Supporting Information

Time-resolved detection of SDS-induced conformational changes in α-synuclein by a micro-stopped-flow system

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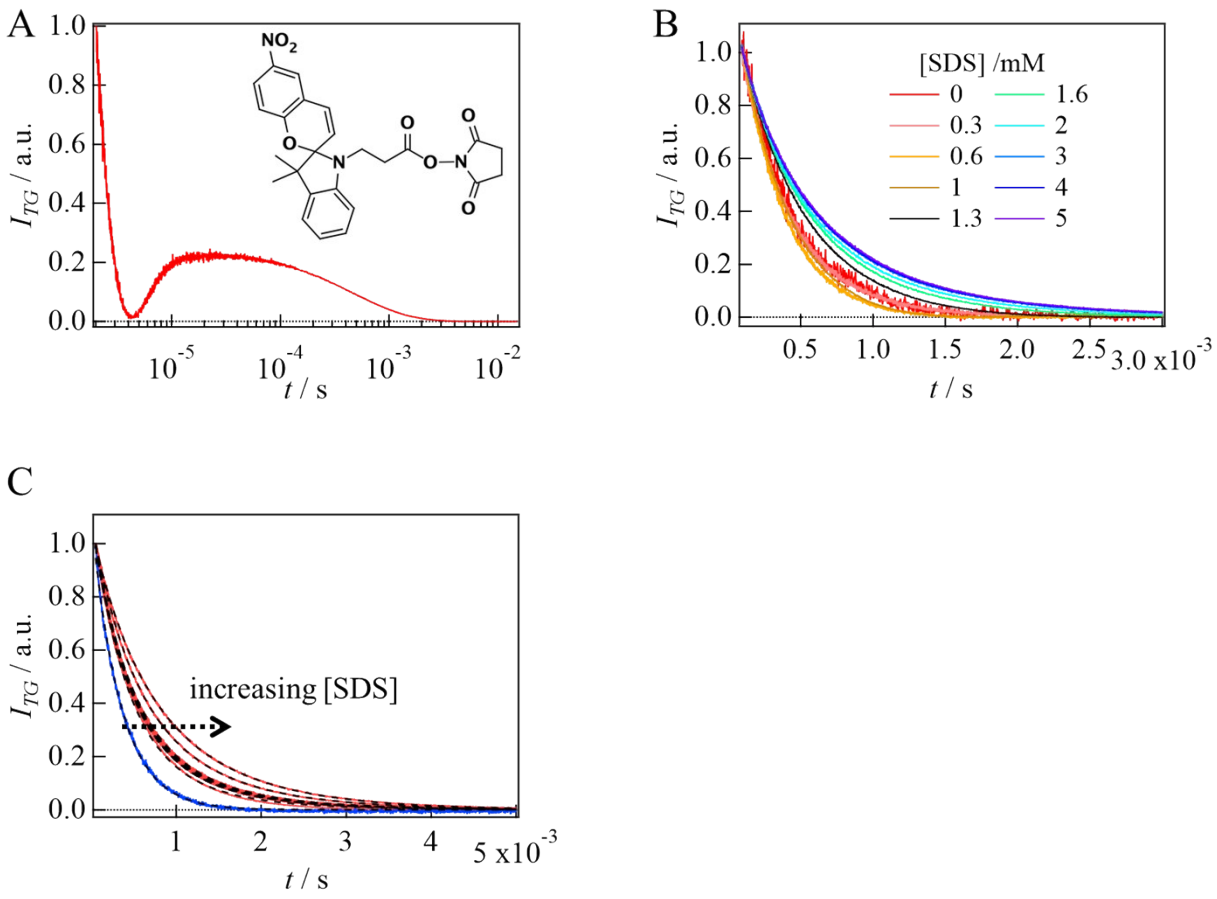

Figure SI-1. (A) Typical TG signal of NSP at 3 mM SDS (q^2 = 3.6 × 10^{12} m^{-2}). Inset: molecular structure of NSP. (B) Dependence of the TG signal on lower [SDS] condition at q^2 = 3.6 × 10^{12} m^{-2}. (C) The TG signals of NSP at 0 mM (blue), and 2, 3, 4, 5, 6, 7, 8, 9, 10, 25, 50 mM SDS used for calculation of D of the SDS micelle (red) at q^2 = 3.9 × 10^{12} m^{-2}. The broken lines show fitting curves based on Eq. (2).

