Full wwPDB X-ray Structure Validation Report (i)

Oct 10, 2023 – 12:02 AM EDT

PDB ID	:	7R6T
Title	:	Human EXOG complexed with dRP-containing DNA
Authors	:	Szymanski, M.R.; Yin, Y.W.
Deposited on	:	2021-06-23
Resolution	:	2.90 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 (1)) were used in the production of this report:

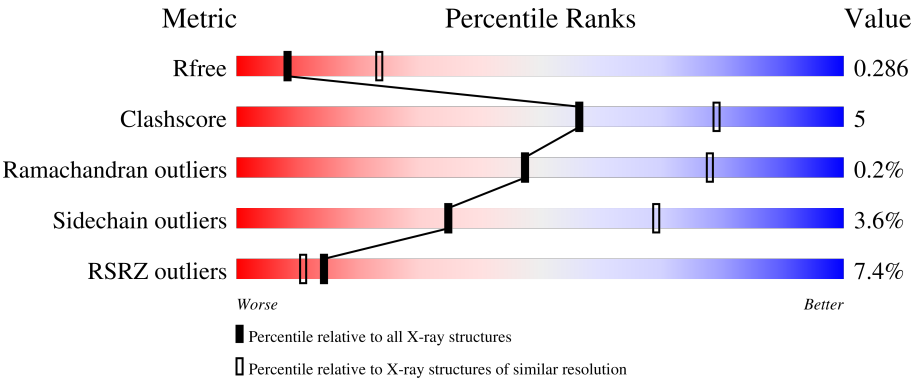
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 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	C	311	4% 81% 11% • 7%
1	D	311	% 83% 9% 8%
1	L	311	14% 80% 10% • 7%
2	E	10	10% 50% 30% 10% 10%
2	F	10	20% 40% 50% 10%

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Mol	Chain	Length	Quality of chain
2	M	10	10% 10% 60% 30%
3	A	11	18% 9% 73% 18%
3	B	11	18% 64% 18% 18%
3	K	11	9% 27% 36% 36%

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
4	MG	L	401	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7809 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 Nuclease EXOG, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	287	Total	C	N	O	S	0	0	0
			2269	1446	384	429	10			
1	C	290	Total	C	N	O	S	0	0	0
			2240	1424	383	423	10			
1	L	288	Total	C	N	O	S	0	0	0
			2272	1444	385	432	11			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	140	ALA	HIS	engineered mutation	UNP Q9Y2C4
C	140	ALA	HIS	engineered mutation	UNP Q9Y2C4
L	140	ALA	HIS	engineered mutation	UNP Q9Y2C4

- Molecule 2 is a DNA chain called DNA (5'-D(3DR)P*CP*TP*GP*AP*CP*GP*TP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	9	Total	C	N	O	P	0	0	0
			183	87	33	54	9			
2	E	9	Total	C	N	O	P	0	0	0
			176	83	30	54	9			
2	M	7	Total	C	N	O	P	0	0	0
			140	68	25	41	6			

- Molecule 3 is a DNA chain called DNA (5'-D(*CP*GP*CP*AP*CP*GP*TP*CP*AP*GP* A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	9	Total	C	N	O	P	0	0	0
			185	87	36	53	9			

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	B	9	Total C N O P 184 87 36 52 9	0	0	0
3	K	7	Total C N O P 144 68 28 41 7	0	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	1	Total Mg 1 1	0	0
4	A	1	Total Mg 1 1	0	0
4	E	1	Total Mg 1 1	0	0
4	L	1	Total Mg 1 1	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Na 1 1	0	0

- Molecule 6 is water.

