Startling Temperature Effect on Proteins when Confined: Single Molecular Level Behaviour of Human Serum Albumin in Reverse Micelle

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Supplementary Information

Figure S1: Circular dichroism spectra of (a) tagged (4.96 μM) and untagged (5.03 μM) human serum albumin in buffer. (b) tagged human serum albumin (HSA) in buffer (3.74 μM) and in water-pool of AOT reverse micelle W_0=20 (overall concentration of HSA is 1.65 μM).

Figure S2: Fluorescence autocorrelation spectra of TMR tagged human serum albumin (HSA) in buffer and in AOT reverse micelle (W_0=46). Solid black lines indicate best fits of the corresponding data.

Figure S3: Experimental fluorescence autocorrelation curve of TMR tagged HSA in the water-pool of AOT reverse micelle of different W_0 values at 298 K and its fitting with (i) 1 diffusion model (green line), (ii) 1 diffusion + 1 conformational relaxation component model (violet line), (iii) Gaussian distribution on diffusion model (cyan line), (iv) Gaussian distribution on diffusion + 1 conformational relaxation component model (brown line), and (v) Gaussian distribution on diffusion + Gaussian distribution on conformational relaxation component model (black line). Upper panel shows the residuals of the corresponding fits.

Figure S4: Normalized fits of autocorrelation curves of TMR tagged HSA in buffer at different temperatures.

Figure S5: Normalized fits of autocorrelation curves of TMR tagged HSA in W_0=20 AOT reverse micelle at different temperatures.

Figure S6: Normalized fits of autocorrelation curves of TMR tagged HSA in W_0=25 AOT reverse micelle at different temperatures.

Figure S7: Normalized fits of autocorrelation curves of TMR tagged HSA in W_0=30 AOT reverse micelle at different temperatures.

Figure S8: A comparison of the fluorescence autocorrelation curve of TMR tagged HSA in the water-pool of AOT reverse micelle (W_0=25) and untagged HSA along with Rhodamine 6G in the water-pool of AOT reverse micelle of same dimension at different temperatures.

Figure S1: Circular dichroism spectra of (a) TMR-tagged and untagged human serum albumin in buffer. (b) human serum albumin in buffer and in water-pool of AOT reverse micelle W_0=20 (overall concentration of HSA is maintained at 5 μM).

