



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 01:20 PM UTC

PDB ID : 2HHV / pdb_00002hhv
Title : T:O6-methyl-guanine in the polymerase-2 basepair position
Authors : Warren, J.J.; Forsberg, L.J.; Beese, L.S.
Deposited on : 2006-06-28
Resolution : 1.55 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

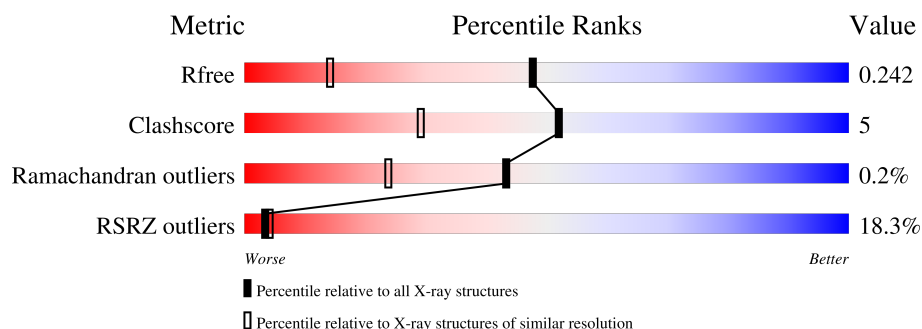
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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	2145 (1.56-1.56)
Clashscore	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
RSRZ outliers	180081	2146 (1.56-1.56)

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	B	12	67% 50% 50%
2	C	16	50% 50% 38% 6% 6%
3	A	580	16% 87% 13%
4	D	2	50% 50%
4	E	2	100%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 5909 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 DNA chain called 5'-D(*GP*CP*GP*AP*TP*CP*AP*GP*CP*TP*TP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	12	Total	C	N	O	P	0	0	0
			244	117	45	71	11			

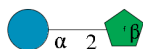
- Molecule 2 is a DNA chain called 5'-D(*GP*TP*AP*CP*(6OG)P*AP*GP*CP*TP*GP*AP*TP*CP*GP*CP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	15	Total	C	N	O	P	0	0	0
			306	147	58	87	14			

- Molecule 3 is a protein called DNA Polymerase I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	580	Total	C	N	O	S	0	0	0
			4650	2956	807	870	17			

- Molecule 4 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	D	2	Total	C	O	0	0	0
			23	12	11			
4	E	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

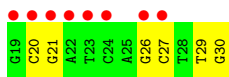
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	13	Total	O	0	0
			13	13		
7	C	35	Total	O	0	0
			35	35		
7	A	589	Total	O	0	0
			589	589		

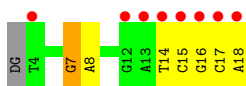
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

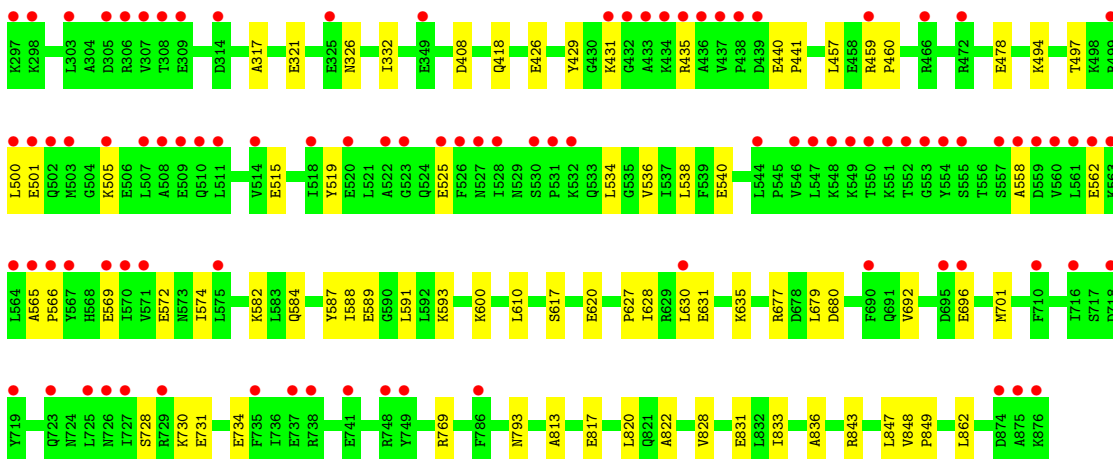
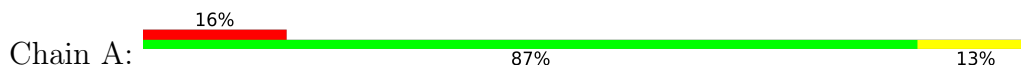
- Molecule 1: 5'-D(*GP*CP*GP*AP*TP*CP*AP*GP*CP*TP*TP*G)-3'



