



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 12:23 pm BST

PDB ID : 6JFU
Title : Crystal structure of Nme2Cas9 in complex with sgRNA and target DNA (AG-GCCC PAM)
Authors : Sun, W.; Yang, J.; Cheng, Z.; Liu, C.; Wang, K.; Huang, X.; Wang, Y.
Deposited on : 2019-02-12
Resolution : 3.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

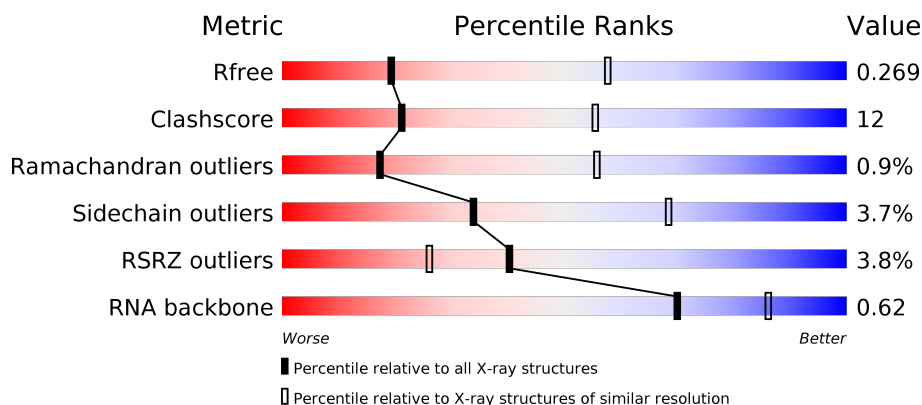
1 Overall quality at a glance

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	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 $\leq 5\%$. 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	1083	<div> <div>4%</div> <div>63%</div> <div>17%</div> <div>•</div> <div>18%</div> </div>
2	B	135	<div> <div>%</div> <div>30%</div> <div>39%</div> <div>9%</div> <div>22%</div> </div>
3	C	35	<div> <div>49%</div> <div>51%</div> </div>
4	D	11	<div> <div>45%</div> <div>55%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	EDO	C	101	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9476 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	884	Total	C	N	O	S	0	0	0
			6312	3968	1167	1156	21			

- Molecule 2 is a RNA chain called sgRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	105	Total	C	N	O	P	0	0	0
			2214	990	375	744	105			

- Molecule 3 is a DNA chain called target-strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	35	Total	C	N	O	P	0	0	0
			720	344	139	203	34			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	11	Total	C	N	O	P	0	0	0
			222	107	43	62	10			

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).

