Supporting materials

**NMR Structure, Localization and Vesicle Fusion of Chikungunya Virus
Fusion Peptide**

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Figure S1

Figure S1: Stern-Volmer plots showing quenching by acrylamide of the Trp residue of VT18 in free solution (square) and in the presence of DMPC vesicles (circle). Quenching experiments were carried out by a step wise addition of acrylamide (0.025 M-0.2 M), from a stock solution of 2 M, into solutions containing 5 μ M VT18 either in the free solution or in the presence of 100 μ M LUVs of DPMC. Samples were prepared in solutions of 10 mM sodium phosphate buffer, pH 5.0. The quenching data were examined by fitting to the Stern-Volmer equation, $F_0/F=1+K_{SV}[Q]$, where, F_0 and F are the fluorescence intensities at the λ_{max} of the fluorophore in the absence and presence of acrylamide, respectively, K_{SV} is the Stern-Volmer quenching constant and $[Q]$ is the molar quencher concentration. A lower K_{SV} of Trp in the presence of LUVs of DMPC, in comparison to that of in the free solution, indicated limited exposure of the Trp to aqueous solution.

Figure S2

Figure S2: Vesicle fusion of VT18AAA peptide: Plot shows fluorescence intensity of NBD-PE at 530 nm in vesicle fusion assays carried out for the VT18AAA peptide at pHs 5.0 and 7.5. No detectable changes of NBD-PE fluorescence, in either pHs, indicated absence of vesicle fusion or lipid mixing for the mutant peptide. Peptide was purchased from GL-Biochem (Shanghai, China) and purified by HPLC. Experiments were carried out as described for the native VT18 peptide (see Materials and Methods).

Table S1: Key long-range NOEs used to determine DPC micelle bound 3-D structure of the VT18 peptide

94 CYS HN	87 PHE H δ
87 PHE HN	93 TYR H ϵ
93 TYR H α	87 PHE H δ
88 MET H β s	95 PHE H ζ
85 TYR H ϵ	95 PHE H ζ
87 PHE H δ	95 PHE H β s
87 PHE H δ	95 PHE H δ
87 PHE H δ	95 PHE H ϵ
87 PHE HN	95 TYR H ϵ
87 PHE H δ	93 TYR H α
87 PHE H ϵ	93 TYR H δ