

Table S1. Data collection and refinement statistics of Δ NC and E202Y.

Data collection		
Protein	Δ NC-Fab complex	E202Y
Space group	C2 (a=232.3 , b=97.5 , c=173.96 ; β =132.9 $^\circ$)	C2 (a=92.1 , b=84.9 , c=100.9 ; β =102.9 $^\circ$)
Beamline	ALS 8.2.1.	ALS 5.0.2.
Resolution (\AA) ^a	25.0 – 2.5 (2.64 – 2.5)	25.0 – 3.2 (3.26-3.2)
Unique reflections	96398	12142
I/ σ I	10.0 (1.4)	38.9 (5.1)
Multiplicity	6.0 (6.0)	7.3 (7.2)
Completeness (%)	98.0 (97.6)	99.0 (99.9)
R _{merge} ^b	0.09 (1.1)	0.16 (0.59)
Refinement		
Resolution (\AA)	25.0 – 2.5	25.0 – 3.2
Number of reflections	96236	12132
R _{work} (%)	23.3	23.4
R _{free} (%)	26.5	31.3
B factor	49.8	92.1
Ramachandran plot ^c	94.0 / 5.1 / 0.7	89.1 / 10.0 / 0.9
r.m.s.d. bond length (\AA)	0.01	0.01
r.m.s.d. bond angle ($^\circ$)	1.3	1.6

^a numbers in parentheses represent values for the highest resolution shell.

^b $R_{\text{merge}} = \sum |I_i - \langle I_i \rangle| / \sum I_i$, where $\langle I_i \rangle$ is the mean intensities.

^c percentage of residues in the favored / allowed / disallowed region.