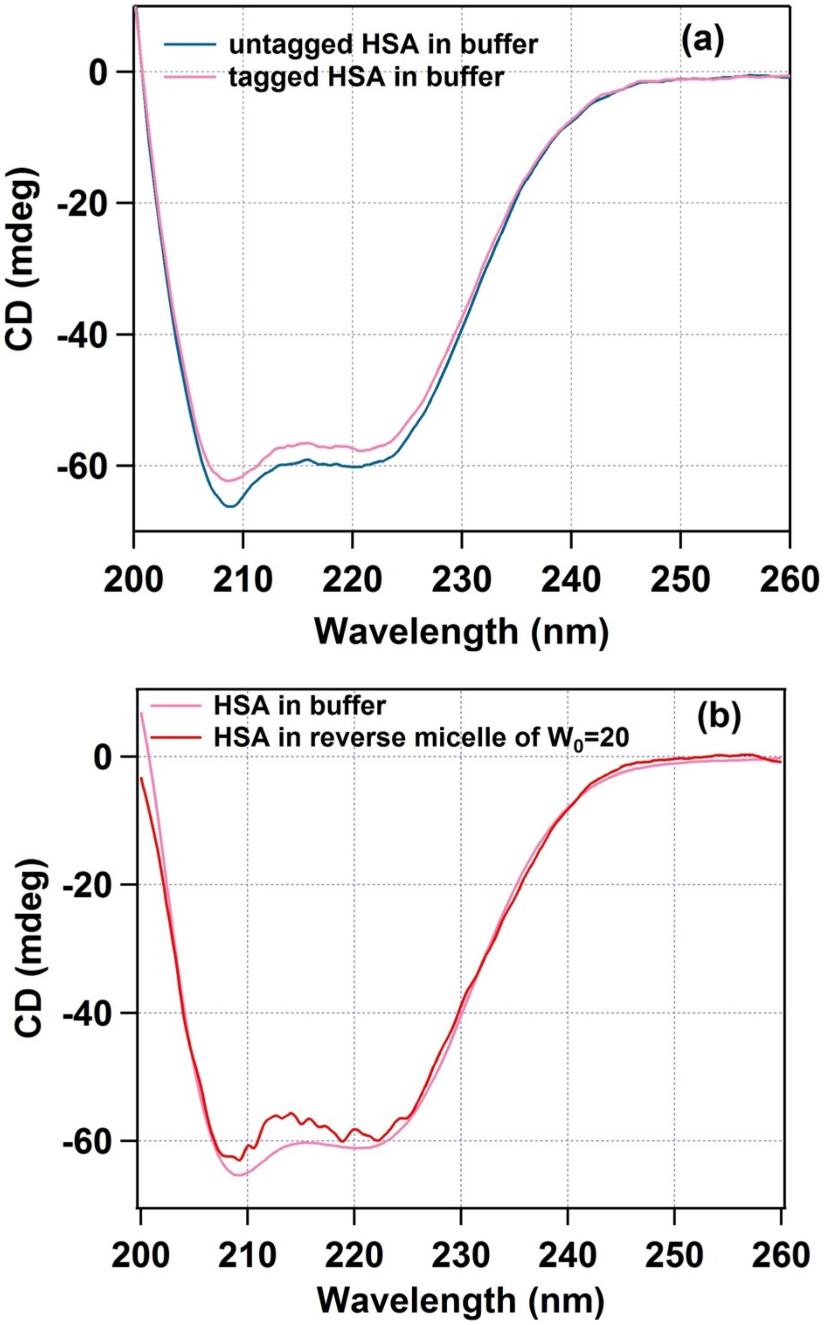


Figure S2: Fluorescence autocorrelation spectra of TMR tagged human serum albumin (HSA) in buffer and in AOT reverse micelle (W_0=46). Solid black lines indicate best fits of the corresponding data.