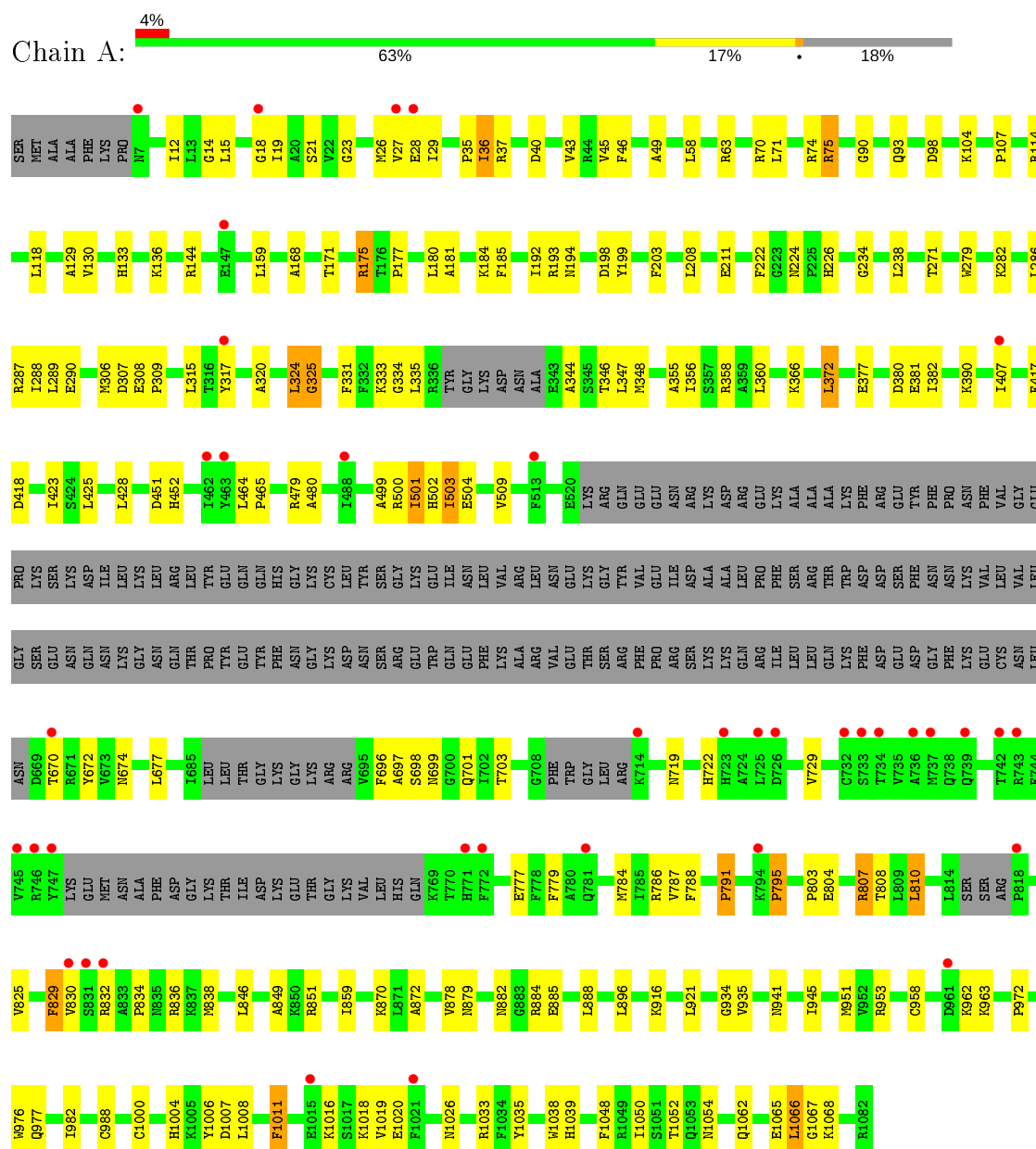


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		

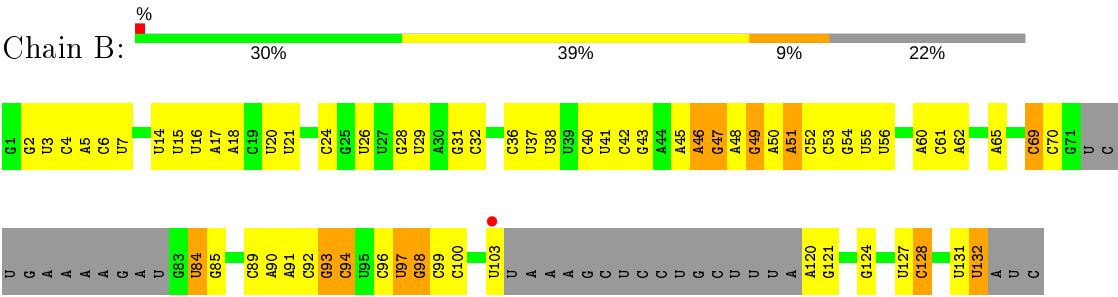
3 Residue-property plots

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.

