# Supporting Information for "Protein diffusion in a bicontinuous microemulsion: Inducing sub-diffusion by tuning the water domain size"

**Ralph Neubauer,[a] Sebastian Höhn,[a,b] Martin Dulle[a], Alain Lapp[c], Christoph Schulreich,[b] and Thomas Hellweg*[a]**

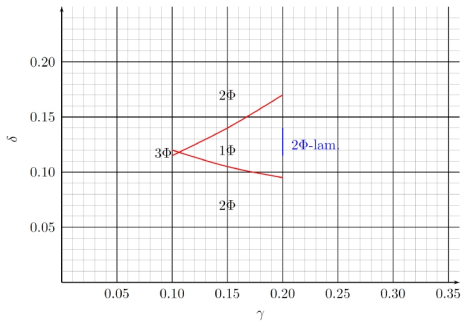


**Fig. S1** Phase diagram of the second used $C_9G_2$ batch. The X-point is shifted to slightly higher values of $\gamma$. It is not unusual that such differences occur when a new batch is used.

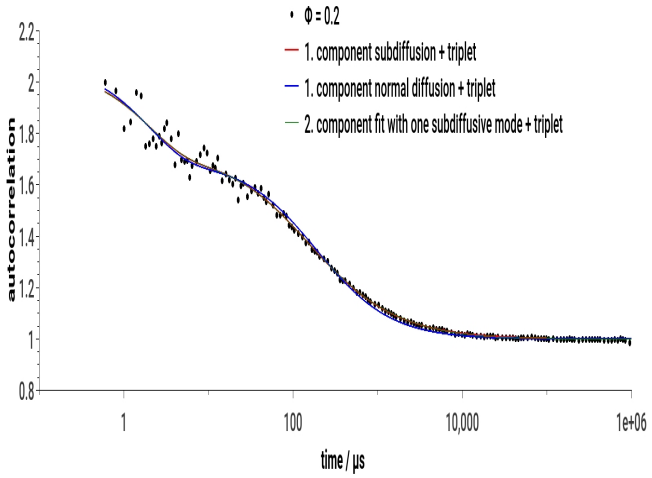


**Fig. S2** Comparison of the fit using the normal diffusion model, the sub-diffusion model, and the sub-diffusion model with an addition normal diffusion mode. It is obvious that the normal diffusion model (eq. 1) does not fit the data correctly.

## 1 Supporting Information

For the preparation of the microemulsions two different batches of $C_9G_2$ were used. Fig. S1 shows the phase diagram for the second batch which we used for the FCS and the small angle scattering experiments. This diagram was obtained for $\Phi = 0.5$.

To describe the diffusion of GFP+ in the bicontinuous microemulsion we first tried a normal diffusion model (eq. 1) going back to the work of Rigler and Mets. However, this model exhibits systematic deviations from the data. These deviations were found for all microemulsions used. Below you can see the fit result for a microemulsion with $\Phi = 0.2$ with GFP+ as tracer. The red line which corresponds to the sub-diffusive model already gives a significantly better description of the data (eq. 3). However, in addition we have chosen a model which contains an additional normal diffusion term to account for a slower mode arising from spurious amounts of a second fluorescent species associated to the microemulsion matrix (eq. 4). The difference is hard to see and the obtained diffusion times are very similar (see fig. 7 of the manuscript). It has to be pointed out that in the 2 component fit 3 parameters were fixed. This is the diffusion time of the microemulsion mode which was set to the value found by the measurement on the pure microemulsion, the triplet relaxation time which was set to 2 microseconds, and the S parameter which was set to 5 based on the calibration.