

Aqueous Self-Assembly of a Protein-Mimetic Ampholytic Block Copolypeptide

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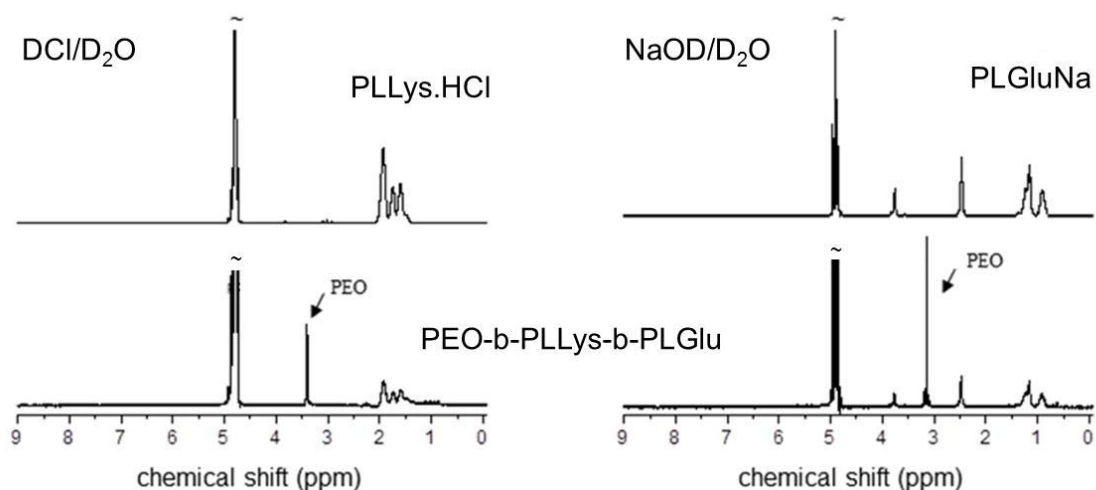


Figure S1. ¹H NMR spectra (400.1 MHz, r.t.) of PLLys and PEO₄₂-*b*-PLLys₆₁-*b*-PLGlu₆₂ in 0.9 M DCI in D₂O (left) and PLGlu and PEO₄₂-*b*-PLLys₆₁-*b*-PLGlu₆₂ in 1.0 M NaOD in D₂O (right).

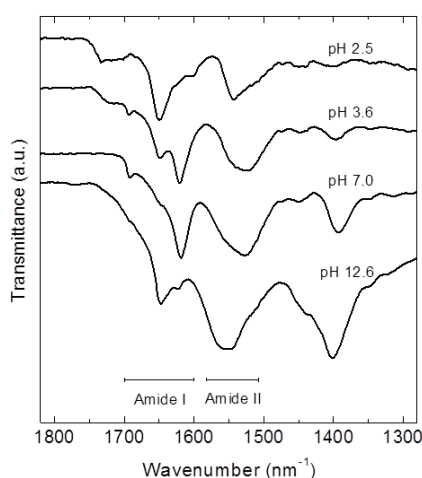


Figure S2. FT-IR spectra of freeze-dried samples of 0.2 wt% PEO₄₂-PLLys₆₁-PLGlu₆₂ in water at pH 2.5–12.6.

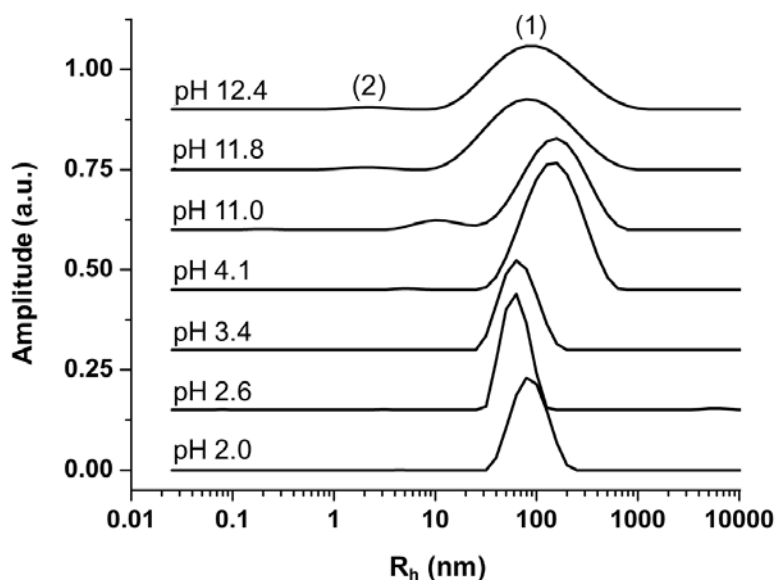


Figure S3. Normalized distributions of hydrodynamic radii (R_h) observed in ~ 0.1 wt% solutions of PEO₄₂-*b*-PLLYS₆₁-*b*-PLGlu₆₂ in 0.5 M NaCl at various pH. Data measured at scattering angle 90° at room temperature. (1) and (2) denote slow and fast modes, respectively.