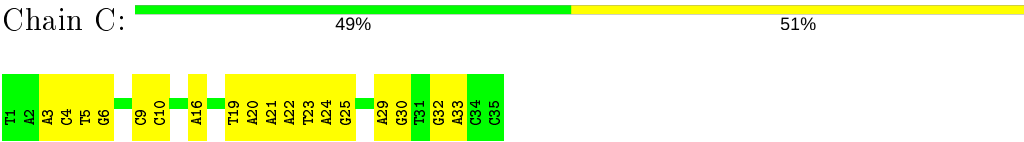
- Molecule 1: CRISPR-associated endonuclease Cas9



- Molecule 2: sgRNA



• Molecule 3: target-strand DNA



• Molecule 4: non-target strand



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	153.48Å 166.93Å 179.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.68 – 3.20 48.68 – 3.20	Depositor EDS
% Data completeness (in resolution range)	83.1 (48.68-3.20) 83.1 (48.68-3.20)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.17 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.14_3247: ???)	Depositor
R, R_{free}	0.254 , 0.271 0.255 , 0.269	Depositor DCC
R_{free} test set	1528 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	55.7	Xtriage
Anisotropy	0.804	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 16.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	9476	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% 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

5.1 Standard geometry

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

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	0.28	0/6418	0.51	4/8719 (0.0%)
2	B	0.22	0/2466	0.87	4/3831 (0.1%)
3	C	0.54	0/810	0.90	0/1250
4	D	0.55	0/249	0.89	0/383
All	All	0.30	0/9943	0.67	8/14183 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	795	PRO	N-CA-CB	8.10	113.02	103.30
2	B	84	U	C2-N1-C1'	6.91	126.00	117.70
2	B	84	U	N1-C2-O2	6.62	127.44	122.80
2	B	84	U	N3-C2-O2	-6.23	117.84	122.20
1	A	791	PRO	N-CA-CB	5.91	110.39	103.30
1	A	325	GLY	N-CA-C	5.51	126.88	113.10
2	B	69	C	C2-N1-C1'	5.44	124.79	118.80
1	A	335	LEU	CA-CB-CG	5.44	127.81	115.30

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	6312	0	5675	150	0
2	B	2214	0	1128	51	0
3	C	720	0	392	23	0
4	D	222	0	122	3	0
5	B	4	0	6	0	0
5	C	4	0	6	0	0
All	All	9476	0	7329	204	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 12.

