



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:15 AM UTC

PDB ID : 4DO5 / pdb_00004do5
Title : Pharmacological chaperones for human alpha-N-acetylgalactosaminidase
Authors : Clark, N.E.; Garman, S.C.
Deposited on : 2012-02-09
Resolution : 1.51 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

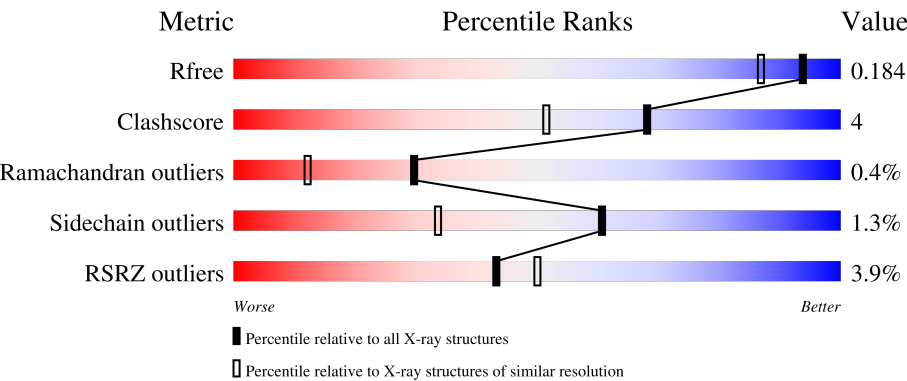
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.51 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	5890 (1.54-1.50)
Clashscore	190562	6116 (1.54-1.50)
Ramachandran outliers	187476	6002 (1.54-1.50)
Sidechain outliers	187428	5999 (1.54-1.50)
RSRZ outliers	180081	5891 (1.54-1.50)

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	A	400	2% 91% 6%
1	B	400	6% 94% 5%
2	C	2	50% 50%
2	E	2	100%
3	D	5	60% 40%

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Mol	Chain	Length	Quality of chain
3	F	5	20% 80%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7745 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 Alpha-N-acetylgalactosaminidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	0	9	0
			3152	2012	533	578	29			
1	B	400	Total	C	N	O	S	0	5	0
			3233	2060	551	592	30			

There are 14 discrepancies between the modelled and reference sequences:

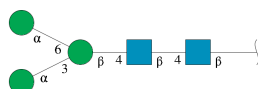
Chain	Residue	Modelled	Actual	Comment	Reference
A	201	GLN	ASN	engineered mutation	UNP P17050
A	412	HIS	-	expression tag	UNP P17050
A	413	HIS	-	expression tag	UNP P17050
A	414	HIS	-	expression tag	UNP P17050
A	415	HIS	-	expression tag	UNP P17050
A	416	HIS	-	expression tag	UNP P17050
A	417	HIS	-	expression tag	UNP P17050
B	201	GLN	ASN	engineered mutation	UNP P17050
B	412	HIS	-	expression tag	UNP P17050
B	413	HIS	-	expression tag	UNP P17050
B	414	HIS	-	expression tag	UNP P17050
B	415	HIS	-	expression tag	UNP P17050
B	416	HIS	-	expression tag	UNP P17050
B	417	HIS	-	expression tag	UNP P17050

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



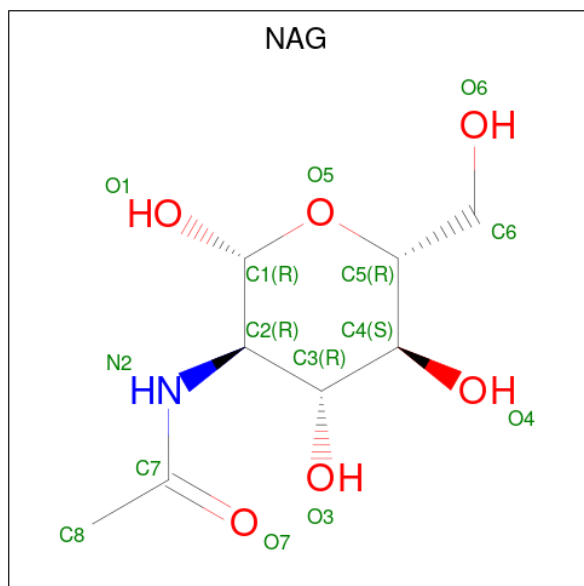
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



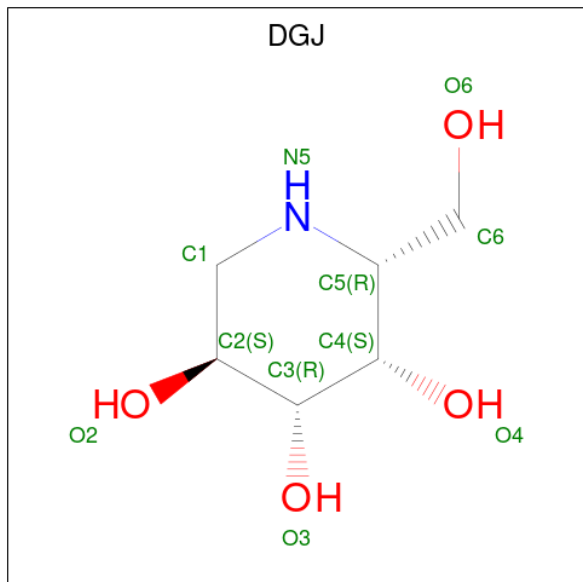
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	5	Total	C	N	O	0	0	0
			61	34	2	25			
3	F	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



