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**Supplemental Information**

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synaptotagmin-1 C2A and C2B dynamics: Insights  
from experiments and simulations**

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## Supplementary Information

### Ca<sup>2+</sup>-Dependent Lipid Preferences Shape Synaptotagmin-1 C2A and C2B Dynamics: Insights from Experiments and Simulations

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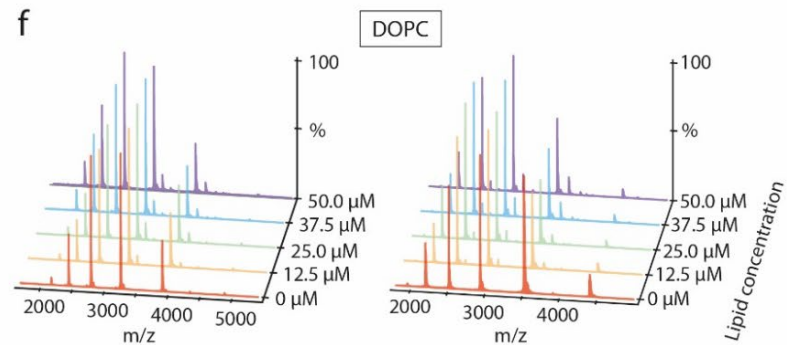
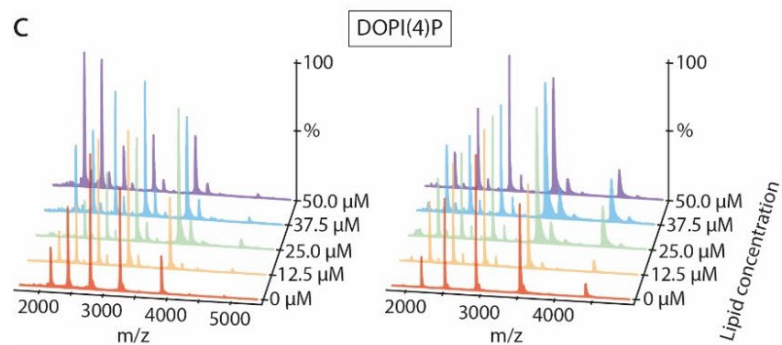
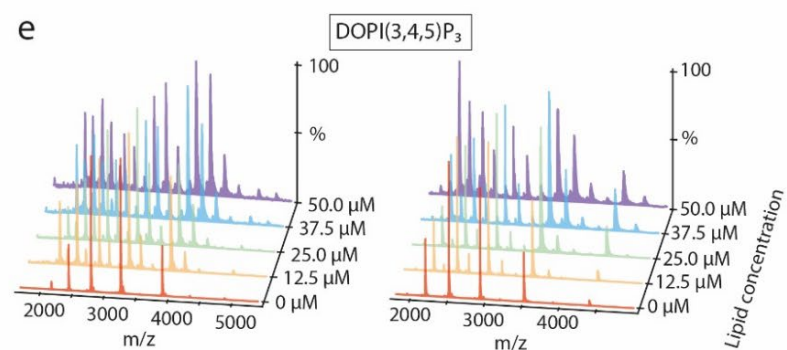
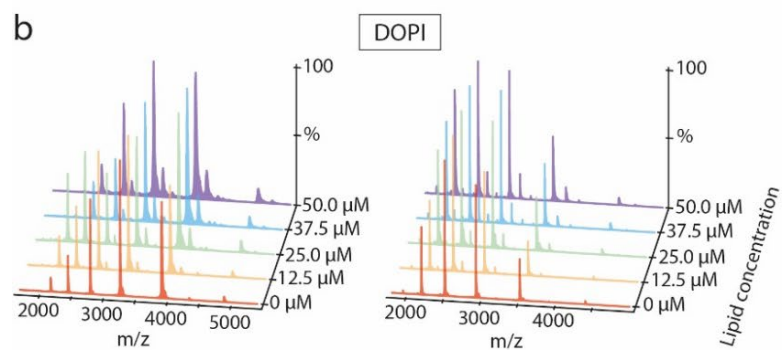
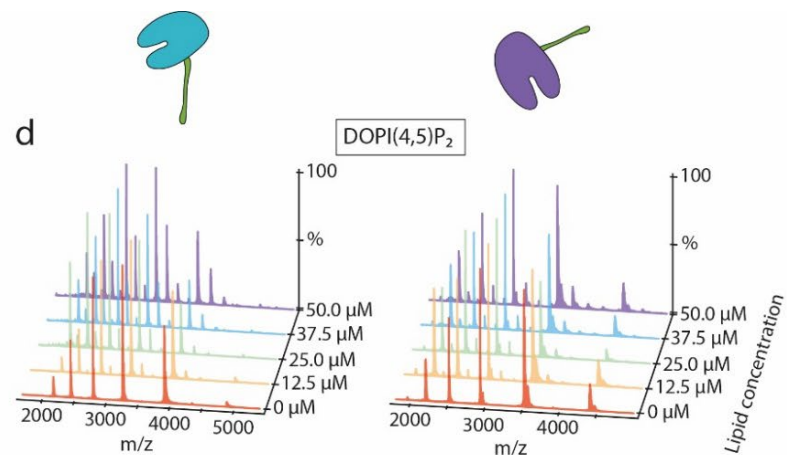