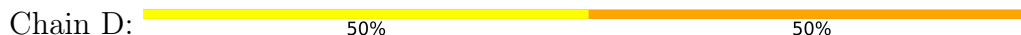
- Molecule 2: 5'-D(*GP*TP*AP*CP*(6OG)P*AP*GP*CP*TP*GP*AP*TP*CP*GP*CP*A)-3',



- Molecule 3: DNA Polymerase I



- Molecule 4: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose



GLC1
FRU2

- Molecule 4: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain E:

100%

GLC1
FRU2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.96Å 93.36Å 106.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.55 50.00 – 1.55	Depositor EDS
% Data completeness (in resolution range)	86.4 (50.00-1.55) 86.4 (50.00-1.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 1.55Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.216 , 0.239 0.218 , 0.242	Depositor DCC
R_{free} test set	5499 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	15.4	Xtriage
Anisotropy	0.429	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 42.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5909	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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: FRU, GLC, MG, SO4, 6OG

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	B	0.27	0/273	0.61	0/420
2	C	0.27	0/316	0.56	0/483
3	A	0.34	0/4734	0.82	12/6398 (0.2%)
All	All	0.33	0/5323	0.80	12/7301 (0.2%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	321	GLU	N-CA-C	7.21	120.28	109.25
3	A	680	ASP	N-CA-C	-6.87	99.25	109.15
3	A	317	ALA	N-CA-C	-5.79	99.85	109.46
3	A	769	ARG	N-CA-C	-5.62	102.58	110.50
3	A	862	LEU	N-CA-C	-5.52	100.70	109.59
3	A	332	ILE	N-CA-C	-5.51	99.95	107.99
3	A	538	LEU	N-CA-C	5.41	117.03	111.03
3	A	847	LEU	N-CA-C	5.27	116.83	111.14
3	A	617	SER	N-CA-C	-5.13	101.57	109.52
3	A	457	LEU	N-CA-C	5.07	119.32	113.18
3	A	478	GLU	N-CA-C	5.02	116.44	111.07
3	A	793	ASN	N-CA-C	5.00	117.84	111.69

