



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:41 PM UTC

PDB ID : 7ZO1 / pdb_00007zo1
Title : SpCas9 bound to CD34 off-target9 DNA substrate
Authors : Pacesa, M.; Jinek, M.
Deposited on : 2022-04-23
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

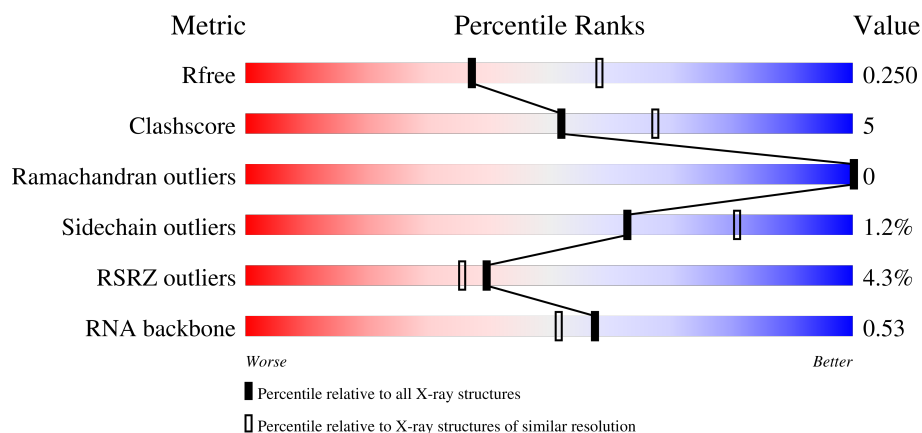
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)
RNA backbone	3983	1155 (2.70-2.10)

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 $\leq 5\%$. 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	85	 49% 45% 6%
2	B	1368	 4% 76% 10% 15%
3	C	28	 57% 43%
4	D	12	 25% 58% 17%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12407 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 CD34 sgRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	85	Total	C	N	O	P	0	0	1
			1794	801	335	574	84			

- Molecule 2 is a protein called CRISPR-associated endonuclease Cas9/Csn1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1169	Total	C	N	O	S	0	1	0
			9559	6107	1650	1783	19			

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 CD34 off-target9 DNA target strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	28	Total	C	N	O	P	0	0	0
			555	270	90	168	27			

- Molecule 4 is a DNA chain called CD34 off-target9 DNA non-target strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	10	Total	C	N	O	P	0	0	0
			205	100	35	61	9			

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Mg	0	0
			2	2		

- Molecule 6 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total 3	K 3	0	0
6	B	5	Total 5	K 5	0	0

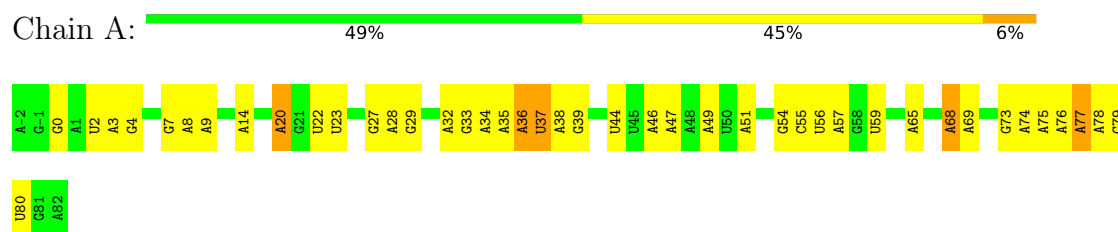
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	110	Total 110	O 110	0	0
7	B	166	Total 166	O 166	0	0
7	C	5	Total 5	O 5	0	0
7	D	3	Total 3	O 3	0	0

