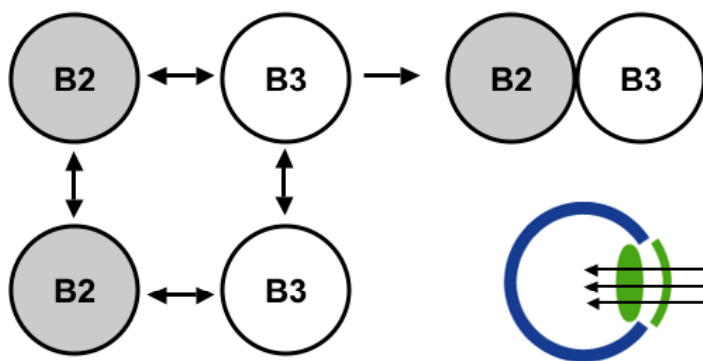


INTERACTION OF THE SUBUNITS OF BETA-CRYSTALLIN BY RADICAL PROBE MASS SPECTROMETRY (RP-MS)

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In the lens of the eye in animals, populations of oligomeric and monomeric crystallin proteins are packed together forming concentration gradients of importance to the optical characteristics of the eye and vision. Beta-crystallins are the most complex lens proteins in terms of the many ways in which subunits of the proteins combine and interact. Two basic subunits beta B2 and B3 have been shown to self-associate and associate with one another to form homo and heterodimers (see figure). Although the latter has been crystallised [1], there is as yet no crystal structure obtained for the dimer. It has been reported, however, that the structure of the beta-crystallin dimer is stabilized through interactions between the N-terminal "arms" of the subunits.



We report here the application of RP-MS, pioneered in the late 1990s [2-4], to study the interaction of the beta B2 and B3 subunits. The approach involves the limited oxidation of the complex through the application of an electrical discharge and measuring the level of oxidation across segments of both subunits by LC-MS. A combination of ESI-TOF, ESI-QTOF, MALDI-TOF/TOF mass spectrometry data will be presented in describing the results [5]. The significance of this data in understanding the interaction of the subunits the context of protecting the eye from cataractogenesis will be discussed.

References:

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