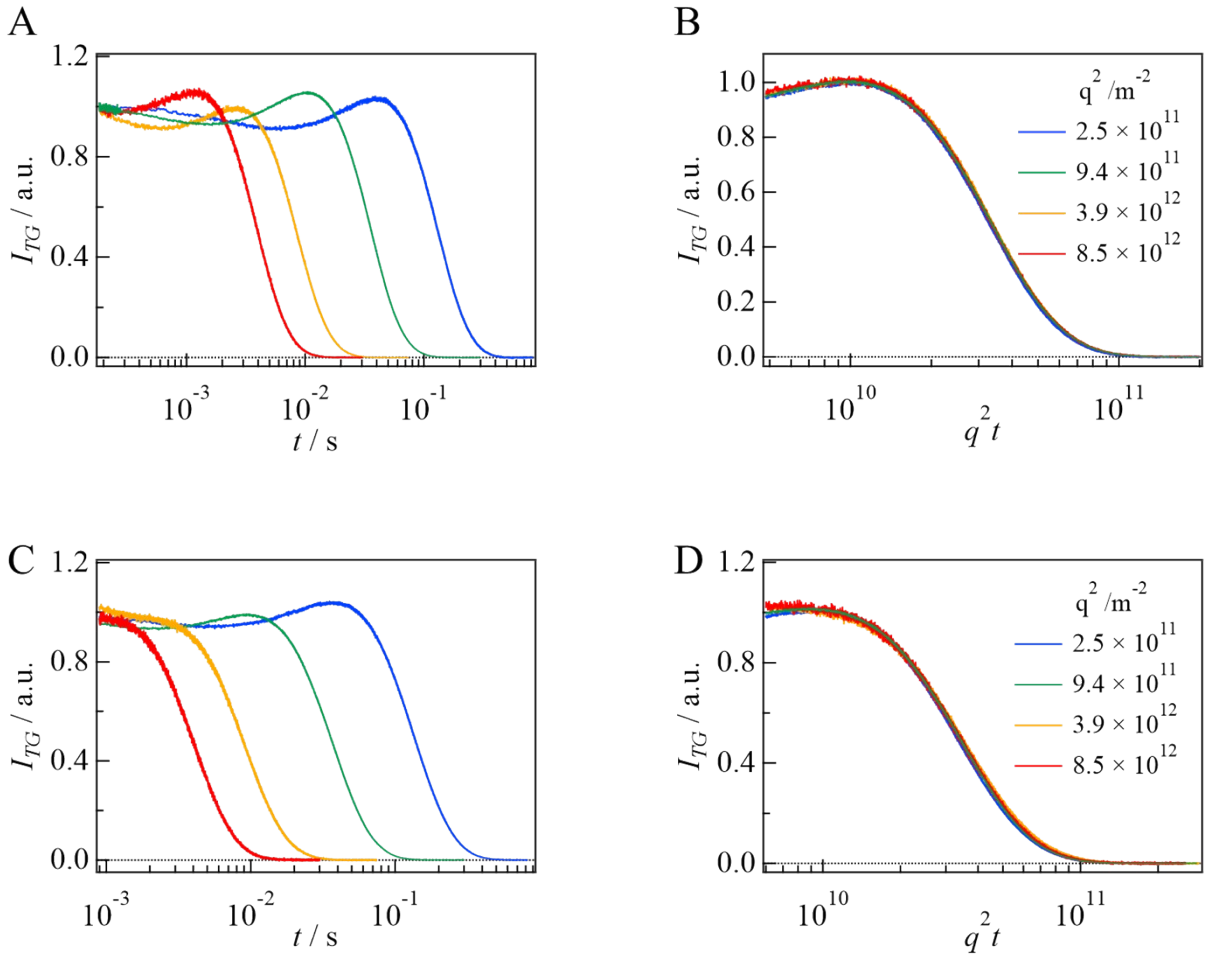

Figure SI-2. q^2 dependence of the TG signal of αSyn in the presence of 2 mM SDS (A). The q^2 values are 8.5 × 10^{12} m^{-2}, 3.9 × 10^{12} m^{-2}, 9.4 × 10^{11} m^{-2}, and 2.5 × 10^{11} m^{-2}, from left to right. (B) q^2t plot of the rise-decay profiles at 2 mM SDS. (C) The q^2 dependence at 1 mM SDS. The q^2 values are the same as that of (A). (D) The q^2t plot of the rise-decay profiles at 1 mM SDS.

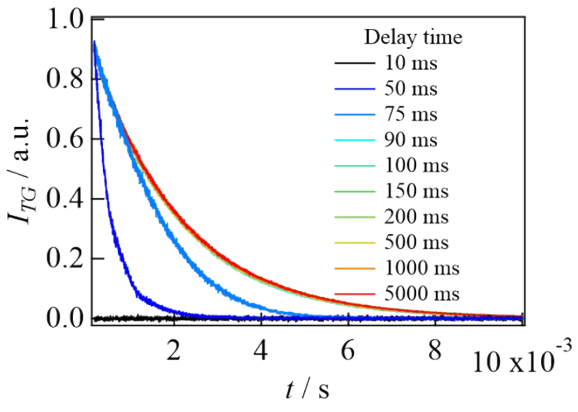

Figure SI-3. Diffusion signals of Bovine Serum Albumin labeled with NSP at several delay times after mixing two identical solutions containing 20 μM protein in PBS buffer ($q^2 = 3.8\times10^{12}$ m^{-2}).