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	B	244	0	137	7	0
2	C	306	0	172	9	0
3	A	4650	0	4695	39	0
4	D	23	0	21	1	0
4	E	23	0	21	0	0
5	A	25	0	0	0	0
6	A	1	0	0	0	0
7	A	589	0	0	1	0
7	B	13	0	0	1	0
7	C	35	0	0	0	0
All	All	5909	0	5046	53	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 (53) 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:C:15:DC:H2''	2:C:16:DG:H5'	1.66	0.76
3:A:631:GLU:OE2	3:A:635:LYS:HE3	1.88	0.73
3:A:692:VAL:HG21	3:A:701:MET:HE1	1.75	0.68
3:A:408:ASP:HB2	4:D:2:FRU:H11	1.79	0.65
3:A:500:LEU:HD11	3:A:591:LEU:HD23	1.79	0.65
3:A:813:ALA:O	3:A:817:GLU:HG3	1.98	0.64
3:A:534:LEU:HD11	3:A:574:ILE:HD13	1.82	0.61
3:A:426:GLU:OE2	3:A:431:LYS:HD2	2.02	0.59
3:A:558:ALA:O	3:A:562:GLU:HG3	2.02	0.59
3:A:326:ASN:HD22	3:A:620:GLU:CD	2.12	0.57
3:A:459:ARG:HB3	3:A:460:PRO:HD3	1.85	0.57
3:A:497:THR:O	3:A:501:GLU:HG3	2.05	0.56
2:C:16:DG:H2''	2:C:17:DC:H5'	1.88	0.54
2:C:14:DT:H2''	2:C:15:DC:C5	2.43	0.54
3:A:494:LYS:NZ	3:A:600:LYS:HB2	2.23	0.53
3:A:565:ALA:HB3	3:A:566:PRO:HD3	1.91	0.53
3:A:589:GLU:O	3:A:593:LYS:HG3	2.09	0.53
1:B:26:DG:H2'	1:B:27:DC:C6	2.45	0.52
3:A:494:LYS:HZ2	3:A:600:LYS:HB2	1.75	0.51
3:A:584:GLN:O	3:A:589:GLU:HG3	2.11	0.51
2:C:7:6OG:H3	2:C:8:DA:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:15:DC:H2''	2:C:16:DG:C5'	2.41	0.50
3:A:848:VAL:HB	3:A:849:PRO:HD3	1.94	0.47
3:A:500:LEU:HD22	3:A:588:ILE:HD13	1.95	0.47
3:A:833:ILE:N	3:A:833:ILE:HD12	2.30	0.47
3:A:630:LEU:HD12	3:A:630:LEU:N	2.29	0.47
3:A:519:TYR:CD1	3:A:525:GLU:HA	2.49	0.47
3:A:536:VAL:O	3:A:540:GLU:HB2	2.16	0.46
1:B:20:DC:H2'	1:B:21:DG:C8	2.50	0.46
3:A:440:GLU:N	3:A:441:PRO:HD2	2.31	0.45
3:A:610:LEU:HD23	3:A:610:LEU:C	2.42	0.45
3:A:459:ARG:O	3:A:459:ARG:HD3	2.17	0.45
3:A:418:GLN:HA	7:A:2575:HOH:O	2.16	0.45
3:A:501:GLU:O	3:A:505:LYS:HG3	2.16	0.45
1:B:29:DT:O4	2:C:7:6OG:H2	2.17	0.44
1:B:20:DC:H2''	1:B:21:DG:H5'	1.98	0.44
1:B:29:DT:H2'	1:B:30:DG:C8	2.53	0.44
3:A:429:TYR:O	3:A:435:ARG:HA	2.18	0.43
3:A:828:VAL:HB	3:A:831:GLU:CG	2.48	0.43
3:A:728:SER:OG	3:A:731:GLU:HG3	2.19	0.43
2:C:17:DC:H2''	2:C:18:DA:C8	2.53	0.43
1:B:21:DG:H2'	7:B:3330:HOH:O	2.19	0.42
3:A:587:TYR:CE2	3:A:627:PRO:HD3	2.54	0.42
3:A:730:LYS:O	3:A:734:GLU:HG3	2.20	0.42
3:A:677:ARG:HB2	3:A:679:LEU:HG	2.01	0.41
3:A:822:ALA:CB	3:A:836:ALA:HB2	2.51	0.41
3:A:569:GLU:O	3:A:572:GLU:HG2	2.21	0.41
1:B:27:DC:H2''	3:A:582:LYS:HG2	2.04	0.40
2:C:16:DG:H2'	2:C:17:DC:O4'	2.20	0.40
3:A:692:VAL:HB	3:A:696:GLU:HB2	2.02	0.40
3:A:820:LEU:HD21	3:A:843:ARG:CZ	2.51	0.40
2:C:16:DG:H2'	2:C:17:DC:C6	2.56	0.40
3:A:515:GLU:HG2	3:A:519:TYR:CE2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries

of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	A	578/580 (100%)	563 (97%)	14 (2%)	1 (0%)	43 24

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	628	ILE

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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	6OG	C	7	2,1	22,25,26	1.88	2 (9%)	31,36,39	2.77	6 (19%)

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	6OG	C	7	2,1	-	3/9/23/24	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	7	6OG	O6-C6	-6.28	1.25	1.35
2	C	7	6OG	C6-N1	5.60	1.40	1.32

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	7	6OG	C5-C6-N1	-9.00	111.46	123.49
2	C	7	6OG	O6-C6-C5	8.39	127.29	117.17
2	C	7	6OG	C2-N1-C6	6.51	125.01	115.96
2	C	7	6OG	C4-C5-C6	3.95	119.11	115.22
2	C	7	6OG	C6-C5-N7	-3.22	130.05	133.82
2	C	7	6OG	C-O6-C6	2.04	119.11	117.20

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	7	6OG	O4'-C1'-N9-C4
2	C	7	6OG	O4'-C1'-N9-C8
2	C	7	6OG	C2'-C1'-N9-C8

