Supporting Information

Worm-Like Superparamagnetic Nanoparticle Clusters for Enhanced Adhesion and Magnetic Resonance Relaxivity

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Simulation of HPG structure: We simulate the structure of the HPG by 'building' the structure in a fashion informed by the ring-opening synthesis of the molecules in experiment. A random chain end (at the start of the simulation setup, this includes both beads in a starting dimer) is chosen, and two beads are added. If either of these new beads overlaps with *any* other bead in the molecule, these beads are removed and another random chain end is chosen. Otherwise, the beads become two new chain ends that are available to branch further. This procedure is carried out until the desired molecular weight is attained. Each bead roughly corresponds to the single acetal monomer ($-CH_2OCH_2-$) that exists between branching points, such that (for example) HPG_{30k} constitutes 1,136 beads. Alkyl chain beads representing three carbon backbone atoms ($-CH_2CH_2CH_2-$) are subsequently added to randomly chosen chain ends. Typical Monte Carlo translational update moves are used to find a typical equilibrium conformation, with bonds free to have distances between 0.8-1.2σ, where σ is the bead diameter. Overlap distances less than 0.8 σ are not allowed.

Determining the number of peptides per iron dose: The weight percent of HPG in the clusters was estimated by thermogravimetric analysis (TGA) using a Cahn Thermax 500 thermogravimetric analyzer (Thermo Fisher, USA), which yielded values of 59% and 26% HPG by weight in the case of worm-like and spherical clusters, respecteively. Noting that the number of peptides per mass of targeted HPG_{3k} was 0.457 mmol/g as described in the text, the number of peptides per molar amount of iron is estimated as described below, and found to be approximately 1:112 for worm-like clusters and 1:36 for spherical clusters.

For worm-like clusters (with 3:1 HPG_{50k}:targeted HPG_{3k}):

$$\text{weight fraction of targeted } HPG_{3k} \approx \left(\frac{1\text{ mol}\times(3{,}000\text{ g/mol target\_}HPG_{3k})}{1\text{ mol}\times(3{,}000\text{ g/mol target\_}HPG_{3k}) + 3\text{ mol}\times(50{,}000\text{ g/mol }HPG_{50k})}\right) = 0.0196$$

$$\text{mol peptides per mol Fe} = \frac{(0.457\text{ mmol peptide/g target\_}HPG_{3k})\times(0.59\text{ g }HPG_{total})\times 0.0196}{[(0.41\text{ g }Fe_3O_4)/(0.2315\text{ g/mmol }Fe_3O_4)]/3} \approx \frac{1}{112}$$

For spherical clusters (with 3:1 HPG_{3k}:targeted HPG_{3k}):

$$\text{weight fraction of targeted } HPG_{3k} \approx \left(\frac{1\text{ mol}\times(3{,}000\text{ g/mol target\_}HPG_{3k})}{1\text{ mol}\times(3{,}000\text{ g/mol target\_}HPG_{3k}) + 3\text{ mol}\times(3{,}000\text{ g/mol }HPG_{3k})}\right) = 0.25$$

$$\text{mol peptides per mol Fe} = \frac{(0.457\text{ mmol peptide/g }HPG_{3k})\times(0.26\text{ g }HPG_{total})\times 0.25}{[(0.74\text{ g }Fe_3O_4)/(0.2315\text{ g/mmol }Fe_3O_4)]/3} \approx \frac{1}{36}$$