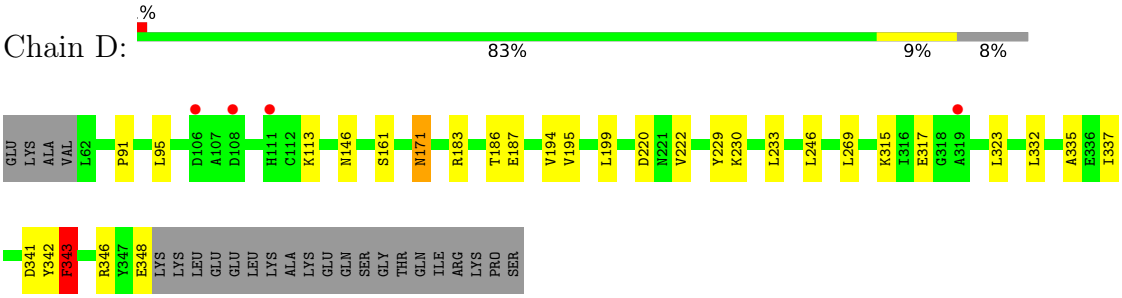
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	D	6	Total O 6 6	0	0
6	C	5	Total O 5 5	0	0

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.

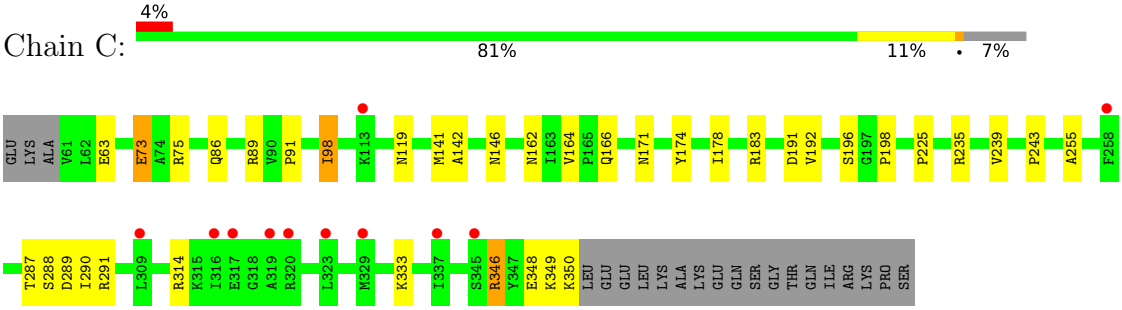
• Molecule 1: Nuclease EXOG, mitochondrial

Chain D:



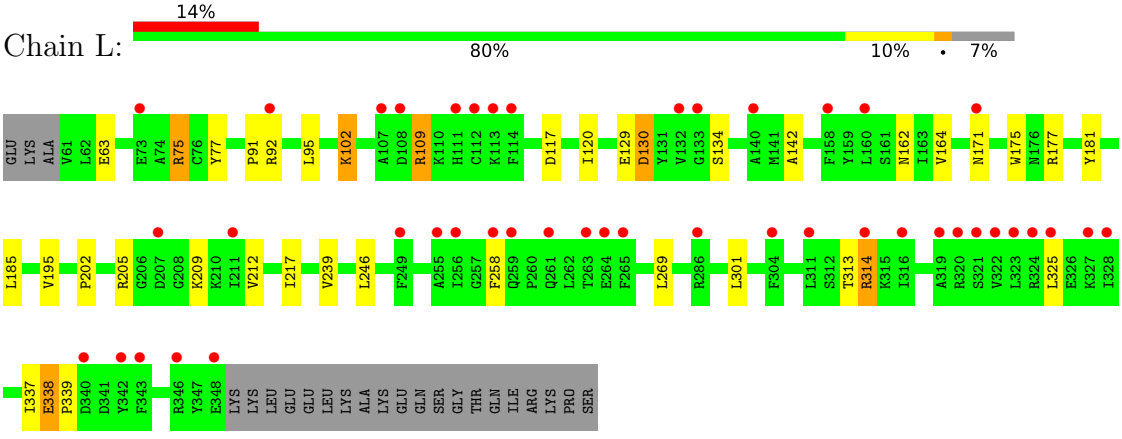
• Molecule 1: Nuclease EXOG, mitochondrial

