

Supplementary Information for: Colloid supported lipid bilayers for self-assembly

Melissa Rinaldin^{*,1,2}, Ruben W. Verweij^{*,1}, Indrani Chakraborty³,
and Daniela J. Kraft¹

^{*}These authors contributed equally to the work.

¹Huygens-Kamerlingh Onnes Lab, Universiteit Leiden, P. O. Box 9504, 2300 RA Leiden,
The Netherlands

²Instituut-Lorentz, Universiteit Leiden, P.O. Box 9506, 2300 RA Leiden, The
Netherlands

³School of Chemistry, Raymond and Beverly Sackler Faculty of Exact Sciences, Tel Aviv
University, Tel Aviv 69978, Israel

Corresponding email: kraft@physics.leidenuniv.nl

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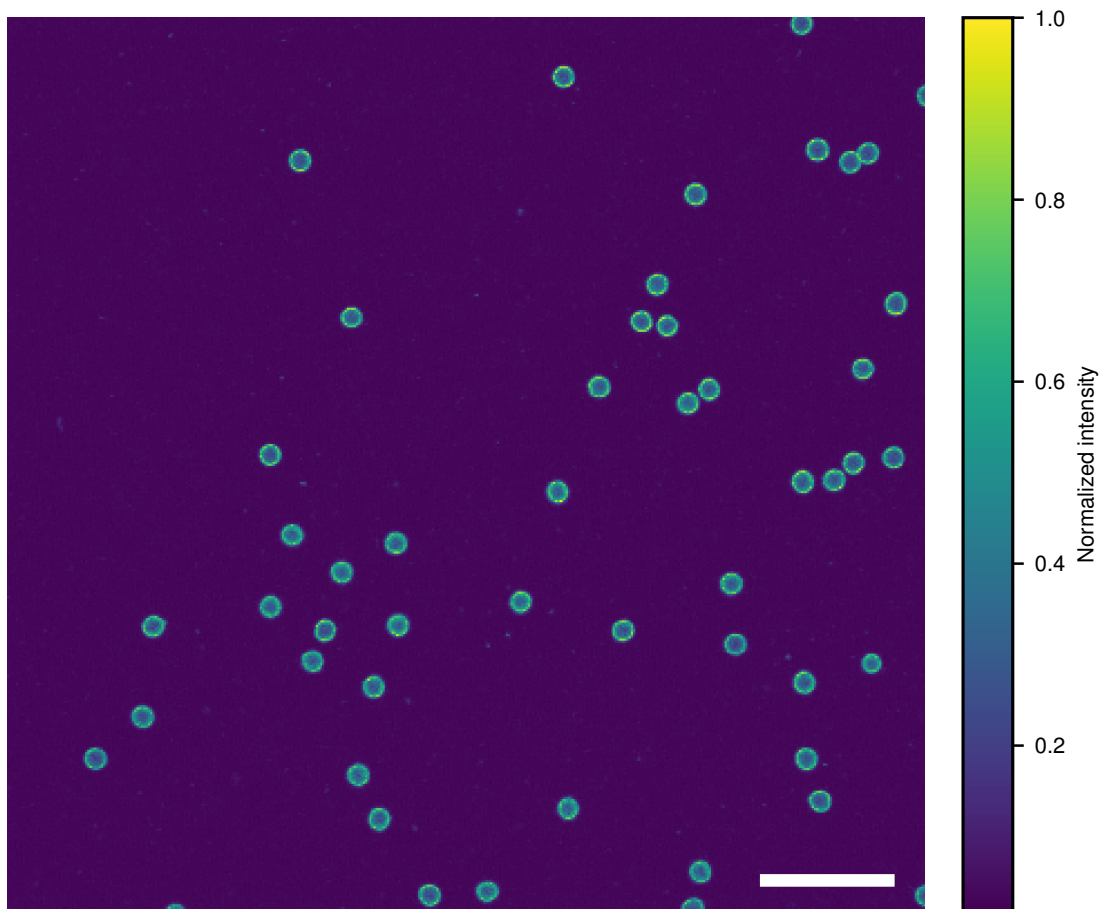


Figure S1: Overview picture showing the homogeneity of the lipid bilayer for CSLBs containing 1 mol % DOPE-PEG(2000). The scale bar is 15 μm .

