



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:52 PM UTC

PDB ID : 2HHQ / pdb_00002hhq
Title : O6-methyl-guanine:T pair in the polymerase-10 basepair position
Authors : Warren, J.J.; Forsberg, L.J.; Beese, L.S.
Deposited on : 2006-06-28
Resolution : 1.80 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

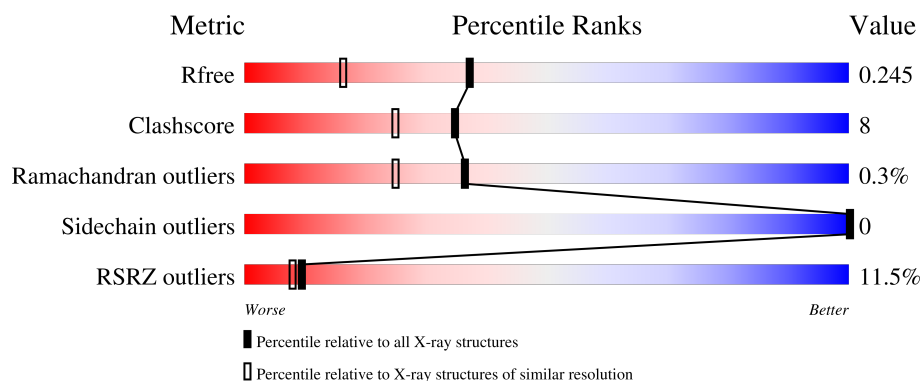
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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.



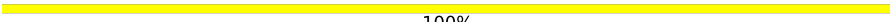
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	13	31% 31% 62% 8%
2	C	15	40% 33% 67%
3	A	580	10% 84% 15%
4	D	2	50% 50%
4	E	2	100%

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Mol	Chain	Length	Quality of chain
4	F	2	 100%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5844 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(*CP*AP*TP*(6OG)P*CP*GP*AP*GP*TP*CP*AP*GP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	13	Total	C	N	O	P	0	0	0
			268	128	53	75	12			

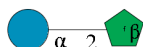
- Molecule 2 is a DNA chain called 5'-D(*GP*CP*CP*TP*GP*AP*CP*TP*CP*GP*TP*AP*TP*GP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	15	Total	C	N	O	P	0	0	0
			304	146	55	89	14			

- Molecule 3 is a protein called DNA polymerase I.

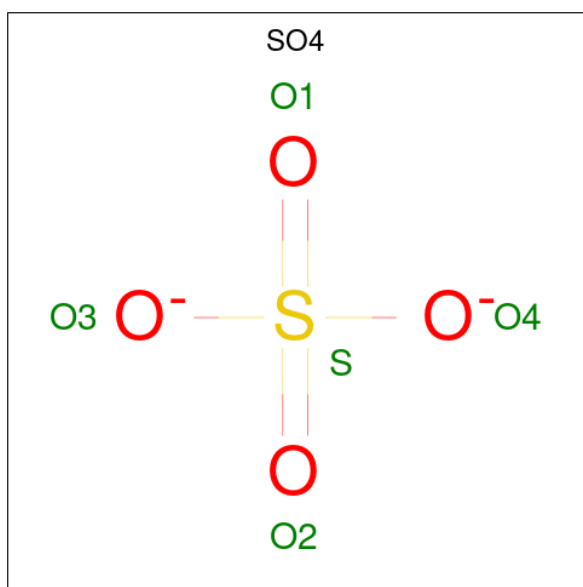
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	580	Total	C	N	O	S	0	0	0
			4650	2956	807	870	17			

- 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			
4	F	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		

- 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		

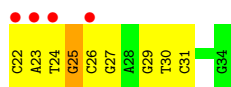
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	23	Total	O	0	0
			23	23		
7	C	28	Total	O	0	0
			28	28		
7	A	486	Total	O	0	0
			486	486		

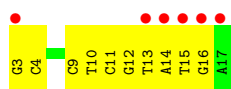
3 Residue-property plots

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.

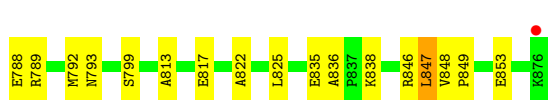
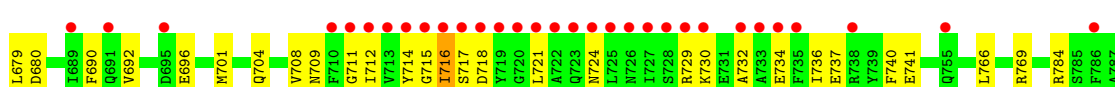
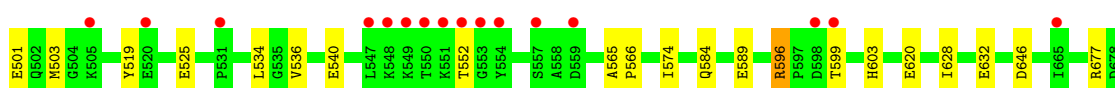
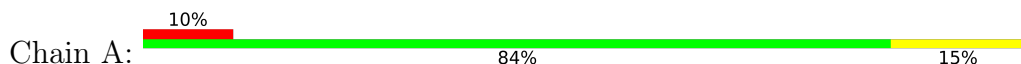
- Molecule 1: 5'-D(*CP*AP*TP*(6OG)P*CP*GP*AP*GP*TP*CP*AP*GP*G)-3'