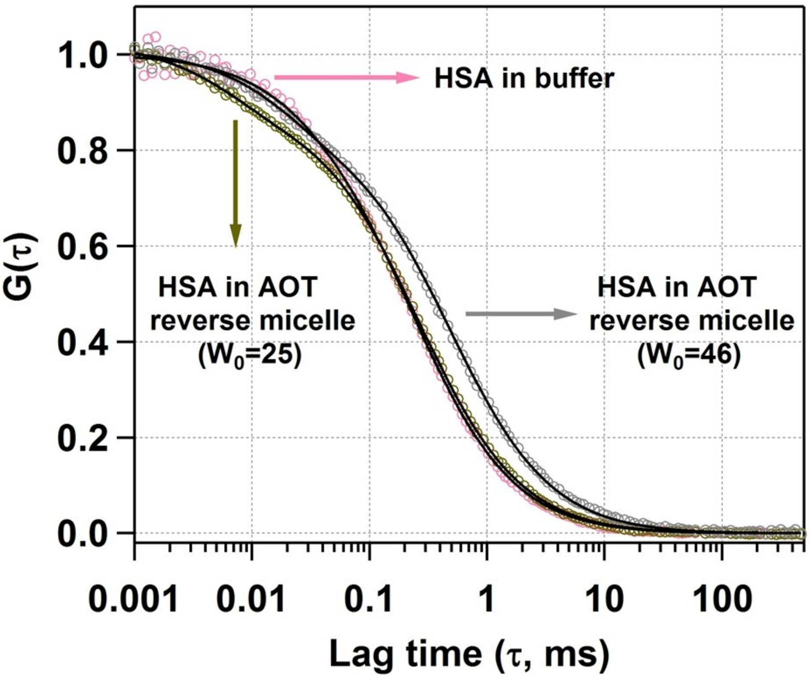
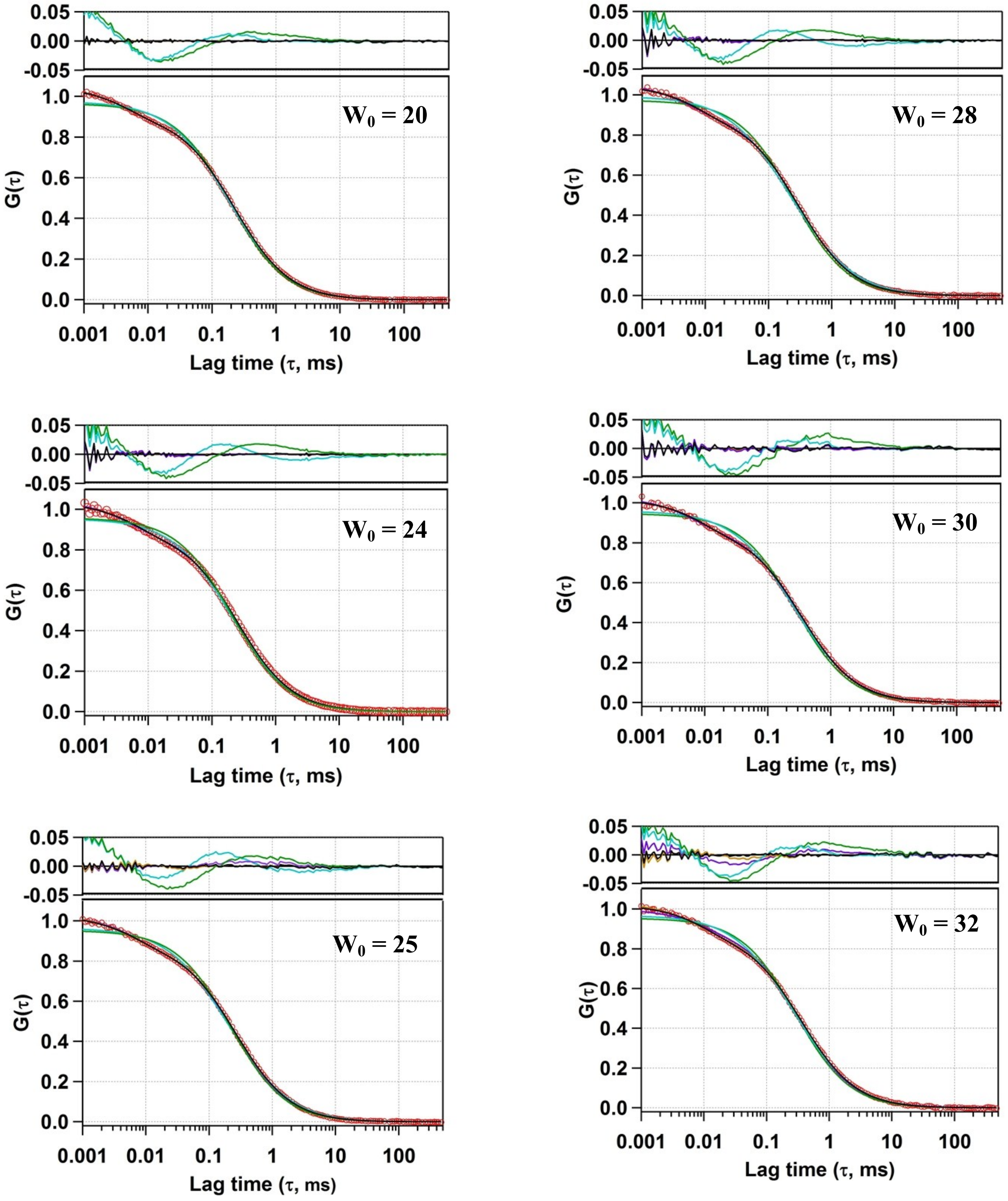
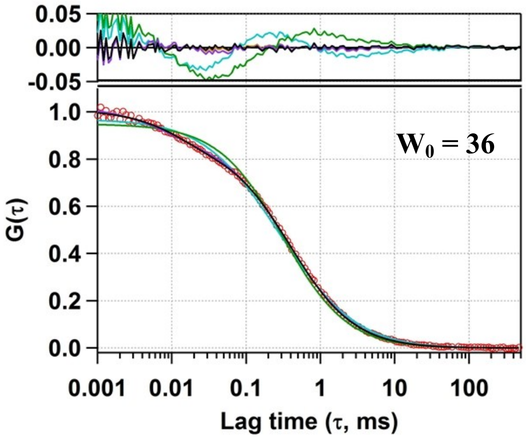
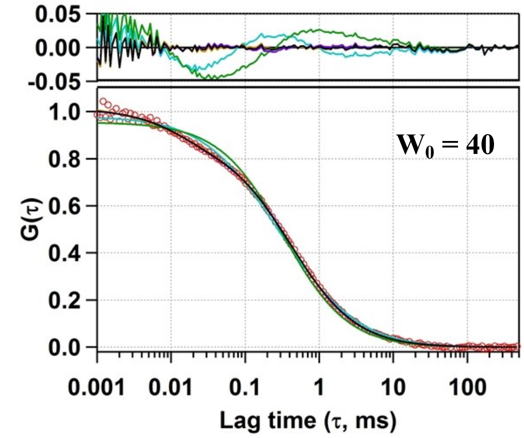


