W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

Jan 3, 2024 – 10:59 am GMT

PDB ID	:	4UN4
Title	:	Crystal structure of Cas9 bound to PAM-containing DNA target with mismatches at positions 1-2
Authors	:	Anders, C.; Niewoehner, O.; Duerst, A.; Jinek, M.
Deposited on	:	2014-05-25
Resolution	:	2.37 Å(reported)

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

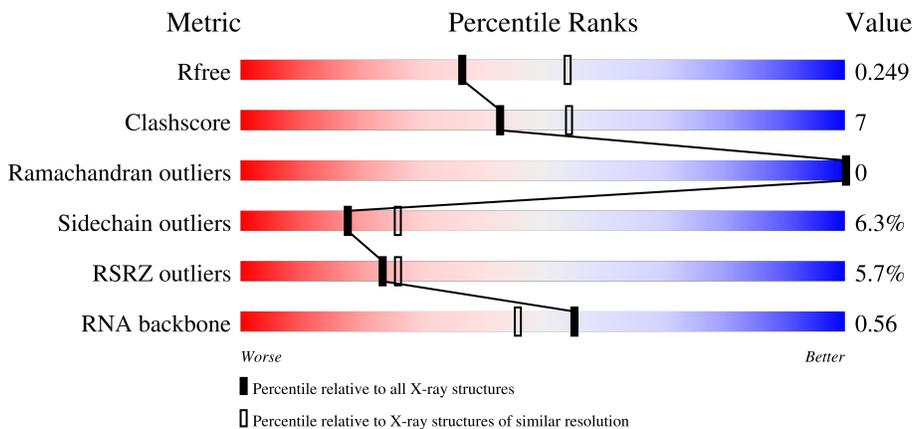|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.37 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		0.249
Clashscore		7
Ramachandran outliers		0
Sidechain outliers		6.3%
RSRZ outliers		5.7%
RNA backbone		0.56

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	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)
RNA backbone	3102	1017 (2.76-2.00)

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	A	83	8% / 59% 30% 10% ·
2	B	1372	5% / 77% 17% · 5%
3	C	11	18% / 55% 27% 18%
4	D	11	18% / 73% 18% 9%

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Mol	Chain	Length	Quality of chain
5	E	17	71% 29%

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 13914 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 SGRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	82	Total	C	N	O	P	0	0	1
			1733	778	318	556	81			

- Molecule 2 is a protein called CRISPR-ASSOCIATED ENDONUCLEASE CAS9/CSN1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1310	Total	C	N	O	S	0	0	0
			10716	6832	1860	2002	22			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP Q99ZW2
B	-2	ALA	-	expression tag	UNP Q99ZW2
B	-1	ALA	-	expression tag	UNP Q99ZW2
B	0	SER	-	expression tag	UNP Q99ZW2
B	10	ALA	ASP	engineered mutation	UNP Q99ZW2
B	840	ALA	HIS	engineered mutation	UNP Q99ZW2

- Molecule 3 is a DNA chain called TARGET DNA STRAND PROXIMAL FRAGMENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	11	Total	C	N	O	P	0	0	0
			218	106	41	61	10			

- Molecule 4 is a DNA chain called NON-TARGET DNA STRAND.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	10	Total	C	N	O	P	0	0	0
			206	100	35	62	9			

- Molecule 5 is a DNA chain called TARGET DNA STRAND DISTAL FRAGMENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	17	Total 346	C 169	N 59	O 102	P 16	0	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	4	Total 4	Mg 4	0	0
6	B	4	Total 4	Mg 4	0	0

- Molecule 7 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	204	Total 204	O 204	0	0
7	B	451	Total 451	O 451	0	0
7	C	7	Total 7	O 7	0	0
7	D	4	Total 4	O 4	0	0
7	E	21	Total 21	O 21	0	0

