
Preface

The chaperonin field has captured the attention of numerous scientists in recent years. A rapidly increasing number of reviews and articles have tried to elucidate the mechanisms by which these multimeric complexes drive the folding of newly synthesized and denatured proteins.

An obvious common theme of chaperonin research first arose from the study of their structural features. All members of this class consist of multiple subunits that form cylindrical structures, which encage proteins in a cave-like environment where folding of proteins takes place according to the current view. Since the chaperonin structures are found even in very primitive organisms, the archaeobacteriae, this “cave scheme” seems to be an evolutionarily successful feature that was conserved and that appears among evolutionarily distinct organisms.

Interestingly, almost all chaperonins have specific cofactors that are involved in the folding process. Even for the eukaryotic cylinder TRiC or CCT, a cofactor called prefoldin or GimC was recently discovered. Only for the archaeal chaperonins cofactors have not yet been discovered, although there seem to be GimC-like homologs in some archaeal species (unpublished observations by M. Leroux).

One key aspect of this volume is the purification of chaperonins along with their corresponding cofactors from different species, with examples ranging from archaee to higher eukaryotes. As there are of course many other species from which chaperonins could be purified, the focus here is to give a representative overview. Many proteins are purified today as recombinant proteins in *E. coli*, which makes the purification protocols easier and less time consuming than in previous years. The protocols are also not the sole protocols for chaperonin purification. Individual labs most likely utilize slightly different techniques, preferring one column over another, etc. However, the protocols described here have been used successfully by the authors and are described in a detailed way to be as reproducible as possible. The notes section especially is intended to reflect the experience of the experimenter with the procedure and should be an important source of troubleshooting for the user of this book.

Chaperonin activity assays for *in vivo* as well as *in vitro* work are the second main focus of this volume. Many assays are given for GroEL, as this is

one of the best characterized and most investigated chaperonin. These assays can also be applied to mitochondrial Hsp60, for example. There are some protocols that describe assays specifically for the eukaryotic chaperonin TRiC. The reason for using more specific protocols for this chaperonin is that it has very specific substrates, such as tubulin and actin. But some of the protocols, for example the method for preparing labeled probes, can be also used for different purposes and might be helpful for numerous other protocols. The addition of purification protocols for the very recently discovered new cofactor of TRiC/CCT, called prefoldin in mammals and GimC in yeast, results from the very recent developments in the field.

I am grateful to series editor John Walker who offered me the opportunity to edit this book and to try something I have never done before. Without his helpful support and advice and without the patience and the encouragement of Tom Lanigan and his staff at Humana Press, I would not have had the opportunity to participate in this enjoyable project. Last but not least, I want to thank all the authors for their enthusiasm in writing the protocols. Their clear and careful descriptions of the protocols contribute to making chaperonin research a less mysterious field.

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