Figure S3. Experimental fluorescence autocorrelation curve of TMR tagged HSA in the water-pool of AOT reverse micelle of different W_0 values at 298 K and its fitting with (i) 1 diffusion model (green line), (ii) 1 diffusion + 1 conformational relaxation component model (violet line), (iii) Gaussian distribution on diffusion model (cyan line), (iv) Gaussian distribution on diffusion + 1 conformational relaxation component model (brown line), and (v) Gaussian distribution on diffusion + Gaussian distribution on conformational relaxation component model (black line). Upper panel shows the residuals of the corresponding fits.




0.05
0.00
-0.05
1.0
0.8
0.6
0.4
0.2
0.0
G(τ)
W₀ = 36
0.001
0.01
0.1
1
10
100
Lag time (τ, ms)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0.8
0.6
0.4
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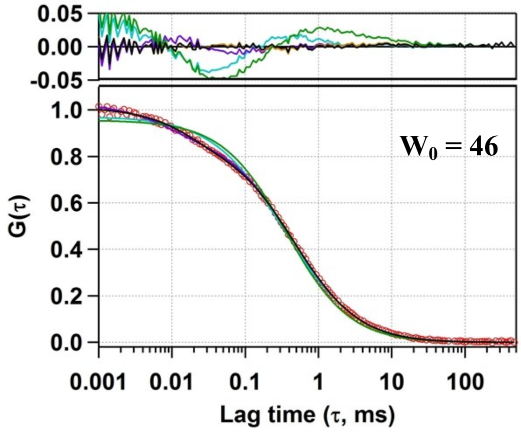
0.1
1
10
100
Lag time (τ, ms)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0.00
-0.05
1.0
0.8
0.6
0.4
0.2
0.0
G(τ)
W₀ = 46
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0.01
0.1
1
10
100
Lag time (τ, ms)

Figure S4: Normalized fits of autocorrelation curves of TMR tagged HSA in buffer at different temperatures.

