Electronic Supplementary Material (ESI) for Nanoscale.

Supplementary Figure

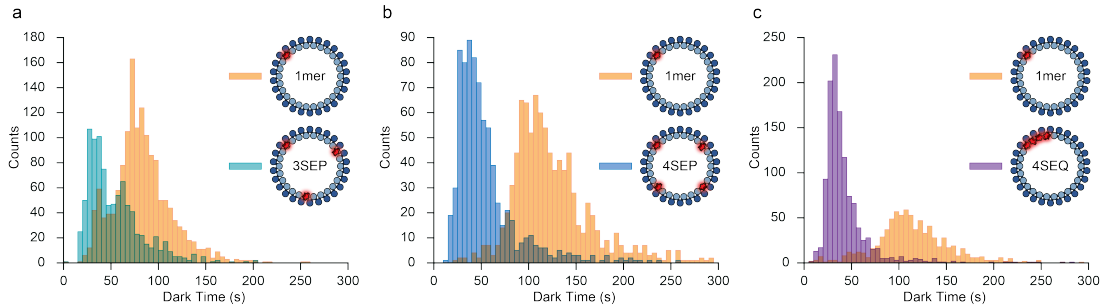

Figure S1. Histograms of dark times prior to normalisation. Histograms of dark times for all DNA origami nanotubes imaged in samples containing (a) 3SEP, (b) 4SEP and (c) 4SEQ. Dark times for nanotubes with a single docking site (1mer) for normalization are shown in orange. The total number of particles analysed was 1480 monomer and 905 trimer clusters for 3SEP, 916 monomer and 781 tetramer clusters for 4SEP and 806 monomer and 1168 trimer clusters for 4SEQ

