wwPDB X-ray Structure Validation Summary Report (i)

Apr 14, 2025 – 04:48 PM JST

PDB ID	:	8KAG / pdb_00008kag
Title	:	Crystal structure of SpyCas9 in complex with sgRNA and target RNA
Authors	:	Chen, Y.; Chen, J.; Liu, L.
Deposited on	:	2023-08-03
Resolution	:	3.88 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

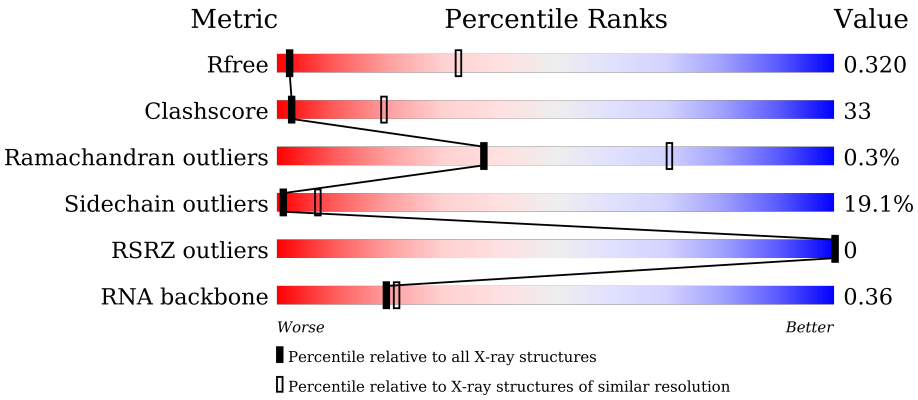
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

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 3.88 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1075 (4.06-3.70)
Clashscore	180529	1137 (4.06-3.70)
Ramachandran outliers	177936	1094 (4.06-3.70)
Sidechain outliers	177891	1087 (4.06-3.70)
RSRZ outliers	164620	1075 (4.06-3.70)
RNA backbone	3690	1135 (4.76-3.00)

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 of 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	B	1368	40% 46% 11% .
2	A	98	28% 47% 24% .
3	C	23	39% 43% . 13%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 13444 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 protein called CRISPR-associated endonuclease Cas9/Csn1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	1346	Total	C	N	O	S	0	0	0
			10926	6963	1889	2051	23			

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 2 is a RNA chain called RNA (98-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	98	Total	C	N	O	P	0	0	0
			2095	937	377	683	98			

- Molecule 3 is a RNA chain called RNA (5'-R(*CP*CP*AP*CP*UP*UP*CP*AP*AP*UP*UP*AP*GP*AP*AP*CP*AP*CP*GP*GP*AP*CP*C)-3').

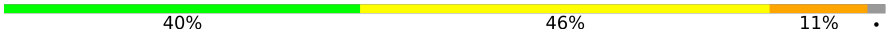
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	20	Total	C	N	O	P	0	0	0
			423	190	76	137	20			

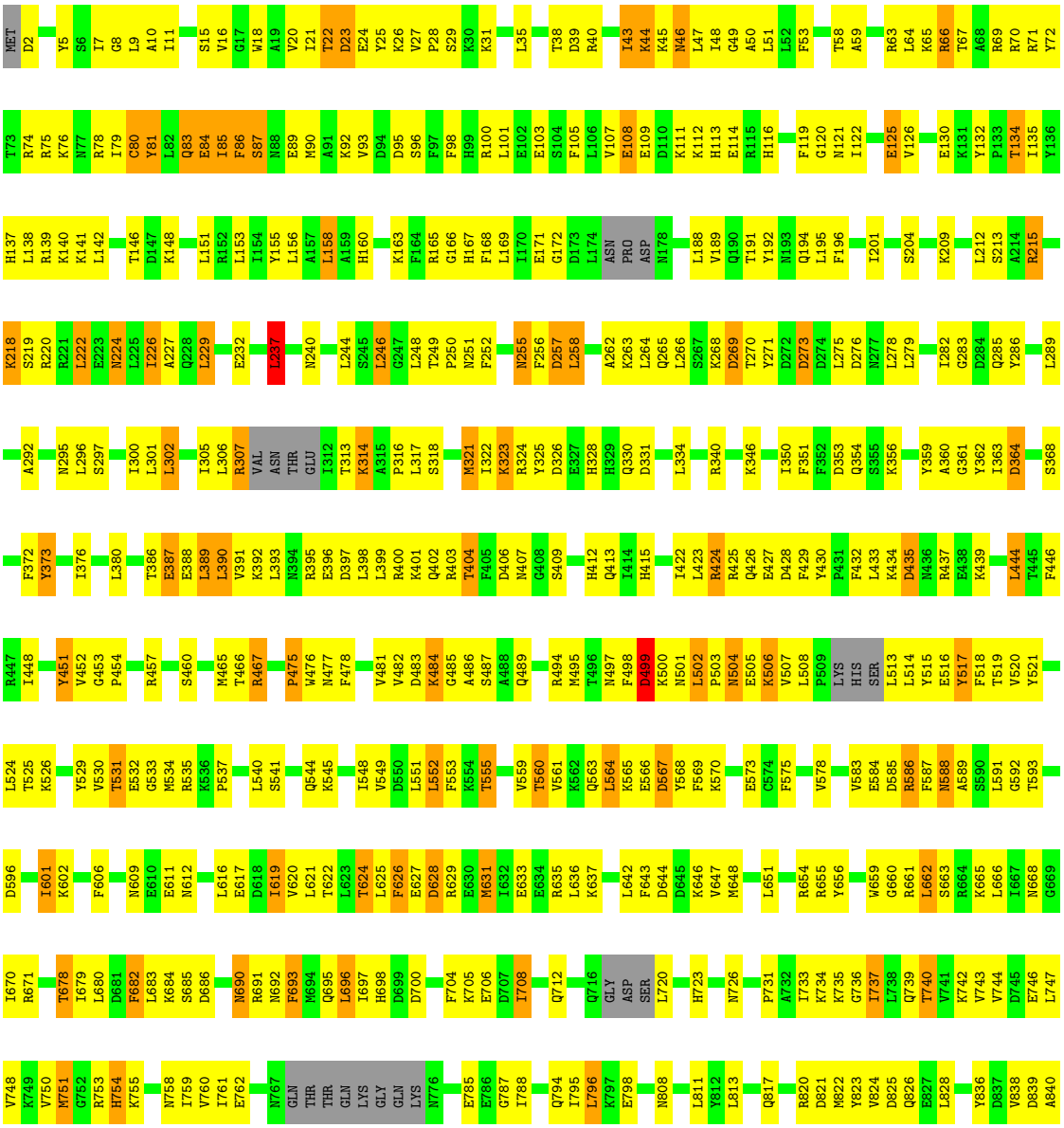
3 Residue-property plots (i)