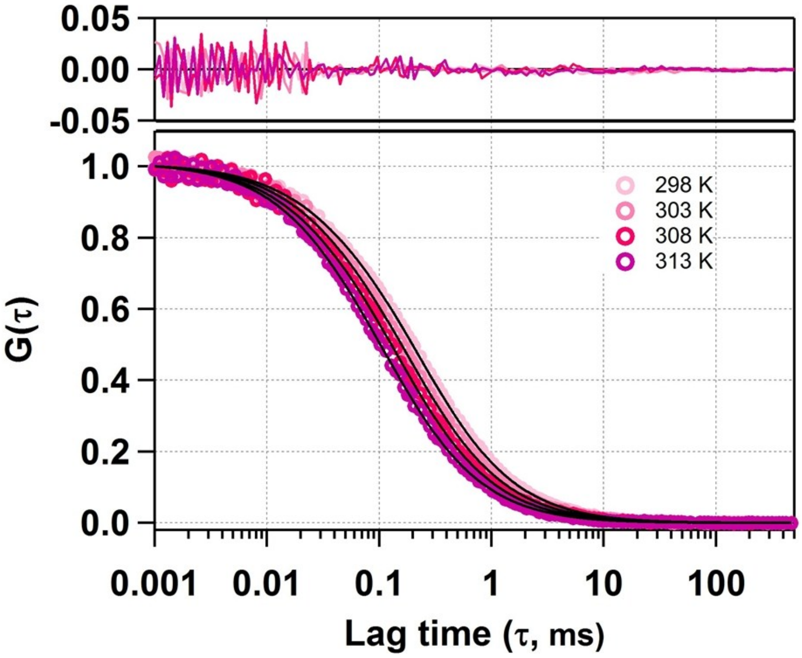

Figure S5: Normalized fits of autocorrelation curves of TMR tagged HSA in W_0=20 AOT reverse micelle at different temperatures.

