**Supplementary** **file 2. Statistics of data collection and refinement**

CC1/2 (%) 99.7 (75.7)

No. unique reflection 30628 (4843)

Multiplicity 6.6 (6.5)

Structure refinement

Rwork / Rfree (%) 20.1 / 26.3

Statistics for the highest-resolution shell are shown in parentheses

Data collection

Resolution range(Å) 43.5 - 2.6 (2.7 - 2.6)

Cell dimension(Å) 70.8 107.6 128.3

Space group *P*212121

Number of unique reflections 30622 (3000)

Completeness (%) 99.9 (99.6)

Multiplicity 6.6 (6.5)

Rmerge (%)a 12.7 (97.1)

<I/sigma(I)> 13.3 (2.05)

CC1/2(%) 99.7 (75.7)

Number of Sld3CBD-Cdc45 in ASU 1

Wilson B factor 43.9

Refinement

Resolution range(Å) 43.5 - 2.6

Rfree/Rwork (%)b 26.2 / 21.9

Total number of atoms 6516

Protein atoms 6476

Water atoms 40

Others 0

Averaged B factor 55.0

 RMS deviations

Bonds (Å) 0.0026

Angles (º) 0.63

Ramachandran plot (%)

　　 Favored 94.1

 Allowed 4.62

Outliers　 　　　　　　　　 1.28

Favored 94.1

Allowed 4.62

Outliers 1.28

 PDB code 8J09

a $R\_{merge}={\sum\_{hkl}^{}\sum\_{i}^{}\left|I\_{i}\left(hkl\right)-\left〈I\_{i}\left(hkl\right)\right〉\right|}/{\sum\_{hkl}^{}\sum\_{i}^{}I\_{i}\left(hkl\right)}$, where *i* is the number of observations of a given reflection and *I(hkl)* is the average intensity of the *i* observations.

b $R={\sum\_{}^{}\left|\left|F\_{0}\right|-\left|F\_{c}\right|\right|}/{\sum\_{}^{}\left|F\_{0}\right|}$. |$F\_{0}$| and |$F\_{c}$| are amplitudes of the observed and calculated structure factors, respectively. $R\_{work}$is the R value for reflections used in the refinement, whereas $R\_{free}$ is the R value for 5% of the reflections, which are selected in thin shells and are not included in the refinement.