Full wwPDB X-ray Structure Validation Report (i)

Nov 14, 2023 – 10:43 PM JST

PDB ID	:	6AI6
Title	:	Crystal structure of SpCas9-NG
Authors	:	Nishimasu, H.; Hirano, S.; Ishitani, R.; Nureki, O.
Deposited on	:	2018-08-21
Resolution	:	2.70 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 (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:

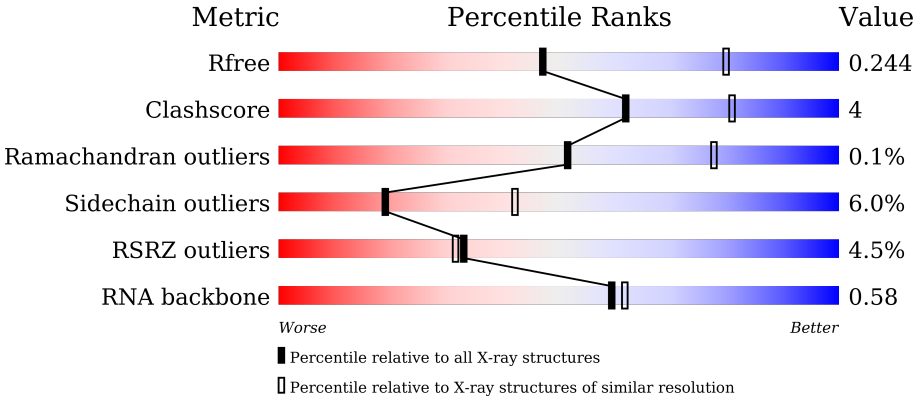
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)
RNA backbone	3102	1159 (3.00-2.40)

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	1372	5% 81% 13% • •
2	B	81	% 83% 17%
3	C	28	64% 36%
4	D	8	100%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 13060 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
			Total	C	N	O	S			
1	A	1322	10535	6721	1822	1970	22	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q99ZW2
A	-2	SER	-	expression tag	UNP Q99ZW2
A	-1	GLY	-	expression tag	UNP Q99ZW2
A	0	HIS	-	expression tag	UNP Q99ZW2
A	863	ALA	ASN	engineered mutation	UNP Q99ZW2
A	1111	ARG	LEU	engineered mutation	UNP Q99ZW2
A	1135	VAL	ASP	engineered mutation	UNP Q99ZW2
A	1218	ARG	GLY	engineered mutation	UNP Q99ZW2
A	1219	PHE	GLU	engineered mutation	UNP Q99ZW2
A	1322	ARG	ALA	engineered mutation	UNP Q99ZW2
A	1335	VAL	ARG	engineered mutation	UNP Q99ZW2
A	1337	ARG	THR	engineered mutation	UNP Q99ZW2

- Molecule 2 is a RNA chain called RNA (81-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	81	1739	778	319	561	81	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	C	28	561	269	103	162	27	0	0	0

- Molecule 4 is a DNA chain called DNA (8-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
4	D	8	164	80	28	49	7	0	0	0

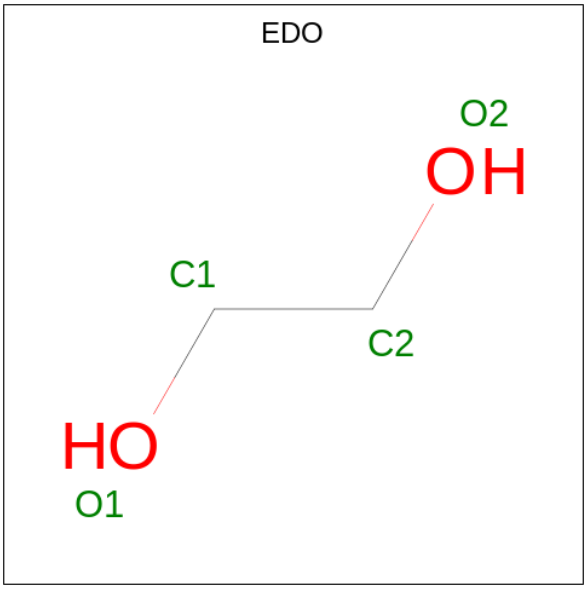
- Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	K		
5	A	9	9	9	0	0
			Total	K		
5	B	1	1	1	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
6	A	1	1	1	0	0
			Total	Mg		
6	B	2	2	2	0	0