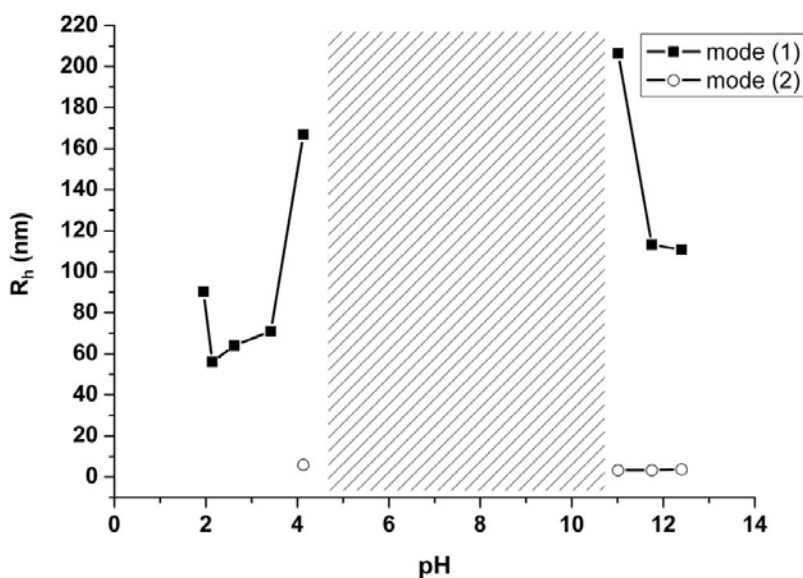


Figure S4. Dependence of hydrodynamic radii (R_h) observed in ~ 0.1 wt% solutions of PEO₄₂-*b*-PLLYS₆₁-*b*-PLGlu₆₂ in 0.5 M NaCl at various solution pH. Data measured at scattering angle 90° at room temperature. The hatched area represents an unstable region where all solutions demonstrate tendency to precipitate. Mode (1) is related to the major, slow diffusive mode of large aggregates, while mode (2) identifies the fast dynamic process of coupled diffusion of polyions and counterions or single chains.

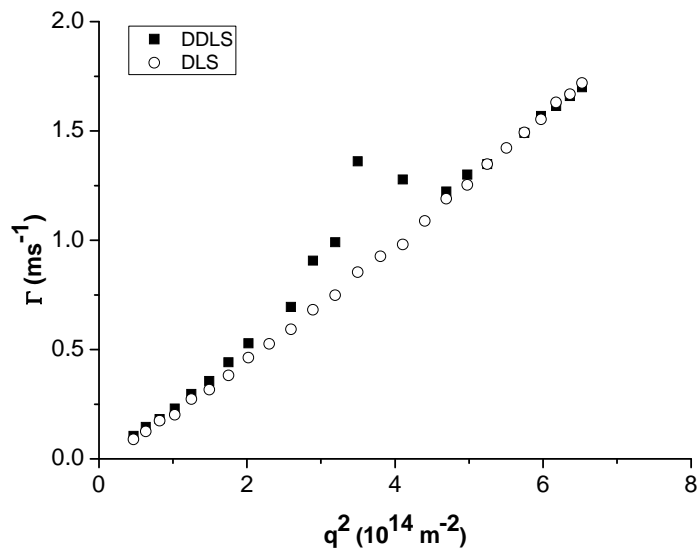


Figure S5. Relaxation rates (Γ) obtained by DLS and DDLS as a function of the square of the scattering vector (q^2) for the ~ 0.1 wt% solutions of PEO₄₂-PLLys₆₁-PLGlu₆₂ in 0.5 M aqueous NaCl at pH 2.0.

DLS and DDLS gives linear dependence of decay rate with square of the scattering vector passing the origin [0,0]. The observable deviation around scattering angle of $\sim 90^\circ$ might be caused by either simultaneous presence of two diffusional effects with similar correlation times, which cannot be distinguished by the fitting algorithm, or deviation of the shape of the scattered objects from an ideal sphere. However, as there is not shift in the Γ -axis, which would indicate a contribution of rotational diffusion (Lehner et al. *Langmuir* **2000**, *16*, 1689-1695), the scattered objects are considered to be spherical in shape.

