Supporting Information

Investigation of the Curvature Induction and Membrane Localization of the Influenza Virus M2 Protein Using Static and Off-Magic-Angle Spinning Solid-State NMR of Oriented Bicelles

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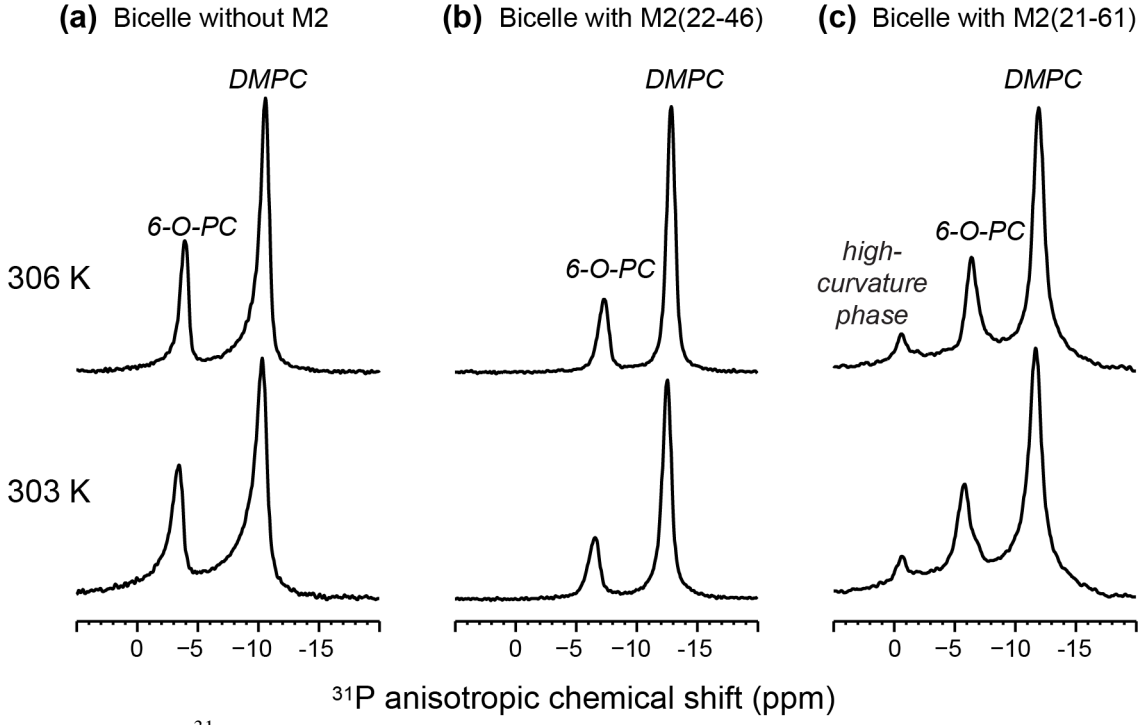

Figure S1. Static ^{31}P spectra of DMPC/6-O-PC bicelles. (a) Control sample without M2. (b) M2(22-46)-containing bicelles. (c) M2(21-61)-containing bicelles. M2(21-61) causes an isotropic peak that is absent in the M2(22-46) sample.

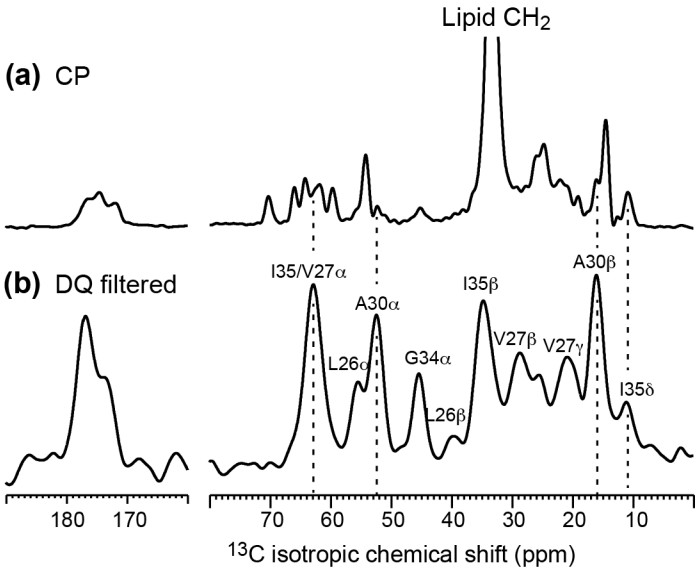

Figure S2. 1D ^{13}C CP (a) and double-quantum filtered (b) spectra of M2(21-61)-containing DMPC/DHPC bicelles at 253 K under 5 kHz MAS. The ^{13}C isotropic chemical shifts of the TM residues correspond to α-helical conformations, indicating that the TM domain adopts the same helical structure in the bicelle as in multilamellar liposomes.

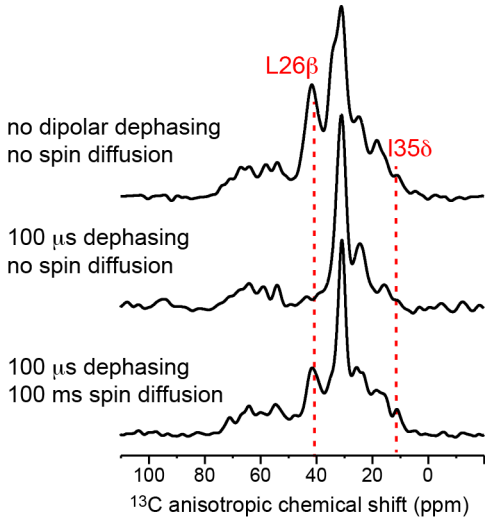

Figure S3. Dephasing of peptide signals by ^{13}C-^{1}H dipolar coupling. A 100 μs dipolar filter removed the L26 Cβ signal and significantly suppressed the I35 Cδ1 intensity. A mixing period (t_m) of 100 ms restored the peptide ^{13}C signals by transferring ^{1}H magnetization from lipids to peptide.