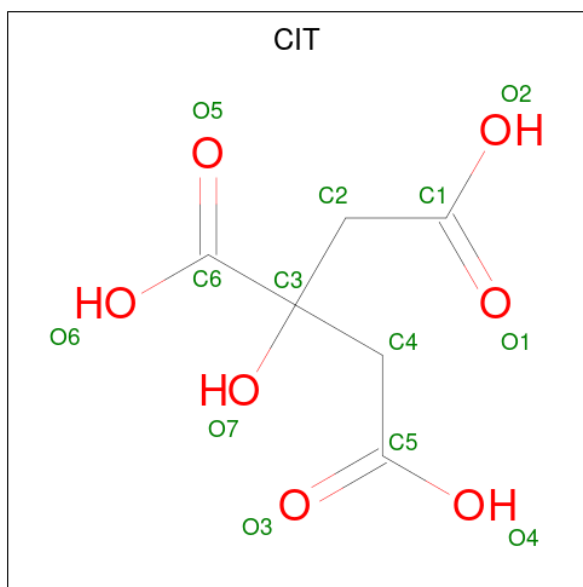
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is (2R,3S,4R,5S)-2-(hydroxymethyl)piperidine-3,4,5-triol (CCD ID: DGJ) (formula: $C_6H_{13}NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			11	6	1	4		
5	B	1	Total	C	N	O	0	0
			11	6	1	4		

- Molecule 6 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			13	6	7		
6	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		

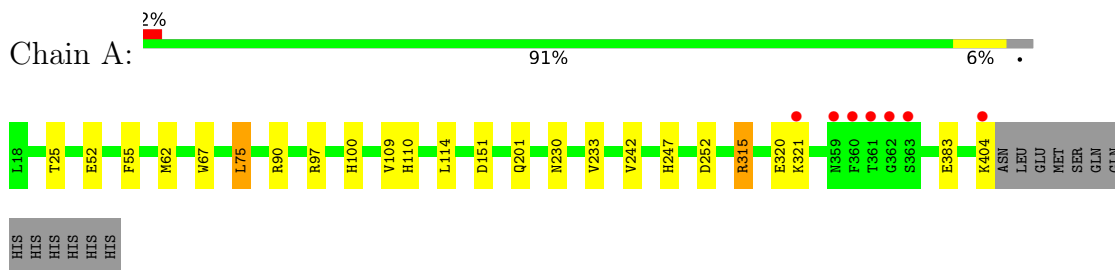
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	569	Total	O	0	0
			569	569		
8	B	453	Total	O	0	0
			453	453		

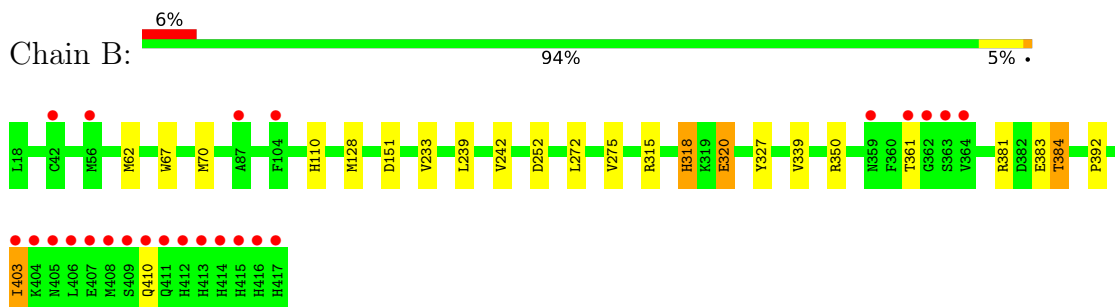
3 Residue-property plots [i](#)

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: Alpha-N-acetylgalactosaminidase



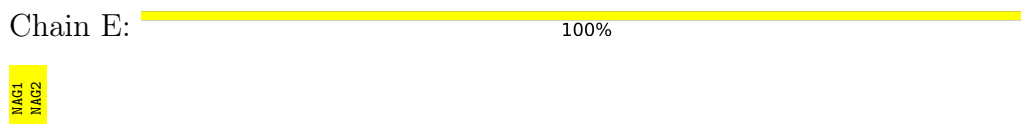
- Molecule 1: Alpha-N-acetylgalactosaminidase



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



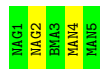
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

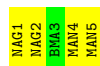
nose

Chain D:  60% 40%



• Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  20% 80%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	154.35Å 114.51Å 68.55Å 90.00° 95.64° 90.00°	Depositor
Resolution (Å)	31.89 – 1.51 31.89 – 1.51	Depositor EDS
% Data completeness (in resolution range)	95.6 (31.89-1.51) 96.1 (31.89-1.51)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.159 , 0.178 0.166 , 0.184	Depositor DCC
R_{free} test set	9434 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	18.6	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7745	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% 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: DGJ, MAN, BMA, CIT, GOL, NAG

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	0.63	0/3237	0.76	2/4401 (0.0%)
1	B	0.57	0/3324	0.76	0/4520
All	All	0.60	0/6561	0.76	2/8921 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	THR	CA-C-N	-5.64	115.54	119.66
1	A	25	THR	C-N-CA	-5.64	115.54	119.66