3 Residue-property plots ⓘ

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: SGRNA

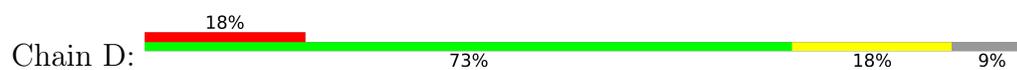- Molecule 2: CRISPR-ASSOCIATED ENDONUCLEASE CAS9/CSN1
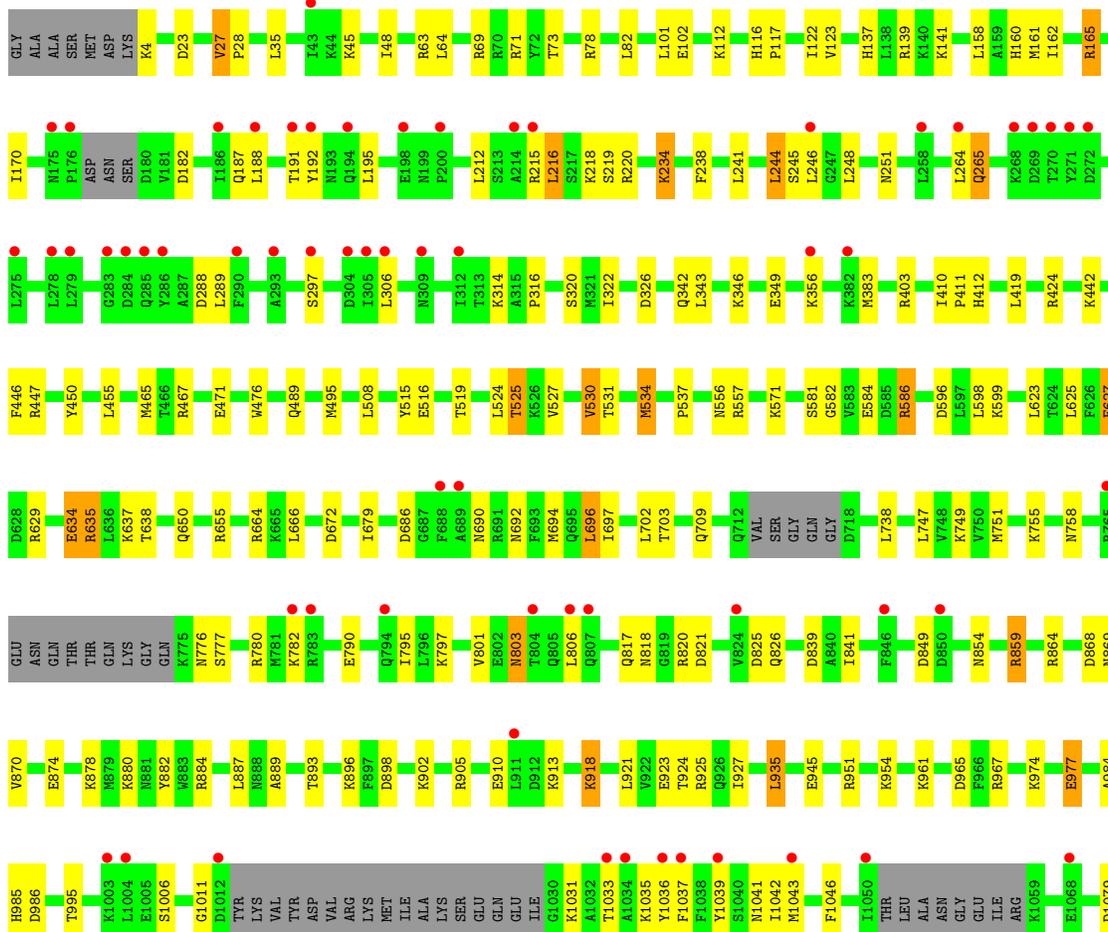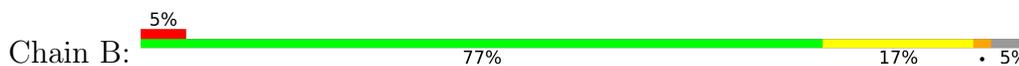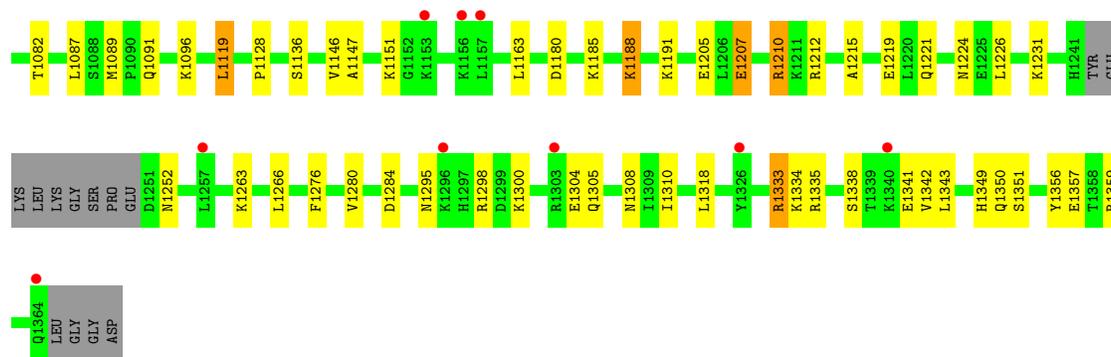
● Molecule 3: TARGET DNA STRAND PROXIMAL FRAGMENT