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



- Molecule 3: DNA polymerase I



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



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

Chain E:  100%

GLC1
FRU2

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

Chain F:  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	86.79Å 93.27Å 106.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.80 50.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (50.00-1.80) 100.0 (50.00-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 1.54Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.212 , 0.244 0.214 , 0.245	Depositor DCC
R_{free} test set	6442 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	14.8	Xtriage
Anisotropy	0.630	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5844	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% 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: MG, FRU, GLC, 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	0.28	0/274	0.62	0/419
2	C	0.29	0/340	0.67	0/523
3	A	0.35	0/4734	0.85	12/6398 (0.2%)
All	All	0.34	0/5348	0.83	12/7340 (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	680	ASP	N-CA-C	-6.96	99.13	109.15
3	A	475	VAL	N-CA-C	6.80	117.59	110.72
3	A	321	GLU	N-CA-C	6.37	119.89	109.76
3	A	317	ALA	N-CA-C	-5.75	99.91	109.46
3	A	478	GLU	N-CA-C	5.63	117.10	111.07
3	A	769	ARG	N-CA-C	-5.61	102.58	110.50
3	A	847	LEU	N-CA-C	5.54	117.13	111.14
3	A	793	ASN	N-CA-C	5.53	118.49	111.69
3	A	620	GLU	CB-CA-C	-5.40	107.36	111.20
3	A	596	ARG	CA-C-N	5.26	125.58	119.47
3	A	596	ARG	C-N-CA	5.26	125.58	119.47
3	A	332	ILE	N-CA-C	-5.21	100.39	107.99

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	B	268	0	149	12	0
2	C	304	0	171	19	0
3	A	4650	0	4695	58	0
4	D	23	0	21	1	0
4	E	23	0	21	0	0
4	F	23	0	21	0	0
5	A	15	0	0	0	0
6	A	1	0	0	0	0
7	A	486	0	0	7	0
7	B	23	0	0	0	0
7	C	28	0	0	0	0
All	All	5844	0	5078	78	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 8.