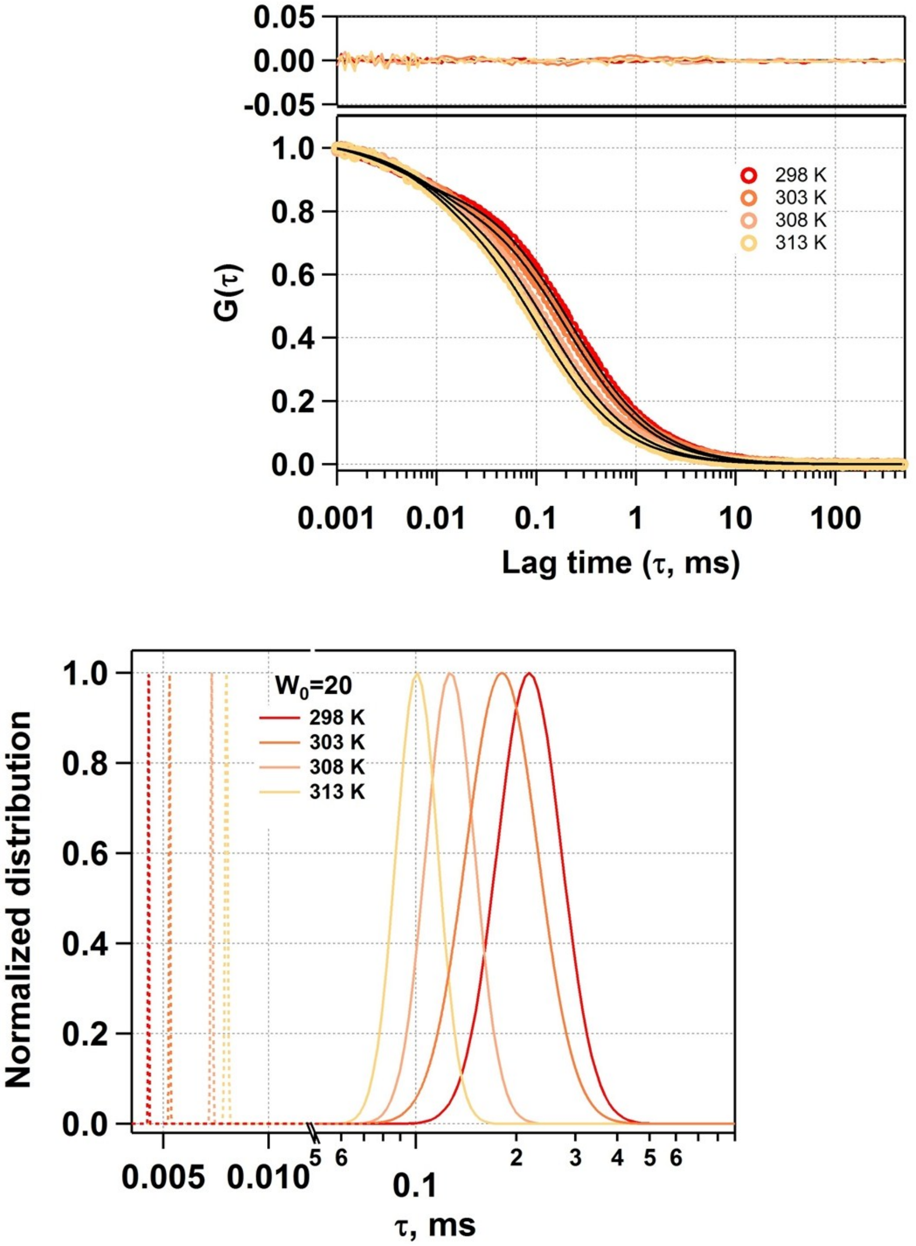

Figure S6: Normalized fits of autocorrelation curves of TMR tagged HSA in W_0=25 AOT reverse micelle at different temperatures.

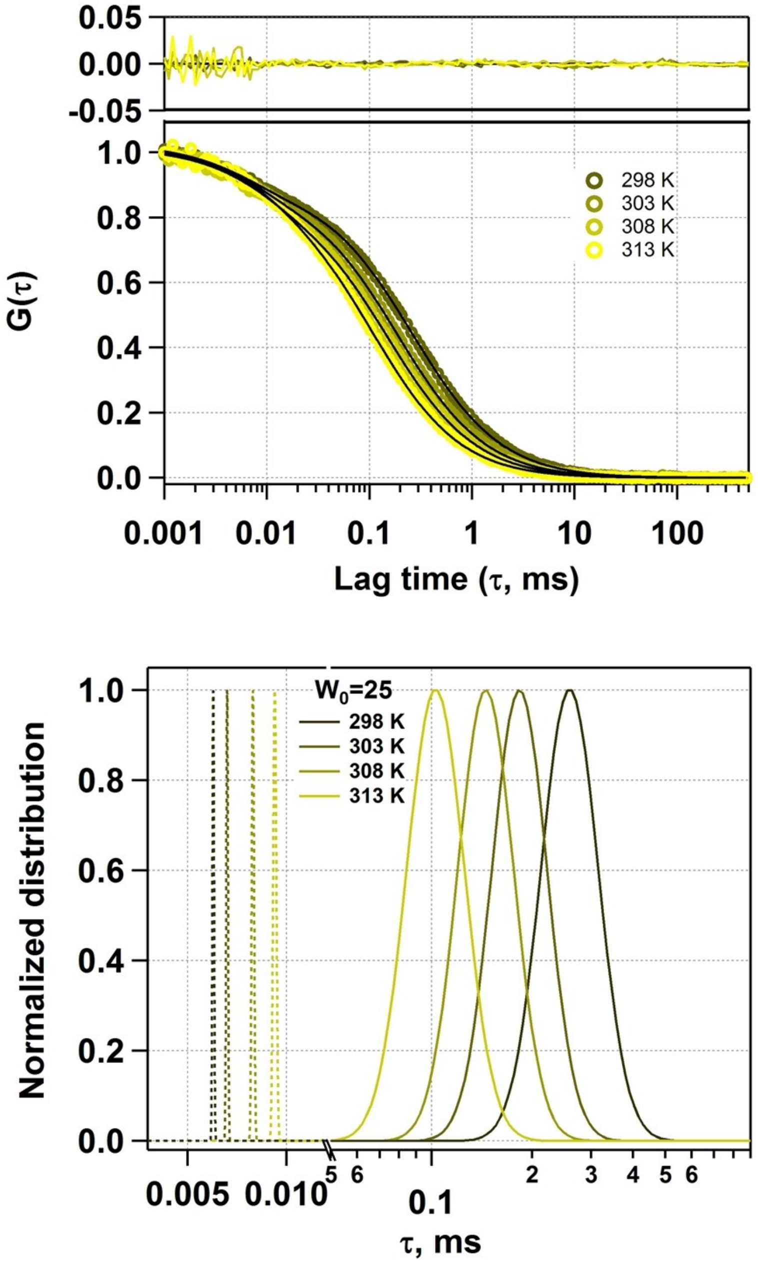

Figure S7: Normalized fits of autocorrelation curves of TMR tagged HSA in W_0=30 AOT reverse micelle at different temperatures.

