W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

May 16, 2020 – 11:05 am BST

PDB ID	:	6K3Z
Title	:	Crystal structure of dCas9 in complex with sgRNA and DNA (TGA PAM)
Authors	:	Chen, W.; Zhang, H.; Zhang, Y.; Wang, Y.; Gan, J.; Ji, Q.
Deposited on	:	2019-05-22
Resolution	:	3.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.

Metric	Percentile Ranks	Value
Rfree		0.277
Clashscore		16
Ramachandran outliers		3.0%
Sidechain outliers		14.6%
RSRZ outliers		2.2%
RNA backbone		0.34

Worse   *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution
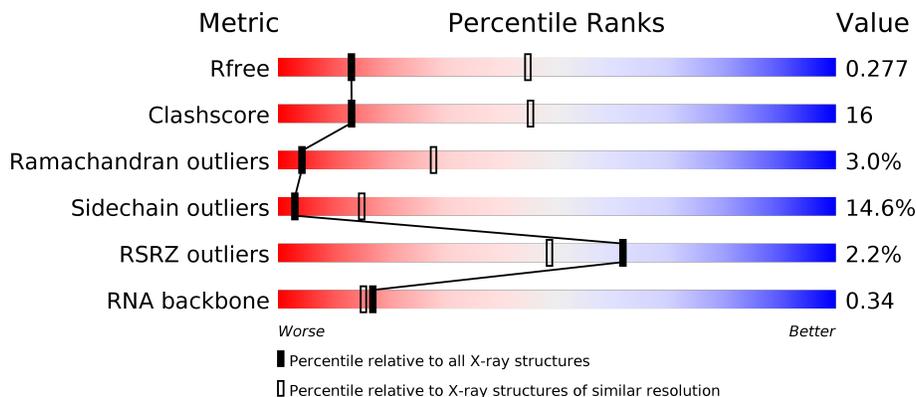
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)
RNA backbone	3102	1010 (3.50-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	83	27% 41% 25% 5% ·
2	B	1368	2% / 58% 32% 6% ·
3	C	28	7% / 39% 61%
4	D	12	8% / 33% 58% 8%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 13284 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called RNA (81-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	81	Total 1732	C 778	N 318	O 555	P 81	0	0	0

- Molecule 2 is a protein called CRISPR-associated endonuclease Cas9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1315	Total 10758	C 6858	N 1865	O 2013	S 22	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	10	ALA	ASP	engineered mutation	UNP Q99ZW2
B	840	ALA	HIS	engineered mutation	UNP Q99ZW2

- Molecule 3 is a DNA chain called DNA (28-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	28	Total 568	C 277	N 95	O 169	P 27	0	0	0

