Effect of Ionic Liquids on the Solution Structure of Human Serum Albumin

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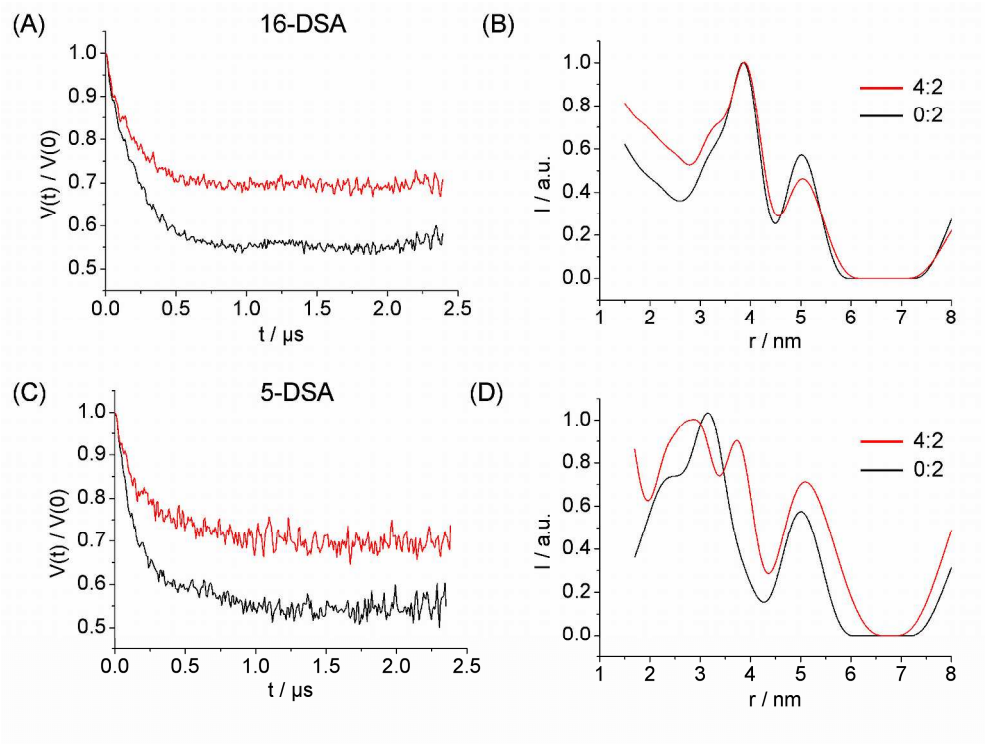

Figure S1. Intramolecular part of the DEER time-domain data (A, C) and extracted distance distributions by Tikhonov regularization (B, D) of spin labeled FAs complexed in HSA/buffer/20% (v/v) choline dhp with different numbers of reduced FAs and two EPR active FAs per protein molecule: black (0:2) and red (4:2). The data from 16-DSA are shown on top (A, B) and 5-DSA on the bottom (C, D).

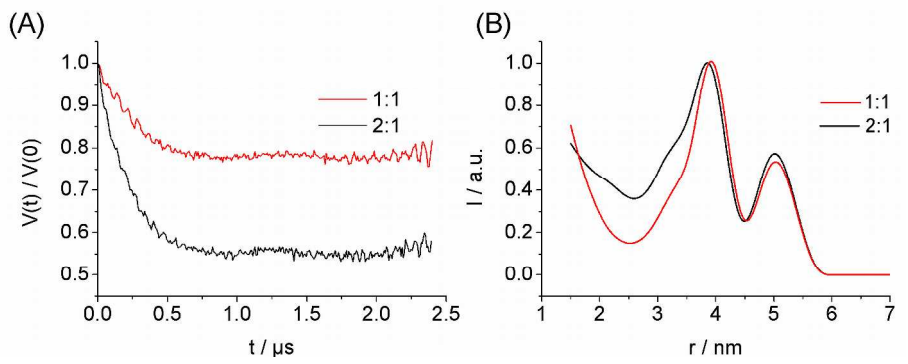

Figure S2. Intramolecular part of the DEER time-domain data (A) and extracted distance distributions by Tikhonov regularization (B) of 16-DSA complexed in HSA/buffer/20% (v/v) choline dhp with different ratios of 16-DSA/HSA: red (1:1) and black (2:1).

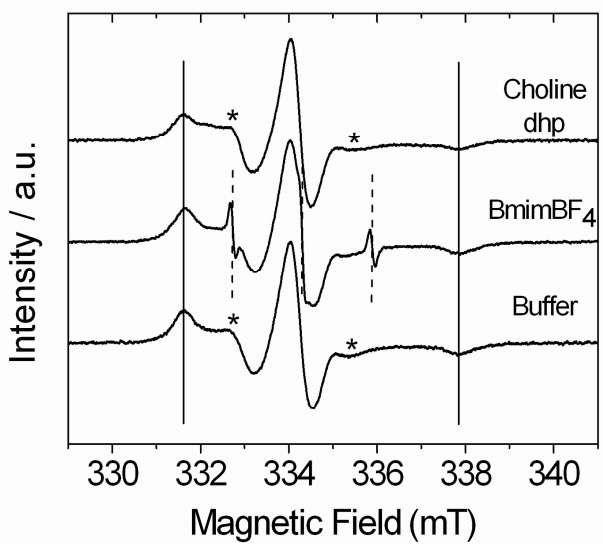

Figure S3. CW EPR spectra of 16-DSA/HSA (2/1) in a purely aqueous buffered medium and after addition of 20% (v/v) $BmimBF_4$, or choline dhp. The characteristic signals of bound 16-DSA to albumin are marked by solid lines. The three lines characteristic for freely tumbling 16-DSA are marked by dashed lines. Asterisks mark spectral component corresponding to 16-DSA bound to less strongly immobilized binding sites of HSA.