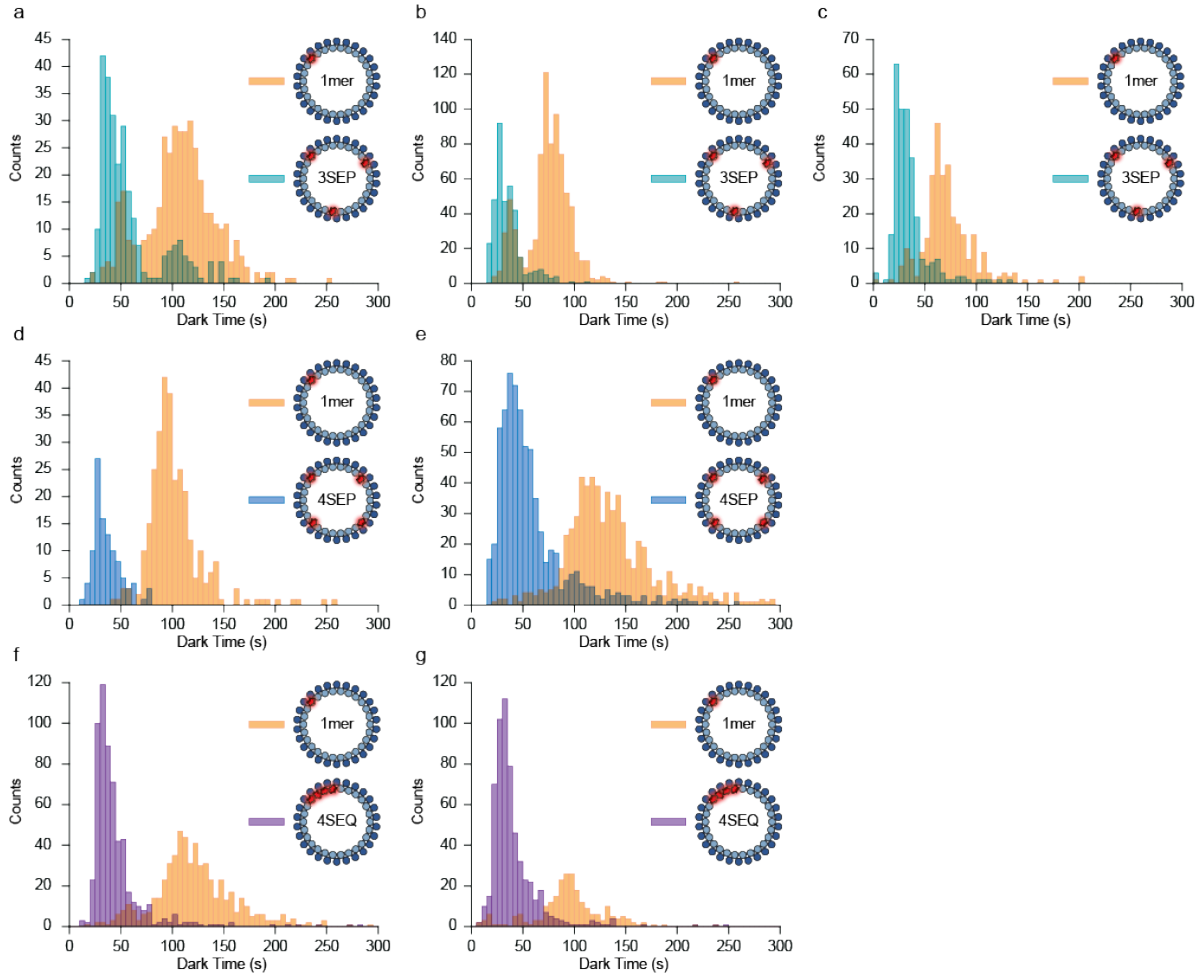

Figure S2. Histograms of dark times for all samples prior to pooling and normalisation. Histograms of dark times for all DNA origami nanotubes separated for (a/b/c) three samples analysed for 3SEP, and two samples for (d/e) 4SEP and (e/f) 4SEQ.

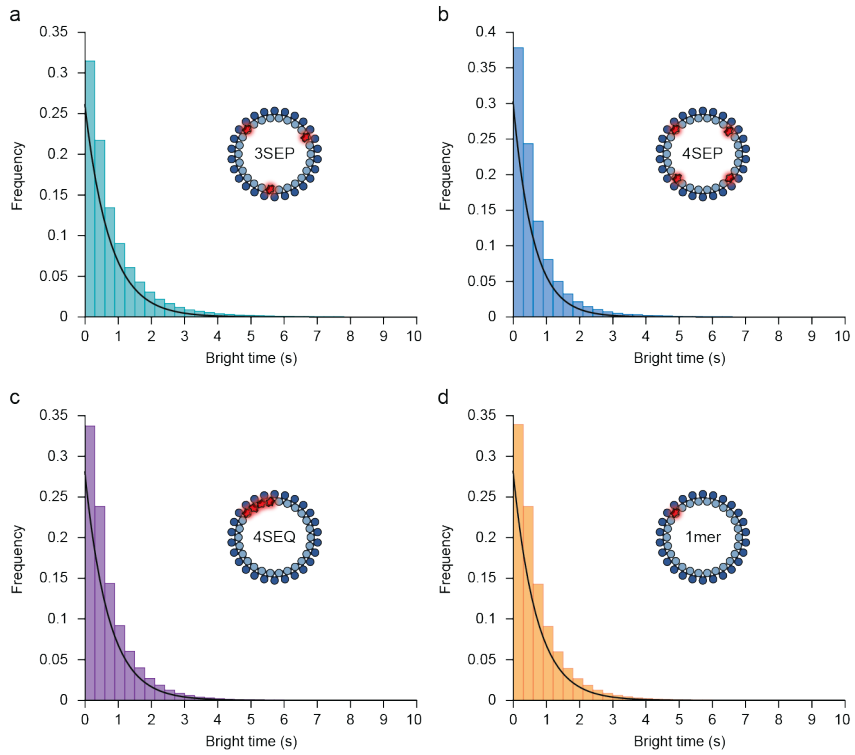

Figure S3: Histogram of bright-time (bound, 'on'-time of imager to docker) for each sample. Distribution of bright-time shown for (a) 3SEP, (b) 4SEP, (c) 4SEQ and (d) monomer. Histograms are generated from pooled data across every sample and measurement. Monoexponential fits ($F = Ae^{-bt}$) are overlaid in black. Decay constants for each sample (± 95% CI) are: $\tau_{4SEP} = 1.65 \pm 0.04\ s^{-1}$, $\tau_{4SEQ} = 1.41 \pm 0.04\ s^{-1}$, $\tau_{3SEP} = 1.34 \pm 0.03\ s^{-1}$, $\tau_{1mer} = 1.42 \pm 0.04\ s^{-1}$ respectively.