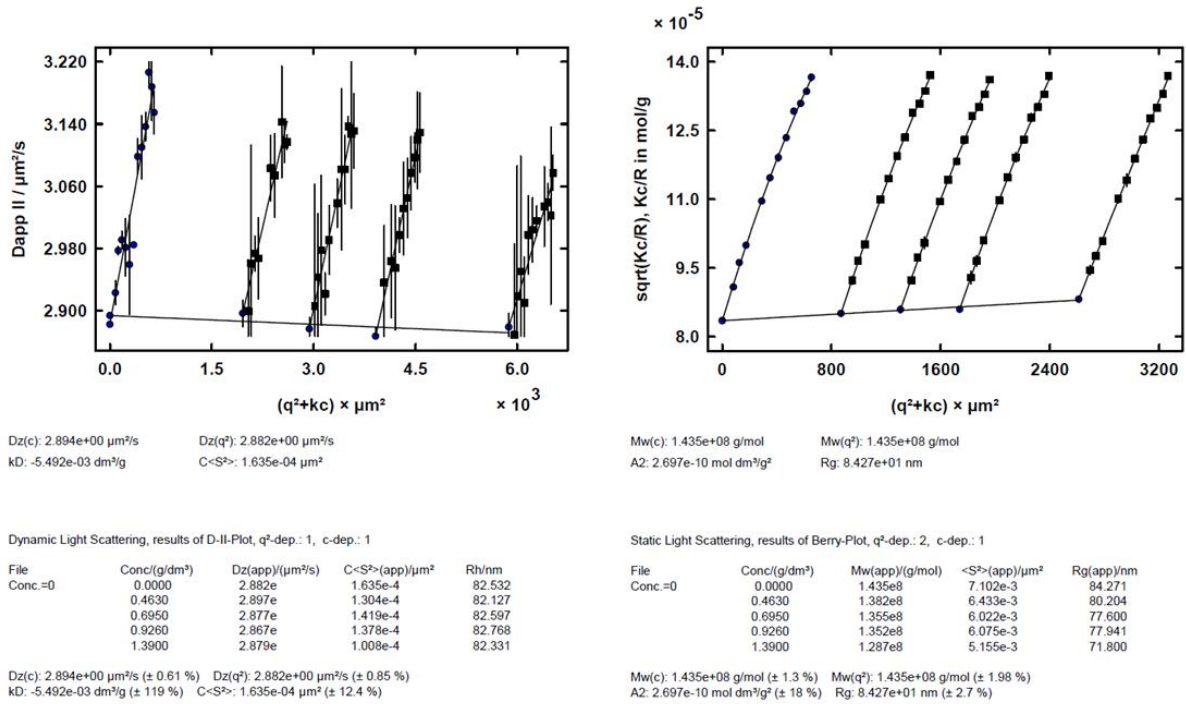


Figure S6. Concentration- and angle-dependent DLS (left) and SLS (right) data for 0.05–0.14 wt% PEO₄₂-PLLys₆₁-PLGlu₆₂ in 0.5 M aqueous NaCl at pH 2.0 at room temperature.

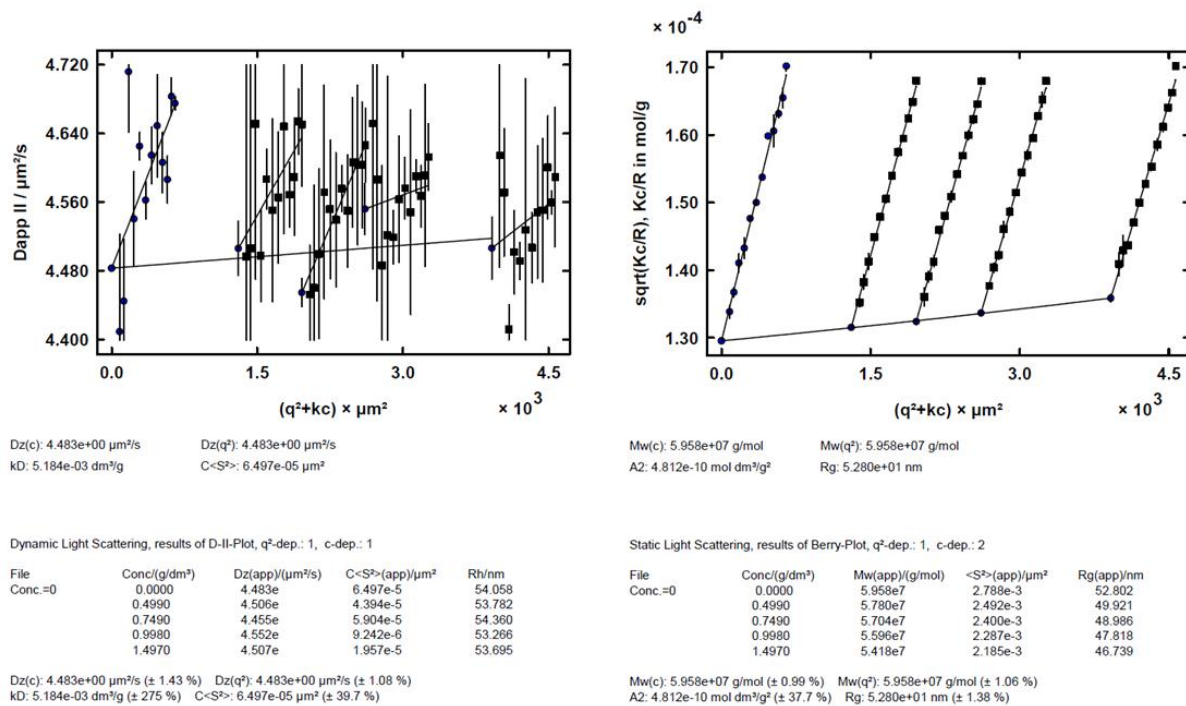


Figure S7. Concentration- and angle-dependent DLS (left) and SLS (right) data for 0.05–0.15 wt% PEO₄₂-PLLys₆₁-PLGlu₆₂ in 0.5 M aqueous NaCl at pH 2.2 at room temperature.