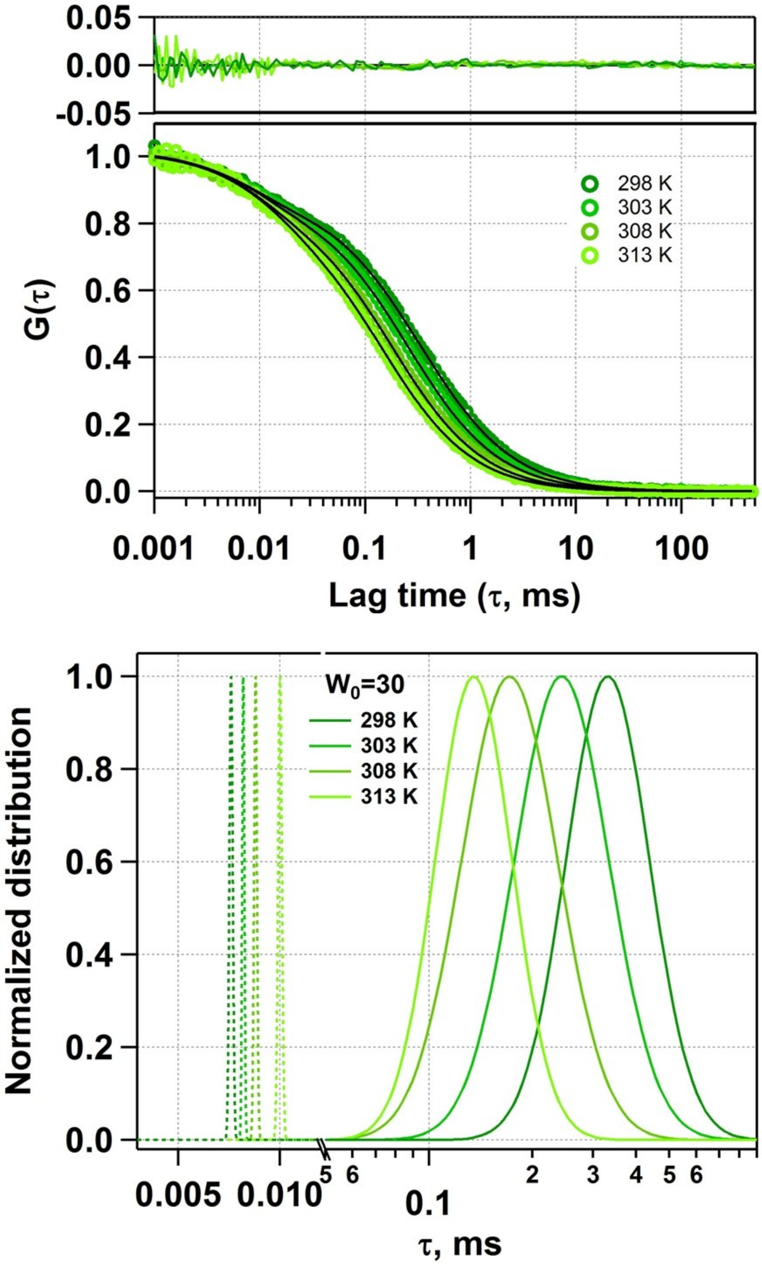

Figure S8: A comparison of the fluorescence autocorrelation curve of TMR tagged HSA in the water-pool of AOT reverse micelle (W_0=25) and untagged HSA along with Rhodamine 6G in the water-pool of AOT reverse micelle of same dimension at different temperatures.