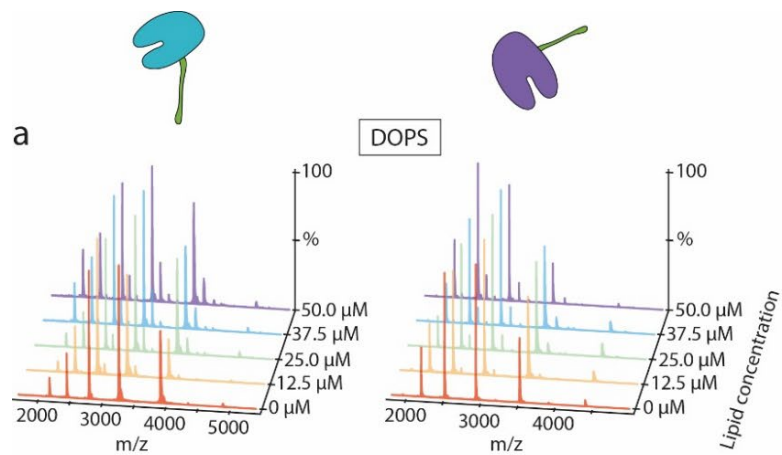
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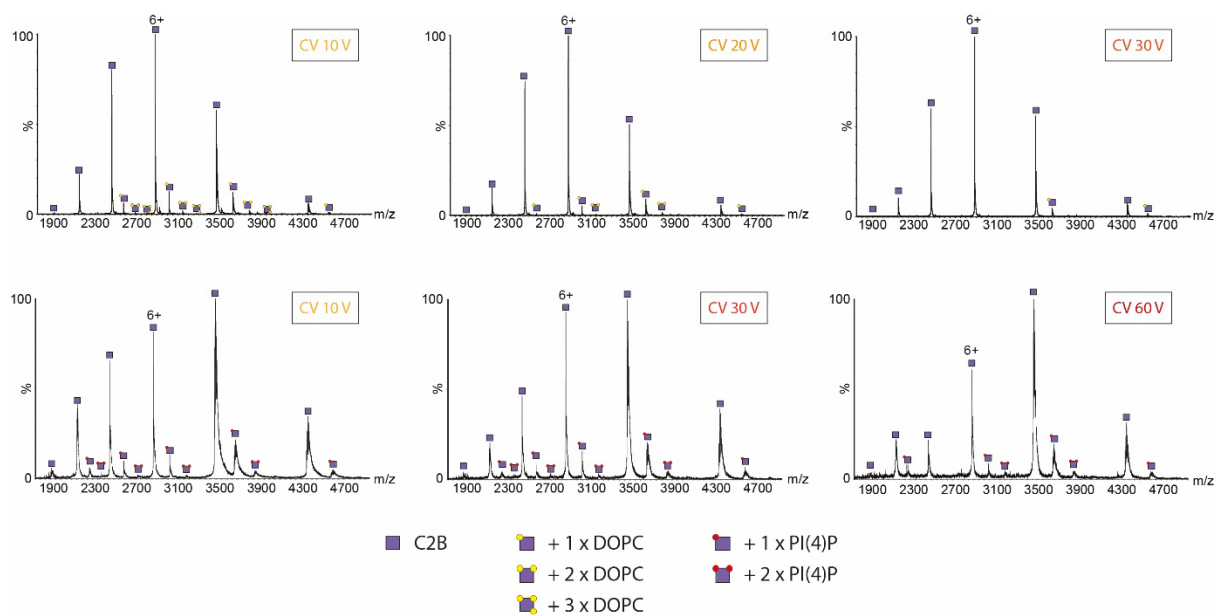
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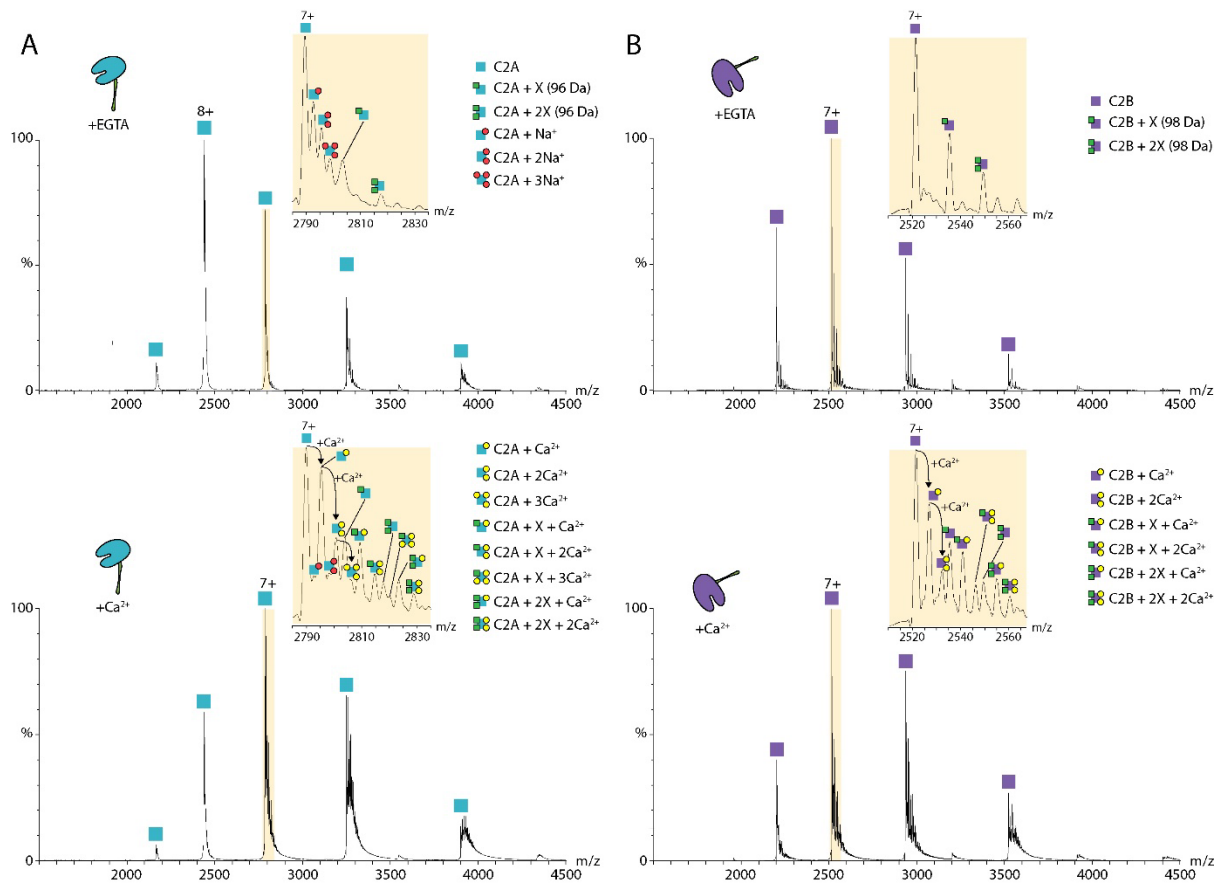
## Supplementary Figures



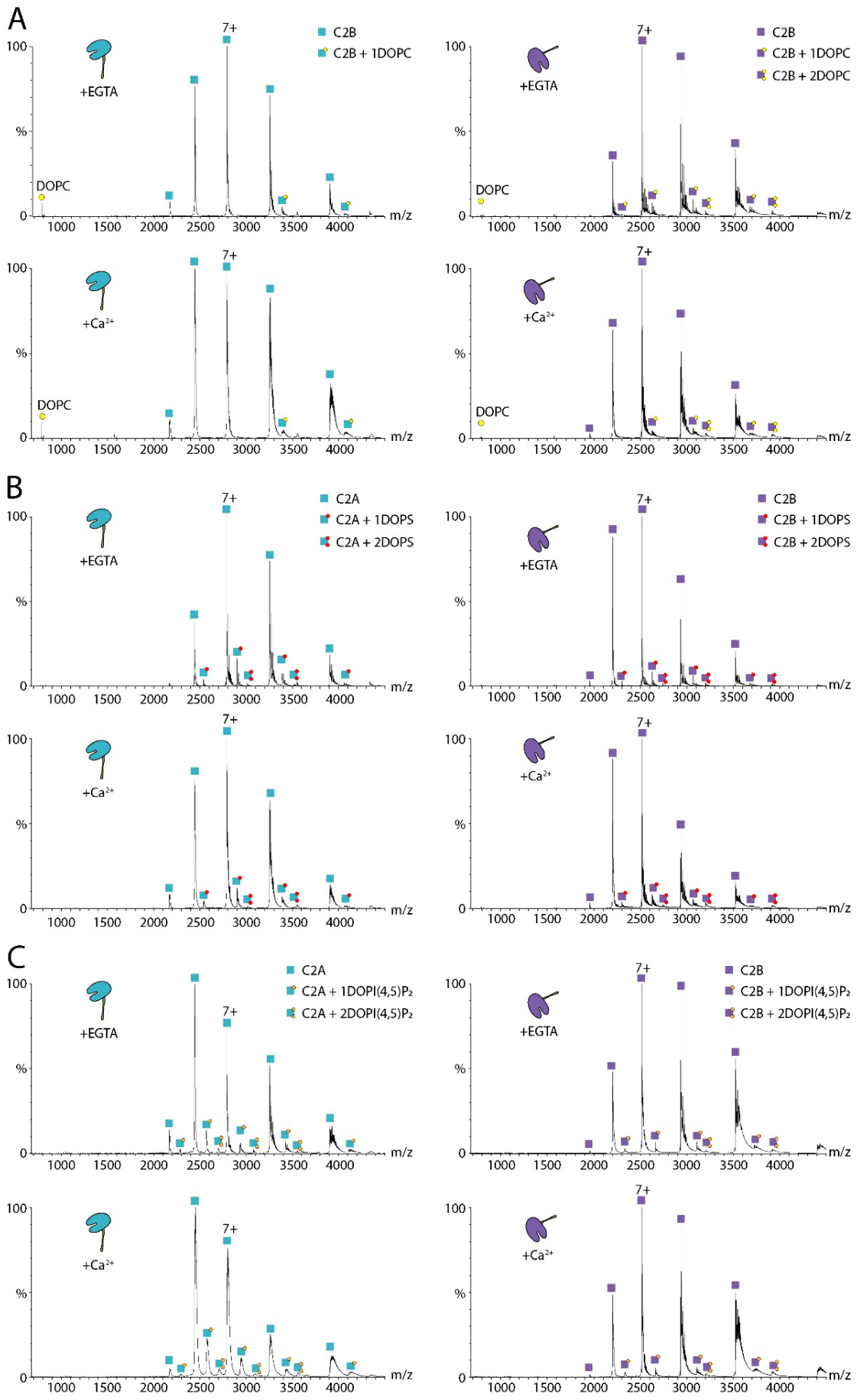