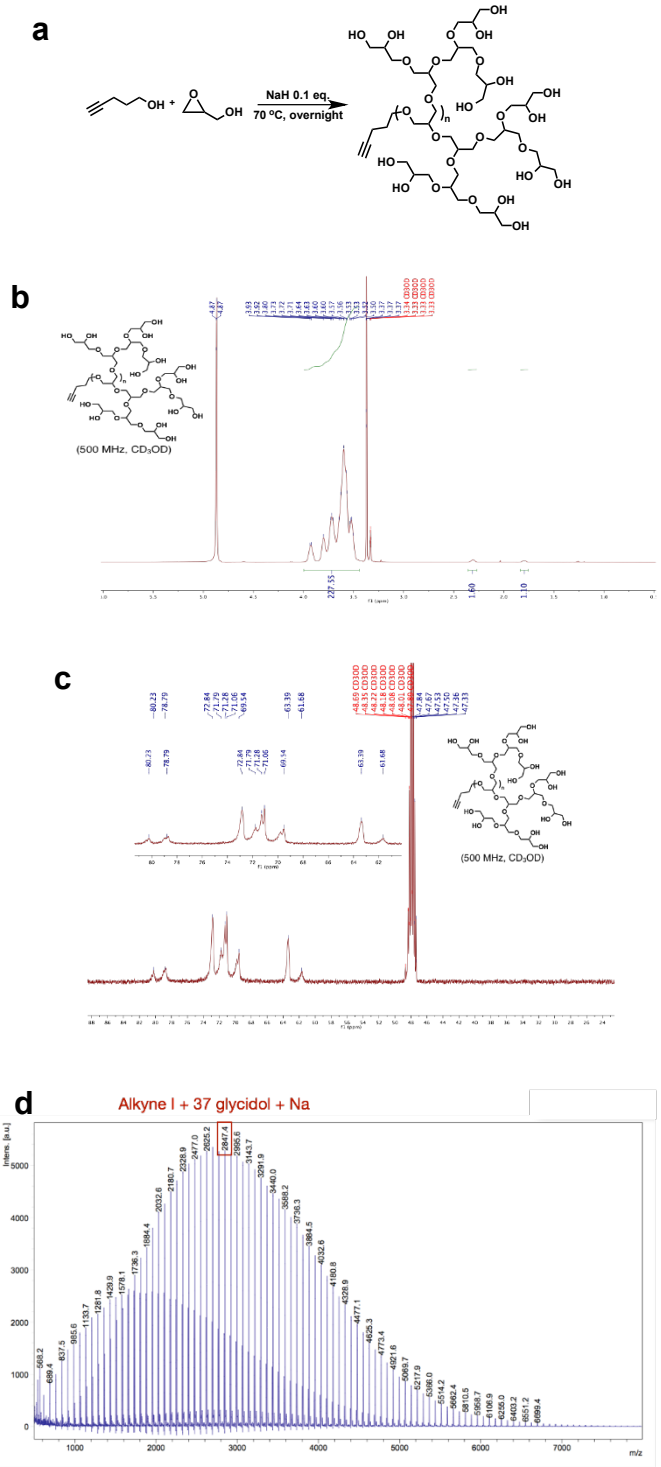

Figure S1. Synthesis (a) and characterization of HPG_{3k} by (b) ^{1}H NMR analysis of HPG_{3k}, (c) ^{13}C NMR analysis of HPG_{3k}, and (d) MALDI-TOF.