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	3152	0	3049	19	0
1	B	3233	0	3106	26	0
2	C	28	0	25	2	0
2	E	28	0	25	0	0
3	D	61	0	52	0	0
3	F	61	0	52	0	0
4	A	14	0	13	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	14	0	13	0	0
5	A	11	0	13	0	0
5	B	11	0	13	0	0
6	A	13	0	5	0	0
6	B	13	0	5	0	0
7	A	48	0	64	1	0
7	B	36	0	48	4	0
8	A	569	0	0	11	0
8	B	453	0	0	8	0
All	All	7745	0	6483	47	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 (47) 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:233:VAL:HG23	8:A:1152:HOH:O	1.49	1.11
1:B:233:VAL:HG23	8:B:1023:HOH:O	1.57	1.04
1:B:128:MET:HE2	1:B:128:MET:HA	1.58	0.86
1:A:55:PHE:HD1	1:A:75[A]:LEU:HD11	1.54	0.73
1:A:233:VAL:CG2	8:A:1152:HOH:O	2.21	0.73
1:B:233:VAL:CG2	8:B:1023:HOH:O	2.22	0.72
1:B:110:HIS:HD2	8:B:719:HOH:O	1.74	0.71
1:A:75[A]:LEU:C	1:A:75[A]:LEU:HD13	2.16	0.71
1:A:52:GLU:OE2	1:A:100:HIS:HD2	1.74	0.70
1:B:381:ARG:H	1:B:384:THR:CG2	2.03	0.69
1:A:110:HIS:HE1	1:A:151:ASP:OD2	1.75	0.69
8:A:1137:HOH:O	2:C:2:NAG:H82	1.94	0.67
1:A:230:ASN:HB2	7:A:517:GOL:O1	1.94	0.66
1:A:110:HIS:HD2	8:A:672:HOH:O	1.80	0.64
1:B:381:ARG:H	1:B:384:THR:HG23	1.65	0.61
1:A:97:ARG:NH2	8:A:1156:HOH:O	2.33	0.61
1:B:110:HIS:HE1	1:B:151:ASP:OD2	1.85	0.60
1:B:128:MET:HE3	7:B:512:GOL:H11	1.82	0.59
1:A:109:VAL:HG13	1:A:114:LEU:HB2	1.87	0.55
1:A:75[A]:LEU:C	1:A:75[A]:LEU:CD1	2.80	0.55
8:A:1154:HOH:O	2:C:1:NAG:H83	2.07	0.54
1:B:403:ILE:HG23	1:B:403:ILE:O	2.08	0.54
1:A:201:GLN:NE2	8:A:1135:HOH:O	2.32	0.53
1:B:128:MET:HE3	7:B:512:GOL:C1	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:TYR:HH	7:B:511:GOL:HO1	1.54	0.52
1:B:128:MET:HA	1:B:128:MET:CE	2.37	0.52
1:B:350:ARG:NH1	8:B:905:HOH:O	2.43	0.50
1:B:275[A]:VAL:HG11	1:B:339:VAL:HG23	1.93	0.50
1:B:410:GLN:HG3	8:B:1024:HOH:O	2.11	0.50
1:B:239:LEU:O	1:B:242:VAL:HG22	2.12	0.49
1:A:383:GLU:O	4:A:508:NAG:H82	2.14	0.47
1:B:381:ARG:N	1:B:384:THR:HG23	2.29	0.47
1:B:381:ARG:H	1:B:384:THR:HG21	1.79	0.46
8:A:971:HOH:O	1:B:392:PRO:HB2	2.16	0.46
1:B:327:TYR:OH	7:B:511:GOL:O1	2.30	0.46
1:A:55:PHE:CD1	1:A:75[A]:LEU:HD11	2.42	0.44
1:A:315[A]:ARG:HG3	8:A:748:HOH:O	2.18	0.43
1:B:361:THR:O	8:B:909:HOH:O	2.21	0.42
1:B:272:LEU:HA	1:B:275[A]:VAL:HG22	2.01	0.42
1:A:90[A]:ARG:NH1	8:A:1019:HOH:O	2.52	0.41
1:A:100:HIS:HE1	8:A:827:HOH:O	2.03	0.41
1:B:70:MET:HE3	8:B:1043:HOH:O	2.20	0.41
1:B:315:ARG:NH2	8:B:808:HOH:O	2.52	0.41
1:A:242:VAL:O	1:A:247:HIS:HD2	2.04	0.41
1:B:62:MET:HA	1:B:67:TRP:HB2	2.02	0.41
1:A:62:MET:HA	1:A:67:TRP:HB2	2.02	0.40
1:B:318:HIS:ND1	1:B:320:GLU:OE1	2.54	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	394/400 (98%)	384 (98%)	9 (2%)	1 (0%)	36 18
1	B	403/400 (101%)	388 (96%)	13 (3%)	2 (0%)	24 8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	797/800 (100%)	772 (97%)	22 (3%)	3 (0%)	30 12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	252	ASP
1	B	252	ASP
1	B	403	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	342/346 (99%)	335 (98%)	7 (2%)	48 19
1	B	351/346 (101%)	347 (99%)	4 (1%)	65 40
All	All	693/692 (100%)	682 (98%)	11 (2%)	61 27