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	7	6OG	2	0

5.5 Carbohydrates

4 monosaccharides 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	$\# Z > 2$
4	GLC	D	1	4	11,11,12	3.25	4 (36%)	15,15,17	1.54	2 (13%)
4	FRU	D	2	4	11,12,12	1.39	1 (9%)	10,18,18	0.78	0
4	GLC	E	1	4	11,11,12	3.29	4 (36%)	15,15,17	1.52	2 (13%)
4	FRU	E	2	4	11,12,12	1.49	1 (9%)	10,18,18	0.73	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
4	GLC	D	1	4	-	0/2/19/22	0/1/1/1
4	FRU	D	2	4	-	0/5/24/24	0/1/1/1
4	GLC	E	1	4	-	0/2/19/22	0/1/1/1
4	FRU	E	2	4	-	0/5/24/24	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1	GLC	C2-C3	9.70	1.67	1.52
4	D	1	GLC	C2-C3	9.60	1.67	1.52
4	E	2	FRU	O2-C2	4.13	1.47	1.40
4	D	2	FRU	O2-C2	4.00	1.47	1.40
4	E	1	GLC	O5-C5	2.73	1.48	1.43
4	D	1	GLC	O5-C1	2.62	1.48	1.43
4	E	1	GLC	O5-C1	2.61	1.48	1.43
4	D	1	GLC	O5-C5	2.50	1.48	1.43
4	D	1	GLC	C4-C5	2.30	1.57	1.53
4	E	1	GLC	C4-C5	2.17	1.57	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1	GLC	C1-O5-C5	4.17	117.77	112.19
4	E	1	GLC	C1-O5-C5	4.02	117.58	112.19
4	E	1	GLC	C1-C2-C3	-2.86	105.49	109.64
4	D	1	GLC	C1-C2-C3	-2.80	105.57	109.64

There are no chirality outliers.

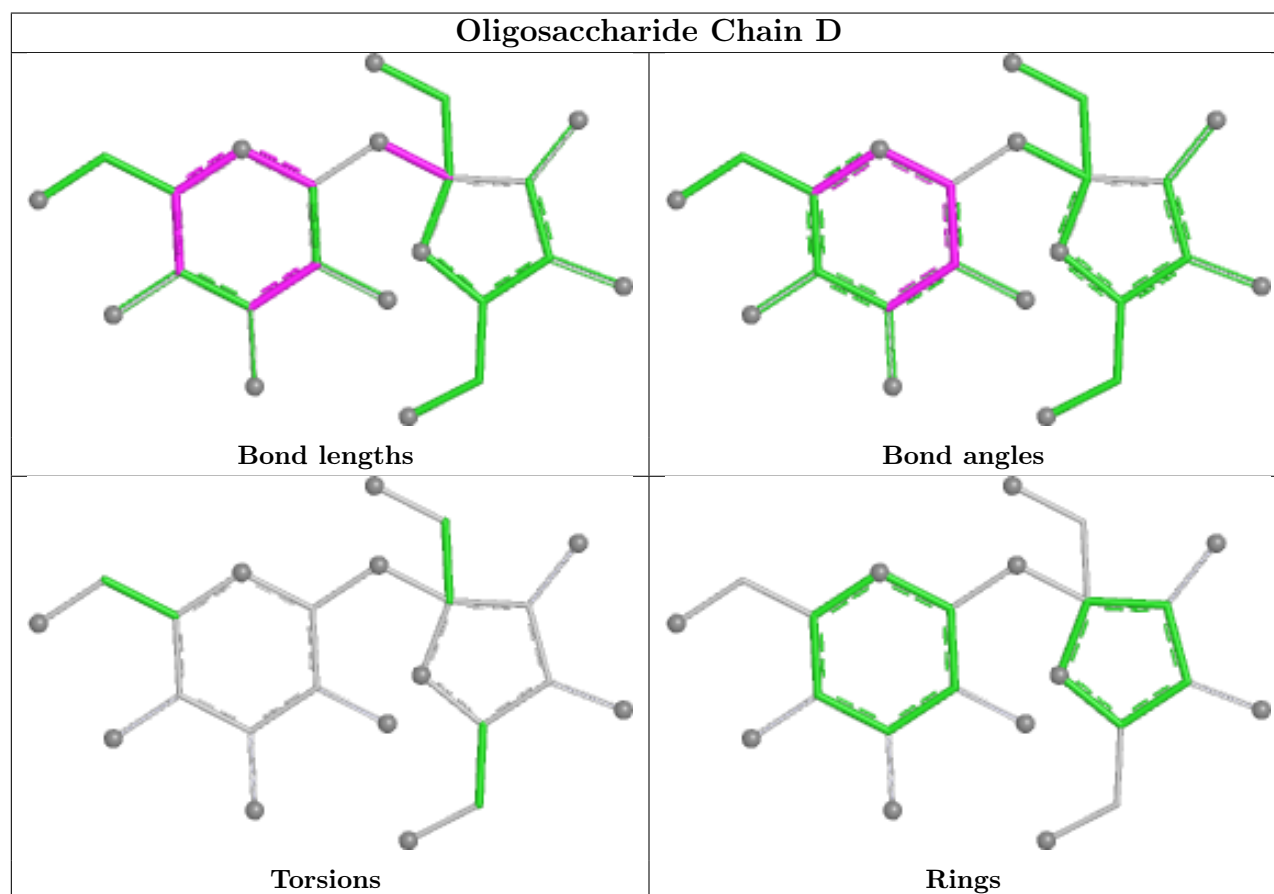
There are no torsion outliers.