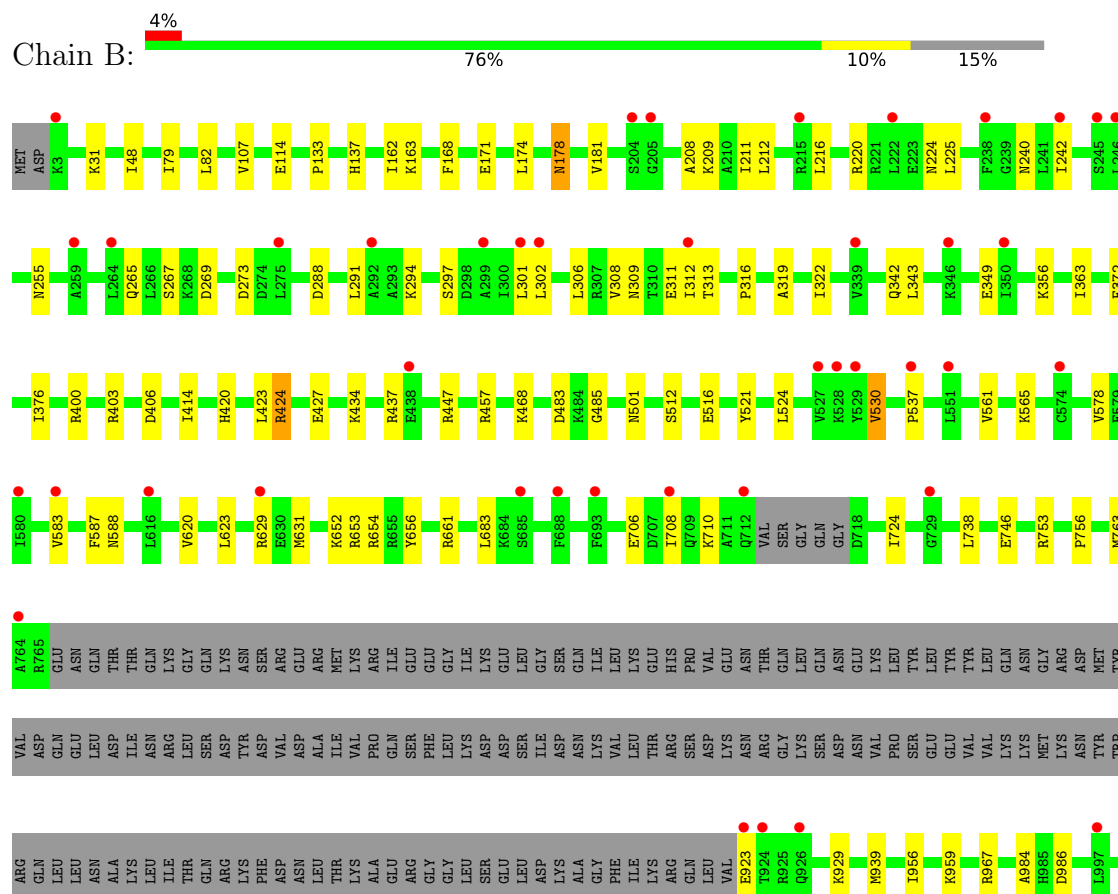
3 Residue-property plots [i](#)

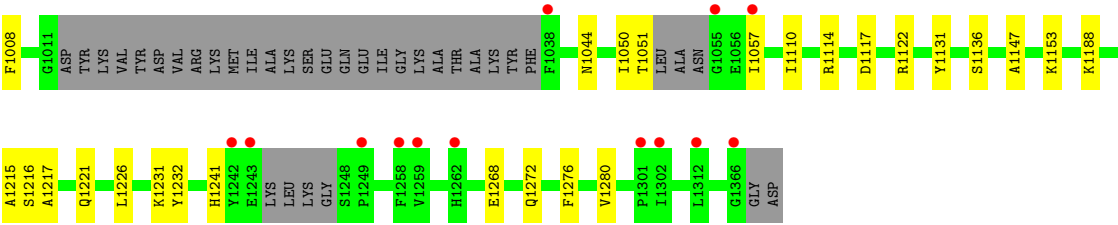
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: CD34 sgRNA



