

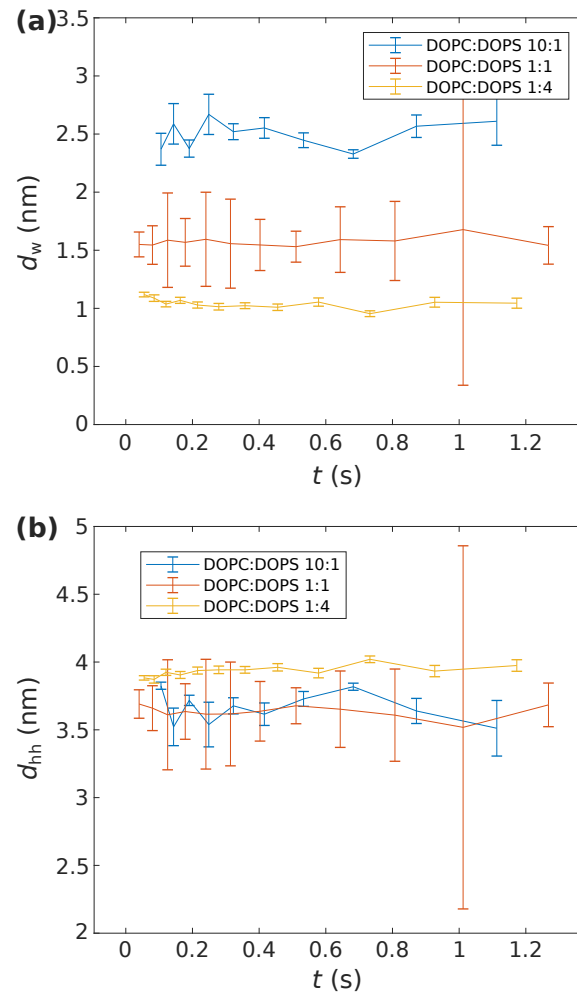
Supplementary information:  
Vesicle adhesion in the strong coupling regime studied by  
time-resolved small-angle x-ray scattering

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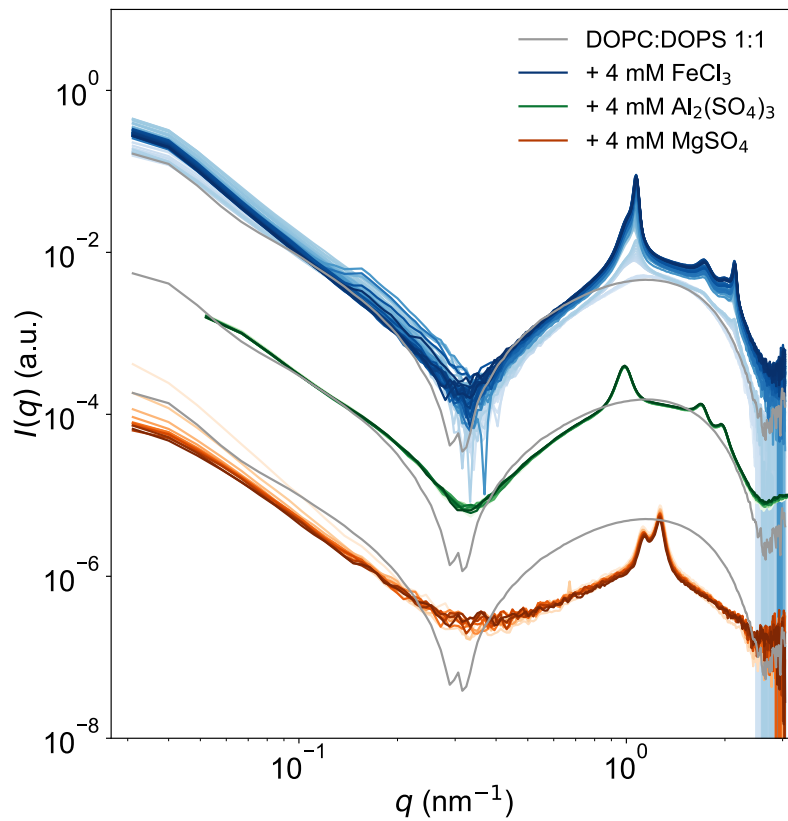
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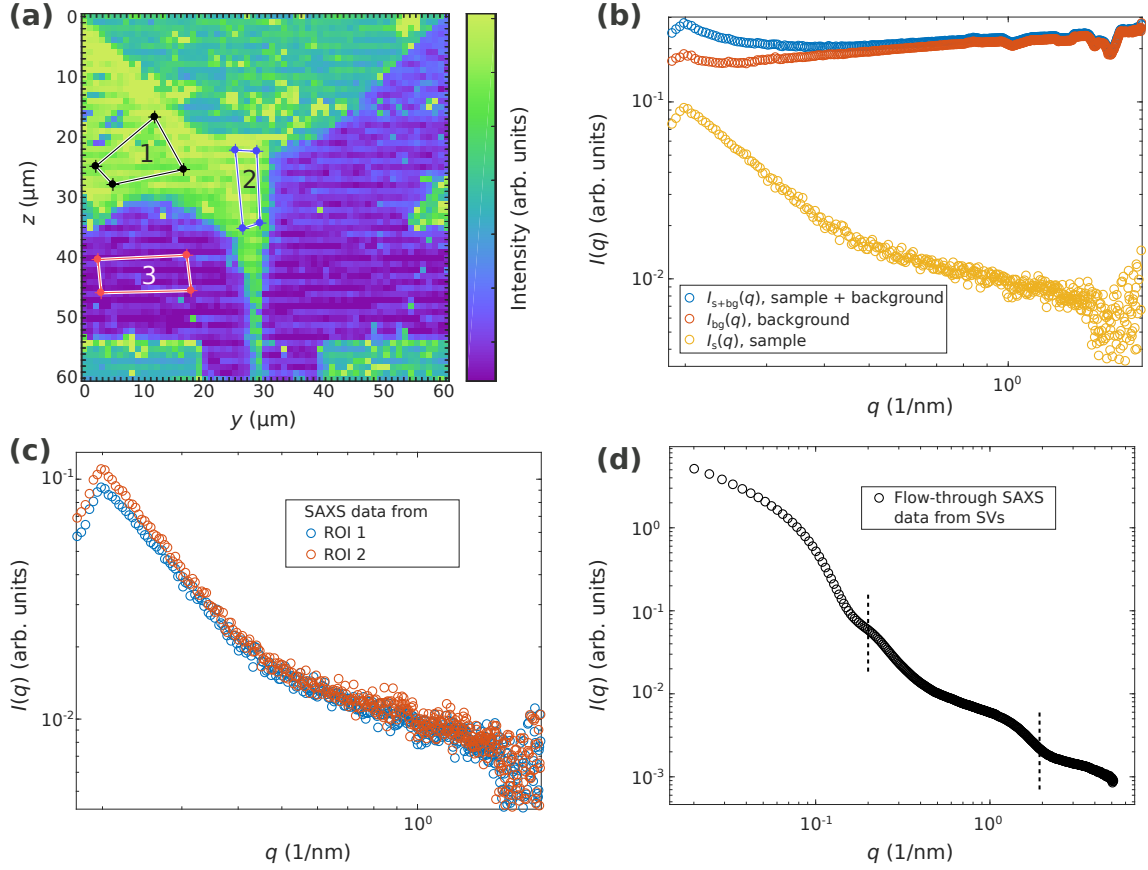
As supplemental figures, we include a plot of the bilayer structure parameters, obtained from the least-squares analysis of the stopped flow reaction as a function of time, see Fig.S1, as well as additional SAXS data on vesicle reactions upon injection of trivalent salts, recorded in the flow-through capillary at ID02/ESRF, see Fig.S2. Finally, as a first test we include a comparison of the SAXS curve as recorded in the flow-through capillary chamber, similar to our previous work in (1), and the SAXS curve as recorded from a SV solution in a microfluidics device (P10/PETRAIII), see Fig.S3. As the comparison shows, the accessible  $q$ -range has to be extended by different improvements in background reduction.