All (78) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:692:VAL:HG21	3:A:701:MET:HE1	1.60	0.83
3:A:499:ARG:HG2	3:A:503:MET:HE2	1.61	0.82
2:C:10:DT:H2''	2:C:11:DC:H5'	1.68	0.75
3:A:534:LEU:HD11	3:A:574:ILE:HD13	1.78	0.66
3:A:813:ALA:O	3:A:817:GLU:HG3	1.96	0.64
2:C:10:DT:H2''	2:C:11:DC:C5'	2.28	0.64
3:A:847:LEU:C	3:A:847:LEU:HD23	2.24	0.61
2:C:13:DT:H2'	2:C:14:DA:C8	2.36	0.60
3:A:730:LYS:O	3:A:734:GLU:HG3	2.01	0.59
2:C:3:DG:C6	3:A:711:GLY:HA3	2.37	0.59
1:B:23:DA:H61	2:C:14:DA:H61	1.50	0.59
3:A:500:LEU:HA	3:A:503:MET:HE3	1.85	0.58
3:A:784:ARG:O	3:A:788:GLU:HG3	2.03	0.58
3:A:464:GLU:O	3:A:467:ARG:HG2	2.04	0.57
1:B:29:DG:OP1	3:A:552:THR:HG22	2.03	0.57
1:B:26:DC:H2''	1:B:27:DG:H5'	1.87	0.56
3:A:718:ASP:HB2	3:A:729:ARG:HG2	1.87	0.56
3:A:692:VAL:HB	3:A:696:GLU:HB2	1.88	0.55
3:A:766:LEU:HD13	3:A:799:SER:OG	2.06	0.55
2:C:9:DC:H2'	2:C:10:DT:H72	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:485:LEU:O	3:A:489:GLU:HG3	2.07	0.55
2:C:15:DT:H2''	2:C:16:DG:C8	2.41	0.55
3:A:709:ASN:O	3:A:712:ILE:HG22	2.07	0.54
1:B:30:DT:H2''	1:B:31:DC:H5'	1.89	0.54
3:A:690:PHE:CD2	3:A:701:MET:HE3	2.43	0.53
3:A:646:ASP:HB3	3:A:838:LYS:HZ3	1.74	0.53
3:A:789:ARG:HA	3:A:792:MET:HE3	1.89	0.53
3:A:497:THR:O	3:A:501:GLU:HG3	2.10	0.52
1:B:23:DA:N6	2:C:14:DA:H61	2.07	0.52
2:C:3:DG:C8	3:A:717:SER:HB3	2.44	0.52
1:B:25:6OG:H3	2:C:12:DG:C6	2.45	0.52
1:B:30:DT:H2''	1:B:31:DC:C5'	2.39	0.52
3:A:632:GLU:HG3	7:A:3111:HOH:O	2.09	0.51
3:A:825:LEU:HD11	3:A:835:GLU:HB3	1.93	0.51
3:A:408:ASP:HB2	4:D:2:FRU:H11	1.91	0.51
3:A:692:VAL:CG2	3:A:701:MET:HE1	2.35	0.51
2:C:3:DG:H2'	2:C:3:DG:N3	2.26	0.50
3:A:677:ARG:HB2	3:A:679:LEU:HG	1.93	0.50
2:C:10:DT:H2'	2:C:11:DC:C6	2.48	0.49
3:A:646:ASP:HB3	3:A:838:LYS:NZ	2.26	0.49
3:A:847:LEU:HD23	3:A:847:LEU:O	2.12	0.49
3:A:716:ILE:HG21	3:A:740:PHE:CZ	2.47	0.49
3:A:690:PHE:CB	3:A:701:MET:HE3	2.43	0.48
3:A:536:VAL:O	3:A:540:GLU:HB2	2.14	0.48
2:C:4:DC:O4'	3:A:714:TYR:HB3	2.13	0.48
1:B:26:DC:H2'	1:B:27:DG:C8	2.49	0.47
3:A:308:THR:OG1	3:A:311:MET:HE3	2.14	0.47
3:A:848:VAL:HB	3:A:849:PRO:HD3	1.95	0.47
1:B:23:DA:H2''	1:B:24:DT:H5'	1.97	0.47
3:A:690:PHE:CG	3:A:701:MET:HE3	2.49	0.47
3:A:565:ALA:HB3	3:A:566:PRO:HD3	1.98	0.46
3:A:704:GLN:O	3:A:708:VAL:HG23	2.16	0.45
3:A:847:LEU:C	3:A:847:LEU:CD2	2.89	0.44
3:A:440:GLU:HB3	3:A:441:PRO:HD3	2.00	0.43
3:A:737:GLU:O	3:A:741:GLU:HG3	2.19	0.43
2:C:3:DG:N2	3:A:724:ASN:OD1	2.50	0.43
3:A:584:GLN:O	3:A:589:GLU:HG3	2.18	0.43
3:A:846:ARG:HG2	7:A:3423:HOH:O	2.19	0.43
1:B:22:DC:H42	2:C:16:DG:N2	2.17	0.43
3:A:596:ARG:HG3	3:A:603:HIS:HD2	1.84	0.42
3:A:721:LEU:HD22	3:A:736:ILE:HD11	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:459:ARG:HB3	3:A:460:PRO:CD	2.49	0.42
3:A:388:CYS:SG	7:A:3347:HOH:O	2.44	0.42
3:A:519:TYR:CD1	3:A:525:GLU:HA	2.54	0.42
1:B:23:DA:H61	2:C:14:DA:N6	2.17	0.42
1:B:22:DC:H42	2:C:16:DG:H22	1.68	0.41
2:C:3:DG:N3	2:C:3:DG:H5''	2.35	0.41
3:A:418:GLN:HA	7:A:2858:HOH:O	2.18	0.41
3:A:732:ALA:O	3:A:736:ILE:HG12	2.20	0.41
3:A:849:PRO:O	3:A:853:GLU:HG3	2.20	0.41
2:C:9:DC:C2'	2:C:10:DT:H72	2.49	0.41
3:A:467:ARG:HD2	7:A:3475:HOH:O	2.20	0.41
3:A:822:ALA:CB	3:A:836:ALA:HB2	2.51	0.40
3:A:483:SER:O	3:A:487:GLU:HG3	2.22	0.40
3:A:599:THR:HG21	7:A:2328:HOH:O	2.22	0.40
3:A:459:ARG:HA	3:A:459:ARG:NE	2.36	0.40
3:A:457:LEU:O	3:A:460:PRO:HG2	2.21	0.40
3:A:715:GLY:HA2	7:A:3198:HOH:O	2.22	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%)	559 (97%)	17 (3%)	2 (0%)	36 25

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	628	ILE
3	A	716	ILE

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	
3	A	495/497 (100%)	495 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	529	ASN
3	A	624	GLN
3	A	704	GLN
3	A	755	GLN
3	A	768	HIS

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$
1	6OG	B	25	1,2	22,25,26	1.82	2 (9%)	31,36,39	2.81	5 (16%)

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
1	6OG	B	25	1,2	-	0/9/23/24	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	25	6OG	O6-C6	-6.07	1.25	1.35
1	B	25	6OG	C6-N1	5.39	1.40	1.32

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	25	6OG	C5-C6-N1	-9.14	111.27	123.49
1	B	25	6OG	O6-C6-C5	8.92	127.93	117.17
1	B	25	6OG	C2-N1-C6	6.64	125.20	115.96
1	B	25	6OG	C4-C5-C6	3.71	118.87	115.22
1	B	25	6OG	C6-C5-N7	-2.99	130.31	133.82

