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CORRIGENDUM

Corrigendum to "Crystal Structures of α-Crystallin Domain Dimers of αB-Crystallin and Hsp20" [*J. Mol. Biol.* (2009) 392, 1242–1252]

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The authors wish to note that a model for the solution dimer structure of human αA-crystallin had been proposed previously by Berengian *et al.*, 1997, and Koteiche *et al.*, 1999. This model was based on electron paramagnetic resonance and site-directed spin labeling in which an extended edge β-strand makes an interaction with an equivalent strand across a subunit interface involving residues topologically equivalent to I114, R116, E117, and F118 of αB-crystallin. This is, therefore, consistent with the X-ray structure of the α-crystallin domain dimer of αB-crystallin.

The complete references are as follows:

Berengian, A. R., Bova, M. P. & Mchaourab, H. S. (1997). Structure and function of the conserved domain in alpha A-crystallin. Site-directed spin labeling identifies abeta-strand located near a subunit interface. *Biochemistry*, 36, 9951–9957.

Koteiche, H. A. & Mchaourab, H. S. (1999). Folding pattern of the alpha-crystallin domain in alpha A-crystallin determined by site-directed spin labeling. *J. Mol. Biol.* 294, 561–577.

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