**Fig. S1:** Structural parameters (a)  $d_w$  and (b)  $d_{hh}$  as a function of time as obtained from docking model fits to SAXS data measured by the stopped-flow technique.



**Fig. S2:** Additional flow-through SAXS data measured at ID02/ESRF using trivalent salts. SAXS curves  $I(q)$  vs.  $q$  from DOPC:DOPS (1:1) vesicles mixed with 4 mM  $\text{FeCl}_3$  (blue), 4 mM  $\text{Al}_2(\text{SO}_4)_3$  (green), and 4 mM  $\text{MgSO}_4$  are shown. No signature attributed to docking of vesicles can be observed, instead, phase transitions to multilamellar states can be inferred from the Bragg peaks.



**Fig. S3:** Scanning-SAXS combined with microfluidics for the investigation of the reaction of synaptic vesicles in buffer (150 mM KCl, 20 mM HEPES, pH 7.4) with 2 mM  $\text{CaCl}_2$  in a microfluidic flow. The purification of synaptic vesicles was described in (2, 3). (a) Darkfield of the microfluidic device obtained by scanning-SAXS. The exposure time was 1 s for each pixel. The SAXS data within the marked areas (black: SVs from the inlet, blue: SVs mixed with  $\text{CaCl}_2$  from the point of stagnation, and red: buffer from the side-inlet) were averaged to obtain a stronger SAXS signal. (b) Example of a background corrected SAXS signal  $I(q) = I_{s+bg}(q) - I_{bg}(q)$ . Here, the averaged SAXS data from the inlet was used, and background corrected by the averaged SAXS data from the buffer. (c) Comparison of SVs in the inlet and of SVs in the point of stagnation (averaged SAXS signals from ROI 1 and ROI 2 in (a)). (d) For comparison, flow-through SAXS data (obtained at ID02/ESRF) is shown, covering a much larger  $q$ -space. The two vertical lines indicate the measured  $q$ -region by microfluidics SAXS shown in (a-c).

## Supporting References

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3. Takamori, S., M. Holt, K. Stenius, E. A. Lemke, M. Gronborg, D. Riedel, H. Urlaub, S. Schenck, B. Brügger, P. Ringler, S. A. Müller, B. Rammner, F. Gräter, J. S. Hub, B. L. D. Groot, G. Mieskes, Y. Moriyama, J. Klingauf, H. Grubmüller, J. Heuser, F. Wieland, and R. Jahn. 2006. Molecular Anatomy of a Trafficking Organelle. *Cell.* 127:831–846.