All (204) 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:289:LEU:HA	1:A:331:PHE:CB	1.27	1.64
1:A:503:ILE:HG22	1:A:696:PHE:O	1.31	1.23
1:A:289:LEU:CA	1:A:331:PHE:CB	2.21	1.17
1:A:290:GLU:H	1:A:331:PHE:HA	1.12	1.13
1:A:503:ILE:HG21	1:A:697:ALA:CA	1.80	1.10
1:A:503:ILE:HG23	1:A:698:SER:H	1.12	1.08
1:A:503:ILE:CG2	1:A:698:SER:H	1.68	1.06
1:A:503:ILE:CG2	1:A:697:ALA:HA	1.87	1.04
1:A:290:GLU:H	1:A:331:PHE:CA	1.75	0.97
1:A:1011:PHE:HB2	1:A:1020:GLU:O	1.66	0.95
1:A:503:ILE:CG2	1:A:696:PHE:O	2.15	0.95
1:A:1011:PHE:HB3	1:A:1020:GLU:HB2	1.49	0.94
1:A:14:GLY:HA2	1:A:502:HIS:CB	2.00	0.91
1:A:503:ILE:HG21	1:A:697:ALA:HA	0.94	0.90
1:A:290:GLU:N	1:A:331:PHE:HA	1.89	0.87
1:A:15:LEU:H	1:A:502:HIS:CB	1.91	0.84
1:A:958:CYS:N	1:A:1000:CYS:SG	2.54	0.81
1:A:503:ILE:CG2	1:A:698:SER:N	2.43	0.81
1:A:288:ILE:CB	1:A:333:LYS:HB2	2.14	0.77
2:B:99:C:O2	2:B:124:G:N2	2.13	0.75
1:A:804:GLU:HA	1:A:807:ARG:HE	1.54	0.72
2:B:99:C:N3	2:B:124:G:N1	2.33	0.71
1:A:12:ILE:HG13	1:A:27:VAL:HG23	1.73	0.69
1:A:1052:THR:HG21	3:C:4:DC:OP2	1.91	0.69
1:A:15:LEU:N	1:A:502:HIS:CB	2.57	0.67
1:A:503:ILE:HG23	1:A:698:SER:N	1.97	0.67
1:A:12:ILE:HG22	1:A:499:ALA:HB3	1.77	0.66
1:A:878:VAL:O	1:A:882:ASN:ND2	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:ARG:NH2	1:A:211:GLU:OE1	2.26	0.66
1:A:159:LEU:HG	3:C:16:DA:H5''	1.78	0.65
1:A:672:TYR:HA	3:C:23:DT:H4'	1.77	0.65
1:A:309:PRO:HD3	1:A:315:LEU:HD22	1.77	0.65
1:A:884:ARG:NH2	2:B:53:C:O2	2.29	0.65
1:A:1052:THR:CG2	3:C:4:DC:OP2	2.45	0.65
1:A:14:GLY:CA	1:A:502:HIS:CB	2.74	0.64
1:A:703:THR:O	1:A:729:VAL:HG11	1.97	0.64
1:A:962:LYS:HG3	1:A:963:LYS:H	1.63	0.64
1:A:355:ALA:HA	1:A:358:ARG:HE	1.61	0.63
1:A:1011:PHE:CB	1:A:1020:GLU:O	2.45	0.62
1:A:1011:PHE:CB	1:A:1020:GLU:HB2	2.25	0.62
1:A:346:THR:O	1:A:348:MET:N	2.28	0.62
1:A:390:LYS:NZ	1:A:417:PHE:O	2.32	0.62
1:A:870:LYS:HE2	1:A:872:ALA:HB3	1.82	0.61
1:A:503:ILE:HG13	1:A:504:GLU:N	2.15	0.61
1:A:701:GLN:OE1	1:A:701:GLN:N	2.33	0.61
1:A:846:LEU:O	2:B:26:U:O2'	2.18	0.61
2:B:51:A:H2'	2:B:52:C:C6	2.36	0.61
1:A:282:LYS:O	1:A:286:LEU:HB2	2.01	0.60
1:A:851:ARG:HD2	1:A:859:ILE:HD11	1.84	0.60
2:B:90:A:H2'	2:B:91:A:C8	2.36	0.60