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	A	1	4	2	2	0	0
			Total	C	O		
7	A	1	4	2	2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	A	1	4	2	2	0	0

- Molecule 8 is water.

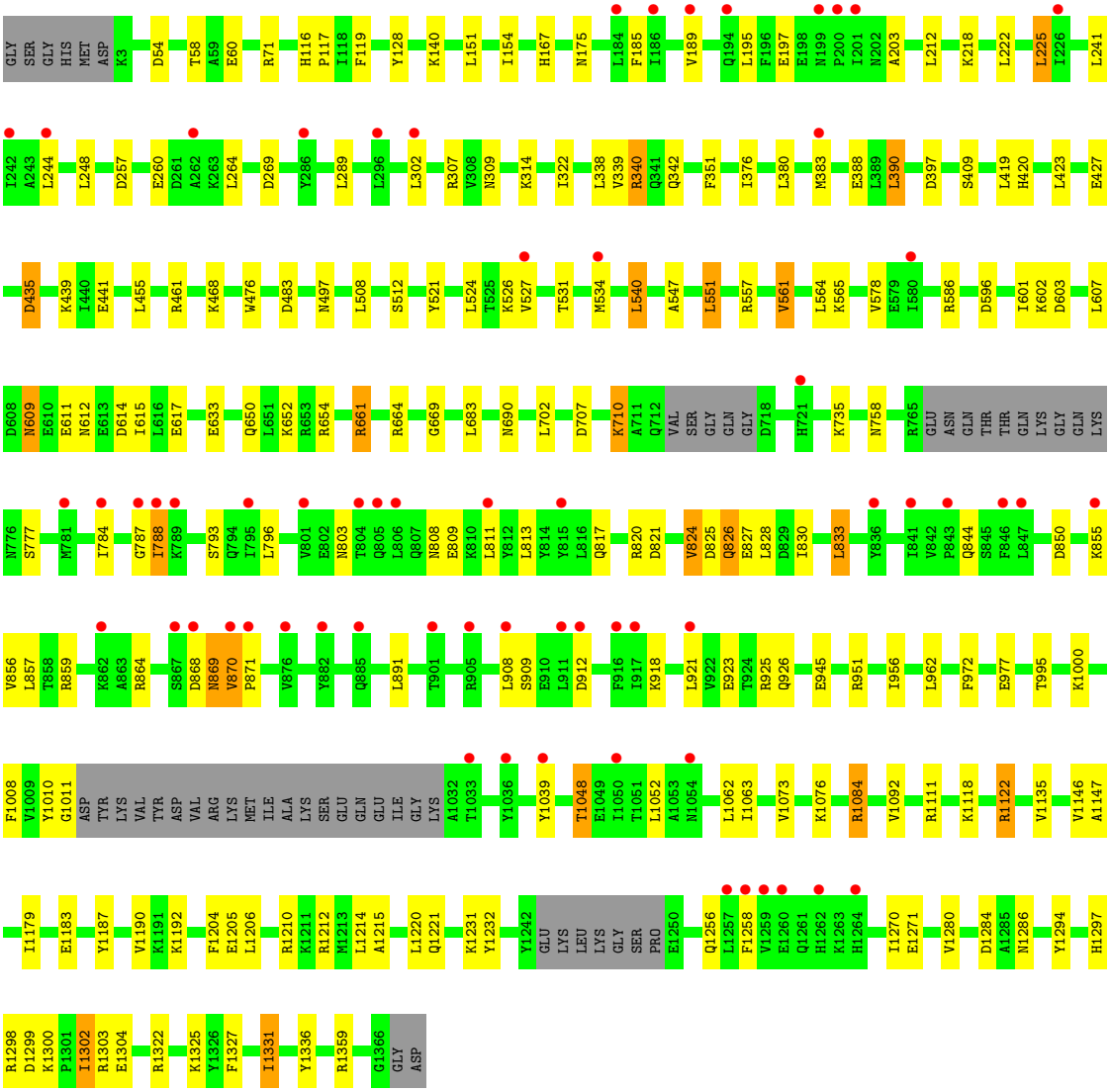
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	A	15	15	15	0	0
			Total	O		
8	B	20	20	20	0	0
			Total	O		
8	C	1	1	1	0	0