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75[A]	LEU
1	A	75[B]	LEU
1	A	315[A]	ARG
1	A	315[B]	ARG
1	A	320	GLU
1	A	321	LYS
1	A	404	LYS
1	B	318	HIS
1	B	320	GLU
1	B	383	GLU
1	B	384	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
1	A	100	HIS
1	A	110	HIS
1	A	214	ASN
1	A	235	HIS
1	A	240	GLN
1	A	247	HIS
1	B	48	ASN
1	B	100	HIS
1	B	110	HIS
1	B	143	GLN
1	B	167	GLN
1	B	214	ASN
1	B	247	HIS
1	B	292	GLN
1	B	416	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

14 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	$\# Z > 2$
2	NAG	C	1	1,2	14,14,15	0.70	0	17,19,21	1.65	6 (35%)
2	NAG	C	2	2	14,14,15	0.59	0	17,19,21	1.00	0
3	NAG	D	1	1,3	14,14,15	0.63	0	17,19,21	0.73	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	D	2	3	14,14,15	0.74	1 (7%)	17,19,21	0.62	0
3	BMA	D	3	3	11,11,12	0.40	0	15,15,17	0.70	0
3	MAN	D	4	3	11,11,12	0.59	0	15,15,17	0.89	1 (6%)
3	MAN	D	5	3	11,11,12	0.59	0	15,15,17	0.85	0
2	NAG	E	1	1,2	14,14,15	0.46	0	17,19,21	0.94	1 (5%)
2	NAG	E	2	2	14,14,15	0.57	0	17,19,21	0.92	1 (5%)
3	NAG	F	1	1,3	14,14,15	0.71	1 (7%)	17,19,21	1.00	1 (5%)
3	NAG	F	2	3	14,14,15	0.68	0	17,19,21	0.89	1 (5%)
3	BMA	F	3	3	11,11,12	0.34	0	15,15,17	0.59	0
3	MAN	F	4	3	11,11,12	0.64	0	15,15,17	0.82	1 (6%)
3	MAN	F	5	3	11,11,12	0.57	0	15,15,17	0.92	2 (13%)

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	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	BMA	D	3	3	-	2/2/19/22	0/1/1/1
3	MAN	D	4	3	-	2/2/19/22	0/1/1/1
3	MAN	D	5	3	-	0/2/19/22	0/1/1/1
2	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	BMA	F	3	3	-	0/2/19/22	0/1/1/1
3	MAN	F	4	3	-	0/2/19/22	0/1/1/1
3	MAN	F	5	3	-	2/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	1	NAG	O5-C1	-2.12	1.40	1.43
3	D	2	NAG	O5-C1	-2.02	1.40	1.43

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	NAG	O5-C1-C2	3.00	115.93	111.29
2	E	1	NAG	C1-O5-C5	2.95	116.14	112.19
3	F	2	NAG	O4-C4-C3	-2.58	104.29	110.38
2	C	1	NAG	O7-C7-N2	2.56	126.51	121.98
2	C	1	NAG	C2-N2-C7	2.43	126.15	122.90
2	C	1	NAG	C1-O5-C5	2.41	115.42	112.19
2	C	1	NAG	C1-C2-N2	-2.40	106.65	110.43
3	F	5	MAN	C1-C2-C3	2.33	113.04	109.64
3	D	4	MAN	C1-O5-C5	2.32	115.30	112.19
3	F	4	MAN	C1-C2-C3	2.26	112.94	109.64
3	F	5	MAN	C1-O5-C5	2.24	115.19	112.19
2	C	1	NAG	O7-C7-C8	-2.24	118.07	122.05
3	F	1	NAG	C1-C2-N2	2.14	113.80	110.43
2	E	2	NAG	C4-C3-C2	2.13	114.14	111.02

There are no chirality outliers.

All (8) torsion outliers are listed below:

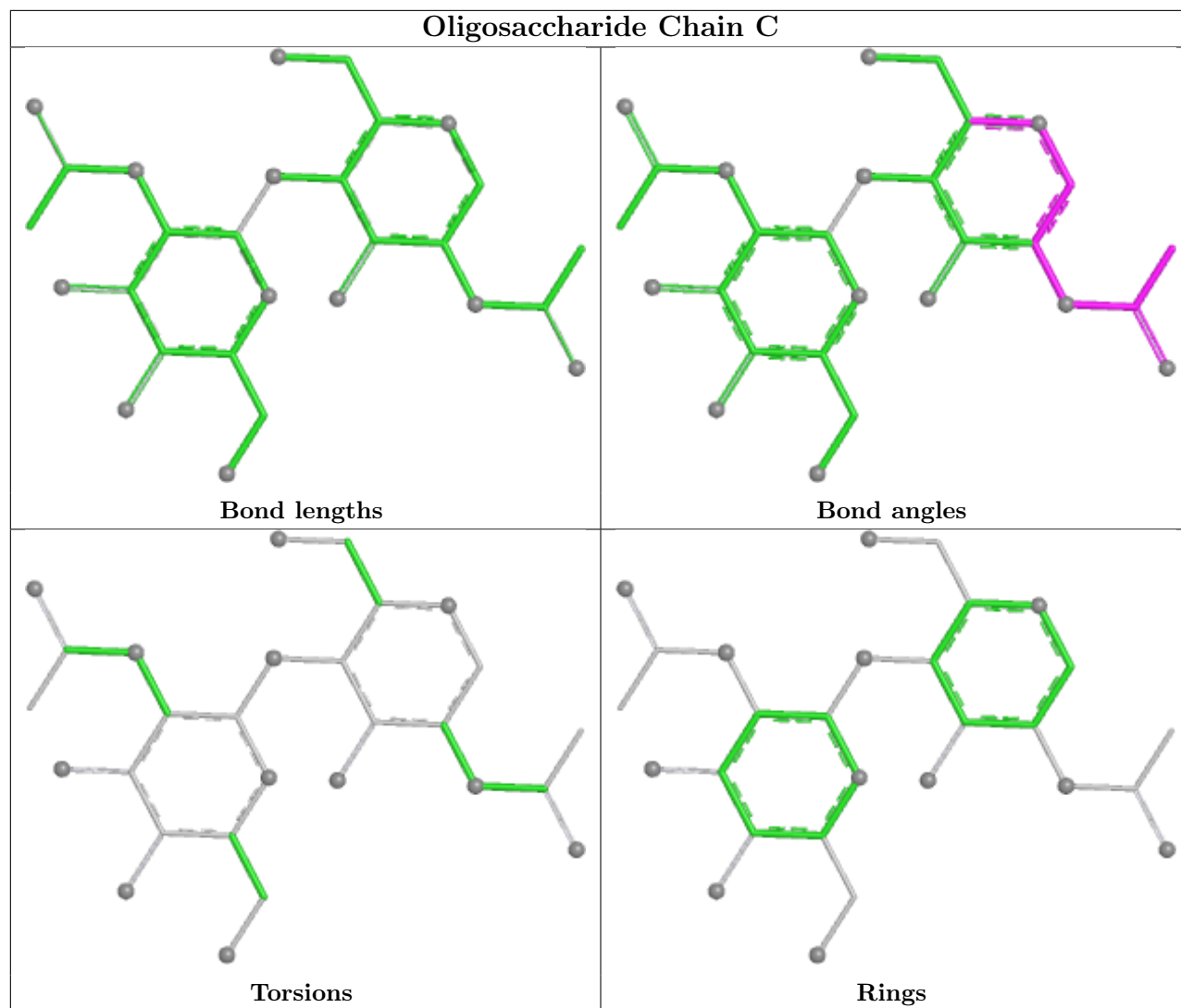
Mol	Chain	Res	Type	Atoms
2	E	2	NAG	O5-C5-C6-O6
3	F	5	MAN	O5-C5-C6-O6
3	D	4	MAN	O5-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
3	F	5	MAN	C4-C5-C6-O6
3	D	4	MAN	C4-C5-C6-O6
3	D	3	BMA	C4-C5-C6-O6
3	D	3	BMA	O5-C5-C6-O6

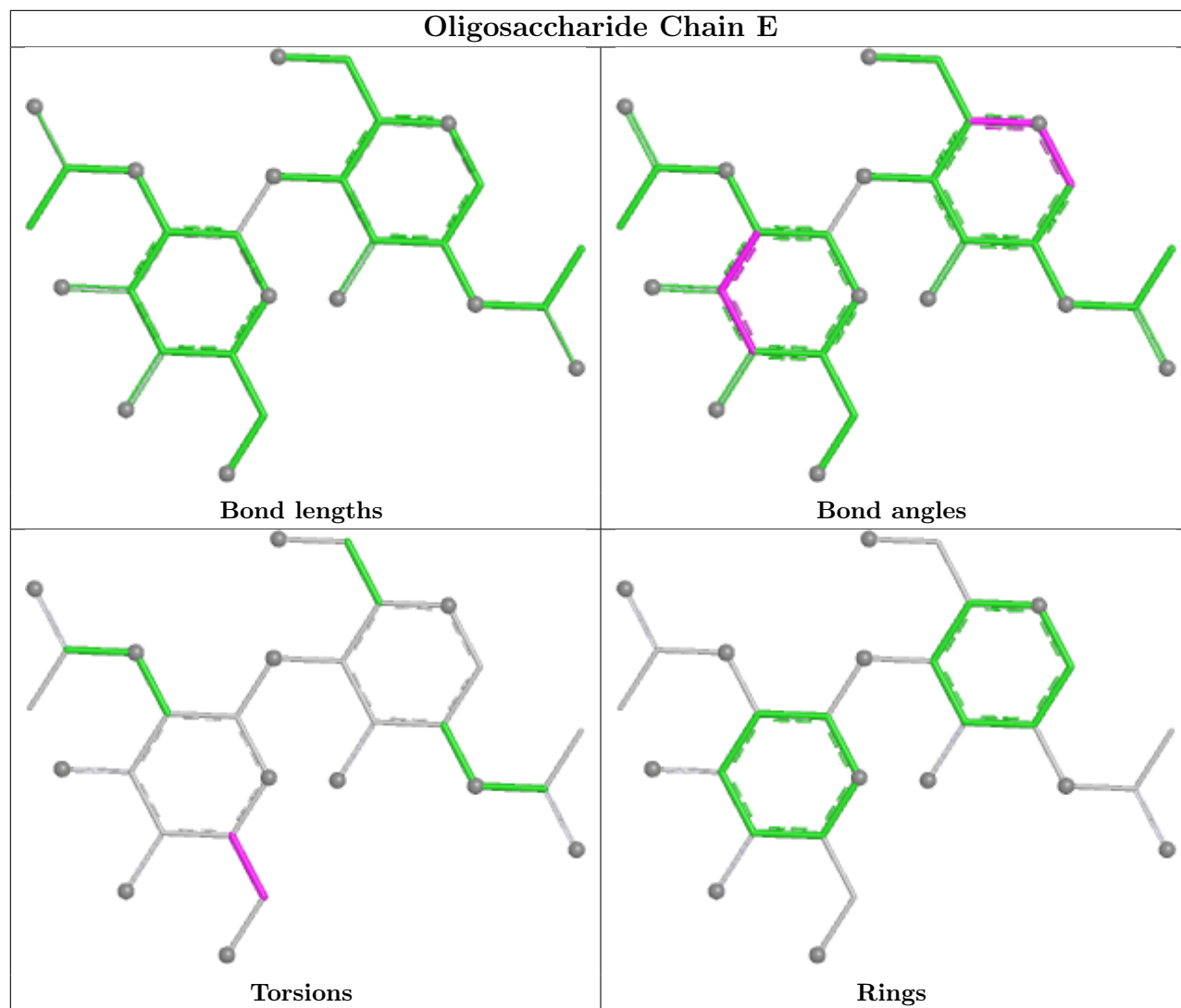
There are no ring outliers.