Table S1: Summary of all DNA strand sequences and their names. Sticky ends are marked in cursive.

No.	Name	Sequence
1	10 nm Single Base	Cholesterol-TEG-3'-GTT-AGC-CCG-ATT-ACA- -GAG-CGT-TCT-TT-3'
2	10 nm Single Inert	Cholesterol-TEG-5'-TTT-GAA-CGC-TCT-GTA- -ATC-GGG-CTA-AC-3'
3	20 nm Single Base	Cholesterol-TEG-3'-TTT-TAG-CGA-TGG-GAA- -GCG-TGT-CAG-TTA-GAT-CTC-TCG-GGA-CGG- -AAT-GC-5'
4	20 nm Single Inert	Cholesterol-TEG-5'-TTT-ATC-GCT-ACC-CTT- -CGC-ACA-GTC-AAT-CTA-GAG-AGC-CCT-GCC- -TTA-CGA-3'
5	20 nm Single Linker A	Cholesterol-TEG-5'-TTT-ATC-GCT-ACC-CTT- -CGC-ACA-GTC-AAT-CTA-GAG-AGC-CCT-GCC- -TTA-CGA- <i>GTA-GAA-GTA-GG</i> -3'-6FAM
6	20 nm Single Linker A'	Cholesterol-TEG-5'-TTT-ATC-GCT-ACC-CTT- -CGC-ACA-GTC-AAT-CTA-GAG-AGC-CCT-GCC- -TTA-CGA- <i>CCT-ACT-TCT-AC</i> -3'-Cy3
7	30 nm Single Base	5'-TCG-TAA-GGC-AGG-GCT-CTC-TAG-ACA-GGG- -CTC-TCT-GAA-TGT-GAC-TGT-GCG-AAG-GTG- -ACT-GTG-CGA-AGG-GTA-GCG-ATT-TT-3'
8	30 nm Single Linker A	Double Stearyl-HEG-5'-TT-TAT-CGC-TAC-CCT- -TCG-CAC-AGT-CAC-CTT-CGC-ACA-GTC-ACA- -TTC-AGA-GAG-CCC-TGT-CTA-GAG-AGC-CCT- -GCC-TTA-CGA- <i>GTA-GAA-GTA-GG</i> -3'-6FAM
9	30 nm Single Linker A'	Double Stearyl-HEG-5'-TT-TAT-CGC-TAC-CCT- -TCG-CAC-AGT-CAC-CTT-CGC-ACA-GTC-ACA- -TTC-AGA-GAG-CCC-TGT-CTA-GAG-AGC-CCT- -GCC-TTA-CGA- <i>CCT-ACT-TCT-AC</i> -3'-Cy3