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
1	B	25	6OG	1	0

5.5 Carbohydrates

6 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	3.26	4 (36%)	15,15,17	1.50	2 (13%)
4	FRU	D	2	4	11,12,12	1.41	1 (9%)	10,18,18	0.80	0
4	GLC	E	1	4	11,11,12	3.22	4 (36%)	15,15,17	1.52	3 (20%)
4	FRU	E	2	4	11,12,12	1.51	1 (9%)	10,18,18	0.75	0
4	GLC	F	1	4	11,11,12	3.29	4 (36%)	15,15,17	1.52	2 (13%)
4	FRU	F	2	4	11,12,12	1.52	1 (9%)	10,18,18	0.70	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	-	1/5/24/24	0/1/1/1
4	GLC	F	1	4	-	1/2/19/22	0/1/1/1
4	FRU	F	2	4	-	0/5/24/24	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	1	GLC	C2-C3	9.72	1.67	1.52
4	D	1	GLC	C2-C3	9.47	1.67	1.52
4	E	1	GLC	C2-C3	9.41	1.66	1.52
4	F	2	FRU	O2-C2	4.18	1.48	1.40
4	E	2	FRU	O2-C2	4.18	1.48	1.40
4	D	2	FRU	O2-C2	4.04	1.47	1.40
4	D	1	GLC	O5-C1	2.89	1.48	1.43
4	F	1	GLC	O5-C5	2.78	1.48	1.43
4	E	1	GLC	O5-C5	2.70	1.48	1.43
4	D	1	GLC	O5-C5	2.67	1.48	1.43
4	E	1	GLC	O5-C1	2.58	1.48	1.43
4	F	1	GLC	O5-C1	2.56	1.48	1.43
4	D	1	GLC	C4-C5	2.46	1.58	1.53
4	E	1	GLC	C4-C5	2.23	1.57	1.53
4	F	1	GLC	C4-C5	2.07	1.57	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	1	GLC	C1-O5-C5	4.09	117.67	112.19
4	E	1	GLC	C1-O5-C5	4.06	117.62	112.19
4	D	1	GLC	C1-O5-C5	4.02	117.57	112.19
4	E	1	GLC	C1-C2-C3	-2.80	105.56	109.64
4	F	1	GLC	C1-C2-C3	-2.78	105.60	109.64
4	D	1	GLC	C1-C2-C3	-2.62	105.83	109.64
4	E	1	GLC	O3-C3-C2	-2.07	105.83	110.05

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	2	FRU	O1-C1-C2-O2
4	F	1	GLC	C4-C5-C6-O6

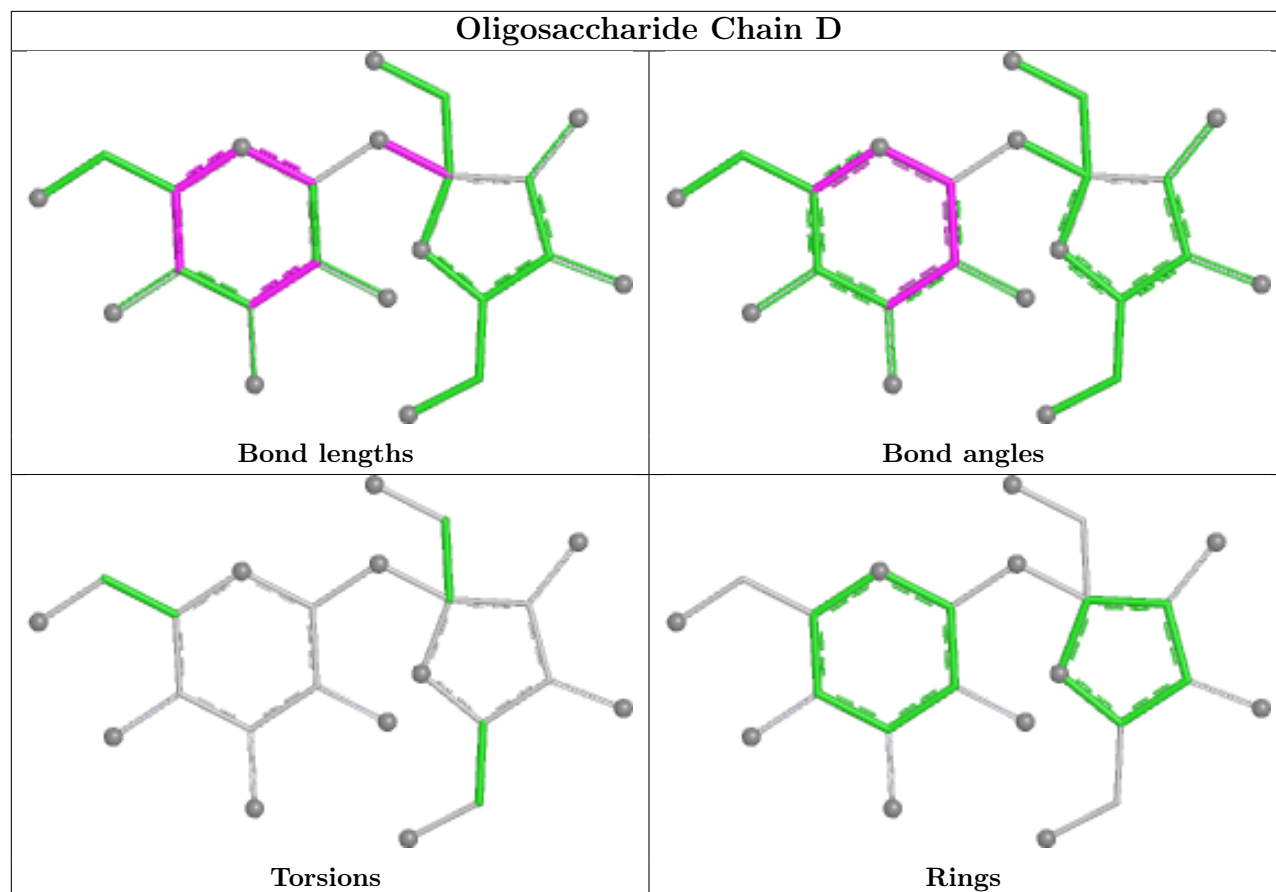
There are no ring outliers.