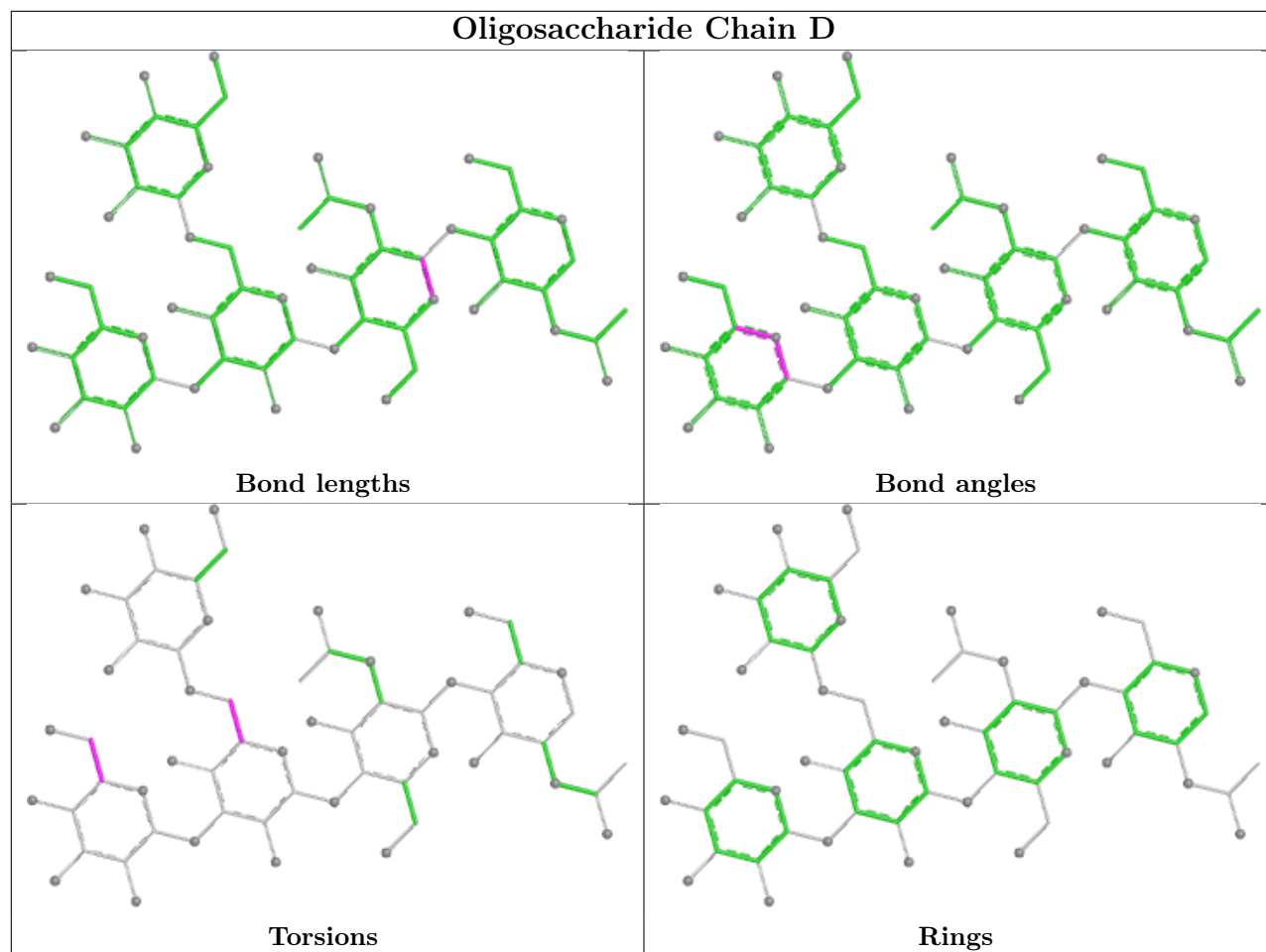
2 monomers are involved in 2 short contacts:

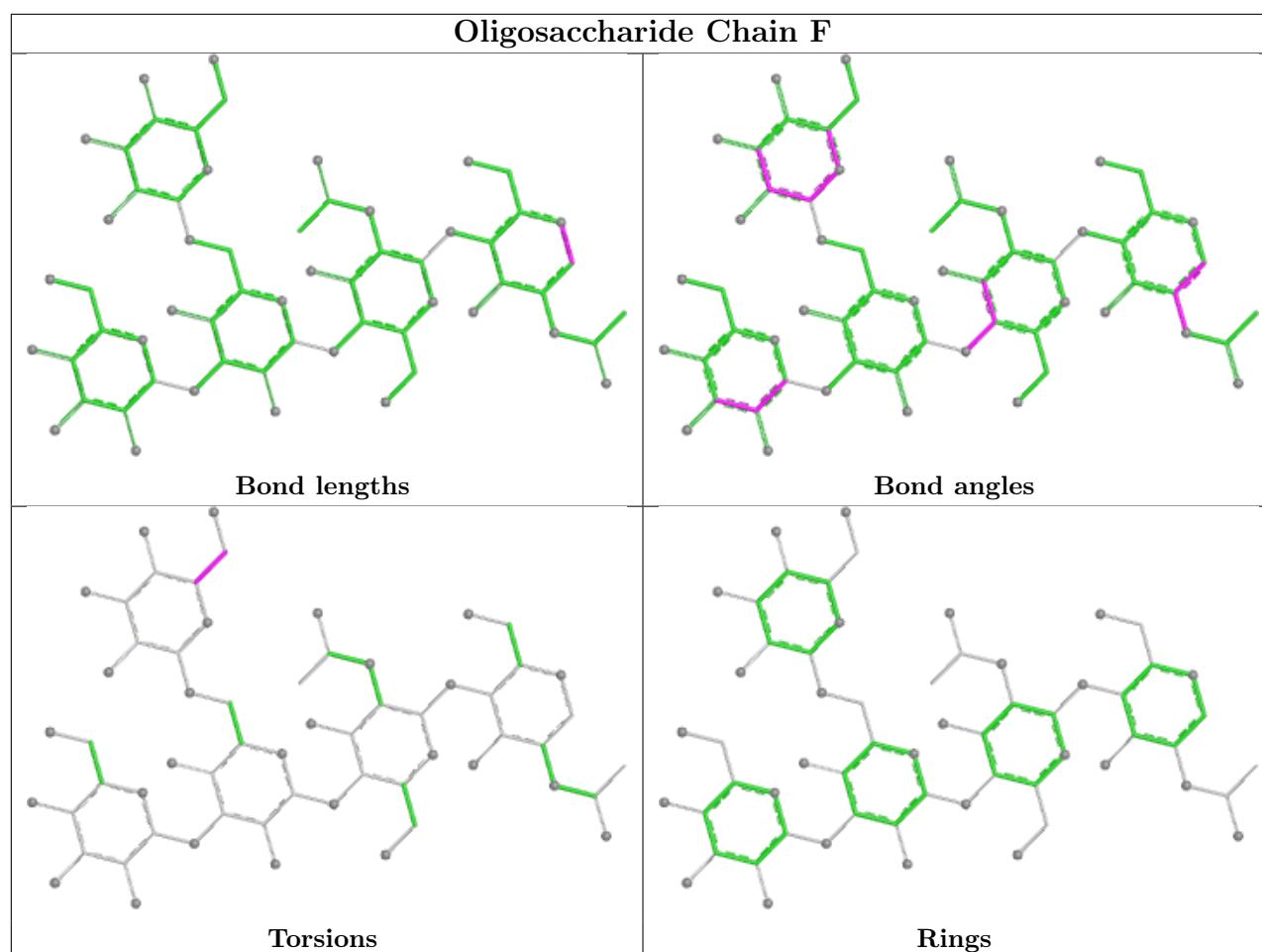
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	1	0
2	C	1	NAG	1	0

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](#)

20 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	GOL	B	511	-	5,5,5	0.32	0	5,5,5	0.49	0
7	GOL	B	515	-	5,5,5	0.38	0	5,5,5	0.42	0
4	NAG	B	508	1	14,14,15	0.49	0	17,19,21	0.82	0
7	GOL	B	513	-	5,5,5	0.37	0	5,5,5	0.25	0
7	GOL	A	512	-	5,5,5	0.36	0	5,5,5	0.49	0
7	GOL	A	518	-	5,5,5	0.40	0	5,5,5	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	CIT	B	510	-	12,12,12	0.94	0	17,17,17	1.55	3 (17%)
6	CIT	A	510	-	12,12,12	1.03	0	17,17,17	1.30	2 (11%)
5	DGJ	B	509	-	11,11,11	0.81	0	13,15,15	1.15	2 (15%)
7	GOL	A	511	-	5,5,5	0.42	0	5,5,5	0.55	0
7	GOL	A	515	-	5,5,5	0.38	0	5,5,5	0.37	0
7	GOL	B	512	-	5,5,5	0.59	0	5,5,5	0.45	0
7	GOL	B	516	-	5,5,5	0.35	0	5,5,5	0.43	0
7	GOL	A	516	-	5,5,5	0.37	0	5,5,5	0.13	0
7	GOL	B	514	-	5,5,5	0.37	0	5,5,5	0.29	0
7	GOL	A	514	-	5,5,5	0.43	0	5,5,5	0.19	0
5	DGJ	A	509	-	11,11,11	0.26	0	13,15,15	1.28	2 (15%)
7	GOL	A	517	-	5,5,5	0.35	0	5,5,5	0.38	0
4	NAG	A	508	1	14,14,15	0.52	0	17,19,21	1.22	1 (5%)
7	GOL	A	513	-	5,5,5	0.37	0	5,5,5	0.31	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	GOL	B	511	-	-	0/4/4/4	-
7	GOL	B	515	-	-	2/4/4/4	-
4	NAG	B	508	1	-	1/6/23/26	0/1/1/1
7	GOL	B	513	-	-	2/4/4/4	-
7	GOL	A	512	-	-	0/4/4/4	-
7	GOL	A	518	-	-	4/4/4/4	-
6	CIT	B	510	-	-	0/16/16/16	-
6	CIT	A	510	-	-	4/16/16/16	-
5	DGJ	B	509	-	-	0/2/19/19	0/1/1/1
7	GOL	A	511	-	-	0/4/4/4	-
7	GOL	A	515	-	-	1/4/4/4	-
7	GOL	B	512	-	-	0/4/4/4	-
7	GOL	B	516	-	-	0/4/4/4	-
7	GOL	A	516	-	-	2/4/4/4	-
7	GOL	B	514	-	-	0/4/4/4	-
7	GOL	A	514	-	-	0/4/4/4	-
5	DGJ	A	509	-	-	0/2/19/19	0/1/1/1
7	GOL	A	517	-	-	2/4/4/4	-
4	NAG	A	508	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	GOL	A	513	-	-	1/4/4/4	-