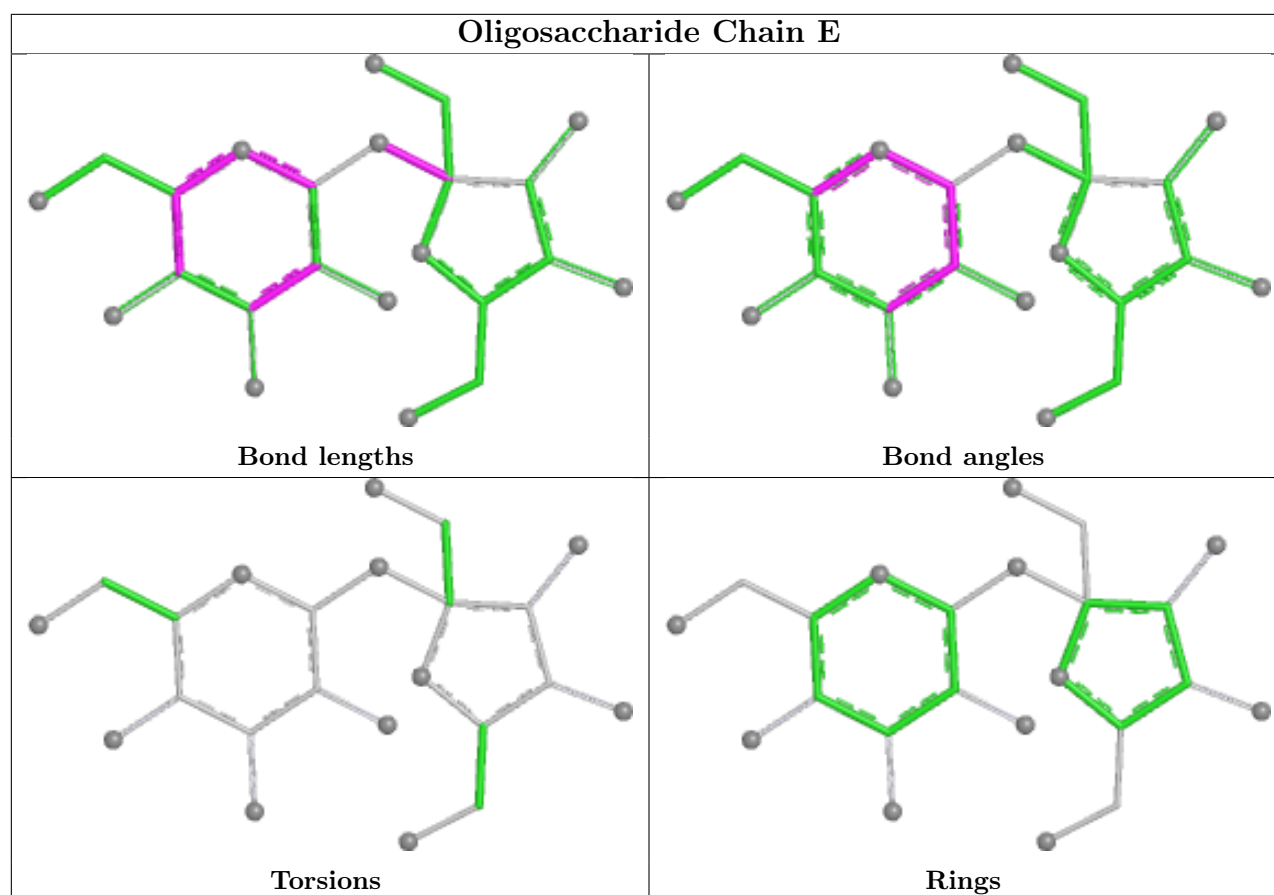
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	2	FRU	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	$\# Z > 2$
5	SO4	A	912	-	4,4,4	0.36	0	6,6,6	0.09	0
5	SO4	A	914	-	4,4,4	0.37	0	6,6,6	0.07	0
5	SO4	A	911	-	4,4,4	0.37	0	6,6,6	0.10	0
5	SO4	A	913	-	4,4,4	0.37	0	6,6,6	0.07	0
5	SO4	A	910	-	4,4,4	0.37	0	6,6,6	0.06	0

