Preface

Study of the septin family of proteins comes with many challenges due to their heteromeric nature with 2–13 genes in an organism plus many splice variants and posttranslational modifications that can tune their properties. Septins are conserved from single-celled eukaryotes to humans, where they are increasingly linked to many human diseases including afflictions of the nervous system and cancer. At the cell level, they act in morphogenesis, cytokinesis, and membrane shape and dynamics. The drive to decipher the conserved features and functions of this heterogeneous group of proteins has required ingenuity and been a source of experimental advancements. There are many unexplored questions, poorly understood mechanisms, and elusive functions for septins leaving ample room for new labs to join the septin community.

This is the first compilation of septin methods for the field, and my goal for this project was to assemble a guidebook to welcome new investigators into the world of septins and a handbook to allow established septin researchers to tackle new questions. The collection includes approaches specific to a variety of model systems including yeast, filamentous fungi, flies, fish, and mammals so that people can readily find approaches appropriate to their preferred experimental systems. The volume also spans a variety of genetic, cell biological, and biochemical approaches to provide entry points into the community from diverse starting points.

The book begins with detailed identification of putative septin genes outside of the typical model systems revealing how much remains to be explored and discovered about septin form and function. This chapter was appropriately written by the founding father of the septin field, John Pringle, along with Masayuki Onishi. John's career-long study of septins from the isolation of the first mutant alleles as conditional cell division cycle mutants in yeast, to the naming and first localization of the proteins and further work on septin assembly and function have launched the field. Similarly, my hope for John's chapter on septins across the tree of eukaryotes is to inspire investigation of diverse forms and functions of septins.

I am grateful to all who contributed to the volume and all the funding agencies around the world that have supported the work of this small community. This is a collaborative and collegial assembly of groups using varied approaches and systems. I also want to thank Sarah Lay for excellent support in the production. With this volume, we share approaches with the goal of facilitating further discovery of this important family of filament forming proteins.

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