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.

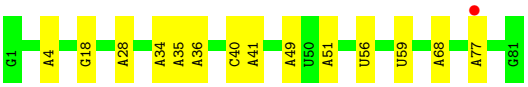
- Molecule 1: CRISPR-associated endonuclease Cas9/Csn1

Chain A:



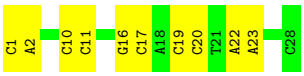
- Molecule 2: RNA (81-MER)

Chain B:

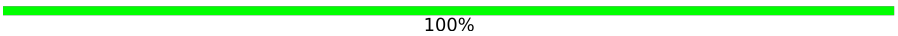


• Molecule 3: DNA (28-MER)

Chain C:



• Molecule 4: DNA (8-MER)

Chain D: 

There are no outlier residues recorded for this chain.

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	177.38Å 68.57Å 187.97Å 90.00° 111.51° 90.00°	Depositor
Resolution (Å)	48.17 – 2.70 48.17 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.17-2.70) 100.0 (48.17-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.95 (at 2.69Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.218 , 0.243 0.218 , 0.244	Depositor DCC
R_{free} test set	2899 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	61.8	Xtriage
Anisotropy	0.724	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 46.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	13060	wwPDB-VP
Average B, all atoms (Å^2)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, K, 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	0.24	0/10726	0.40	0/14476
2	B	0.17	0/1949	0.71	0/3037
3	C	0.56	0/628	0.92	0/964
4	D	0.56	0/183	1.06	0/282
All	All	0.26	0/13486	0.52	0/18759

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	10535	0	10413	99	0
2	B	1739	0	870	7	0
3	C	561	0	315	6	0
4	D	164	0	94	0	0
5	A	9	0	0	0	0
5	B	1	0	0	0	0
6	A	1	0	0	0	0
6	B	2	0	0	0	0
7	A	12	0	17	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	15	0	0	0	0
8	B	20	0	0	0	0
8	C	1	0	0	0	0
All	All	13060	0	11709	106	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 4.