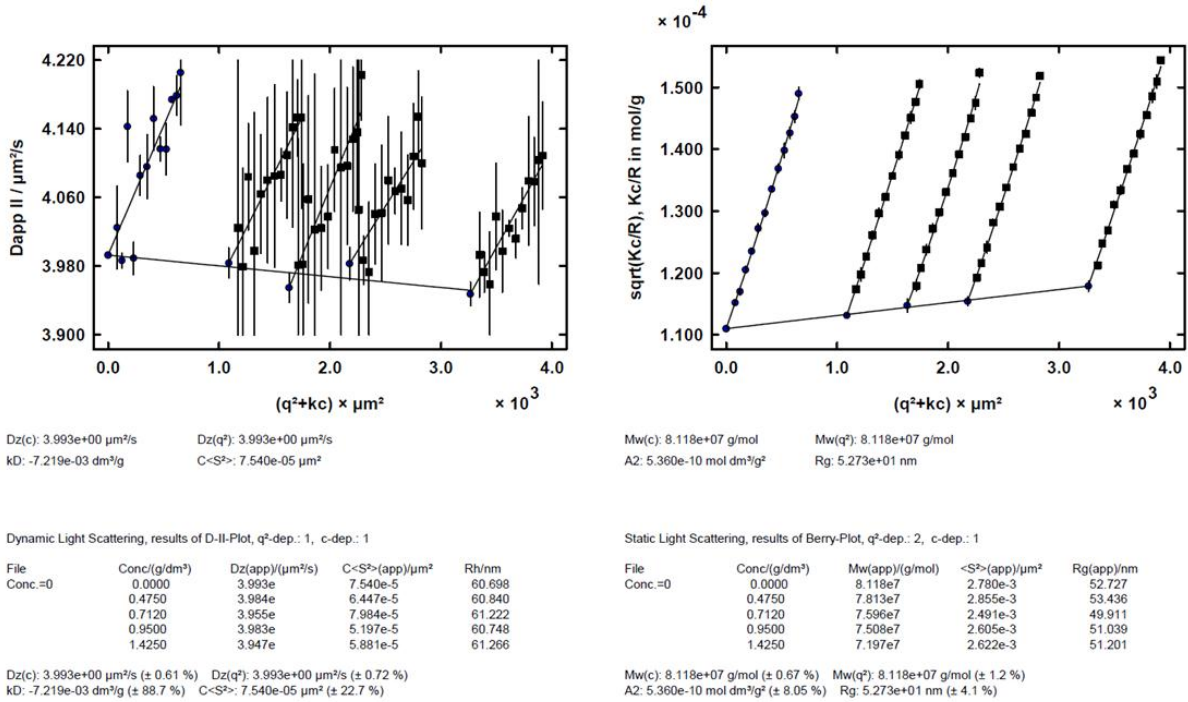


Figure S8. Concentration- and angle-dependent DLS (left) and SLS (right) data for 0.05–0.14 wt% PEO₄₂-PLLys₆₁-PLGlu₆₂ in 0.5 M aqueous NaCl at pH 2.6 at room temperature.

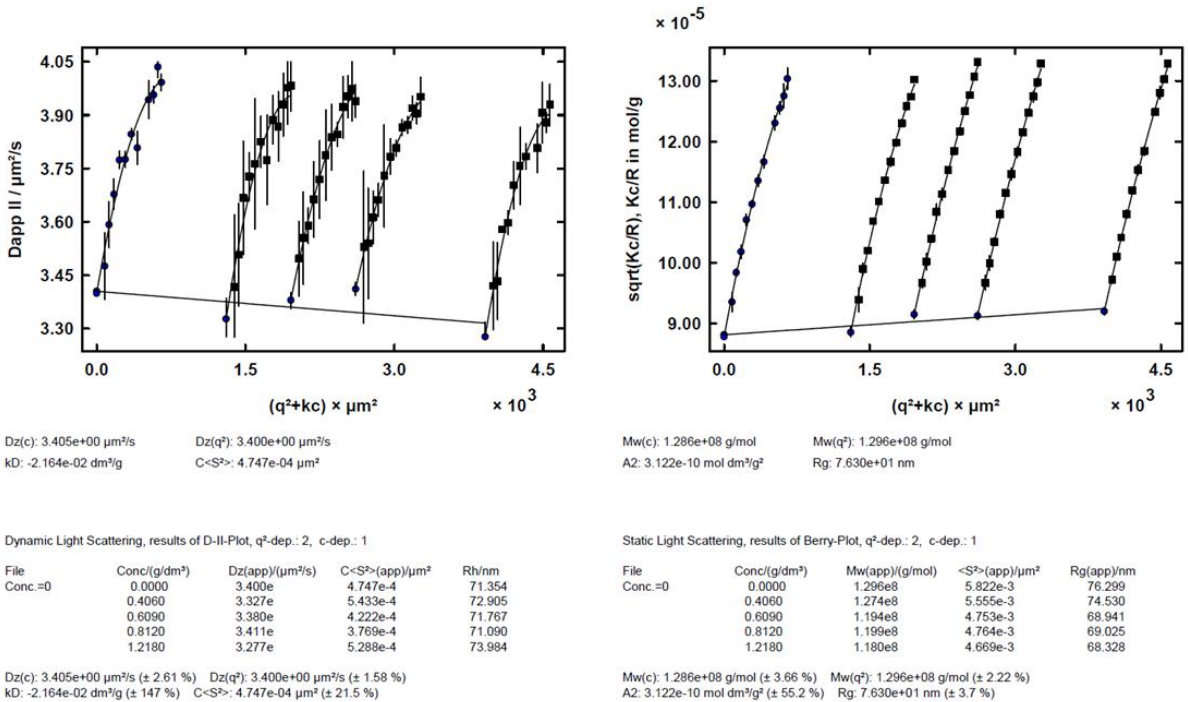


Figure S9. Concentration- and angle-dependent DLS (left) and SLS (right) data for 0.04–0.12 wt% PEO₄₂-PLLys₆₁-PLGlu₆₂ in 0.5 M aqueous NaCl at pH 3.4 at room temperature.