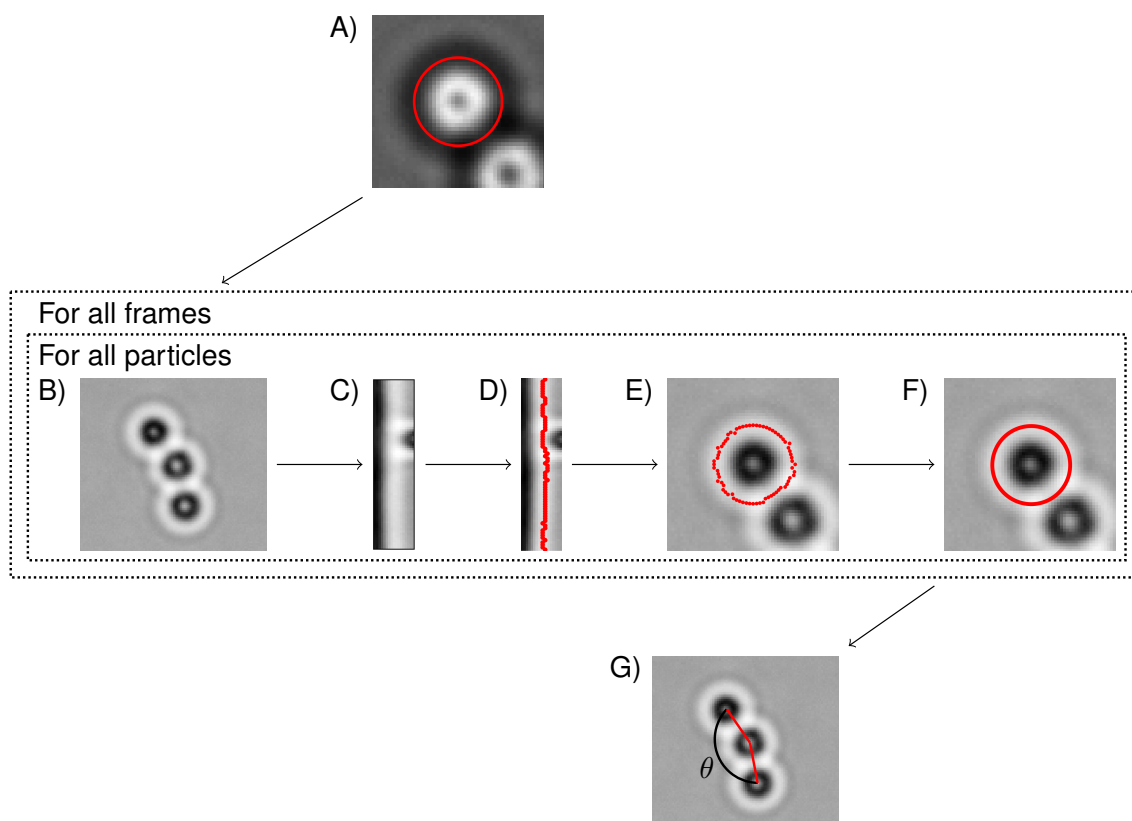


Figure S2: The algorithm used for tracking particles in bright-field movies depicted graphically. **A)** The user is asked to manually select the particles that need to be tracked from the first frame using a Matplotlib [1] interface. **B)** The current frame is inverted so that the dark ring around features becomes bright. **C)** The frame is interpolated and converted to polar coordinates with the current provisional particle position at the origin. **D)** For each row (corresponds to each polar angle), the position with the maximum intensity is found (for intensities higher than a set threshold). **E)** The coordinates that were found are then converted to the original Cartesian coordinates. **F)** A circle is fit to the coordinates using a least squares method. **G)** The opening angle between the three particles is determined using simple trigonometry, whilst keeping the particle order the same for all frames.

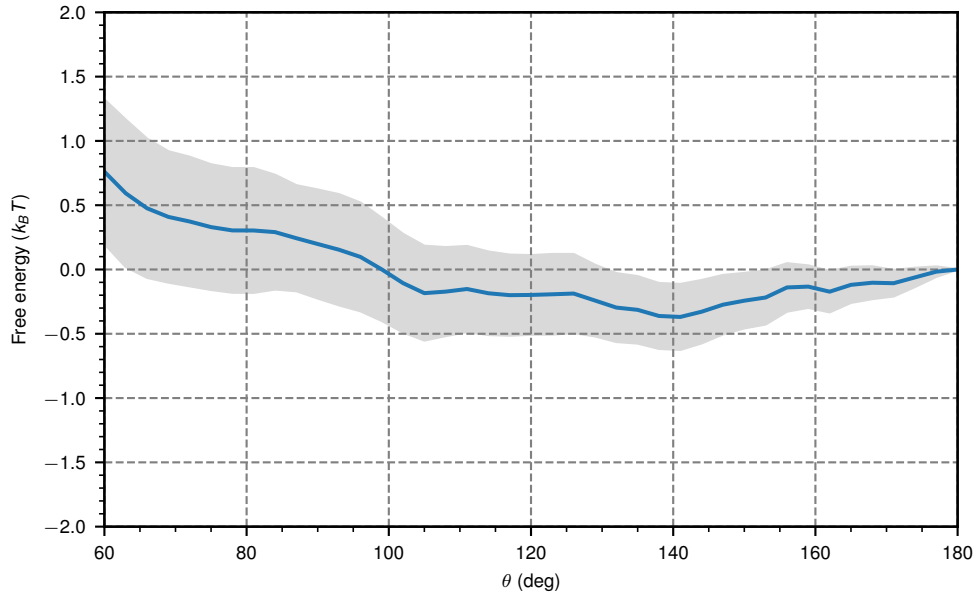


Figure S3: In [2], we measured a preferred angle of 140° with a magnitude of roughly $0.9 K_B T$. When we analyze this data using the angular displacement method outlined in this work, we see that the observed preference is within the experimental error (indicated by the shaded gray area).