All (106) 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:869:ASN:HD22	1:A:870:VAL:H	1.36	0.73
1:A:565:LYS:NZ	1:A:578:VAL:O	2.24	0.70
1:A:869:ASN:HD21	1:A:908:LEU:H	1.40	0.70
1:A:909:SER:H	1:A:912:ASP:HB2	1.58	0.67
1:A:189:VAL:HG21	1:A:203:ALA:HB2	1.76	0.67
1:A:71:ARG:NH2	2:B:18:G:N7	2.43	0.67
1:A:58:THR:HG23	1:A:60:GLU:H	1.60	0.66
1:A:1000:LYS:HB2	1:A:1073:VAL:HG11	1.77	0.66
1:A:244:LEU:HD11	1:A:264:LEU:HB2	1.79	0.64
1:A:758:ASN:HD22	1:A:995:THR:HG22	1.61	0.63
1:A:423:LEU:O	1:A:427:GLU:HB2	1.99	0.62
1:A:633:GLU:HB2	1:A:652:LYS:HD2	1.80	0.62
1:A:1212:ARG:NH2	1:A:1280:VAL:O	2.32	0.62
1:A:788:ILE:HG13	1:A:793:SER:HB3	1.81	0.62
1:A:951:ARG:NH1	1:A:1010:TYR:O	2.33	0.61
1:A:340:ARG:NH1	2:B:41:A:OP2	2.33	0.61
1:A:526:LYS:NZ	1:A:690:ASN:O	2.34	0.59
1:A:1205:GLU:OE1	1:A:1359:ARG:NH2	2.36	0.58
1:A:824:VAL:HG23	1:A:826:GLN:HE22	1.68	0.58
1:A:1220:LEU:HB2	1:A:1336:TYR:HB2	1.86	0.57
1:A:218:LYS:HB3	1:A:248:LEU:HD11	1.86	0.57
1:A:921:LEU:HD22	1:A:962:LEU:HD13	1.87	0.56
1:A:1286:ASN:HB3	1:A:1331:ILE:HD11	1.87	0.56
1:A:527:VAL:HB	1:A:540:LEU:HD11	1.88	0.56
1:A:1302:ILE:H	1:A:1302:ILE:HD13	1.71	0.55
1:A:531:THR:HG22	1:A:534:MET:HG2	1.88	0.55
1:A:870:VAL:HG12	1:A:871:PRO:HD2	1.89	0.55
1:A:339:VAL:HG11	1:A:351:PHE:HE2	1.74	0.53
1:A:972:PHE:HE1	1:A:1084:ARG:HD2	1.74	0.52
1:A:435:ASP:N	1:A:435:ASP:OD1	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:LYS:HD3	1:A:322:ILE:HD12	1.92	0.52
1:A:54:ASP:O	1:A:735:LYS:NZ	2.38	0.51
1:A:212:LEU:HD21	1:A:225:LEU:HD12	1.93	0.51
1:A:869:ASN:HD22	1:A:870:VAL:HG23	1.76	0.51
1:A:777:SER:OG	1:A:803:ASN:O	2.30	0.50
1:A:808:ASN:HB3	1:A:811:LEU:HB3	1.92	0.50
1:A:241:LEU:HD11	1:A:289:LEU:HD21	1.94	0.50
1:A:1204:PHE:HE2	1:A:1214:LEU:HG	1.77	0.50
1:A:151:LEU:HA	1:A:154:ILE:HD12	1.94	0.50
3:C:16:DG:H2'	3:C:17:DC:C6	2.47	0.50
1:A:557:ARG:NH1	1:A:596:ASP:OD1	2.38	0.49
1:A:821:ASP:OD2	1:A:859:ARG:N	2.44	0.49
1:A:977:GLU:OE2	1:A:977:GLU:N	2.46	0.48
1:A:609:ASN:HB3	1:A:612:ASN:ND2	2.28	0.48
1:A:1084:ARG:H	1:A:1084:ARG:HG2	1.42	0.48
1:A:813:LEU:O	1:A:817:GLN:HG3	2.13	0.48
1:A:787:GLY:HA3	1:A:891:LEU:HD21	1.96	0.47
1:A:521:TYR:HB3	1:A:683:LEU:HB3	1.96	0.47
3:C:10:DC:H2'	3:C:11:DC:H6	1.80	0.47
1:A:561:VAL:HA	1:A:564:LEU:HB3	1.97	0.47
1:A:809:GLU:OE2	1:A:855:LYS:NZ	2.32	0.47
1:A:376:ILE:O	1:A:380:LEU:HD12	2.15	0.47
1:A:820:ARG:NH1	1:A:825:ASP:OD1	2.49	0.46
1:A:1304:GLU:HG3	1:A:1327:PHE:HE1	1.79	0.46