- Molecule 2: CRISPR-associated endonuclease Cas9/Csn1

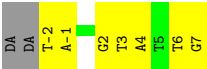




● Molecule 3: CD34 off-target9 DNA target strand



● Molecule 4: CD34 off-target9 DNA non-target strand



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	177.41Å 69.20Å 188.46Å 90.00° 111.77° 90.00°	Depositor
Resolution (Å)	46.51 – 2.40 46.51 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.51-2.40) 88.4 (46.51-2.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.68 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.212 , 0.250 0.212 , 0.250	Depositor DCC
R_{free} test set	4739 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	45.6	Xtriage
Anisotropy	0.408	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 56.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12407	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: K, 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	0.13	0/2013	0.32	0/3140
2	B	0.12	0/9735	0.28	0/13083
3	C	0.21	0/618	0.44	0/948
4	D	0.20	0/229	0.48	0/353
All	All	0.13	0/12595	0.30	0/17524

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1794	0	891	30	0
2	B	9559	0	9709	82	0
3	C	555	0	320	8	0
4	D	205	0	117	6	0
5	A	2	0	0	0	0
6	A	3	0	0	0	0
6	B	5	0	0	0	0
7	A	110	0	0	2	0
7	B	166	0	0	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	5	0	0	0	0
7	D	3	0	0	0	0
All	All	12407	0	11037	116	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 5.