1:A:118:LEU:HD13	1:A:175:ARG:HD2	1.84	0.60
1:A:503:ILE:O	1:A:503:ILE:HG23	2.02	0.59
1:A:28:GLU:O	1:A:36:ILE:N	2.36	0.58
1:A:670:THR:HA	3:C:24:DA:H4'	1.86	0.57
1:A:934:GLY:HA3	1:A:945:ILE:HD11	1.86	0.57
4:D:6:DC:H2''	4:D:7:DA:C8	2.39	0.57
1:A:1054:ASN:HD22	3:C:3:DA:H5'	1.68	0.57
1:A:803:PRO:O	1:A:807:ARG:HG3	2.04	0.57
1:A:500:ARG:O	1:A:501:ILE:O	2.22	0.57
1:A:181:ALA:HA	1:A:184:LYS:HG2	1.86	0.56
2:B:96:C:N3	2:B:128:C:O2'	2.36	0.56
1:A:49:ALA:HB2	1:A:479:ARG:HD2	1.88	0.56
2:B:97:U:O2'	2:B:98:G:OP1	2.22	0.56
1:A:63:ARG:NH2	2:B:18:A:OP2	2.32	0.55
1:A:177:PRO:HG2	1:A:208:LEU:HD12	1.89	0.54
3:C:23:DT:H2'	3:C:24:DA:H8	1.70	0.54
2:B:97:U:H2'	2:B:98:G:C8	2.42	0.54
1:A:972:PRO:HD3	1:A:988:CYS:SG	2.48	0.54
2:B:49:G:H2'	2:B:50:A:H8	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:21:DA:H2'	3:C:22:DA:H8	1.73	0.53
1:A:1066:LEU:O	1:A:1068:LYS:N	2.41	0.53
1:A:1054:ASN:ND2	3:C:3:DA:H5'	2.24	0.53
1:A:360:LEU:HD11	1:A:407:ILE:HG22	1.90	0.53
1:A:884:ARG:NH1	2:B:36:C:O2	2.42	0.53
1:A:37:ARG:HA	1:A:779:PHE:CE2	2.44	0.52
1:A:324:LEU:CD2	1:A:324:LEU:N	2.73	0.52
1:A:133:HIS:CD2	2:B:60:A:H5''	2.44	0.52
1:A:423:ILE:HG23	1:A:428:LEU:HG	1.91	0.52
1:A:464:LEU:HD12	1:A:465:PRO:HD2	1.91	0.52
1:A:838:MET:HE1	1:A:953:ARG:HD3	1.92	0.52
1:A:180:LEU:HD23	1:A:203:PHE:HE1	1.75	0.51
1:A:503:ILE:CG2	1:A:697:ALA:CA	2.64	0.51
1:A:324:LEU:CD2	1:A:324:LEU:H	2.24	0.51
1:A:719:ASN:HA	1:A:722:HIS:HB3	1.91	0.51
2:B:4:C:H2'	2:B:5:A:C8	2.46	0.51
2:B:4:C:H2'	2:B:5:A:H8	1.76	0.51
3:C:22:DA:H2'	3:C:23:DT:C6	2.46	0.51
3:C:5:DT:H2''	3:C:6:DG:C8	2.46	0.51
2:B:93:G:H2'	2:B:94:C:C6	2.46	0.50
1:A:43:VAL:HG23	1:A:830:VAL:HA	1.93	0.50
1:A:1026:ASN:HB2	1:A:1035:TYR:HB2	1.92	0.50
2:B:99:C:H2'	2:B:100:C:C6	2.47	0.50
1:A:962:LYS:HG3	1:A:963:LYS:N	2.26	0.49
2:B:61:C:H2'	2:B:62:A:H8	1.77	0.49
1:A:1050:ILE:O	1:A:1050:ILE:HD12	2.13	0.49
3:C:23:DT:H2'	3:C:24:DA:C8	2.47	0.49
1:A:333:LYS:O	1:A:334:GLY:C	2.48	0.49
2:B:54:G:H2'	2:B:55:U:O4'	2.12	0.49
1:A:320:ALA:O	1:A:324:LEU:CD2	2.61	0.49
2:B:3:U:H2'	2:B:4:C:C6	2.47	0.49
3:C:21:DA:H2'	3:C:22:DA:C8	2.47	0.49
1:A:308:GLU:N	1:A:309:PRO:HD2	2.28	0.48