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, 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	B	12/12 (100%)	3.20	8 (66%) 0 0	22, 37, 75, 77	0
2	C	14/16 (87%)	2.78	8 (57%) 0 0	16, 33, 72, 74	0
3	A	580/580 (100%)	0.85	95 (16%) 4 5	8, 17, 35, 52	0
All	All	606/608 (99%)	0.94	111 (18%) 3 4	8, 18, 37, 77	0

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	552	THR	10.9
3	A	550	THR	7.1
1	B	21	DG	7.0
1	B	19	DG	6.6
3	A	549	LYS	6.6
2	C	16	DG	6.2
2	C	17	DC	6.1
3	A	559	ASP	6.1
2	C	18	DA	6.0
3	A	547	LEU	5.9
3	A	553	GLY	5.7
2	C	15	DC	5.4
2	C	4	DT	5.3
3	A	433	ALA	5.2
3	A	551	LYS	5.2
3	A	719	TYR	5.2
1	B	20	DC	5.1
3	A	695	ASP	4.6
3	A	531	PRO	4.6
1	B	22	DA	4.4
3	A	466	ARG	4.4
3	A	507	LEU	4.1
3	A	554	TYR	4.1

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Mol	Chain	Res	Type	RSRZ
3	A	558	ALA	4.0
3	A	526	PHE	3.9
3	A	876	LYS	3.8
3	A	548	LYS	3.7
3	A	520	GLU	3.7
3	A	431	LYS	3.7
3	A	459	ARG	3.6
3	A	502	GLN	3.6
2	C	14	DT	3.5
3	A	309	GLU	3.5
3	A	528	ILE	3.4
3	A	729	ARG	3.4
3	A	305	ASP	3.4
3	A	508	ALA	3.4
3	A	561	LEU	3.2
3	A	562	GLU	3.2
1	B	23	DT	3.1
3	A	439	ASP	3.1
3	A	509	GLU	3.1
3	A	349	GLU	3.0
3	A	530	SER	3.0
3	A	726	ASN	3.0
3	A	436	ALA	3.0
3	A	523	GLY	3.0
3	A	514	VAL	3.0
3	A	303	LEU	3.0
3	A	564	LEU	3.0
1	B	24	DC	2.9
3	A	716	ILE	2.9
3	A	434	LYS	2.9
3	A	741	GLU	2.9
3	A	505	LYS	2.9
3	A	297	LYS	2.8
3	A	565	ALA	2.8
3	A	532	LYS	2.8
3	A	432	GLY	2.8
3	A	786	PHE	2.8
3	A	567	TYR	2.7
3	A	546	VAL	2.7
3	A	560	VAL	2.7
3	A	738	ARG	2.7
2	C	13	DA	2.6