**Supplementary Figure 1. Lipid binding of C2A (cyan) and C2B (purple) explored by native mass spectrometry.** Related to Figure 2. Mixed detergent-lipid micelles containing increasing lipid concentrations were prepared and mixed with the two C2 domains. Lipid binding was then analysed by native mass spectrometry. **(a)** DOPS, **(b)** DOPI, **(c)** DOPI(4)P, **(d)** DOPI(4,5)P<sub>2</sub>, **(e)** DOPI(3,4,5)<sub>3</sub>, **(f)** DOPC.



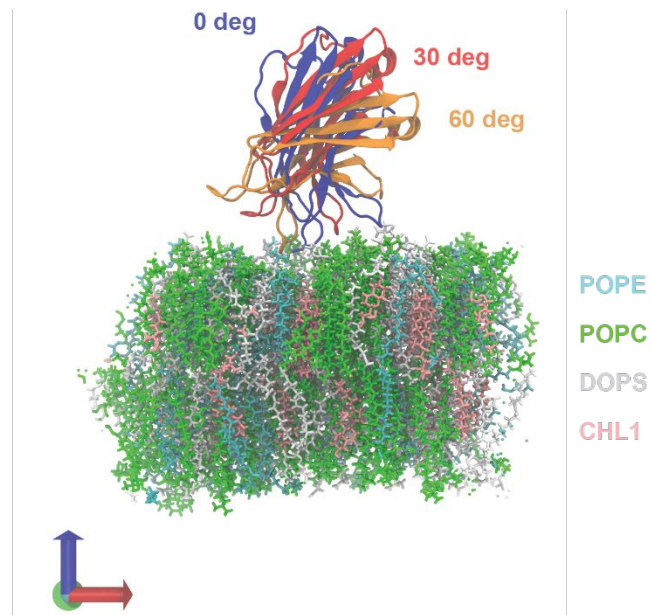
**Supplementary Figure 2. Dissociation of C2B-lipid complexes.** Related to Figure 2. Increasing the collisional voltage from 10 to 30 V caused loss of all associated DOPC molecules (upper row), while PI(4)P binding to C2B was still observed at 60 V (lower row).