1:A:1215:ALA:HB2	1:A:1221:GLN:HG3	1.97	0.46
1:A:420:HIS:ND1	1:A:441:GLU:OE2	2.36	0.46
1:A:923:GLU:OE2	1:A:925:ARG:NE	2.47	0.46
1:A:1231:LYS:HE3	1:A:1232:TYR:CZ	2.50	0.46
1:A:1297:HIS:HD2	1:A:1300:LYS:HE2	1.81	0.45
1:A:1179:ILE:HD11	1:A:1192:LYS:HG3	1.98	0.45
1:A:439:LYS:HG2	1:A:476:TRP:CD1	2.51	0.45
1:A:951:ARG:HH12	1:A:1011:GLY:HA3	1.82	0.45
1:A:784:ILE:O	1:A:788:ILE:HG22	2.16	0.44
1:A:167:HIS:HA	2:B:18:G:H4'	1.99	0.44
1:A:342:GLN:HB2	1:A:383:MET:HE3	2.00	0.44
1:A:1048:THR:HG23	1:A:1076:LYS:HD3	1.99	0.44
1:A:307:ARG:NH1	1:A:397:ASP:OD2	2.38	0.44
1:A:601:ILE:HG13	1:A:603:ASP:H	1.83	0.44
1:A:1298:ARG:HB3	1:A:1298:ARG:NH1	2.33	0.44
1:A:821:ASP:HB2	1:A:828:LEU:HD21	1.99	0.44
1:A:956:ILE:HG23	1:A:1008:PHE:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1122:ARG:NH2	2:B:49:A:N3	2.65	0.44
1:A:497:ASN:HD21	3:C:19:DC:P	2.41	0.43
1:A:547:ALA:O	1:A:551:LEU:HB2	2.17	0.43
3:C:19:DC:H2'	3:C:20:DC:H6	1.82	0.43
1:A:833:LEU:HD13	1:A:833:LEU:HA	1.87	0.43
1:A:338:LEU:HB3	1:A:383:MET:HE2	2.00	0.43
1:A:601:ILE:HD11	1:A:607:LEU:HG	2.00	0.43
1:A:707:ASP:HA	1:A:710:LYS:HE3	2.01	0.43
1:A:390:LEU:HD13	1:A:390:LEU:HA	1.90	0.43
1:A:918:LYS:HD2	1:A:1039:TYR:HE2	1.84	0.43
1:A:1062:LEU:HD23	1:A:1062:LEU:HA	1.88	0.43
2:B:35:A:H2'	2:B:36:A:C8	2.54	0.43
1:A:309:ASN:OD1	1:A:309:ASN:N	2.52	0.42
3:C:22:DA:H2"	3:C:23:DA:H8	1.84	0.42
1:A:1183:GLU:HA	1:A:1187:TYR:O	2.20	0.42
1:A:314:LYS:HB2	1:A:314:LYS:HE3	1.82	0.42
3:C:1:DC:H2'	3:C:2:DA:C8	2.55	0.42
1:A:508:LEU:HD21	1:A:664:ARG:HB2	2.02	0.42
1:A:820:ARG:HG3	1:A:826:GLN:O	2.20	0.42
1:A:1206:LEU:HD13	1:A:1210:ARG:CZ	2.49	0.42
1:A:116:HIS:HA	1:A:117:PRO:HD3	1.92	0.42
2:B:34:A:H2'	2:B:35:A:O4'	2.20	0.42
1:A:661:ARG:HD3	2:B:4:A:OP1	2.20	0.41
1:A:307:ARG:HH12	1:A:397:ASP:CG	2.23	0.41
1:A:1270:ILE:HG13	1:A:1294:TYR:CE2	2.56	0.41
1:A:185:PHE:O	1:A:189:VAL:HG13	2.20	0.41
1:A:468:LYS:HE3	1:A:483:ASP:HA	2.02	0.41
1:A:512:SER:OG	1:A:617:GLU:OE1	2.31	0.41
1:A:1118:LYS:HD2	1:A:1118:LYS:HA	1.84	0.41
1:A:1000:LYS:HA	1:A:1073:VAL:HG21	2.02	0.40
1:A:1147:ALA:HB2	1:A:1190:VAL:HA	2.03	0.40
1:A:119:PHE:HE2	1:A:128:TYR:HB2	1.86	0.40
1:A:439:LYS:HG2	1:A:476:TRP:NE1	2.36	0.40
1:A:534:MET:HG2	1:A:534:MET:H	1.70	0.40
1:A:817:GLN:OE1	1:A:857:LEU:N	2.52	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	1312/1372 (96%)	1274 (97%)	37 (3%)	1 (0%)	51 78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	669	GLY