1 monomer is involved in 1 short contact:

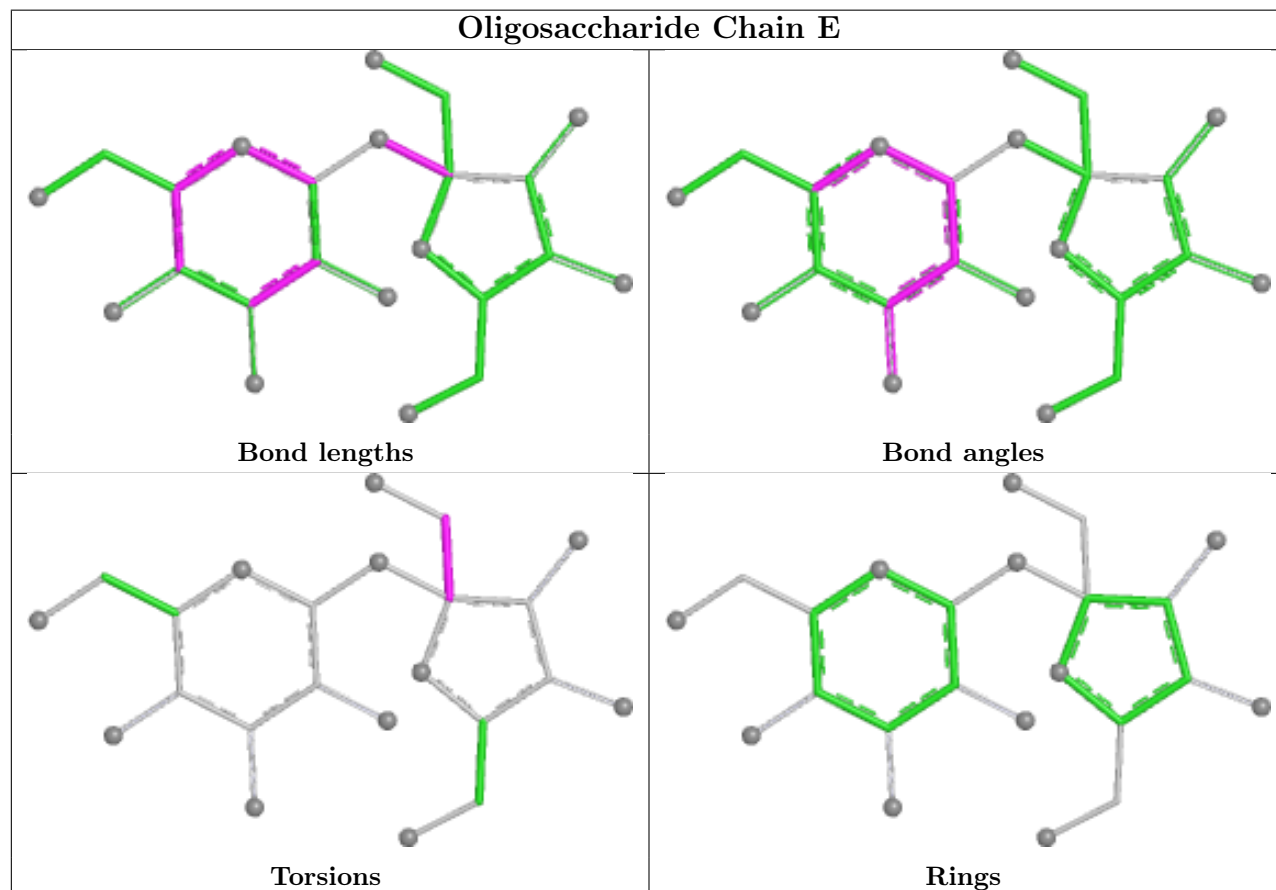
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	2	FRU	1	0

