

Table S1Data collection and refinement statistics for HIV-1 CA^N:CPSF6₃₁₃₋₃₂₇**Data collection**

Space group	$P2_12_12_1$
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	40.6, 46.4, 80.8
<i>a</i> , <i>b</i> , <i>c</i> (°)	90.0, 90.0, 90.0
Resolution (Å)	36 – 1.8
<i>R</i> _{sym}	0.044 (0.311)*
<i>I</i> / <i>σI</i>	14.5 (3.2)
Completeness (%)	95.8 (91.1)
Redundancy	3.4 (3.2)

Refinement

Resolution (Å)	1.8
No. reflections	12,982
<i>R</i> _{work} / <i>R</i> _{free}	0.22/0.27
No. atoms	
Protein	1,076
Ligand/ion	110
Water	94
B-factors	
Protein	29.9
Ligand/ion	40.5
Water	35.0
R.m.s deviations	
Bond lengths (Å)	0.023
Bond angles (°)	1.8

*Numbers in parentheses represent the value in the highest resolution shell.