Chain C:



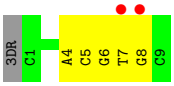
• Molecule 1: Nuclease EXOG, mitochondrial

Chain L:



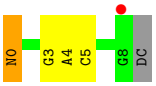
• Molecule 2: DNA (5'-D(3DR)P*CP*TP*GP*AP*CP*GP*TP*GP*C)-3')

Chain F:



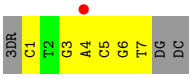
• Molecule 2: DNA (5'-D(3DR)P*CP*TP*GP*AP*CP*GP*TP*GP*C)-3')

Chain E:



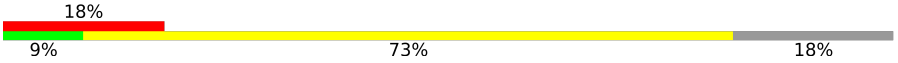
• Molecule 2: DNA (5'-D(3DR)P*CP*TP*GP*AP*CP*GP*TP*GP*C)-3')

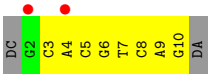
Chain M:



• Molecule 3: DNA (5'-D(*CP*GP*CP*AP*CP*GP*TP*CP*AP*GP*A)-3')

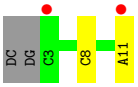
Chain A:





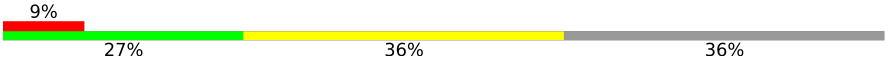
• Molecule 3: DNA (5'-D(*CP*GP*CP*AP*CP*GP*TP*CP*AP*GP*A)-3')

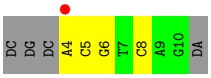
Chain B:



• Molecule 3: DNA (5'-D(*CP*GP*CP*AP*CP*GP*TP*CP*AP*GP*A)-3')

Chain K:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, α, β, γ	73.25Å 100.06Å 174.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.97 – 2.90 37.97 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.0 (37.97-2.90) 91.3 (37.97-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.27 (at 2.90Å)	Xtriage
Refinement program	PHENIX 1.17	Depositor
R, R_{free}	0.229 , 0.286 0.229 , 0.286	Depositor DCC
R_{free} test set	1998 reflections (7.47%)	wwPDB-VP
Wilson B-factor (Å^2)	67.3	Xtriage
Anisotropy	0.810	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 56.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	7809	wwPDB-VP
Average B, all atoms (Å^2)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 3DR, NA

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	C	0.26	0/2294	0.44	0/3117
1	D	0.27	0/2325	0.44	0/3156
1	L	0.25	0/2326	0.42	0/3156
2	E	0.54	0/184	0.90	0/282
2	F	0.57	0/203	0.90	0/309
2	M	0.53	0/156	0.92	0/239
3	A	0.51	0/207	0.79	0/317
3	B	0.50	0/206	0.81	0/315
3	K	0.55	0/161	0.81	0/246
All	All	0.31	0/8062	0.52	0/11137