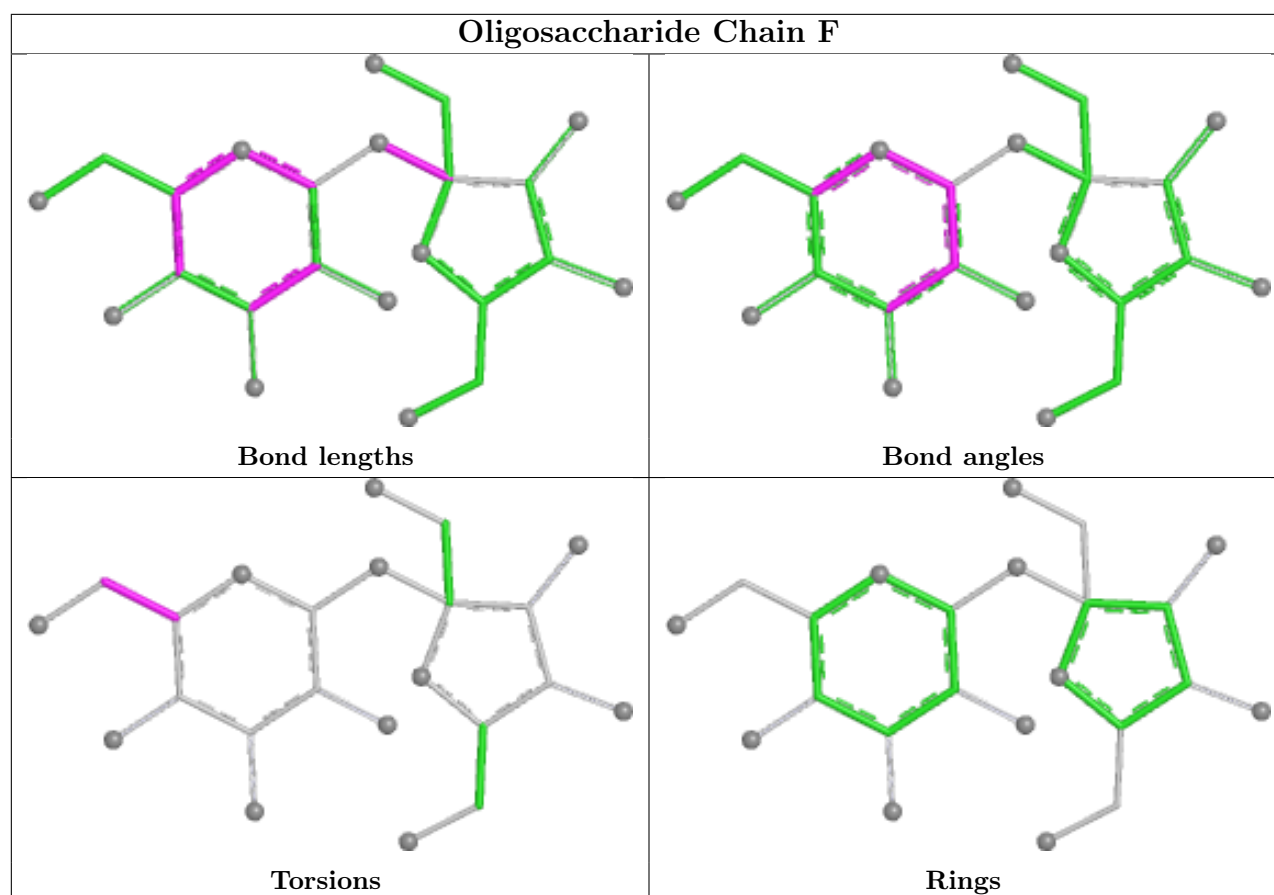
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

Oligosaccharide Chain D



Oligosaccharide Chain E





5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is 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	$\# Z > 2$
5	SO4	A	906	-	4,4,4	0.38	0	6,6,6	0.06	0
5	SO4	A	905	-	4,4,4	0.37	0	6,6,6	0.08	0
5	SO4	A	904	-	4,4,4	0.36	0	6,6,6	0.12	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	12/13 (92%)	1.06	4 (33%)  	19, 26, 81, 83	0
2	C	15/15 (100%)	1.78	6 (40%)  	19, 29, 83, 83	0
3	A	580/580 (100%)	0.40	60 (10%)  	10, 20, 40, 57	0
All	All	607/608 (99%)	0.45	70 (11%)  	10, 20, 45, 83	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	716	ILE	10.1
3	A	714	TYR	7.4
3	A	433	ALA	6.4
3	A	710	PHE	6.0
3	A	551	LYS	5.7
3	A	552	THR	5.5
2	C	3	DG	5.1
3	A	719	TYR	4.9
3	A	735	PHE	4.9
3	A	549	LYS	4.9
3	A	297	LYS	4.5
2	C	17	DA	4.3
3	A	713	VAL	4.3
2	C	16	DG	4.1
1	B	22	DC	4.1
3	A	550	THR	4.0
3	A	715	GLY	3.9
2	C	14	DA	3.9
3	A	431	LYS	3.6
2	C	13	DT	3.5
3	A	727	ILE	3.5
3	A	712	ILE	3.4
3	A	718	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
3	A	729	ARG	3.3
1	B	24	DT	3.3
3	A	722	ALA	3.2
1	B	23	DA	3.2
3	A	876	LYS	3.1
3	A	432	GLY	3.1
3	A	726	ASN	3.0
3	A	723	GLN	2.9
2	C	15	DT	2.9
3	A	298	LYS	2.9
3	A	717	SER	2.9
3	A	554	TYR	2.8
3	A	732	ALA	2.8
3	A	305	ASP	2.8
3	A	553	GLY	2.7
3	A	599	THR	2.7
1	B	26	DC	2.6
3	A	733	ALA	2.6
3	A	459	ARG	2.5
3	A	755	GLN	2.5
3	A	738	ARG	2.5
3	A	598	ASP	2.5
3	A	520	GLU	2.4
3	A	559	ASP	2.4
3	A	665	ILE	2.4
3	A	724	ASN	2.4
3	A	720	GLY	2.4
3	A	548	LYS	2.4
3	A	730	LYS	2.4
3	A	725	LEU	2.3
3	A	711	GLY	2.3
3	A	531	PRO	2.2
3	A	306	ARG	2.2
3	A	689	ILE	2.2
3	A	786	PHE	2.1
3	A	691	GLN	2.1
3	A	728	SER	2.1
3	A	547	LEU	2.1
3	A	734	GLU	2.1
3	A	505	LYS	2.1
3	A	721	LEU	2.1
3	A	557	SER	2.1

