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## Towards crowding in the eye lens: dynamics in aqueous solutions of crystallin proteins

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The function of the eye is dependent on a transparent, refractive, and deformable eye lens. These physical properties are realized by a crowded mixture of mainly crystallin proteins within the eye lens cells. The underlying biophysical mechanisms are not only of fundamental interest, but highly relevant to better understand and treat eye conditions such as presbyopia and cataract.

We present experimental and simulation data on nanosecond dynamics in solutions of  $\alpha$ ,  $\beta$  and  $\gamma$  crystallins as model systems for the cytoplasm in the eye lens. While cage diffusion and gradient diffusion in  $\alpha$  crystallin solutions are consistent with hard sphere systems [1,2], solutions of  $\gamma$  crystallins show short-range attraction, resulting in a significantly reduced cage diffusion [1], and critical slowing down of the gradient diffusion [3].  $\beta$  crystallins appear to have only weak attractive interactions, causing smaller effects than for  $\gamma$  crystallin.

Based on the dynamics characterised in mono-component solutions, we discuss the effects of mutual protein interaction in mixed solutions of crystallins on the dynamics and arrest behavior. For both mixtures of  $\alpha$  /  $\gamma$  crystallins and  $\beta$  /  $\gamma$  crystallins, non-additive effects of the diffusion are observed, suggesting mutual interaction between the crystallins [4].

[1] S Bucciarelli et al. *Sci.Adv.* 2 (2016) e1601432

[2] G Foffi et al. *PNAS* 111 (2014) 16748

[3] S Bucciarelli et al. *JPLC* 6 (2015) 4470

[4] A Stradner et al. *PRL* 99 (2007) 198103

**Authors:** ROOSEN-RUNGE, Felix (Lund University); MYUNG, Jin Suk (Lund University); SCHURTENBERGER, Peter (Lund University); STRADNER, Anna (Lund University, Division of Physical Chemistry)

**Presenter:** ROOSEN-RUNGE, Felix (Lund University)

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