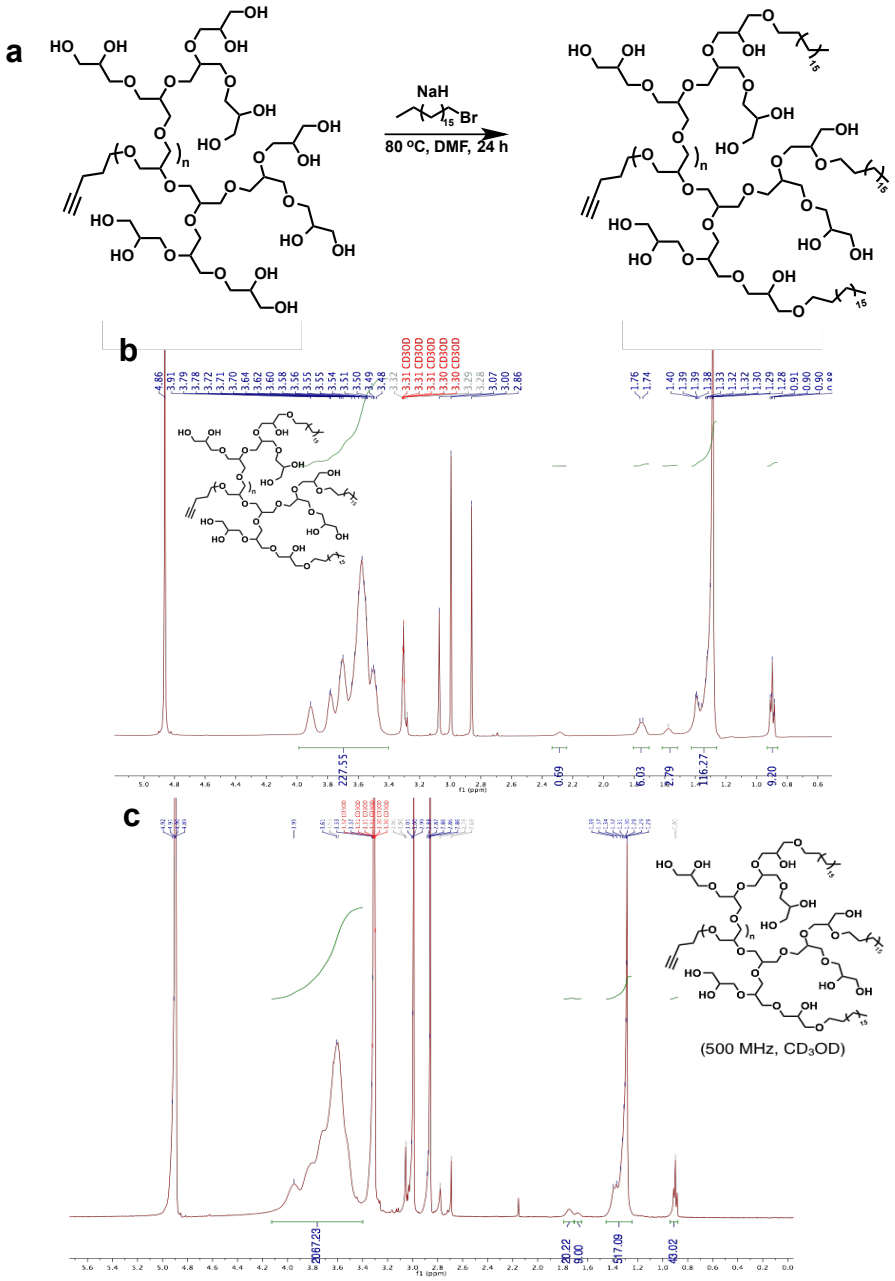

Figure S2. Synthesis (a) and characterization of alkylated HPG. (b) ^{1}H NMR analysis of HPG_{3k}-g-C18(3). (c) ^{1}H NMR analysis of HPG_{50k}-g-C18(15).

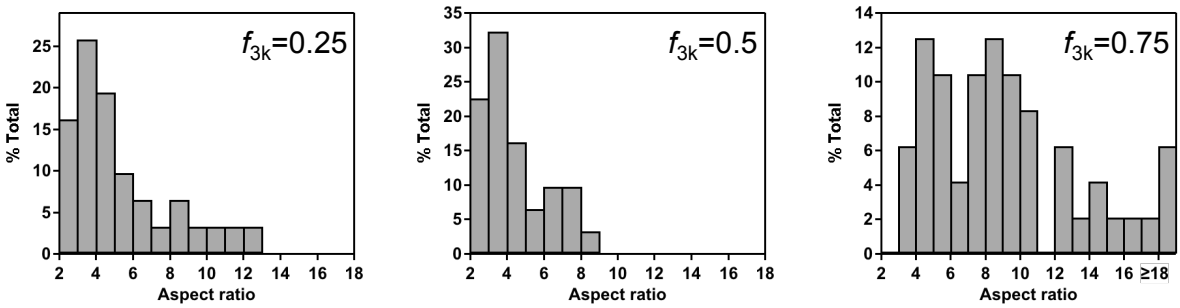

Figure S3. Distribution of aspect ratios across batches of worm-like SPION clusters. Only clusters with aspect ratios greater than 1 (non-spherical) are considered. At least 50 clusters were measured per sample from TEM images.