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Mol	Chain	Res	Type	RSRZ
3	A	304	ALA	2.1
3	A	466	ARG	2.1
3	A	350	THR	2.0
3	A	695	ASP	2.0
3	A	437	VAL	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
1	6OG	B	25	23/24	0.60	0.22	57,63,76,76	0

6.3 Carbohydrates [i](#)

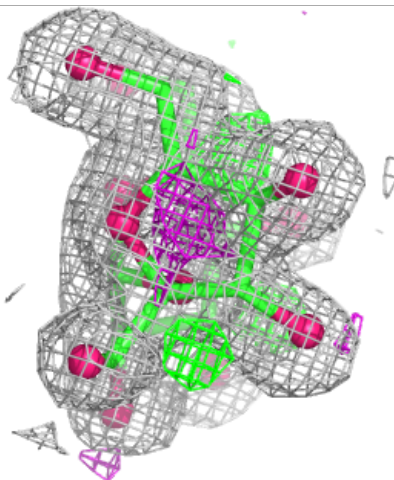
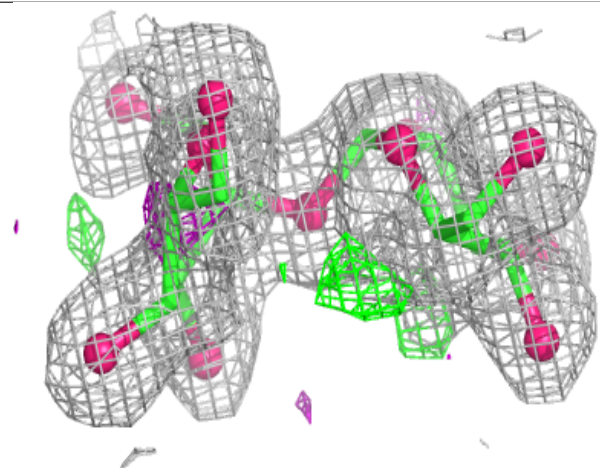
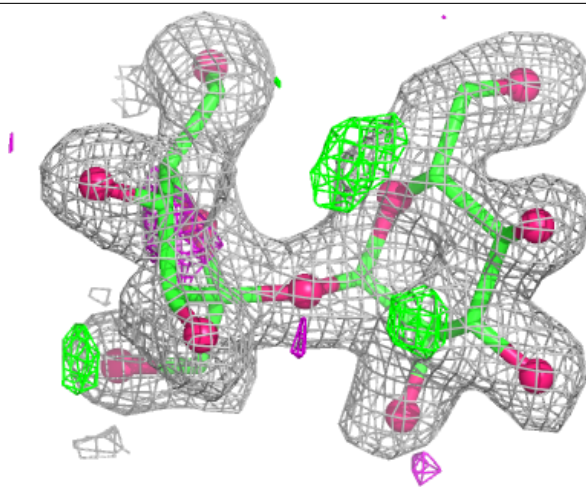
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	0.73	0.21	48,50,52,53	0
4	FRU	E	2	12/12	0.83	0.15	51,53,55,55	0
4	GLC	F	1	11/12	0.83	0.12	29,34,36,37	0
4	GLC	D	1	11/12	0.84	0.11	27,32,33,34	0
4	FRU	F	2	12/12	0.85	0.13	34,37,40,41	0
4	FRU	D	2	12/12	0.87	0.12	21,28,30,30	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.

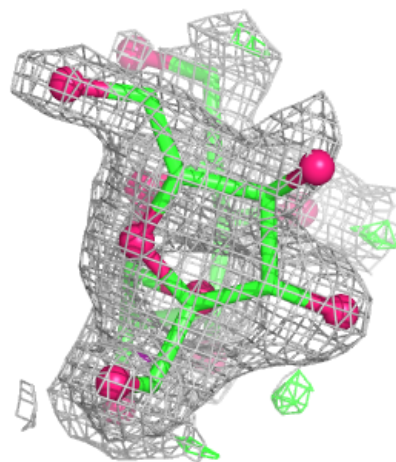
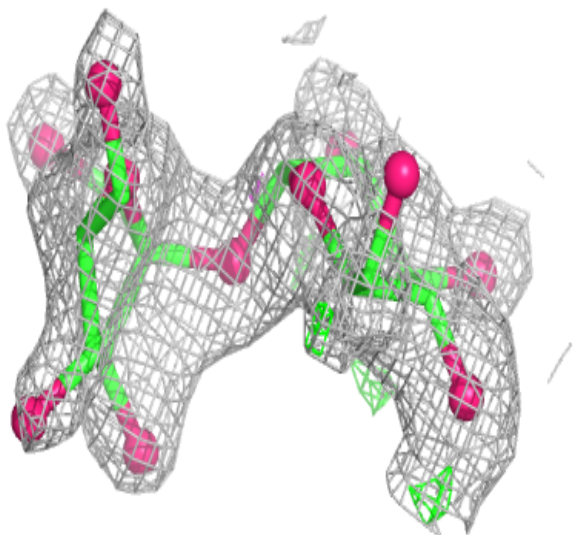
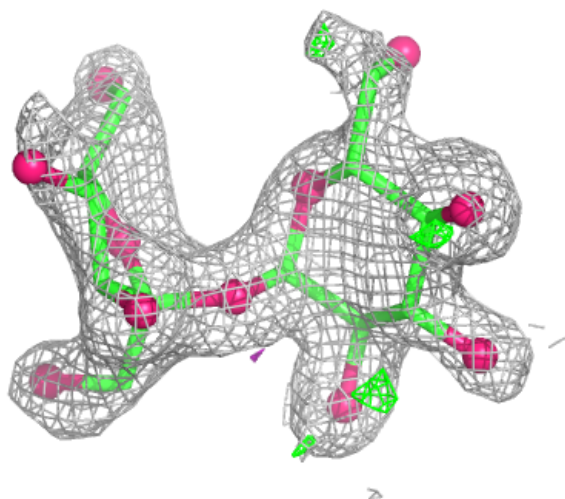
Electron density around Chain D:

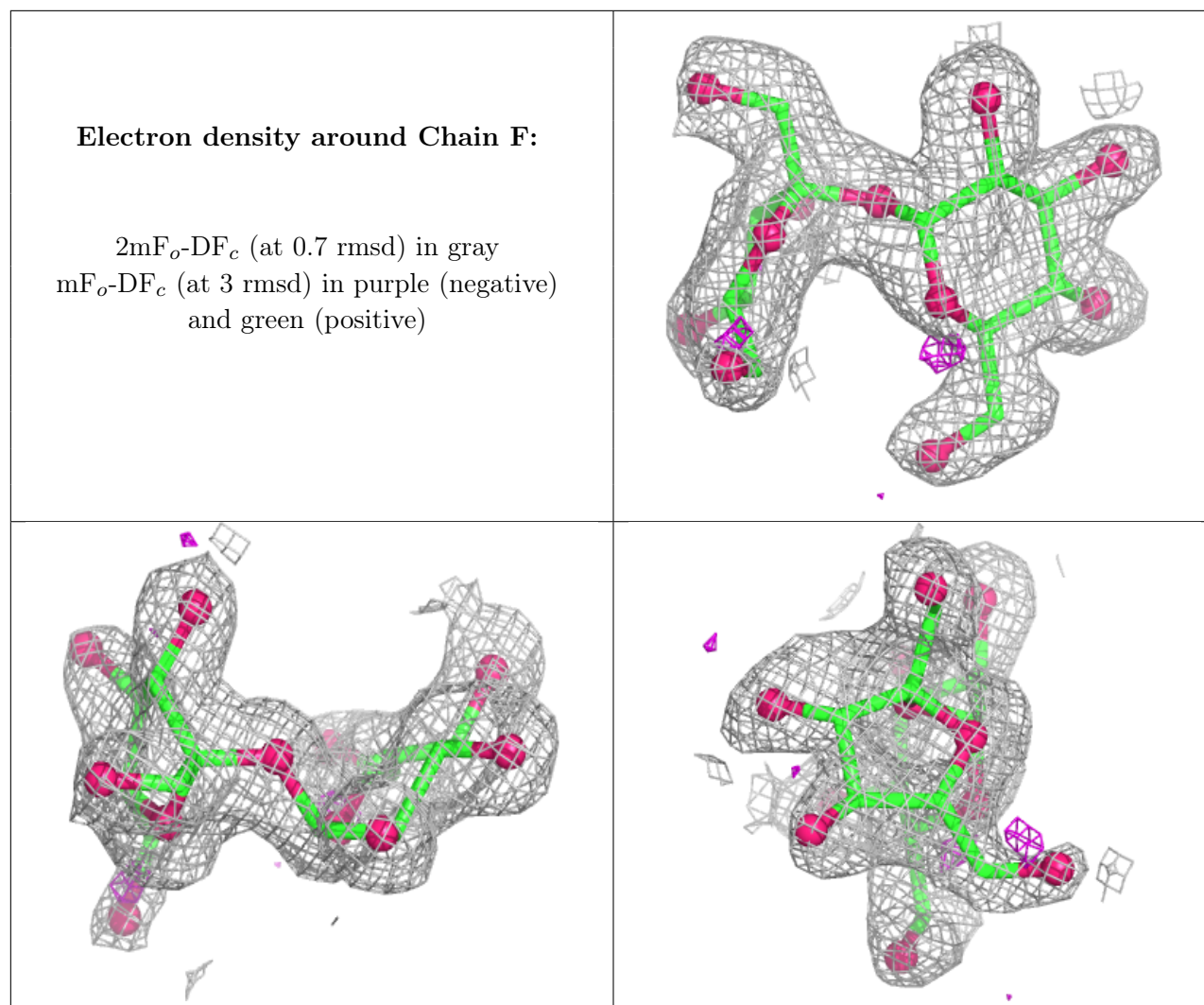
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain E:

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





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	SO4	A	905	5/5	0.86	0.12	51,51,52,52	0
5	SO4	A	904	5/5	0.88	0.13	39,40,41,42	0
6	MG	A	920	1/1	0.94	0.14	35,35,35,35	0
5	SO4	A	906	5/5	0.97	0.08	29,29,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.