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	A	1117/1230 (91%)	1050 (94%)	67 (6%)	19 42

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	175	ASN
1	A	195	LEU
1	A	197	GLU
1	A	222	LEU
1	A	225	LEU
1	A	257	ASP
1	A	260	GLU
1	A	269	ASP
1	A	302	LEU
1	A	340	ARG

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Mol	Chain	Res	Type
1	A	388	GLU
1	A	390	LEU
1	A	409	SER
1	A	419	LEU
1	A	435	ASP
1	A	455	LEU
1	A	461	ARG
1	A	524	LEU
1	A	540	LEU
1	A	551	LEU
1	A	561	VAL
1	A	586	ARG
1	A	602	LYS
1	A	609	ASN
1	A	611	GLU
1	A	614	ASP
1	A	615	ILE
1	A	650	GLN
1	A	654	ARG
1	A	661	ARG
1	A	702	LEU
1	A	710	LYS
1	A	788	ILE
1	A	796	LEU
1	A	824	VAL
1	A	826	GLN
1	A	827	GLU
1	A	830	ILE
1	A	833	LEU
1	A	844	GLN
1	A	850	ASP
1	A	856	VAL
1	A	864	ARG
1	A	868	ASP
1	A	869	ASN
1	A	870	VAL
1	A	926	GLN
1	A	945	GLU
1	A	1048	THR
1	A	1052	LEU
1	A	1063	ILE
1	A	1084	ARG

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Mol	Chain	Res	Type
1	A	1092	VAL
1	A	1111	ARG
1	A	1122	ARG
1	A	1135	VAL
1	A	1146	VAL
1	A	1256	GLN
1	A	1258	PHE
1	A	1271	GLU
1	A	1284	ASP
1	A	1299	ASP
1	A	1302	ILE
1	A	1303	ARG
1	A	1322	ARG
1	A	1325	LYS
1	A	1331	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	HIS
1	A	202	ASN
1	A	609	ASN
1	A	612	ASN
1	A	698	HIS
1	A	826	GLN
1	A	844	GLN
1	A	869	ASN
1	A	926	GLN
1	A	971	GLN
1	A	1264	HIS
1	A	1286	ASN
1	A	1297	HIS
1	A	1311	HIS
1	A	1317	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	80/81 (98%)	7 (8%)	0

All (7) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	28	A
2	B	40	C
2	B	51	A
2	B	56	U
2	B	59	U
2	B	68	A
2	B	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 13 are monoatomic - leaving 3 for Mogul analysis.