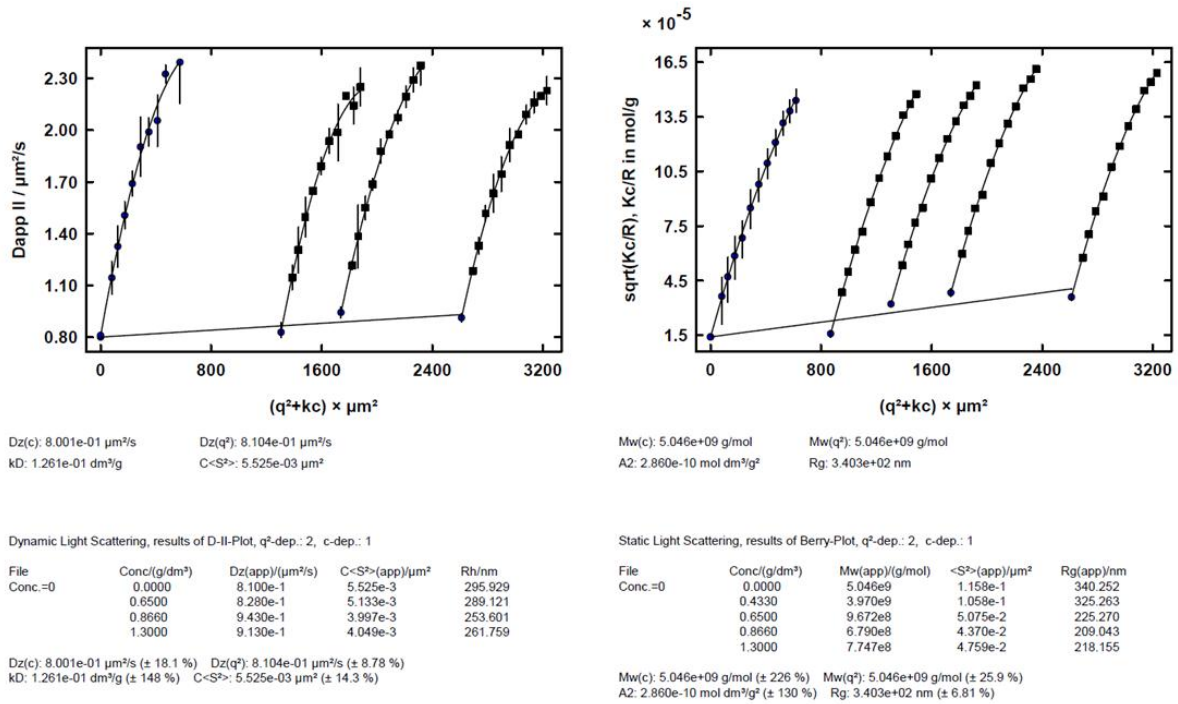


Figure S10. Concentration- and angle-dependent DLS (left) and SLS (right) data for 0.04–0.13 wt% PEO₄₂-PLLys₆₁-PLGlu₆₂ in 0.5 M aqueous NaCl at pH 4.1 at room temperature.

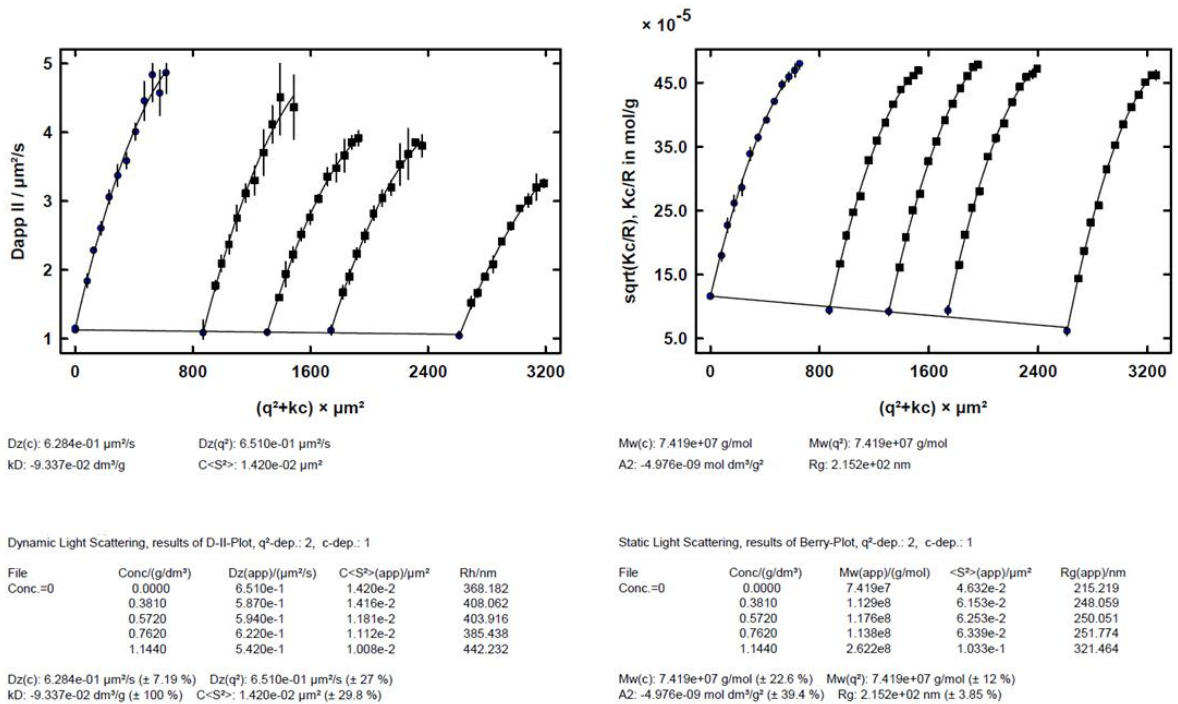


Figure S11. Concentration- and angle-dependent DLS (left) and SLS (right) data for 0.04–0.11 wt% PEO₄₂-PLLys₆₁-PLGlu₆₂ in 0.5 M aqueous NaCl at pH 11.0 at room temperature.