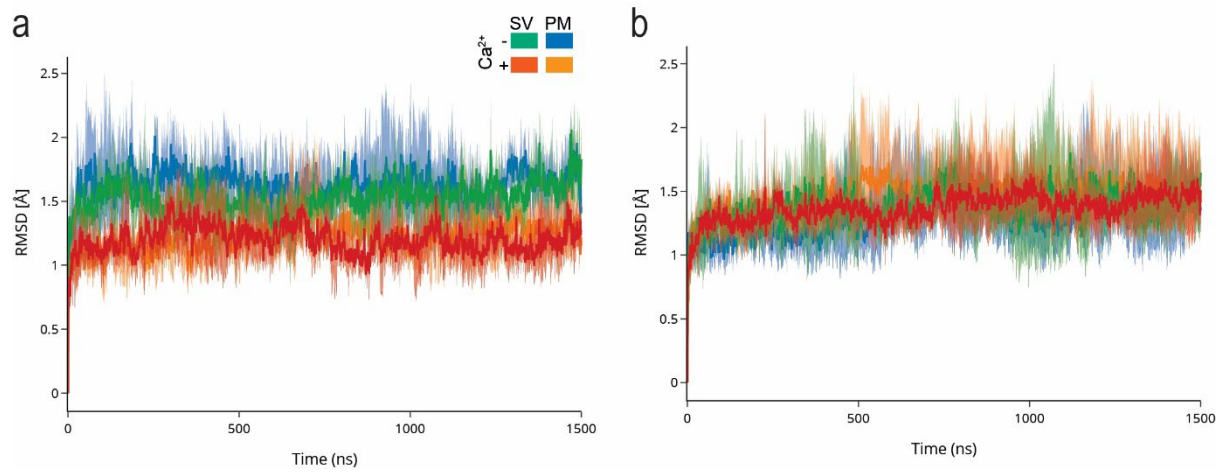
**Supplementary Figure 3.  $\text{Ca}^{2+}$  binding of C2A and C2B domains.** Related to Figure 2. C2A and C2B were incubated with EGTA (upper panels) or  $\text{CaCl}_2$  (lower panels) and analysed by native mass spectrometry. **(A)** In the presence of EGTA, binding of sodium ions (red circles) to C2A (cyan) was observed (upper panel). Upon incubation with  $\text{Ca}^{2+}$ , binding of three  $\text{Ca}^{2+}$  ions (yellow circles) to C2A was observed (lower panel). Note that binding of additional adducts (+96 Da each, green squares) was observed in the absence (+EGTA, upper panel) and in the presence of  $\text{Ca}^{2+}$  (lower panel). This additional adduct likely corresponds to phosphate. Binding of  $\text{Ca}^{2+}$  ions was also observed to the phosphate-bound states. **(B)** Binding of two  $\text{Ca}^{2+}$  ions (yellow circles) to C2B was observed. Again, additional adducts (+98 Da each, green squares) were observed in the absence (+EGTA, upper panel) and in the presence of  $\text{Ca}^{2+}$  (lower panel). Binding of  $\text{Ca}^{2+}$  ions was also observed to the phosphate-bound states.



**Supplementary Figure 4. Phospholipid binding of C2A and C2B domains in the presence of EGTA or Ca<sup>2+</sup>.** Related to Figure 2. C2A (cyan) and C2B (purple) were pre-incubated with EGTA or Ca<sup>2+</sup> and binding of **(A)** DOPC (yellow), **(B)** DOPS (red) and **(C)** DOPI(4,5)P<sub>2</sub> (orange) was subsequently analysed by native mass spectrometry.



**Supplementary Figure 5. Starting orientation of the three starting simulations.** Related to Figures 4, 5, 6 and 7. The C2A domain of Synaptotagmin-1 is placed on the synaptic vesicle membrane in the absence of calcium. Structures corresponding to the different starting orientations (0°, blue; 30°, red; 60°, orange) and membrane lipids (POPE, cyan; POPC, green; DOPS, silver; cholesterol (CHL1), pink) are colour coded.



**Supplementary Figure 6. C $\alpha$  Root-mean-square deviations (RMSDs) of the C2 domains with respect to the first frame of the simulation.** Related to Figures 4, 5, 6 and 7. RMSDs are shown for each C2 domain interacting with the SV membrane in the presence (red) and in the absence (green) of Ca<sup>2+</sup> ions as well as the plasma membrane in the presence (orange) and in the absence (blue) of Ca<sup>2+</sup>. The mean RMSD (solid line) and the range of RMSDs per time step of the three simulations with different starting angles (transparent area) are shown. **(a)** C2A (residues 141-263) **(b)** C2B (residues 272-418).