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	$\#\|Z\| > 2$
7	EDO	A	1411	-	3,3,3	0.49	0	2,2,2	0.27	0
7	EDO	A	1412	-	3,3,3	0.47	0	2,2,2	0.32	0
7	EDO	A	1410	1	3,3,3	0.48	0	2,2,2	0.29	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
7	EDO	A	1411	-	-	0/1/1/1	-
7	EDO	A	1412	-	-	0/1/1/1	-
7	EDO	A	1410	1	-	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 (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	1322/1372 (96%)	0.24	64 (4%) 30 28	37, 83, 147, 185	0
2	B	81/81 (100%)	-0.44	1 (1%) 79 80	41, 67, 167, 210	0
3	C	28/28 (100%)	-0.42	0 100 100	52, 79, 116, 127	0
4	D	8/8 (100%)	-0.17	0 100 100	65, 87, 140, 151	0
All	All	1439/1489 (96%)	0.18	65 (4%) 33 31	37, 82, 148, 210	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	804	THR	5.8
1	A	806	LEU	5.7
1	A	1258	PHE	5.0
1	A	911	LEU	4.0
1	A	841	ILE	3.9
1	A	846	PHE	3.8
1	A	296	LEU	3.7
1	A	805	GLN	3.4
1	A	847	LEU	3.4
1	A	871	PRO	3.3
1	A	784	ILE	3.3
1	A	1036	TYR	3.3
1	A	1257	LEU	3.3
1	A	867	SER	3.2
1	A	908	LEU	3.2
1	A	843	PRO	3.2
1	A	917	ILE	3.2
1	A	1264	HIS	3.2
1	A	200	PRO	3.1
1	A	781	MET	3.0
1	A	885	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	870	VAL	2.9
1	A	882	TYR	2.9
1	A	1033	THR	2.8
1	A	189	VAL	2.7
1	A	905	ARG	2.7
1	A	862	LYS	2.6
2	B	77	A	2.5
1	A	787	GLY	2.5
1	A	244	LEU	2.5
1	A	912	ASP	2.5
1	A	1260	GLU	2.5
1	A	1259	VAL	2.5
1	A	815	TYR	2.5
1	A	836	TYR	2.5
1	A	580	ILE	2.4
1	A	1054	ASN	2.4
1	A	921	LEU	2.4
1	A	186	ILE	2.4
1	A	801	VAL	2.3
1	A	262	ALA	2.3
1	A	242	ILE	2.3
1	A	855	LYS	2.3
1	A	1262	HIS	2.2
1	A	789	LYS	2.2
1	A	868	ASP	2.2
1	A	721	HIS	2.2
1	A	194	GLN	2.2
1	A	286	TYR	2.2
1	A	901	THR	2.2
1	A	226	ILE	2.2
1	A	302	LEU	2.2
1	A	383	MET	2.2
1	A	916	PHE	2.1
1	A	1050	ILE	2.1
1	A	534	MET	2.1
1	A	811	LEU	2.1
1	A	876	VAL	2.1
1	A	788	ILE	2.1
1	A	199	ASN	2.1
1	A	201	ILE	2.1
1	A	527	VAL	2.0
1	A	1039	TYR	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	184	LEU	2.0
1	A	795	ILE	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 monosaccharides 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(Å^2)	Q<0.9
5	K	A	1404	1/1	0.60	0.13	119,119,119,119	0
7	EDO	A	1410	4/4	0.72	0.30	62,63,63,64	0
5	K	A	1408	1/1	0.84	0.14	113,113,113,113	0
5	K	A	1403	1/1	0.85	0.66	120,120,120,120	0
5	K	B	101	1/1	0.91	0.21	77,77,77,77	0
5	K	A	1413	1/1	0.91	0.14	62,62,62,62	0
5	K	A	1406	1/1	0.92	0.23	105,105,105,105	0
6	MG	B	103	1/1	0.92	0.59	59,59,59,59	0
5	K	A	1407	1/1	0.92	0.24	64,64,64,64	0
6	MG	A	1409	1/1	0.93	0.19	52,52,52,52	0
5	K	A	1401	1/1	0.94	0.05	67,67,67,67	0
5	K	A	1405	1/1	0.95	0.14	144,144,144,144	0
7	EDO	A	1411	4/4	0.95	0.40	48,49,50,51	0
7	EDO	A	1412	4/4	0.95	0.43	60,62,64,65	0
6	MG	B	102	1/1	0.96	0.30	67,67,67,67	0
5	K	A	1402	1/1	0.97	0.06	82,82,82,82	0

6.5 Other polymers (i)

There are no such residues in this entry.