

Biological Aging: Methods and Protocols

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This can be a useful book for biogerontologists. The range and variety of experimental model systems and the cellular and molecular methods employed to address questions in basic and applied aging research require a book like this where one can access practical information and advice. Comprised of 25 generally well-written articles, and accompanied by a CD giving high resolution figures from various chapters, this book covers various methods and protocols for studying cellular aging of human cells, yeast cells, and mice. However, one experimental model system which is conspicuous by its absence is the nematode *Caenorhabditis elegans*, which has in recent times proved to be a very powerful system to identify genetic pathways of aging. Similarly, another widely used system for geronto-genetic studies, *Drosophila*, is only discussed in the context of testing the anti-aging and life prolonging effects of certain nutritional factors, and for detecting somatic mutations.

One of the best discussed model systems for which detailed methods and protocols are provided is the Hayflick system of serial passaging and replicative senescence in vitro of normal diploid cells, mostly fibroblasts. Although there is often a lot of repetition in several of these articles, specially in the

introductory parts of these chapters, they cover an impressive range of methods as applied to the study of cellular aging in vitro. These include long term serial passaging and storage, detection of senescence-specific markers, analysis of telomere lengths, methods of cell sorting and telomerase-induced immortalization. Furthermore, potentially useful new methods for studying cellular aging which have been discussed include the use of ribozymes, application of DNA microarrays, subtractive hybridization techniques and induction of cellular senescence by genetic elements and oxidative stress. The other model system that is discussed in more than one chapter is that of the yeast *Saccharomyces cerevisiae*, for studying lifespan dynamics, for calorie restriction studies, and for high-throughput-based screening to identify genes that extend lifespan. Additionally, methods to analyse DNA methyltransferase, evaluating the effects of pharmacological drugs, mapping genetic polymorphisms, and methods for proteomics and metabolomics are also described in the context of aging research.

Finally, despite some glaring omissions in methods and models, this 371st volume in the series titled *Methods in Molecular Biology*, is a welcome source of useful information for researchers intending to find their way into descriptive, analytical and interventional research in biogerontology.

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