Chain C:

● Molecule 4: NON-TARGET DNA STRAND

Chain D:

● Molecule 5: TARGET DNA STRAND DISTAL FRAGMENT

Chain E:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	177.78Å 66.82Å 186.83Å 90.00° 111.39° 90.00°	Depositor
Resolution (Å)	47.49 – 2.37 47.49 – 2.37	Depositor EDS
% Data completeness (in resolution range)	98.7 (47.49-2.37) 99.1 (47.49-2.37)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.22 (at 2.37Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.217 , 0.248 0.217 , 0.249	Depositor DCC
R_{free} test set	4128 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	42.1	Xtriage
Anisotropy	0.274	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 44.9	EDS
L-test for twinning[2]	$<\|L\|> = 0.48$, $<L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	13914	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	0.24	0/1943	0.78	0/3026
2	B	0.24	0/10903	0.40	0/14646
3	C	0.47	0/244	1.19	3/373 (0.8%)
4	D	0.45	0/230	1.31	3/355 (0.8%)
5	E	0.43	0/387	1.16	0/596
All	All	0.26	0/13707	0.56	6/18996 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	10	DA	O4'-C1'-N9	6.00	112.20	108.00
4	D	3	DT	O4'-C1'-N1	5.89	112.12	108.00
3	C	10	DA	C1'-O4'-C4'	-5.54	104.56	110.10
4	D	3	DT	C3'-C2'-C1'	-5.49	95.91	102.50
3	C	4	DT	O4'-C1'-N1	5.31	111.72	108.00

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	1733	0	869	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	10716	0	10887	150	0
3	C	218	0	125	6	0
4	D	206	0	117	2	0
5	E	346	0	197	4	0
6	A	4	0	0	0	0
6	B	4	0	0	0	0
7	A	204	0	0	10	0
7	B	451	0	0	41	0
7	C	7	0	0	1	0
7	D	4	0	0	0	0
7	E	21	0	0	0	0
All	All	13914	0	12195	172	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 7.

The worst 5 of 172 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)
2:B:1043:MET:O	7:B:3344:HOH:O	1.82	0.94
2:B:581:SER:O	7:B:3224:HOH:O	1.91	0.88
2:B:251:ASN:O	7:B:3115:HOH:O	1.97	0.82
1:A:33:G:N2	1:A:36:A:OP2	2.12	0.81
2:B:923:GLU:OE1	7:B:3284:HOH:O	2.00	0.79

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	1296/1372 (94%)	1252 (97%)	44 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2　Protein sidechains ⓘ

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	1175/1226 (96%)	1101 (94%)	74 (6%)	18	26

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	977	GLU
2	B	1334	LYS
2	B	1089	MET
2	B	1210	ARG
2	B	524	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	14	ASN

5.3.3　RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	80/83 (96%)	16 (20%)	3 (3%)

5 of 16 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	24	U
1	A	28	A
1	A	29	G
1	A	34	A
1	A	35	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	27	G
1	A	42	A
1	A	68	A

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 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	82/83 (98%)	0.29	7 (8%)	10	12	16, 32, 117, 164	0
2	B	1310/1372 (95%)	0.35	70 (5%)	26	29	13, 38, 77, 118	0
3	C	11/11 (100%)	0.71	2 (18%)	1	1	35, 48, 131, 137	0
4	D	10/11 (90%)	0.39	2 (20%)	1	1	28, 48, 98, 99	0
5	E	17/17 (100%)	-0.55	0	100	100	24, 28, 35, 36	0
All	All	1430/1494 (95%)	0.34	81 (5%)	23	26	13, 38, 79, 164	0

The worst 5 of 81 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	356	LYS	5.8
2	B	271	TYR	5.4
2	B	269	ASP	5.4
2	B	215	ARG	5.0
2	B	1037	PHE	4.7

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 ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	MG	B	2365	1/1	0.56	0.14	23,23,23,23	0
6	MG	B	2367	1/1	0.69	0.11	33,33,33,33	0
6	MG	B	2368	1/1	0.75	0.14	19,19,19,19	0
6	MG	A	1082	1/1	0.91	0.14	36,36,36,36	0
6	MG	A	1084	1/1	0.92	0.20	6,6,6,6	0
6	MG	A	1083	1/1	0.93	0.14	34,34,34,34	0
6	MG	B	2366	1/1	0.95	0.15	16,16,16,16	0
6	MG	A	1085	1/1	0.99	0.09	13,13,13,13	0

6.5 Other polymers ⓘ

There are no such residues in this entry.