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

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	C	2240	0	2125	21	0
1	D	2269	0	2186	12	0
1	L	2272	0	2197	22	0
2	E	176	0	98	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	183	0	100	5	0
2	M	140	0	81	8	0
3	A	185	0	101	7	0
3	B	184	0	101	2	0
3	K	144	0	79	6	0
4	A	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	L	1	0	0	0	0
5	B	1	0	0	0	0
6	C	5	0	0	0	0
6	D	6	0	0	1	0
All	All	7809	0	7068	71	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 (71) 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:F:6:DG:N2	3:A:5:DC:O2	2.11	0.81
1:L:75:ARG:HH12	1:L:120:ILE:HG12	1.53	0.74
1:C:86:GLN:O	1:C:89:ARG:NH1	2.24	0.70
1:C:287:THR:HG21	1:L:102:LYS:HE2	1.74	0.70
1:L:130:ASP:N	1:L:130:ASP:OD1	2.26	0.68
2:F:8:DG:N2	3:A:3:DC:O2	2.19	0.65
1:C:255:ALA:HB1	3:B:11:DA:H2"	1.78	0.65
2:M:5:DC:O2	3:K:6:DG:N1	2.28	0.63
1:L:246:LEU:HD21	1:L:269:LEU:HD22	1.82	0.61
1:C:63:GLU:N	1:C:63:GLU:OE1	2.36	0.58
1:C:98:ILE:HG13	1:C:192:VAL:HB	1.86	0.56
1:D:233:LEU:HD13	1:D:246:LEU:HD13	1.90	0.54
3:K:6:DG:H5"	3:K:6:DG:H8	1.74	0.53
2:M:6:DG:N1	3:K:5:DC:O2	2.37	0.52
1:D:323:LEU:HD11	1:D:343:PHE:HB3	1.91	0.52
1:D:246:LEU:HD21	1:D:269:LEU:HD22	1.91	0.51
1:C:91:PRO:HD2	1:C:164:VAL:HG12	1.92	0.51
1:C:75:ARG:NH1	1:C:119:ASN:O	2.44	0.51
1:C:141:MET:HB3	1:C:196:SER:HB2	1.93	0.50
1:L:77:TYR:OH	1:L:117:ASP:OD2	2.22	0.50
1:D:91:PRO:HG3	1:D:161:SER:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:8:DG:N1	3:A:3:DC:N3	2.48	0.49
2:E:4:DA:H2"	2:E:5:DC:H5'	1.94	0.49
1:L:337:ILE:HG23	1:L:339:PRO:HD2	1.96	0.48
2:M:3:DG:H1	3:K:8:DC:H42	1.62	0.48
3:A:8:DC:H2'	3:A:9:DA:H8	1.79	0.47
1:C:146:ASN:OD1	1:C:183:ARG:NH1	2.40	0.47
1:C:142:ALA:H	1:C:162:ASN:HD21	1.63	0.47
1:C:243:PRO:HG2	1:C:291:ARG:HD2	1.97	0.46
1:L:202:PRO:HB3	1:L:212:VAL:HG22	1.97	0.46
1:L:177:ARG:HH12	1:L:258:PHE:HA	1.81	0.46
1:L:338:GLU:HG2	1:L:339:PRO:HD3	1.98	0.46
1:C:174:TYR:CE2	1:C:178:ILE:HD11	2.51	0.46
2:E:3:DG:H1	3:B:8:DC:H42	1.63	0.46
1:C:288:SER:HA	1:C:290:ILE:N	2.31	0.45
1:L:95:LEU:HD13	1:L:195:VAL:HG22	1.98	0.45
1:D:183:ARG:O	1:D:186:THR:OG1	2.31	0.45
2:F:7:DT:O2	3:A:4:DA:H2	2.00	0.45
1:C:239:VAL:HA	1:L:239:VAL:HG11	1.98	0.45
2:M:7:DT:H3	3:K:4:DA:H2	1.64	0.44
3:K:6:DG:H5"	3:K:6:DG:C8	2.51	0.44
1:C:198:PRO:HB2	1:C:225:PRO:HB3	1.99	0.44
1:D:171:ASN:ND2	6:D:401:HOH:O	2.50	0.44
1:L:205:ARG:N	1:L:209:LYS:O	2.51	0.44
1:D:113:LYS:HA	1:D:113:LYS:HD3	1.76	0.44
1:C:166:GLN:HB3	1:C:171:ASN:HD22	1.83	0.44
2:F:4:DA:H2"	2:F:5:DC:H5'	2.00	0.43
1:C:191:ASP:OD2	1:C:235:ARG:NH2	2.42	0.43
1:L:142:ALA:HB3	1:L:162:ASN:HD21	1.83	0.43
3:A:9:DA:H2"	3:A:10:DG:H8	1.83	0.43
2:M:7:DT:H6	2:M:7:DT:H2'	1.58	0.43
1:L:313:THR:HG22	1:L:314:ARG:HH21	1.83	0.43
1:C:288:SER:HA	1:C:289:ASP:C	2.39	0.43
1:L:109:ARG:NH2	2:M:3:DG:OP2	2.51	0.42
1:L:134:SER:HB2	1:L:217:ILE:HD12	2.01	0.42
1:D:194:VAL:HG11	1:D:230:LYS:HE3	2.02	0.42
1:L:314:ARG:HG2	2:M:1:DC:C5	2.55	0.42
1:C:346:ARG:HH22	1:C:350:LYS:HB2	1.85	0.42
1:L:129:GLU:OE1	1:L:129:GLU:N	2.44	0.42
1:L:177:ARG:HH21	1:L:301:LEU:HB2	1.85	0.41
2:M:3:DG:H2"	2:M:4:DA:C8	2.55	0.41
1:D:95:LEU:HD13	1:D:195:VAL:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:220:ASP:O	1:D:222:VAL:HG23	2.21	0.41
1:L:91:PRO:HD2	1:L:164:VAL:HG12	2.03	0.41
1:D:146:ASN:OD1	1:D:183:ARG:NH1	2.49	0.41
1:C:73:GLU:H	1:C:73:GLU:CD	2.24	0.41
1:D:199:LEU:HG	1:D:229:TYR:HD2	1.85	0.40
1:L:181:TYR:CZ	1:L:185:LEU:HD21	2.56	0.40
3:A:6:DG:C8	3:A:7:DT:H72	2.57	0.40
1:L:171:ASN:HA	1:L:175:TRP:HB3	2.04	0.40
1:C:314:ARG:HH21	2:E:0:3DR:H1'2	1.85	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	C	288/311 (93%)	277 (96%)	11 (4%)	0	100 100
1	D	285/311 (92%)	270 (95%)	13 (5%)	2 (1%)	22 54
1	L	286/311 (92%)	274 (96%)	12 (4%)	0	100 100
All	All	859/933 (92%)	821 (96%)	36 (4%)	2 (0%)	47 78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	343	PHE
1	D	335	ALA