All (116) 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)
3:C:-7:DC:H2'	3:C:-6:DA:C8	2.28	0.69
2:B:501:ASN:HB3	2:B:708:ILE:HD12	1.74	0.68
2:B:309:ASN:HD21	2:B:311:GLU:HB2	1.60	0.66
1:A:2:U:H2'	1:A:3:A:C8	2.32	0.65
2:B:1215:ALA:HB2	2:B:1221:GLN:HG3	1.81	0.62
1:A:2:U:H2'	1:A:3:A:H8	1.63	0.62
2:B:1051:THR:HG22	2:B:1057:ILE:HG12	1.81	0.62
1:A:46:A:H2'	1:A:47:A:C8	2.35	0.61
2:B:565:LYS:NZ	2:B:578:VAL:O	2.34	0.60
1:A:49:A:N3	2:B:1122:ARG:NH2	2.50	0.60
4:D:6:DT:H2''	4:D:7:DG:H5''	1.83	0.60
2:B:1114:ARG:NH1	4:D:4:DA:OP1	2.35	0.59
2:B:181:VAL:HB	2:B:209:LYS:HG3	1.83	0.59
2:B:623:LEU:HD13	2:B:654:ARG:HG3	1.84	0.58
1:A:22:U:H2'	1:A:23:U:C6	2.38	0.58
1:A:34:A:H2'	1:A:35:A:O4'	2.03	0.57
2:B:561:VAL:HG12	2:B:565:LYS:HD2	1.87	0.56
4:D:-2:DT:H1'	4:D:-1:DA:H5'	1.87	0.56
2:B:306:LEU:HD22	2:B:316:PRO:HB2	1.89	0.55
2:B:956:ILE:HG23	2:B:1008:PHE:HB3	1.88	0.54
3:C:-6:DA:H2''	3:C:-5:DA:C8	2.42	0.54
1:A:35:A:H2'	1:A:36:A:C8	2.42	0.54
1:A:46:A:H2'	1:A:47:A:H8	1.72	0.54
2:B:349:GLU:HG3	2:B:356:LYS:HG3	1.89	0.54
2:B:181:VAL:H	2:B:209:LYS:HE3	1.72	0.54
2:B:1044:ASN:HB3	2:B:1050:ILE:HD13	1.90	0.54
2:B:212:LEU:HD21	2:B:225:LEU:HD22	1.90	0.53
1:A:54:G:H2'	1:A:55:C:C6	2.44	0.53
2:B:240:ASN:ND2	2:B:255:ASN:OD1	2.38	0.53
2:B:1110:ILE:HG23	2:B:1122:ARG:HD2	1.92	0.52
1:A:65:A:N6	7:A:203:HOH:O	2.32	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:273:ASP:HB2	2:B:653:ARG:HH21	1.75	0.52
2:B:216:LEU:HD13	2:B:220:ARG:HG2	1.93	0.51
2:B:1216:SER:OG	2:B:1217:ALA:N	2.43	0.51
2:B:923:GLU:HA	2:B:959:LYS:HE3	1.93	0.51
2:B:168:PHE:CG	2:B:447:ARG:HD2	2.46	0.50
1:A:3:A:OP1	2:B:661:ARG:NH1	2.44	0.50
2:B:756:PRO:HD2	2:B:939:MET:HE2	1.93	0.50
2:B:1051:THR:HA	2:B:1057:ILE:H	1.77	0.50
2:B:82:LEU:HD22	2:B:162:ILE:HD12	1.93	0.50
1:A:77:A:H2'	1:A:78:A:H8	1.77	0.50
1:A:20:A:OP2	2:B:403:ARG:NH1	2.45	0.49
2:B:583:VAL:HG21	2:B:587:PHE:CE1	2.47	0.49
2:B:133:PRO:HG2	2:B:137:HIS:CE1	2.47	0.49
4:D:-2:DT:H2''	4:D:-1:DA:C8	2.47	0.49
2:B:512:SER:HA	2:B:620:VAL:HG11	1.94	0.49
2:B:516:GLU:OE1	7:B:1501:HOH:O	2.20	0.49
1:A:77:A:H2'	1:A:78:A:C8	2.47	0.49
2:B:427:GLU:HB2	2:B:434:LYS:HB2	1.94	0.48
1:A:68:A:C4	1:A:69:A:C8	3.01	0.48
2:B:468:LYS:HE3	2:B:483:ASP:HA	1.95	0.48
1:A:22:U:H2'	1:A:23:U:H6	1.78	0.47
1:A:74:A:H2'	1:A:75:A:O4'	2.14	0.47
3:C:-5:DA:H1'	3:C:-4:DT:H5'	1.95	0.47
2:B:137:HIS:HA	2:B:322:ILE:HD11	1.97	0.47
2:B:265:GLN:HG2	2:B:267:SER:H	1.78	0.47
1:A:27:G:N2	1:A:44:U:OP2	2.47	0.47
2:B:423:LEU:HB3	2:B:437:ARG:HG3	1.97	0.47