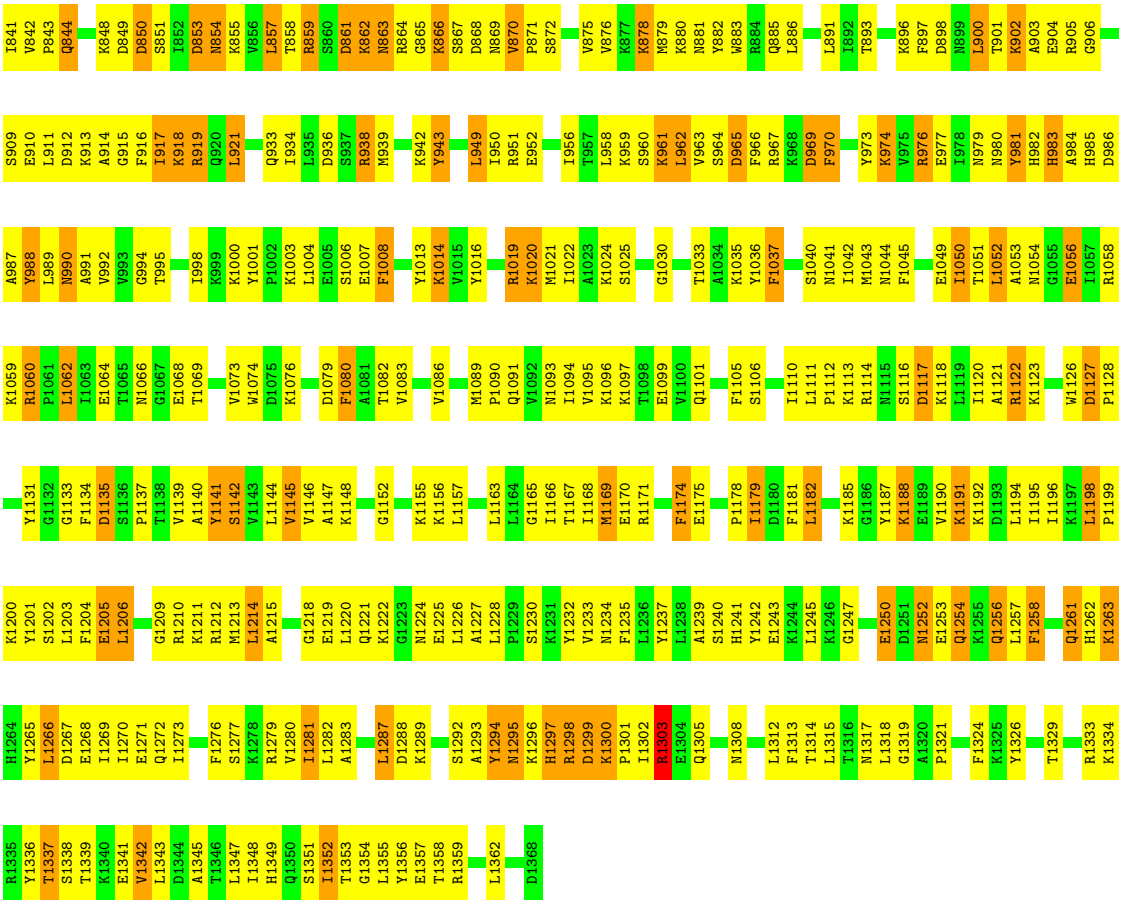
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: CRISPR-associated endonuclease Cas9/Csn1