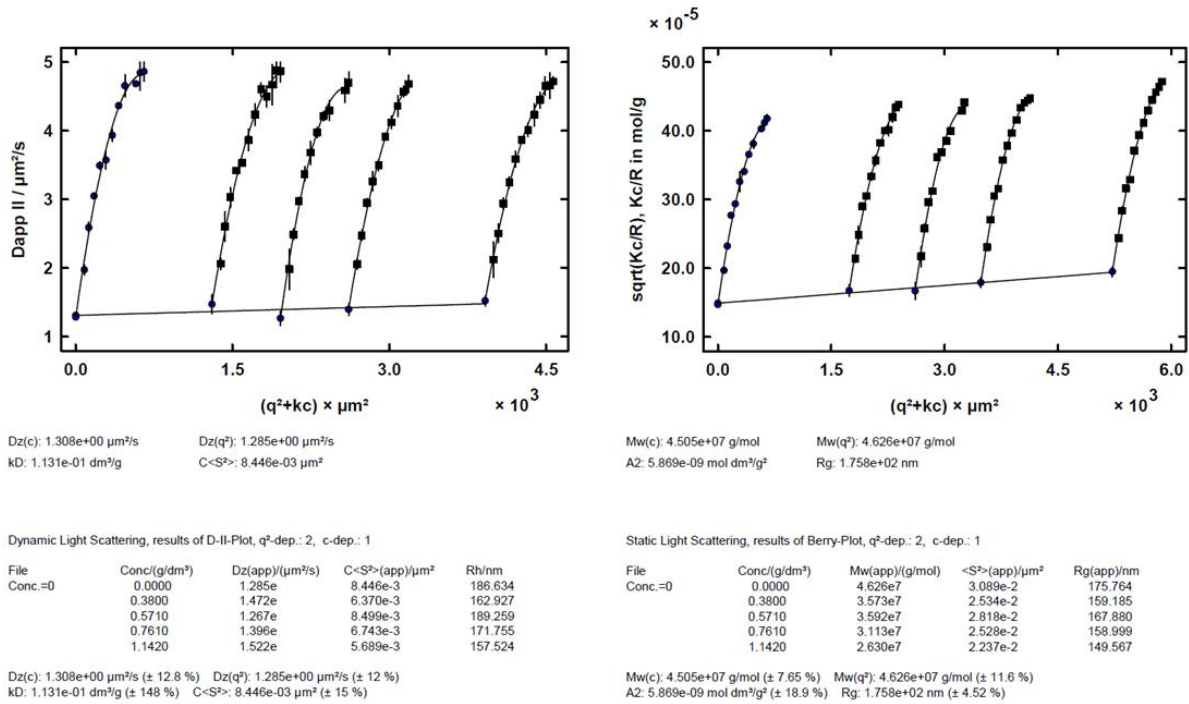


Figure S12. Concentration- and angle-dependent DLS (left) and SLS (right) data for 0.04–0.11 wt% PEO₄₂-PLLys₆₁-PLGlu₆₂ in 0.5 M aqueous NaCl at pH 11.8 at room temperature.