- Molecule 4 is a DNA chain called DNA (5'-D(*AP*AP*AP*TP*GP*AP*TP*AP*TP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	11	Total 226	C 110	N 43	O 63	P 10	0	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: RNA (81-MER)
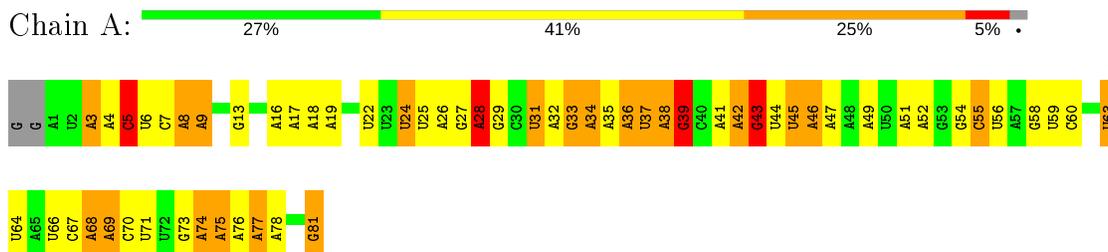
• Molecule 2: CRISPR-associated endonuclease Cas9
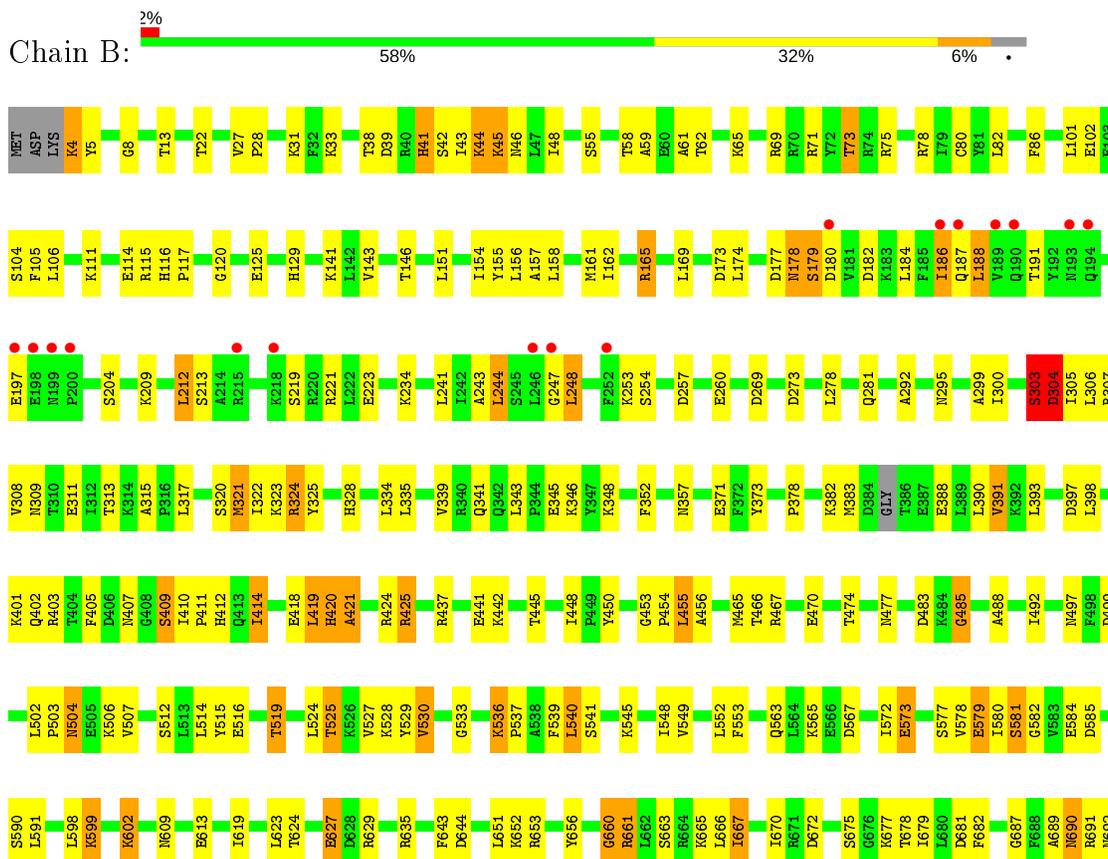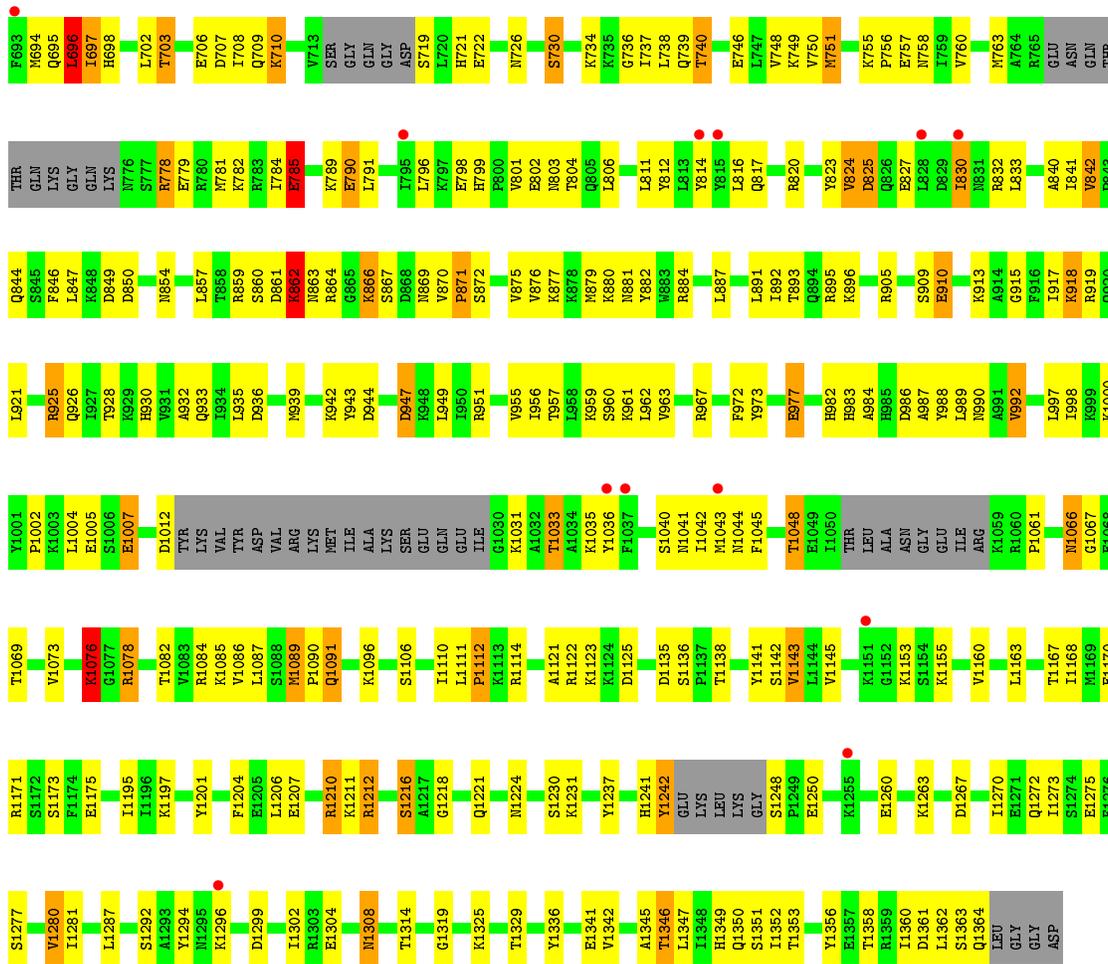
● Molecule 3: DNA (28-MER)