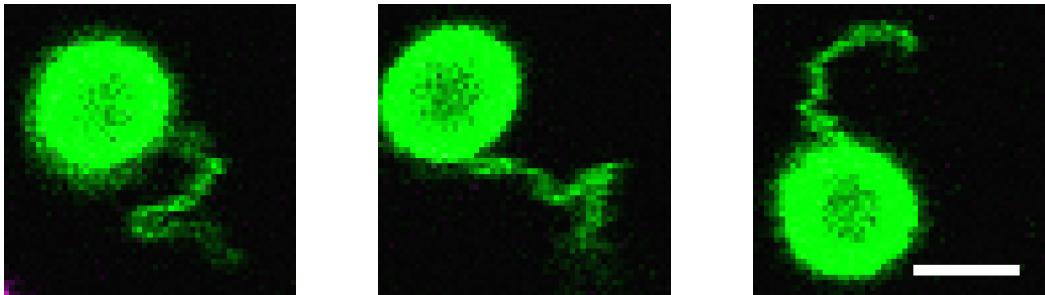


Figure S4: Figure showing the membrane tubes that form at high DNA coating concentrations for three different particles. The scale bar is $2 \mu\text{m}$. The tubes are comparable to the particle size ($2 \mu\text{m}$) and are very floppy. Note that the brightness was increased to show the tubes and as a result the particles are oversaturated.

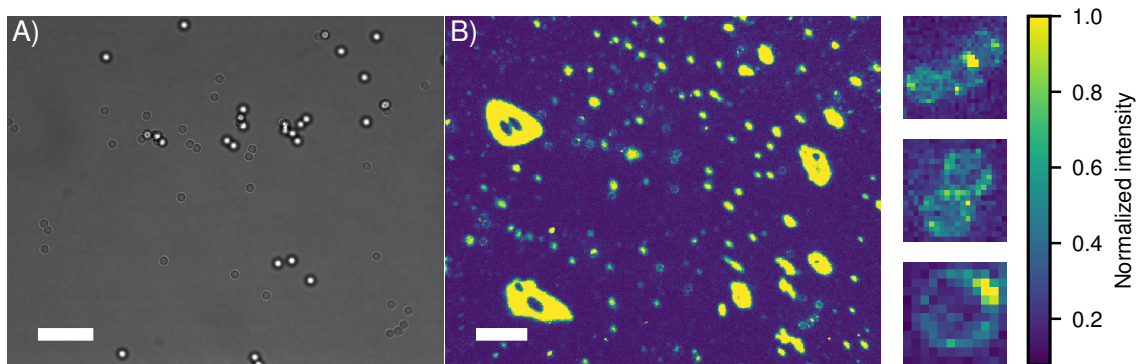


Figure S5: Figure showing particles coated with SUVs that were first incubated with $\sigma_{\text{DNA}} = 413 \mu\text{m}^{-2}$ linker DNA strands and $\sigma_{\text{DNA}} = 1.55 \times 10^5 \mu\text{m}^{-2}$ inert DNA for 1 h. The functionalized SUVs were mixed with the particles for 1 h and then washed three times. Because the SUVs are sterically stabilized by the DNA strands, the spreading of the SUVs on the particle surface is hindered. **A)** A bright field image taken at the same position and focal plane as **B)** a confocal image showing inhomogeneously coated particles and irregular patches where the glass substrate was partially coated with the SUVs that were left in the solution. On the right are three close-ups of particles. Scale bars are $15 \mu\text{m}$. Note that the brightness was increased to show the inhomogeneously coated particles and as a result some pixels are oversaturated.

A References

- [1] Hunter, J. D. Matplotlib: A 2d graphics environment. *Comput. Sci. Eng.* **9**, 90–95 (2007).
- [2] Chakraborty, I., Meester, V., Van der Wel, C. & Kraft, D. J. Colloidal joints with designed motion range and tunable joint flexibility. *Nanoscale* **9**, 7814–7821 (2017).