Chain B:

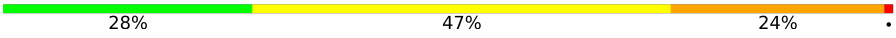


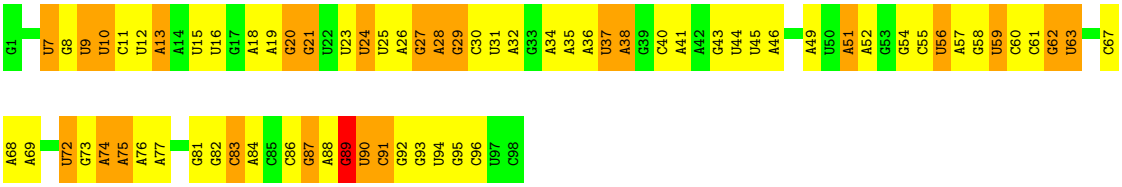




• Molecule 2: RNA (98-MER)

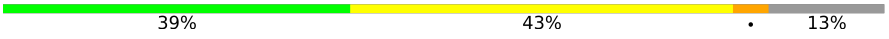
Chain A:

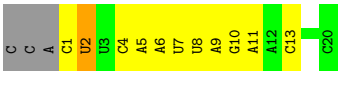




• Molecule 3: RNA (5'-R(*CP*CP*AP*CP*UP*UP*CP*AP*AP*UP*UP*AP*GP*AP*AP*CP *AP*CP*GP*GP*AP*CP*C)-3')

Chain C:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	185.68Å 185.68Å 137.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.92 – 3.88 49.92 – 3.88	Depositor EDS
% Data completeness (in resolution range)	79.6 (49.92-3.88) 79.6 (49.92-3.88)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.06 (at 3.88Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.303 , 0.320 0.303 , 0.320	Depositor DCC
R_{free} test set	958 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å^2)	21.3	Xtriage
Anisotropy	0.927	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 23.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.32$, $< L^2 > = 0.15$	Xtriage
Estimated twinning fraction	0.189 for -h,-k,l	Xtriage
F_o,F_c correlation	0.81	EDS
Total number of atoms	13444	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.17% 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	B	0.38	0/11116	0.61	4/14945 (0.0%)
2	A	0.41	0/2345	1.02	9/3653 (0.2%)
3	C	0.34	0/472	0.99	1/732 (0.1%)
All	All	0.39	0/13933	0.72	14/19330 (0.1%)

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1303	ARG	NE-CZ-NH1	6.84	123.72	120.30
2	A	62	G	N3-C4-C5	6.23	131.71	128.60
2	A	89	G	C5-C6-O6	-6.22	124.87	128.60
2	A	89	G	N9-C4-C5	-6.06	102.97	105.40
2	A	89	G	C6-C5-N7	-5.87	126.88	130.40

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	B	10926	0	11019	789	1
2	A	2095	0	1052	106	0
3	C	423	0	217	13	0
All	All	13444	0	12288	843	1

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 33.

The worst 5 of 843 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:B:1218:GLY:HA2	1:B:1339:THR:N	1.68	1.08
1:B:1218:GLY:H	1:B:1339:THR:HG23	1.19	1.01
1:B:1142:SER:OG	1:B:1214:LEU:HD11	1.58	1.01
1:B:668:ASN:HA	1:B:678:THR:HG21	1.45	0.98
1:B:748:VAL:HB	1:B:753:ARG:HA	1.45	0.94

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:LYS:O	1:B:532:GLU:O[4_565]	2.11	0.09

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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
1	B	1334/1368 (98%)	1265 (95%)	65 (5%)	4 (0%)	37 70

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1052	LEU
1	B	1051	THR
1	B	863	ASN
1	B	870	VAL

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
1	B	1186/1225 (97%)	960 (81%)	226 (19%)	1 7

5 of 226 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	696	LEU
1	B	1337	THR
1	B	921	LEU
1	B	1314	THR
1	B	1250	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1044	ASN
1	B	1091	GLN
1	B	1254	GLN
1	B	1252	ASN
1	B	990	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A	97/98 (98%)	31 (31%)	1 (1%)
3	C	19/23 (82%)	0	0
All	All	116/121 (95%)	31 (26%)	1 (0%)

5 of 31 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A	7	U
2	A	9	U
2	A	13	A

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Mol	Chain	Res	Type
2	A	19	A
2	A	20	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	20	G

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 oligosaccharides 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

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	B	1346/1368 (98%)	-1.22	0	100	100	3, 38, 98, 155	0
2	A	98/98 (100%)	-1.50	0	100	100	10, 69, 178, 219	0
3	C	20/23 (86%)	-1.52	0	100	100	19, 58, 237, 247	0
All	All	1464/1489 (98%)	-1.24	0	100	100	3, 40, 112, 247	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.