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	C	236/275 (86%)	230 (98%)	6 (2%)	47	78
1	D	246/275 (90%)	235 (96%)	11 (4%)	27	61
1	L	248/275 (90%)	239 (96%)	9 (4%)	35	69
All	All	730/825 (88%)	704 (96%)	26 (4%)	35	69

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	171	ASN
1	D	187	GLU
1	D	315	LYS
1	D	317	GLU
1	D	332	LEU
1	D	337	ILE
1	D	341	ASP
1	D	342	TYR
1	D	343	PHE
1	D	346	ARG
1	D	348	GLU
1	C	73	GLU
1	C	98	ILE
1	C	333	LYS
1	C	346	ARG
1	C	348	GLU
1	C	349	LYS
1	L	63	GLU
1	L	75	ARG
1	L	92	ARG
1	L	102	LYS
1	L	109	ARG
1	L	130	ASP
1	L	314	ARG
1	L	325	LEU
1	L	338	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	259	GLN
1	L	259	GLN
1	L	305	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\#\|Z\| > 2$
2	3DR	E	0	1,2	8,11,12	5.28	4 (50%)	9,14,17	1.11	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
2	3DR	E	0	1,2	-	1/3/15/16	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	0	3DR	O4'-C4'	-10.97	1.26	1.44
2	E	0	3DR	O4'-C1'	6.42	1.62	1.42
2	E	0	3DR	C2'-C1'	-6.32	1.34	1.51
2	E	0	3DR	C3'-C4'	3.16	1.61	1.53

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	0	3DR	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	0	3DR	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 5 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