2:B:654:ARG:HD2	2:B:656:TYR:CZ	2.50	0.47
1:A:78:A:H2'	1:A:79:G:H8	1.80	0.46
3:C:-6:DA:H2''	3:C:-5:DA:H8	1.81	0.46
2:B:178:ASN:HD21	2:B:309:ASN:HA	1.81	0.46
1:A:75:A:H2'	1:A:76:A:C8	2.50	0.46
2:B:967:ARG:NH1	2:B:986:ASP:OD1	2.48	0.46
2:B:468:LYS:HG3	2:B:483:ASP:HB2	1.98	0.45
1:A:37:U:H2'	1:A:38:A:C8	2.51	0.45
2:B:269:ASP:HB2	2:B:629:ARG:NH2	2.30	0.45
2:B:312:ILE:HG13	2:B:313:THR:HG22	1.97	0.45
1:A:37:U:H2'	1:A:38:A:H8	1.82	0.45
2:B:308:VAL:HG11	2:B:319:ALA:HB3	1.98	0.45
1:A:0:G:H5''	2:B:929:LYS:HE2	1.99	0.44
2:B:521:TYR:HB3	2:B:683:LEU:HB3	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:A:H2'	1:A:79:G:C8	2.53	0.44
1:A:80:U:OP2	2:B:753:ARG:NH2	2.50	0.44
2:B:420:HIS:CE1	2:B:424:ARG:HD3	2.52	0.44
2:B:1232:TYR:OH	2:B:1268:GLU:OE1	2.32	0.44
4:D:3:DT:H2''	4:D:4:DA:C8	2.52	0.44
2:B:225:LEU:HD23	2:B:242:ILE:HG21	1.99	0.44
2:B:211:ILE:HD11	2:B:224:ASN:HB3	2.00	0.43
2:B:48:ILE:HG12	2:B:984:ALA:HB1	2.00	0.43
2:B:763:MET:HE3	2:B:763:MET:HB2	1.77	0.43
2:B:406:ASP:OD1	2:B:406:ASP:N	2.51	0.43
2:B:706:GLU:HG2	2:B:710:LYS:HZ3	1.83	0.43
2:B:485:GLY:HA2	2:B:631:MET:HE1	2.00	0.43
2:B:706:GLU:HG2	2:B:710:LYS:NZ	2.34	0.43
1:A:14:A:N3	7:A:208:HOH:O	2.37	0.43
2:B:724:ILE:HD12	2:B:738:LEU:HD13	2.01	0.43
1:A:57:A:H5''	2:B:457:ARG:HH21	1.84	0.42
2:B:306:LEU:HD21	2:B:414:ILE:HD13	2.00	0.42
1:A:38:A:H2'	1:A:39:G:C8	2.54	0.42
2:B:1147:ALA:HB1	2:B:1188:LYS:O	2.19	0.42
3:C:5:DC:H2'	3:C:6:DA:H8	1.84	0.42
2:B:79:ILE:HD11	2:B:163:LYS:HB2	2.01	0.42
2:B:288:ASP:HA	2:B:291:LEU:HB3	2.02	0.42
2:B:208:ALA:HA	2:B:211:ILE:HG22	2.02	0.42
2:B:403:ARG:NH1	7:B:1524:HOH:O	2.52	0.41
2:B:372:PHE:O	2:B:376:ILE:HG12	2.19	0.41
2:B:1276:PHE:O	2:B:1280:VAL:HG22	2.20	0.41
3:C:-1:DC:H2''	3:C:0:DA:C8	2.55	0.41
2:B:652:LYS:HB3	2:B:652:LYS:HE2	1.77	0.41
3:C:7:DT:H2'	3:C:8:DC:O4'	2.21	0.41
2:B:211:ILE:HD12	2:B:211:ILE:HA	1.88	0.41
2:B:400:ARG:NH2	2:B:406:ASP:OD2	2.52	0.41
2:B:1136:SER:HA	4:D:2:DG:O3'	2.20	0.41
2:B:297:SER:O	2:B:301:LEU:N	2.53	0.41
2:B:631:MET:HE2	2:B:631:MET:HB3	1.81	0.41
2:B:530:VAL:HG22	2:B:537:PRO:HB3	2.03	0.41
2:B:174:LEU:HD13	2:B:302:LEU:HD11	2.02	0.40
2:B:294:LYS:O	2:B:297:SER:HB3	2.20	0.40
3:C:12:DT:H2'	3:C:13:DT:C6	2.56	0.40
2:B:524:LEU:HD12	2:B:587:PHE:CE1	2.57	0.40
2:B:1226:LEU:HD13	2:B:1276:PHE:CG	2.56	0.40
2:B:31:LYS:HD3	2:B:31:LYS:HA	1.90	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:107:VAL:HG23	2:B:1131:TYR:CE1	2.56	0.40
1:A:44:U:H5'	2:B:363:ILE:HD12	2.03	0.40
1:A:4:G:H21	2:B:588:ASN:ND2	2.19	0.40