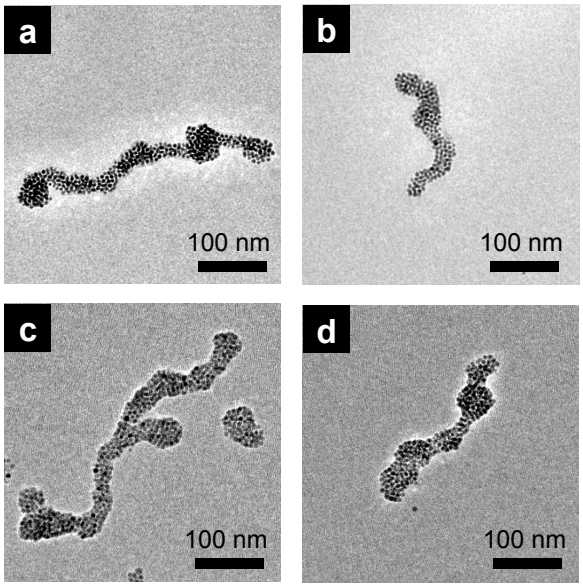

Figure S4. TEM images of worm-like SPION clusters before (a, b) and after (c, d) aging in 10% bovine serum solution.

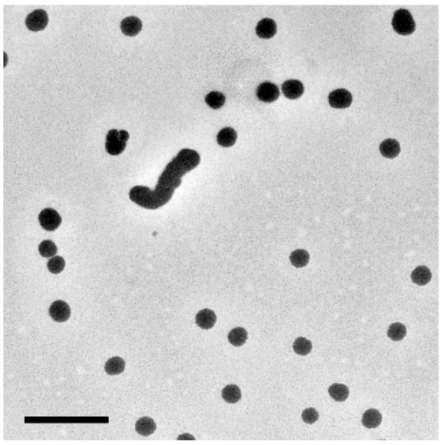

Figure S5. A 3:1 mixture of HPG_{3k}-g-C_{18}(5):HPG_{50k}-g-C_{18}(15) prepared from emulsification with SPION-free chloroform resulted predominantly in spherical structures. The scale bar represents 500 nm.

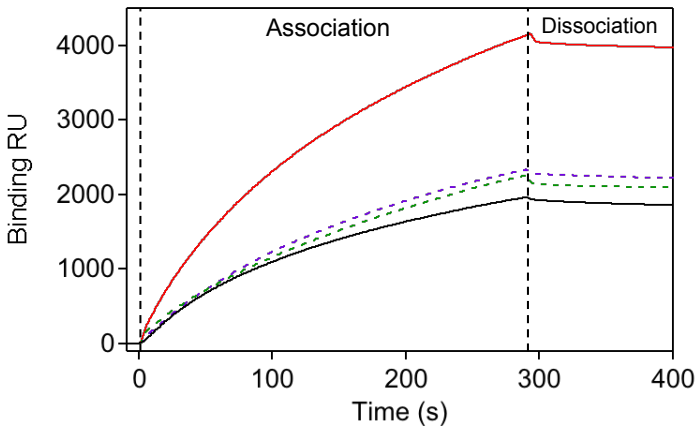

Figure S6. The role of targeting peptide in the binding of worm-like nanoclusters. The binding RU for VHPKQHR peptide-conjugated worm-like SPION clusters (red, solid curve) was higher than that of peptide-free worm-like SPION clusters (green, dotted curve). Additionally, pre-saturating VCAM-1 receptors with free VHPKQHR peptide reduced the binding RU for VHPKQHR peptide-conjugated worm-like SPION clusters (black, solid curve), but had minimal effect on peptide-free worm-like SPION clusters (purple, dotted curve).