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Mol	Chain	Res	Type	RSRZ
3	A	563	LYS	2.6
3	A	306	ARG	2.6
3	A	522	ALA	2.6
3	A	325	GLU	2.5
3	A	710	PHE	2.5
3	A	503	MET	2.5
3	A	298	LYS	2.5
3	A	525	GLU	2.5
3	A	557	SER	2.5
3	A	500	LEU	2.4
1	B	27	DC	2.4
3	A	723	GLN	2.4
3	A	735	PHE	2.4
3	A	875	ALA	2.3
3	A	435	ARG	2.3
3	A	501	GLU	2.3
1	B	26	DG	2.3
3	A	511	LEU	2.3
3	A	727	ILE	2.3
3	A	737	GLU	2.3
3	A	566	PRO	2.2
3	A	718	ASP	2.2
3	A	748	ARG	2.2
3	A	571	VAL	2.2
3	A	438	PRO	2.2
3	A	314	ASP	2.2
3	A	690	PHE	2.2
3	A	630	LEU	2.1
3	A	725	LEU	2.1
3	A	518	ILE	2.1
3	A	308	THR	2.1
3	A	510	GLN	2.1
3	A	307	VAL	2.1
3	A	437	VAL	2.1
3	A	696	GLU	2.1
3	A	570	ILE	2.1
3	A	749	TYR	2.1
3	A	472	ARG	2.1
3	A	499	ARG	2.1
3	A	527	ASN	2.1
3	A	874	ASP	2.1
3	A	575	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
2	C	12	DG	2.0
3	A	569	GLU	2.0
3	A	544	LEU	2.0
3	A	555	SER	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, 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
2	6OG	C	7	23/24	0.95	0.08	17,18,19,22	0

6.3 Carbohydrates [i](#)

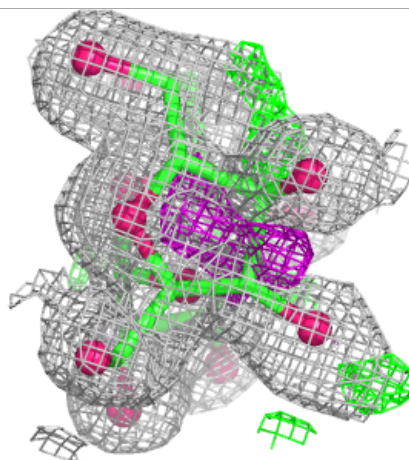
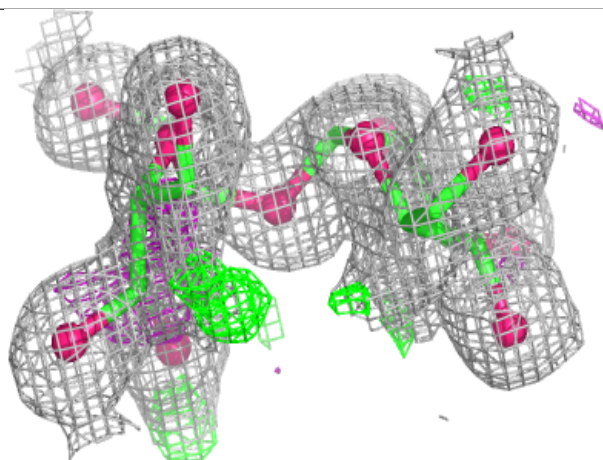
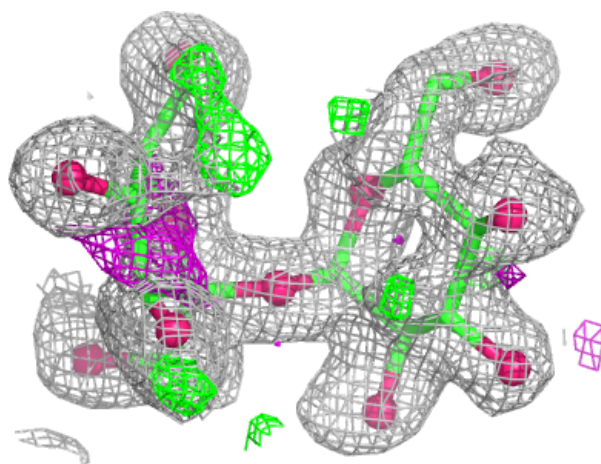
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

