Supplementary information, Table S1. X-ray data collection, processing and refinement statistics.

	ZIKV C protein	
Statistics	Data 1	Data 2
Data Collection		
X-ray Source	SSRF beamline BL18U1	Diamond Beamline I04
Wavelength (Å)	0.97791	0.97950
Space group	$P2_1$	$P2_1$
Unit cell a, b, c, α, β, γ (Å, °)	74.3, 81.4, 77.2, 90.0, 104.8, 90.0	63.1, 223.1, 85.2, 90.0, 110.0, 90.0
Resolution range (Å)	50.0-2.05 (2.09-2.05)*	50.0-2.90 (2.95-2.90)
Unique reflections	55,737 (2,177)	46,037 (2,247)
Completeness (%)	94.7 (75.1)	95.9 (95.2)
Redundancy	4.4 (2.6)	6.1 (5.4)
$I/\sigma(I)$	10.5 (1.0)	5.9 (1.0)
R_{merge} (%)	17.8 (65.0)	23.5 (0.00**)
Refinement		
Resolution range (Å)	48.3-2.05 (2.12-2.05)	45.8-2.91 (3.02-2.91)
Reflections used in refinement	53,145 (4,486)	45,995 (4,406)
Reflections used for R-free	1,912 (174)	2,339 (251)
R_{work} (%)	22.1 (29.7)	20.4 (29.8)
R_{free} (%)	25.4 (31.6)	24.8 (33.8)
Number of non-hydrogen atoms	7,299	13,947
Protein	6,879	13,723
Ligands	46	92
solvent	374	132
Average B-factors	39.6	46.9
Protein	39.5	47.0
Ligands	39.7	34.8
solvent	40.9	38.2
r.m.s. deviations		
Bond lengths (Å)	0.004	0.005
Bond angles (°)	1.06	0.75
Ramachandran		
Favored (%)	98.2	98.9
Allowed (%)	1.8	1.1
Outliers (%)	0.0	0.0

* Numbers in the brackets are for the highest resolution shell.

** R>=1