Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.

Supporting information

Exploring homo-FRET to quantify the oligomer stoichiometry of membrane-bound proteins involved in a cooperative partition equilibrium

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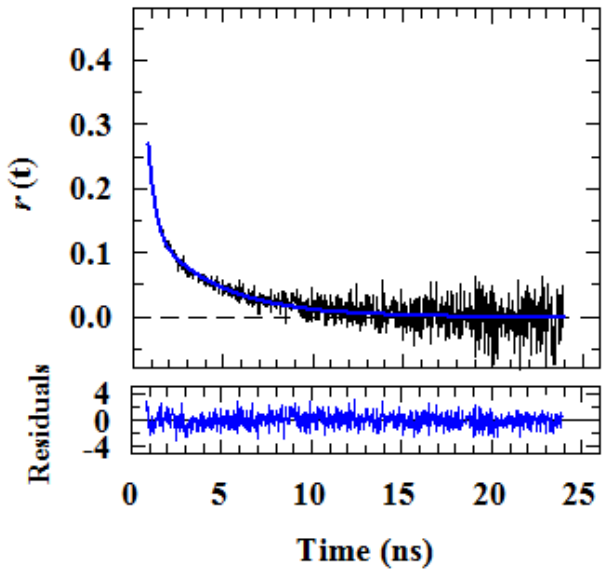

Figure S1 – Fluorescence anisotropy decay from free Lz-BODIPY. The blue solid line is the best fit of eqn (6) to the anisotropy decay obtained for Lz-BODIPY in buffer (1.5 μM, f = 0.53). The residuals of the fit are also shown.

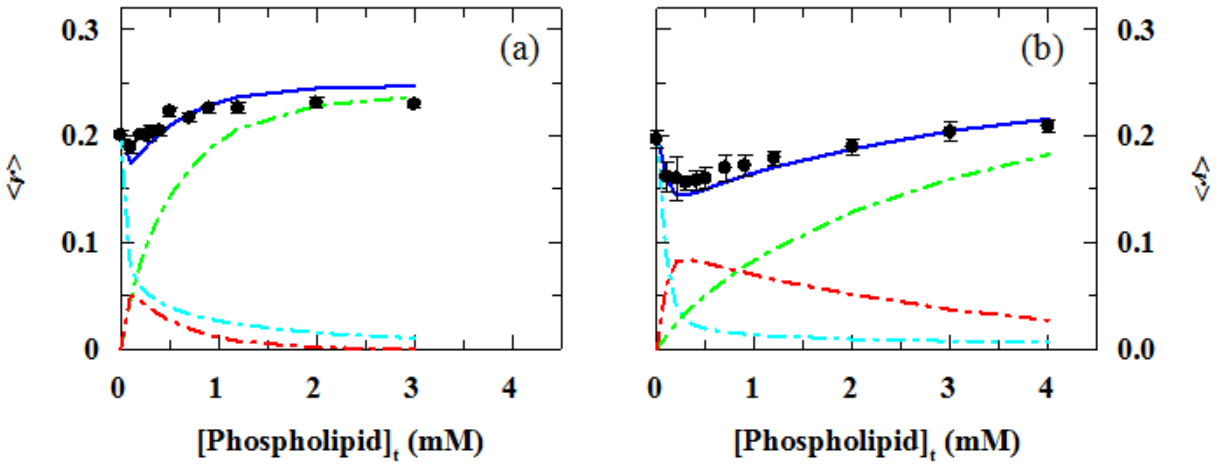

Figure S2 – The extent of homo-FRET critically depends on the membrane surface density of Lz-A488. Changes in the steady-state anisotropy of (a) 0.5 μM and (b) 3 μM lysozyme (f = 0.50) as a function of total phospholipid concentration (POPC:POPS 70:30 LUVs). The blue solid curves are the best-fit of eqn (17) to the steady-state anisotropy data (k = 6 and $K_{ag} = 2 \times 10^{14}$). The cyan, green and red doted dashed lines represent the contribution of the aqueous and membrane–bound monomeric and oligomeric species to the overall anisotropy of the sample, respectively.