1:A:418:ASP:OD1	1:A:418:ASP:N	2.45	0.48
1:A:786:ARG:HD2	1:A:825:VAL:HG21	1.95	0.48
1:A:98:ASP:HA	1:A:104:LYS:HE2	1.96	0.48
1:A:290:GLU:H	1:A:331:PHE:CB	2.25	0.48
1:A:46:PHE:CE2	1:A:480:ALA:HA	2.49	0.48
1:A:804:GLU:O	1:A:808:THR:HG23	2.13	0.48
2:B:31:G:H2'	2:B:32:C:C6	2.49	0.48
2:B:5:A:H2'	2:B:6:C:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:977:GLN:HG2	1:A:982:ILE:HD11	1.97	0.47
3:C:24:DA:H2'	3:C:25:DG:H8	1.79	0.47
3:C:32:DG:H2'	3:C:33:DA:C8	2.50	0.47
1:A:290:GLU:N	1:A:331:PHE:CA	2.59	0.47
2:B:28:G:H2'	2:B:29:U:C6	2.49	0.47
3:C:22:DA:H2'	3:C:23:DT:H6	1.80	0.47
2:B:60:A:H2'	2:B:61:C:C6	2.50	0.47
1:A:234:GLY:O	1:A:238:LEU:HD23	2.15	0.46
1:A:23:GLY:HA3	1:A:43:VAL:HG12	1.96	0.46
1:A:70:ARG:O	1:A:74:ARG:HG3	2.15	0.46
3:C:9:DC:H2'	3:C:10:DC:C6	2.51	0.46
2:B:6:C:H2'	2:B:7:U:C6	2.50	0.46
4:D:10:DT:H2''	4:D:11:DA:C8	2.51	0.46
1:A:346:THR:C	1:A:348:MET:H	2.16	0.46
2:B:91:A:H2'	2:B:92:C:C6	2.51	0.46
1:A:834:PRO:HA	1:A:1006:TYR:HB2	1.96	0.46
1:A:74:ARG:NH2	2:B:20:U:OP1	2.36	0.46
1:A:193:ARG:HB3	2:B:24:C:OP1	2.17	0.45
1:A:177:PRO:HD2	1:A:211:GLU:HB2	1.97	0.45
1:A:271:THR:HG21	1:A:425:LEU:HD21	1.97	0.45
1:A:699:ASN:O	1:A:703:THR:N	2.50	0.45
1:A:286:LEU:O	1:A:288:ILE:N	2.50	0.45
1:A:317:TYR:HB2	1:A:344:ALA:HB1	1.99	0.45
1:A:849:ALA:HB2	1:A:945:ILE:HB	1.98	0.45
1:A:1018:LYS:HG2	1:A:1019:VAL:H	1.80	0.45
1:A:45:VAL:HG22	1:A:832:ARG:HA	1.99	0.45
1:A:888:LEU:HD22	1:A:916:LYS:HE2	1.98	0.45
1:A:935:VAL:HG22	1:A:976:TRP:CE2	2.51	0.45
1:A:1016:LYS:HA	1:A:1016:LYS:HD3	1.68	0.45
1:A:324:LEU:HD23	1:A:325:GLY:H	1.82	0.45
1:A:829:PHE:HB2	1:A:1039:HIS:HB3	1.99	0.44
1:A:289:LEU:HD23	1:A:331:PHE:CB	2.46	0.44
1:A:279:TRP:HE1	1:A:306:MET:HG2	1.82	0.44
1:A:45:VAL:HG21	1:A:832:ARG:HD2	1.98	0.44
1:A:287:ARG:HH22	3:C:29:DA:H4'	1.82	0.44
2:B:132:U:H3'	2:B:132:U:OP2	2.17	0.44
2:B:97:U:H2'	2:B:98:G:H8	1.82	0.44
2:B:98:G:H2'	2:B:99:C:C6	2.51	0.44
1:A:674:ASN:HB3	1:A:677:LEU:HB3	1.99	0.44
1:A:37:ARG:HA	1:A:779:PHE:HE2	1.81	0.44
1:A:114:ARG:HG3	1:A:130:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:ALA:O	1:A:171:THR:HG22	2.18	0.44
1:A:74:ARG:NH1	2:B:21:U:OP2	2.51	0.44