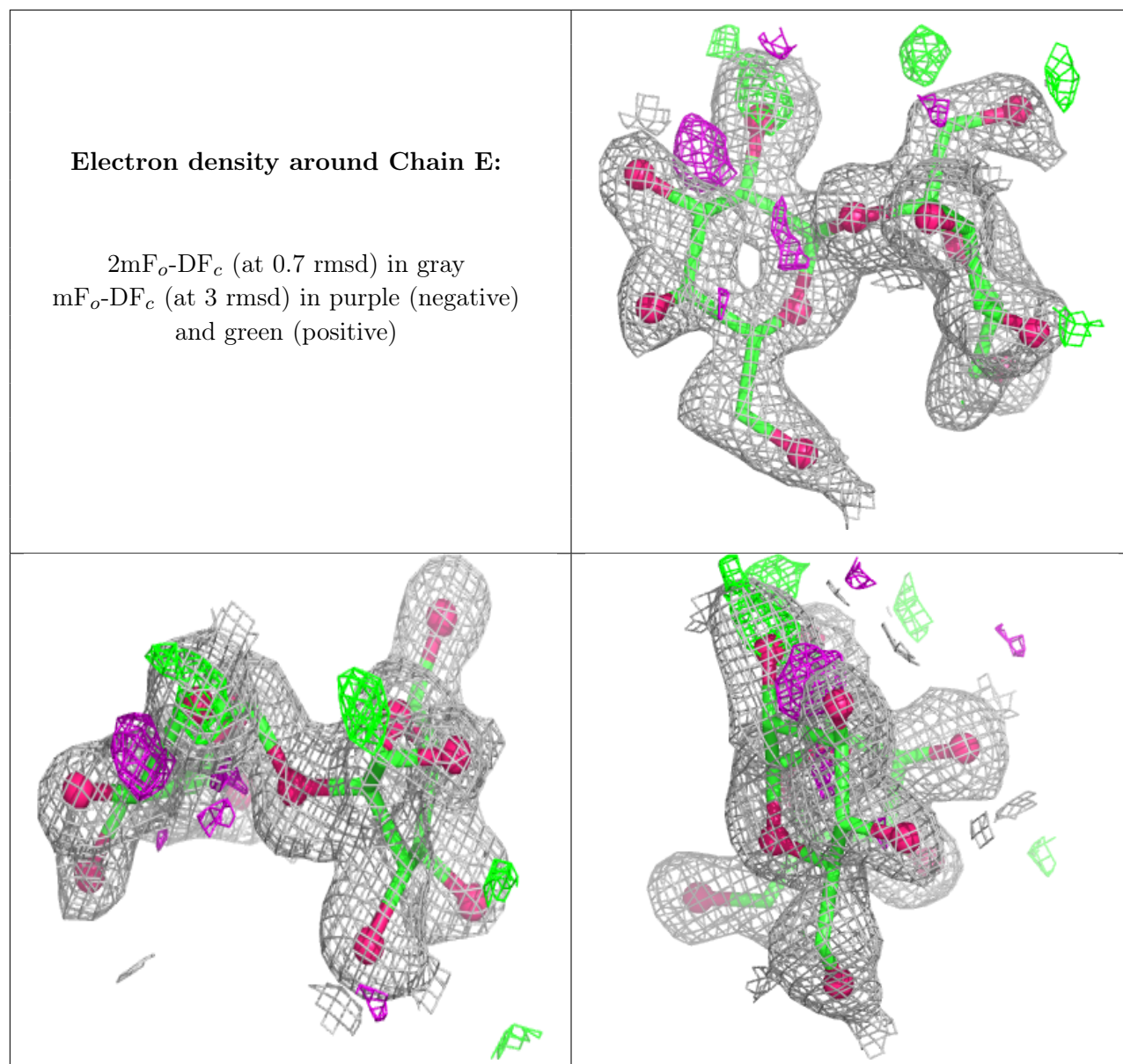
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GLC	E	1	11/12	0.78	0.17	35,36,36,37	0
4	FRU	E	2	12/12	0.84	0.12	36,37,37,37	0
4	GLC	D	1	11/12	0.85	0.13	29,30,31,32	0
4	FRU	D	2	12/12	0.85	0.14	27,29,30,30	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain D:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	SO4	A	914	5/5	0.54	0.21	92,92,92,92	0
5	SO4	A	913	5/5	0.78	0.18	58,58,58,58	0
5	SO4	A	912	5/5	0.90	0.15	42,43,43,43	0
5	SO4	A	910	5/5	0.93	0.10	45,46,46,46	0
5	SO4	A	911	5/5	0.94	0.10	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	MG	A	920	1/1	0.97	0.13	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.