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	C	290/311 (93%)	0.06	11 (3%)	40	36	33, 59, 140, 156	0
1	D	287/311 (92%)	-0.02	4 (1%)	75	75	34, 59, 111, 140	0
1	L	288/311 (92%)	0.91	44 (15%)	2	1	83, 114, 161, 189	0
2	E	8/10 (80%)	-0.17	1 (12%)	3	3	59, 89, 159, 187	0
2	F	9/10 (90%)	1.05	2 (22%)	0	0	63, 89, 227, 229	0
2	M	7/10 (70%)	1.23	1 (14%)	2	2	124, 155, 193, 202	0
3	A	9/11 (81%)	1.27	2 (22%)	0	0	80, 124, 206, 206	0
3	B	9/11 (81%)	1.07	2 (22%)	0	0	108, 138, 184, 209	0
3	K	7/11 (63%)	1.33	1 (14%)	2	2	152, 179, 193, 210	0
All	All	914/996 (91%)	0.35	68 (7%)	14	11	33, 80, 156, 229	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	112	CYS	11.0
1	L	323	LEU	7.9
1	L	322	VAL	7.8
1	L	320	ARG	7.5
1	L	113	LYS	7.1
1	L	261	GLN	6.7
3	A	2	DG	6.3
1	L	319	ALA	6.2
3	K	4	DA	6.1
1	L	321	SER	6.0
3	B	3	DC	5.7
1	L	249	PHE	4.8
1	C	319	ALA	4.5
1	L	259	GLN	4.3
3	B	11	DA	4.3

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Mol	Chain	Res	Type	RSRZ
2	F	7	DT	4.2
1	C	320	ARG	3.8
1	C	337	ILE	3.7
1	L	286	ARG	3.6
1	L	132	VAL	3.5
2	M	4	DA	3.4
1	L	340	ASP	3.3
1	L	311	LEU	3.3
1	L	346	ARG	3.3
1	D	319	ALA	3.3
1	L	258	PHE	3.2
1	L	316	ILE	3.1
1	L	133	GLY	3.1
1	L	265	PHE	3.1
1	D	111	HIS	3.0
1	L	264	GLU	3.0
1	C	316	ILE	2.8
1	C	113	LYS	2.8
3	A	4	DA	2.8
1	L	211	ILE	2.8
1	L	255	ALA	2.8
1	L	328	ILE	2.8
1	C	258	PHE	2.7
1	C	317	GLU	2.7
1	L	263	THR	2.7
1	L	325	LEU	2.7
1	L	348	GLU	2.7
1	L	256	ILE	2.6
1	L	304	PHE	2.5
1	C	323	LEU	2.5
1	L	342	TYR	2.5
1	L	140	ALA	2.4
1	L	324	ARG	2.4
1	L	111	HIS	2.3
1	L	114	PHE	2.3
1	L	327	LYS	2.3
1	L	108	ASP	2.3
1	L	343	PHE	2.3
1	L	107	ALA	2.3
1	L	92	ARG	2.3
1	L	207	ASP	2.2
1	D	106	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	L	171	ASN	2.2
1	C	345	SER	2.2
1	C	309	LEU	2.2
1	L	73	GLU	2.2
2	E	8	DG	2.1
1	L	314	ARG	2.1
1	D	108	ASP	2.0
2	F	8	DG	2.0
1	L	158	PHE	2.0
1	C	329	MET	2.0
1	L	160	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} 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
2	3DR	E	0	11/12	0.79	0.26	106,123,167,178	0

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, 95^{th} 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
4	MG	L	401	1/1	0.79	0.51	95,95,95,95	0
4	MG	E	101	1/1	0.88	0.33	53,53,53,53	0
4	MG	A	101	1/1	0.88	0.07	114,114,114,114	0
5	NA	B	101	1/1	0.88	0.11	148,148,148,148	0
4	MG	F	101	1/1	0.96	0.19	53,53,53,53	0

6.5 Other polymers (i)

There are no such residues in this entry.