1:A:851:ARG:HH22	1:A:878:VAL:HG13	1.82	0.44
4:D:1:DA:H2'	4:D:2:DG:C8	2.53	0.44
1:A:19:ILE:HB	1:A:509:VAL:HA	2.00	0.44
2:B:6:C:H2'	2:B:7:U:H6	1.81	0.44
1:A:12:ILE:HG13	1:A:27:VAL:CG2	2.43	0.43
1:A:366:LYS:CB	1:A:372:LEU:HD21	2.48	0.43
1:A:879:ASN:ND2	1:A:885:GLU:OE1	2.42	0.43
1:A:951:MET:HE2	1:A:951:MET:HB3	1.83	0.43
3:C:23:DT:C2	3:C:24:DA:C8	3.06	0.43
1:A:953:ARG:NH1	2:B:127:U:O4	2.51	0.43
1:A:58:LEU:HD12	1:A:58:LEU:H	1.82	0.43
1:A:777:GLU:HB3	1:A:779:PHE:CE2	2.53	0.43
2:B:16:U:H2'	2:B:17:A:C8	2.54	0.43
2:B:37:U:H2'	2:B:38:U:O4'	2.18	0.43
1:A:787:VAL:HG23	1:A:788:PHE:CD2	2.54	0.43
1:A:1008:LEU:O	1:A:1062:GLN:CB	2.67	0.43
1:A:198:ASP:OD1	1:A:199:TYR:N	2.48	0.43
2:B:131:U:H3'	2:B:132:U:H5'	2.00	0.43
1:A:63:ARG:HD3	2:B:18:A:OP2	2.19	0.43
1:A:290:GLU:N	1:A:331:PHE:CB	2.81	0.42
1:A:185:PHE:CD1	1:A:192:ILE:HG13	2.55	0.42
1:A:377:GLU:O	1:A:381:GLU:HG3	2.19	0.42
1:A:356:ILE:HD13	1:A:382:ILE:HD11	2.01	0.42
2:B:41:U:H2'	2:B:42:C:C6	2.55	0.42
2:B:46:A:HO2'	2:B:47:G:P	2.43	0.42
1:A:90:GLY:O	1:A:226:HIS:NE2	2.53	0.42
1:A:1033:ARG:HD2	3:C:5:DT:H72	2.02	0.42
1:A:271:THR:HG23	1:A:380:ASP:HA	2.02	0.42
2:B:92:C:H2'	2:B:93:G:C8	2.55	0.42
1:A:324:LEU:H	1:A:324:LEU:HD23	1.84	0.42
1:A:836:ARG:HG3	1:A:1004:HIS:CG	2.54	0.42
1:A:107:PRO:HD2	1:A:129:ALA:HB2	2.01	0.42
2:B:41:U:H2'	2:B:42:C:H6	1.85	0.41
2:B:14:U:H2'	2:B:15:U:C6	2.55	0.41
1:A:287:ARG:HH12	3:C:30:DG:P	2.43	0.41
1:A:194:ASN:HB2	2:B:24:C:O5'	2.21	0.41
1:A:921:LEU:O	2:B:56:U:O2'	2.34	0.41
2:B:99:C:H2'	2:B:100:C:H6	1.86	0.41
3:C:19:DT:H2'	3:C:20:DA:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:ARG:NH1	1:A:136:LYS:O	2.54	0.41
2:B:40:C:H2'	2:B:41:U:C6	2.56	0.41
1:A:222:PHE:O	1:A:224:ASN:N	2.47	0.41
2:B:92:C:H2'	2:B:93:G:H8	1.85	0.41
1:A:26:MET:HB2	1:A:40:ASP:H	1.84	0.41
1:A:810:LEU:HD23	1:A:810:LEU:HA	1.79	0.41
1:A:18:GLY:N	1:A:21:SER:O	2.54	0.40
1:A:29:ILE:HA	1:A:35:PRO:HA	2.03	0.40
2:B:14:U:H2'	2:B:15:U:H6	1.86	0.40
1:A:71:LEU:HD11	2:B:21:U:C5	2.57	0.40
2:B:93:G:HO2'	2:B:94:C:P	2.44	0.40
3:C:32:DG:H2'	3:C:33:DA:H8	1.87	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	
1	A	870/1083 (80%)	771 (89%)	91 (10%)	8 (1%)	17	56