● Molecule 4: DNA (5'-D(*AP*AP*AP*TP*GP*AP*TP*AP*TP*TP*G)-3')

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	177.94Å 69.06Å 190.05Å 90.00° 110.21° 90.00°	Depositor
Resolution (Å)	40.89 – 3.20 48.93 – 3.19	Depositor EDS
% Data completeness (in resolution range)	87.0 (40.89-3.20) 87.1 (48.93-3.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	3.11 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.197 , 0.276 0.202 , 0.277	Depositor DCC
R_{free} test set	1567 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å²)	61.0	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol}(e/Å³), B_{sol}(Å²)	0.29 , 27.3	EDS
L-test for twinning[2]	$<|L|> = 0.47$, $<L^2> = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	13284	wwPDB-VP
Average B, all atoms (Å²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[1]Intensities estimated from amplitudes.
[2]Theoretical values of $<|L|>$, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$|Z|$>5	RMSZ	#$|Z|$>5
1	A	0.85	11/1942 (0.6%)	0.95	0/3023
2	B	0.74	0/10947	0.93	0/14709
3	C	0.69	1/635 (0.2%)	0.99	0/978
4	D	0.70	0/254	0.95	0/391
All	All	0.75	12/13778 (0.1%)	0.94	0/19101

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	24	U	O3'-P	-7.28	1.52	1.61
1	A	45	U	O3'-P	-7.06	1.52	1.61
1	A	46	A	O3'-P	-6.82	1.52	1.61
1	A	43	G	O3'-P	-6.33	1.53	1.61
1	A	13	G	O3'-P	-5.84	1.54	1.61

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1732	0	869	95	0
2	B	10758	0	10918	319	0
3	C	568	0	323	29	0
4	D	226	0	127	9	0

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	13284	0	12237	414	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

The worst 5 of 414 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:A:H2'	1:A:42:A:H5"	1.25	1.09
1:A:42:A:H8	1:A:42:A:H5'	1.18	1.07
1:A:81:G:H5'	1:A:81:G:C8	1.91	1.06
1:A:54:G:C6	1:A:55:C:N4	2.25	1.04
1:A:27:G:H5'	1:A:28:A:O5'	1.59	1.02

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	1301/1368 (95%)	1085 (83%)	177 (14%)	39 (3%)	4 28

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	197	GLU
2	B	304	ASP
2	B	690	ASN
2	B	790	GLU
2	B	862	LYS

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	1181/1225 (96%)	1008 (85%)	173 (15%)	3 15

5 of 173 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	635	ARG
2	B	778	ARG
2	B	1248	SER
2	B	651	LEU
2	B	697	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	698	HIS
2	B	726	ASN
2	B	930	HIS
2	B	692	ASN
2	B	1066	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	80/83 (96%)	26 (32%)	3 (3%)

5 of 26 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	C
1	A	6	U
1	A	8	A
1	A	9	A
1	A	28	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	5	C
1	A	28	A
1	A	36	A

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	81/83 (97%)	-0.12	0	100	100	40, 61, 131, 174	0
2	B	1315/1368 (96%)	-0.03	28 (2%)	63	49	41, 76, 115, 145	0
3	C	28/28 (100%)	0.16	2 (7%)	16	9	44, 68, 125, 169	0
4	D	11/12 (91%)	-0.00	1 (9%)	9	5	54, 82, 139, 152	0
All	All	1435/1491 (96%)	-0.03	31 (2%)	62	48	40, 75, 116, 174	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	2	DA	5.9
2	B	197	GLU	4.7
2	B	200	PRO	4.6
2	B	199	ASN	4.5
3	C	1	DC	3.9

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.