There are no symmetry-related clashes.

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	
2	B	1158/1368 (85%)	1110 (96%)	48 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	1048/1225 (86%)	1034 (99%)	14 (1%)	61	80

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	114[A]	GLU
2	B	114[B]	GLU
2	B	171	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	178	ASN
2	B	342	GLN
2	B	343	LEU
2	B	424	ARG
2	B	530	VAL
2	B	746	GLU
2	B	1117	ASP
2	B	1153	LYS
2	B	1231	LYS
2	B	1241	HIS
2	B	1272	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	14	ASN
2	B	175	ASN
2	B	178	ASN
2	B	309	ASN
2	B	407	ASN
2	B	412	HIS
2	B	698	HIS
2	B	1101	GLN
2	B	1297	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	82/85 (96%)	16 (19%)	0

All (16) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	8	A
1	A	9	A
1	A	20	A
1	A	28	A
1	A	29	G
1	A	32	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	33	G
1	A	36	A
1	A	37	U
1	A	51	A
1	A	56	U
1	A	59	U
1	A	68	A
1	A	73	G
1	A	77	A

There are no RNA pucker outliers to report.

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](#)

Of 10 ligands modelled in this entry, 10 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 [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	85/85 (100%)	-0.47	0 100 100	42, 76, 137, 178	0
2	B	1169/1368 (85%)	0.44	55 (4%) 36 32	39, 86, 152, 241	1 (0%)
3	C	28/28 (100%)	-0.09	0 100 100	58, 81, 132, 135	0
4	D	10/12 (83%)	-0.31	0 100 100	60, 87, 137, 142	0
All	All	1292/1493 (86%)	0.36	55 (4%) 40 36	39, 86, 150, 241	1 (0%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	616	LEU	5.1
2	B	529	TYR	4.3
2	B	1259	VAL	4.2
2	B	527	VAL	4.0
2	B	1038	PHE	3.6
2	B	551	LEU	3.4
2	B	1366	GLY	3.3
2	B	537	PRO	3.2
2	B	693	PHE	3.2
2	B	580	ILE	3.2
2	B	242	ILE	2.9
2	B	924	THR	2.9
2	B	764	ALA	2.8
2	B	1243	GLU	2.8
2	B	246	LEU	2.8
2	B	997	LEU	2.8
2	B	688	PHE	2.8
2	B	1057	ILE	2.8
2	B	204	SER	2.7
2	B	222	LEU	2.7
2	B	926	GLN	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	3	LYS	2.6
2	B	1258	PHE	2.6
2	B	275	LEU	2.6
2	B	301	LEU	2.6
2	B	629	ARG	2.5
2	B	583	VAL	2.5
2	B	574	CYS	2.5
2	B	1301	PRO	2.5
2	B	346	LYS	2.5
2	B	292	ALA	2.5
2	B	528	LYS	2.4
2	B	729	GLY	2.4
2	B	1262	HIS	2.3
2	B	259	ALA	2.3
2	B	238	PHE	2.3
2	B	1249	PRO	2.2
2	B	205	GLY	2.2
2	B	350	ILE	2.2
2	B	708	ILE	2.2
2	B	245	SER	2.2
2	B	339	VAL	2.2
2	B	299	ALA	2.2
2	B	264	LEU	2.2
2	B	302	LEU	2.1
2	B	1312	LEU	2.1
2	B	1242	TYR	2.1
2	B	1302	ILE	2.1
2	B	215	ARG	2.1
2	B	1055	GLY	2.1
2	B	438	GLU	2.1
2	B	923	GLU	2.0
2	B	685	SER	2.0
2	B	712	GLN	2.0
2	B	312	ILE	2.0

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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
6	K	B	1405	1/1	0.83	0.11	119,119,119,119	0
6	K	B	1403	1/1	0.85	0.10	133,133,133,133	0
6	K	B	1404	1/1	0.93	0.09	101,101,101,101	0
6	K	B	1401	1/1	0.95	0.07	96,96,96,96	0
6	K	A	104	1/1	0.95	0.08	86,86,86,86	0
6	K	A	103	1/1	0.96	0.06	75,75,75,75	0
6	K	A	105	1/1	0.97	0.06	73,73,73,73	0
6	K	B	1402	1/1	0.98	0.04	83,83,83,83	0
5	MG	A	102	1/1	0.98	0.05	68,68,68,68	0
5	MG	A	101	1/1	0.99	0.08	56,56,56,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.