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	501	ILE
1	A	795	PRO
1	A	347	LEU
1	A	1065	GLU
1	A	1067	GLY
1	A	791	PRO
1	A	1066	LEU
1	A	36	ILE

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
1	A	537/935 (57%)	517 (96%)	20 (4%)	34 68

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	ARG
1	A	93	GLN
1	A	144	ARG
1	A	175	ARG
1	A	307	ASP
1	A	324	LEU
1	A	372	LEU
1	A	451	ASP
1	A	452	HIS
1	A	503	ILE
1	A	784	MET
1	A	807	ARG
1	A	810	LEU
1	A	829	PHE
1	A	896	LEU
1	A	941	ASN
1	A	1007	ASP
1	A	1011	PHE
1	A	1038	TRP
1	A	1048	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	103/135 (76%)	20 (19%)	4 (3%)

All (20) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	2	G
2	B	43	G
2	B	45	A
2	B	47	G
2	B	48	A
2	B	49	G
2	B	51	A
2	B	65	A
2	B	69	C
2	B	70	C
2	B	84	U
2	B	85	G
2	B	89	C
2	B	94	C
2	B	97	U
2	B	98	G
2	B	103	U
2	B	121	G
2	B	128	C
2	B	132	U

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	46	A
2	B	93	G
2	B	97	U
2	B	120	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 carbohydrates in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	EDO	B	201	-	3,3,3	0.46	0	2,2,2	0.34	0
5	EDO	C	101	-	3,3,3	0.45	0	2,2,2	0.32	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	B	201	-	-	0/1/1/1	-
5	EDO	C	101	-	-	0/1/1/1	-

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	884/1083 (81%)	-0.04	38 (4%) 35 22	15, 77, 146, 189	0
2	B	105/135 (77%)	-0.42	1 (0%) 82 72	16, 60, 172, 215	0
3	C	35/35 (100%)	-0.61	0 100 100	27, 49, 80, 86	0
4	D	11/11 (100%)	-0.66	0 100 100	38, 49, 68, 79	0
All	All	1035/1264 (81%)	-0.10	39 (3%) 40 26	15, 71, 150, 215	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	733	SER	11.4
1	A	739	GLN	6.8
1	A	781	GLN	6.1
1	A	743	ARG	4.7
1	A	725	LEU	4.4
1	A	747	TYR	4.2
1	A	746	ARG	3.9
1	A	462	ILE	3.8
1	A	745	VAL	3.7
1	A	742	THR	3.6
1	A	832	ARG	3.3
1	A	7	ASN	3.2
1	A	723	HIS	3.2
1	A	734	THR	3.1
1	A	1021	PHE	3.1
1	A	27	VAL	3.0
1	A	463	TYR	2.9
1	A	670	THR	2.9
1	A	714	LYS	2.8
1	A	830	VAL	2.8
1	A	1015	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	317	TYR	2.7
1	A	513	PHE	2.6
1	A	732	CYS	2.6
1	A	736	ALA	2.5
1	A	28	GLU	2.5
1	A	818	PRO	2.4
1	A	961	ASP	2.4
1	A	794	LYS	2.4
1	A	407	ILE	2.4
1	A	488	ILE	2.4
1	A	831	SER	2.3
1	A	771	HIS	2.2
1	A	772	PHE	2.2
1	A	737	MET	2.2
2	B	103	U	2.2
1	A	18	GLY	2.1
1	A	726	ASP	2.1
1	A	147	GLU	2.0

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](#)

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(\AA^2)	Q<0.9
5	EDO	C	101	4/4	0.76	0.55	46,46,48,50	0
5	EDO	B	201	4/4	0.86	0.18	23,25,26,27	0

6.5 Other polymers ⓘ

There are no such residues in this entry.