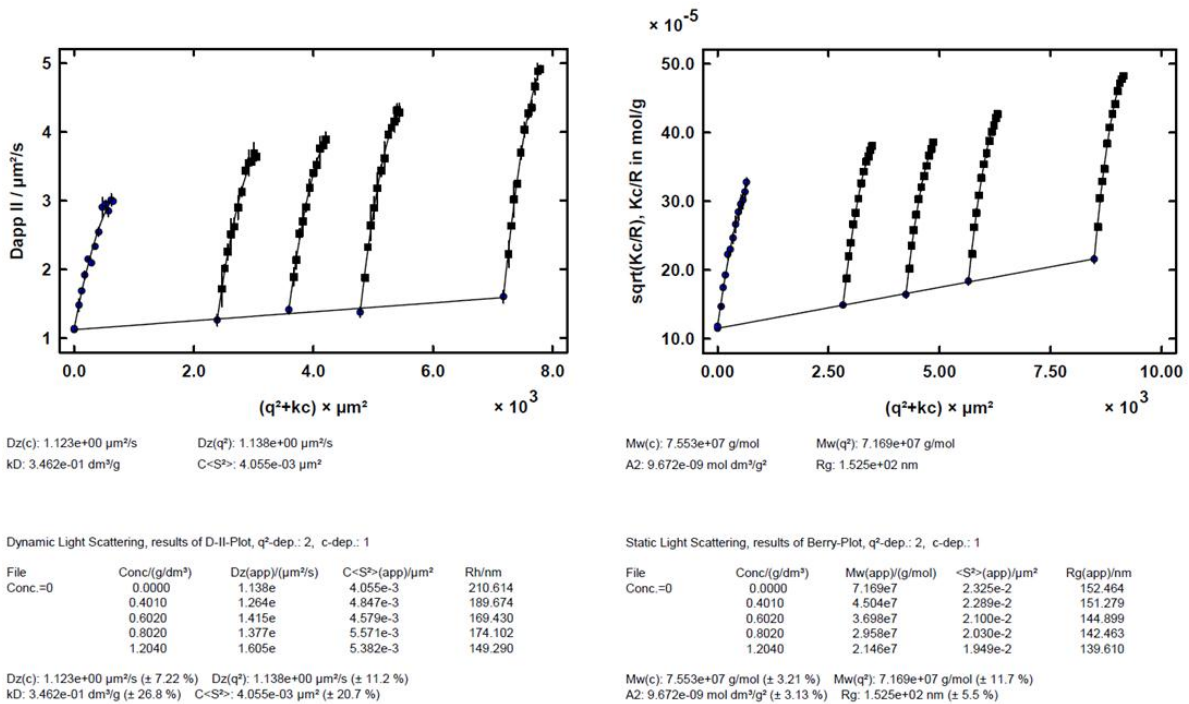


Figure S13. Concentration- and angle-dependent DLS (left) and SLS (right) data for 0.04–0.12 wt% PEO₄₂-PLLys₆₁-PLGlu₆₂ in 0.5 M aqueous NaCl at pH 12.4 at room temperature.

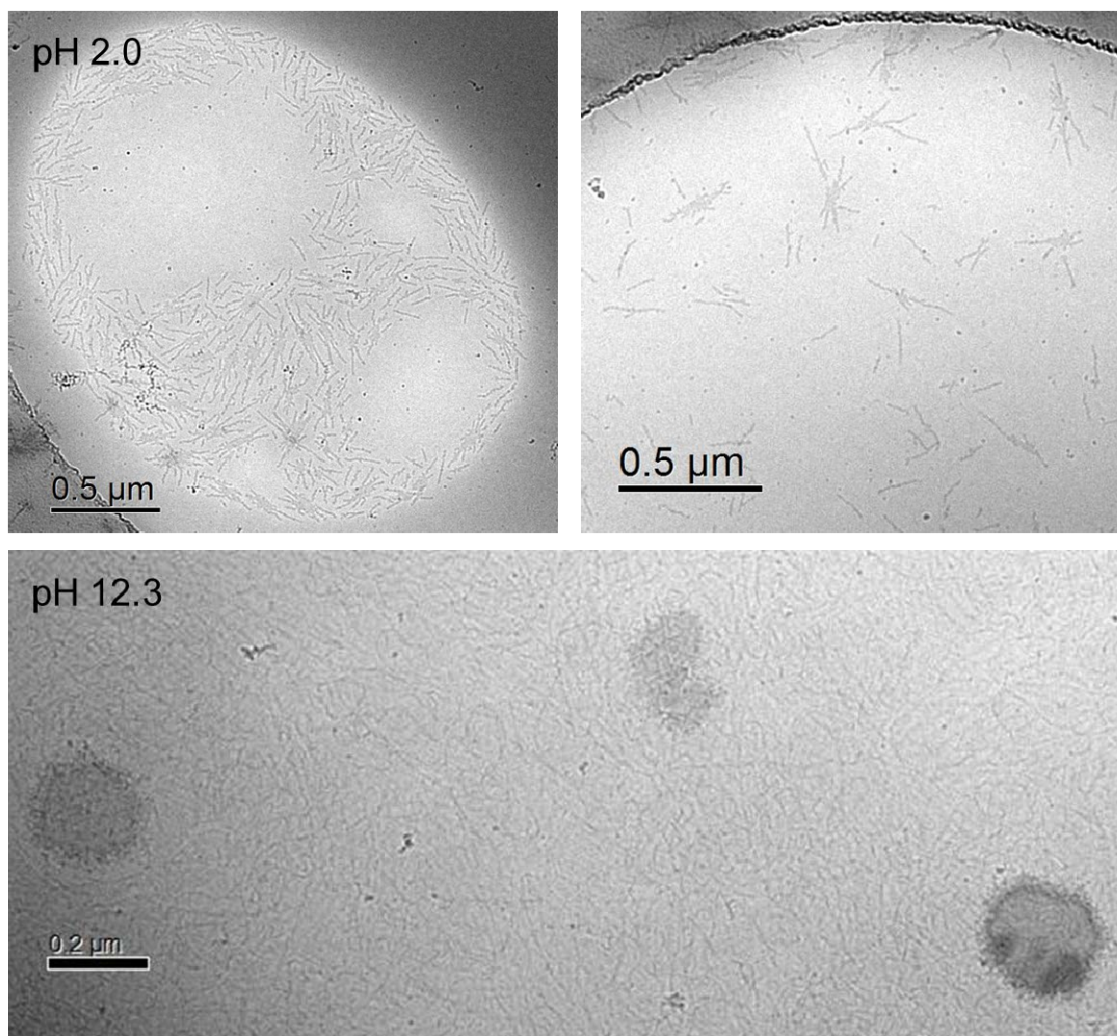


Figure S14. Exemplary cryogenic transmission electron micrographs of aged ~ 0.1 wt% solutions of PEO₄₂-*b*-PLLYS₆₁-*b*-PLGlu₆₂ in 0.5 M NaCl at pH 2.0 (top) and pH 12.4 (bottom), showing either discrete rod-like structures or vesicle-like particles and fibers (instead of vesicles or no aggregates); samples were analyzed ~ 10 months after their preparation.

