

The Pelletier laboratory is interested in various facets of mitotic spindle assembly and centrosome biogenesis. To study these processes we established an imaging pipeline which integrates high-resolution / high-throughput imaging. This microscopy pipeline is compatible with automated imaging of fixed and live cells in 96- and 384-well format and is complimented with a super-resolution microscopy system called OMX, which uses structured-illumination to attain two-fold superior resolution compared to conventional light microscopes. This platform has been used towards the identification and characterization of the human Augmin complex (*Lawo et al, Current Biology, 2009*). Several assays utilizing the aforementioned pipeline have been specifically tailored to study Augmin biology. Briefly, using functional proteomics we identified a novel protein complex composed of eight subunits (HAUS1 -8) that share homology with *Drosophila* Augmin. Depletion of any HAUS subunits leads to defects in mitotic spindle assembly, kinetochore microtubule stability and mitotic spindle pole fragmentation. Defects induced by HAUS depletion are alleviated by NuMA co-depletion suggesting that both factors regulate opposing activities that must be exquisitely balanced to orchestrate robust bipolar mitotic spindle assembly. Recent results on the human Augmin complex and the benefits of super-resolution imaging as applied to the study of mitotic processes will be discussed.