

Table 1. Crystallographic data collection and refinement statistics

Data collection

Sample	BICas9–sgRNA–target DNA
PDB ID	8X5V
Beamline	SPring-8 BL41XU/SLS X06SA
Wavelength (Å)	1.0
Space group	C2
Cell dimensions	
a, b, c (Å)	144.8, 99.2, 119.3
β (°)	97.1
Resolution (Å)	50–2.0 (2.12–2.0)
R_{meas}^*	0.255 (4.186)
$I/\sigma I$	19.01 (1.33)
CC(1/2)*	0.999 (0.649)
Completeness (%)*	99.9 (99.8)
Multiplicity*	28.0 (28.2)

Refinement

No. reflections	107265
$R_{\text{work}}/R_{\text{free}}$	0.1948/0.2333
No. atoms	
Protein	7,172
Nucleic acid	2,983
Others	451
B-factors (Å ²)	
Protein	59.2
Nucleic acid	63.1
Others	59.9
R.m.s. deviations	
Bond lengths (Å)	0.008
Bond angles (°)	1.787
Ramachandran plot (%)	
Favored region	97.28
Allowed region	2.72
Outlier region	0.00

* Friedel pairs are treated as different reflections

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