Experimental procedure. 3 μ L of sample solution was applied on plasma-treated (Gatan Solarus Model 950 Advanced Plasma System, $p = 70$ mTorr, H₂ flow 6.4 sccm, O₂ flow 27.5 sccm, forward RF target 50 W, time 30 s) carbon copper grids (Quantifoil R 3.5/1) in the environmental chamber of FEI Vitrobot having relative air humidity of 100 % and temperature of 22 °C. The excess solution was removed by blotting with filter paper for 1.5–2 seconds followed by 0–30 seconds draining and plunging of the samples into 1:1 mixture of liquid ethane and liquid propane, which was cooled below -170 °C. Vitrified samples were cryo-transferred into Jeol JEM-3200FSC cryo-transmission electron microscope operating at -194 °C. The temperature of the samples was -187 °C during the imaging. The microscope was operating in the bright field mode, using 300 kV acceleration voltage and the in-column energy filter set to 0–20 eV energy-loss range (zero-loss imaging). Micrographs were recorded with Gatan Ultrascan 4000 CCD camera.

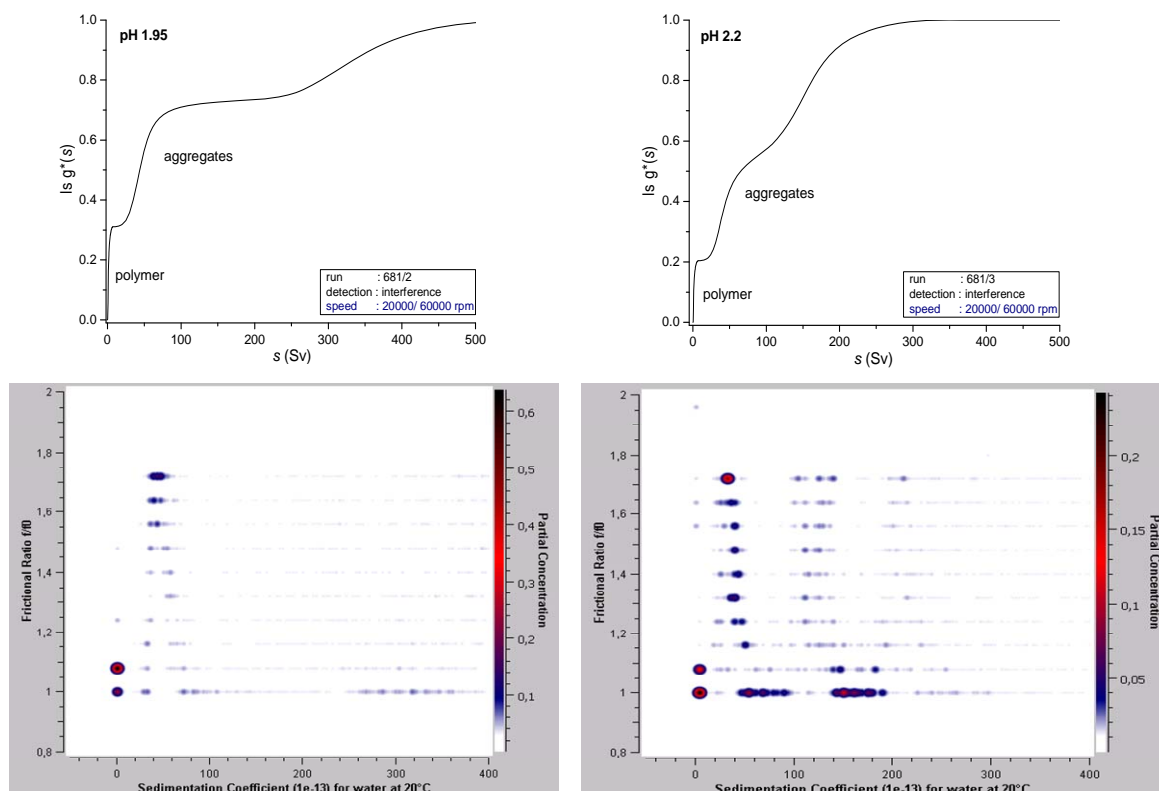


Figure S15. AUC sedimentation coefficient distributions (top) and pseudo 3D plots (UltraScan 2DSA-MC) of frictional ratio (ff_0) vs. sedimentation coefficient (bottom) of aged ~ 0.1 wt% solutions of PEO₄₂-*b*-PLLys₆₁-*b*-PLGlu₆₂ in 0.5 M NaCl at pH 2.0 and pH 2.2; samples were analyzed ~ 3 months after their preparation.

Lamm equation fitting with 2DSA-MC analysis. Sedimentation and diffusion terms are used to generate solutions for the direct modeling of the sedimentation boundary, using the two dimensional spectrum analysis (2DSA) implemented in the software package UltraScan III. The frictional ratio (ff_0), which gives a hint to the morphology of the sedimenting species, is determined with a model-free grid search followed by a Monte Carlo (MC) approach. It can be plotted as a function of the sedimentation coefficient in a pseudo 3D graph where the concentration of each species builds the pseudo z-axis (E. Brookes, W. Cao, B. Demeler, *Eur. Biophys. J.* **2010**, 39, 405). Values of $ff_0 \sim 1$ indicate structures with globular (spherical) shape whereas $ff_0 > 1$ indicate non-globular structures (*e.g.*, rods) (K. E. van Holde, W. C. Johnson, P. S. Ho, *Principles of Physical Biochemistry*, 2nd edition, Intl. ed., Prentice-Hall, EnglewoodCliffs, NJ 2005; C. R. Cantor, P. R. Schimmel, *Biophysical Chemistry*, Freeman Part II, San Francisco, CA 1980.). Exact dimensions of aggregates could not be determined because of different specific volumes of polymer chains and aggregates.

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