppresses dynamics, as microtubules left to their own devices are inherently dynamic.

The loss of EB1 does not, however, have a marked effect on the overall extent of interphase microtubule arrays. Mitosis is another matter. Astral and interpolar microtubules (both of which lack the protective cap present on kinetochore microtubules) are greatly reduced in numbers. The authors suggest that a microtubule-destabilizing factor up-regulated in mitosis may be responsible. Whatever the cause, the upshot is a spindle that wanders far from the center of the cell, as it is no longer braced or tugged into position by astral microtubules that contact the cortex. The loss of interpolar microtubules results in partially collapsed spindles that segregate chromosomes more slowly in anaphase.

Extending the research beyond EB1 will be easier with the cell culture system. Rogers et al. are interested in characterizing several factors, including those that load EB1 at microtubule ends and those that counteract it either by suppressing microtubule dynamics or promoting microtubule destruction.

After proteomic analysis identified 29 different nucleoporins in the yeast nuclear pore complex (NPC), it looked as if the significantly larger and heavier mammalian NPC might contain twice that number of distinct proteins. On page 915, Cronshaw et al. now describe a proteomic analysis of mammalian NPCs that arrives at a surprising tally of mammalian nucleoporins: 29. Despite the numerical similarity, the new work identifies important differences between the two systems and establishes a basis for comparison.

The authors obtained a highly purified NPC fraction from rat liver, and then used mass spectrometry to identify and characterize the proteins making up the NPC. Although the NPCs appear to have remained intact through the purification, only 29 nucleoporins were identified in the final preparation. Two-thirds of the nucleoporins are conserved between yeast and mammalian NPCs, and FG repeat domains are the most highly conserved feature between the two systems. Despite the similarities, six of the mammalian nucleoporins had not been described previously.

The greater abundance and relative mass of some nucleoporins, rather than greater diversity, seems to explain much of the size difference between the yeast and mammalian NPCs. The high degree of similarity between these evolutionarily distant NPCs suggests that the basic functions of the NPC are highly conserved, and that the same basic set of building blocks has evolved to handle specialized functions. Some of those adaptations may also pose risks: of the six previously undescribed nucleoporins the authors identified, one is linked to a human genetic disease known as triple-A syndrome.

On page 855, Wasiak et al. describe another project in the burgeoning field of subcellular proteomics, this one focused on clathrin-coated vesicles. The authors uncovered ten novel proteins in vesicle-enriched preparations, and found that one of them interacts with the clathrin adaptors AP1 and GGA2 and may stimulate clathrin assembly.