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	508	NAG	C1-O5-C5	4.39	118.08	112.19
6	B	510	CIT	O6-C6-C3	4.35	121.48	113.14
6	A	510	CIT	O6-C6-C3	3.09	119.06	113.14
5	A	509	DGJ	C1-C2-C3	-2.83	106.79	110.25
6	B	510	CIT	O5-C6-C3	-2.18	117.87	122.09
5	A	509	DGJ	C4-C5-N5	2.16	113.47	109.12
6	B	510	CIT	O1-C1-C2	-2.11	116.96	122.95
6	A	510	CIT	O3-C5-C4	-2.05	117.14	122.95
5	B	509	DGJ	C2-C3-C4	-2.03	107.29	110.86
5	B	509	DGJ	C1-N5-C5	2.01	114.12	109.71

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	517	GOL	C1-C2-C3-O3
7	A	517	GOL	O2-C2-C3-O3
7	A	518	GOL	O1-C1-C2-C3
7	B	515	GOL	C1-C2-C3-O3
7	B	515	GOL	O2-C2-C3-O3
7	A	516	GOL	C1-C2-C3-O3
7	B	513	GOL	O1-C1-C2-C3
7	A	518	GOL	O1-C1-C2-O2
4	A	508	NAG	C4-C5-C6-O6
7	A	513	GOL	O1-C1-C2-O2
6	A	510	CIT	O1-C1-C2-C3
4	A	508	NAG	O5-C5-C6-O6
6	A	510	CIT	O2-C1-C2-C3
4	B	508	NAG	O5-C5-C6-O6
7	A	516	GOL	O2-C2-C3-O3
7	A	518	GOL	C1-C2-C3-O3
7	B	513	GOL	O1-C1-C2-O2
7	A	515	GOL	O2-C2-C3-O3
7	A	518	GOL	O2-C2-C3-O3
6	A	510	CIT	C3-C4-C5-O3

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Mol	Chain	Res	Type	Atoms
6	A	510	CIT	C3-C4-C5-O4

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	511	GOL	2	0
7	B	512	GOL	2	0
7	A	517	GOL	1	0
4	A	508	NAG	1	0

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	A	387/400 (96%)	-0.28	7 (1%) 67 73	8, 19, 38, 63	9 (2%)
1	B	400/400 (100%)	0.24	24 (6%) 27 32	8, 27, 59, 116	5 (1%)
All	All	787/800 (98%)	-0.01	31 (3%) 43 50	8, 22, 49, 116	14 (1%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	415	HIS	5.9
1	B	414	HIS	5.0
1	B	403	ILE	4.7
1	A	361	THR	4.4
1	B	409	SER	4.4
1	B	412	HIS	4.3
1	B	406	LEU	4.3
1	B	417	HIS	4.2
1	B	361	THR	4.1
1	A	404	LYS	3.9
1	B	405	ASN	3.7
1	B	410	GLN	3.7
1	B	408	MET	3.6
1	B	42	CYS	3.4
1	B	416	HIS	2.9
1	B	364	VAL	2.9
1	B	407	GLU	2.9
1	B	413	HIS	2.8
1	B	362	GLY	2.7
1	B	411	GLN	2.6
1	A	363	SER	2.6
1	B	56[A]	MET	2.6
1	B	404	LYS	2.6
1	A	359	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	360	PHE	2.5
1	B	363	SER	2.4
1	B	87	ALA	2.3
1	B	359	ASN	2.3
1	B	104	PHE	2.2
1	A	362	GLY	2.2
1	A	321	LYS	2.2

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](#)

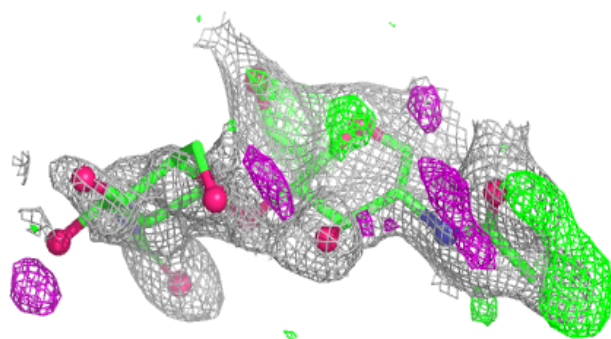
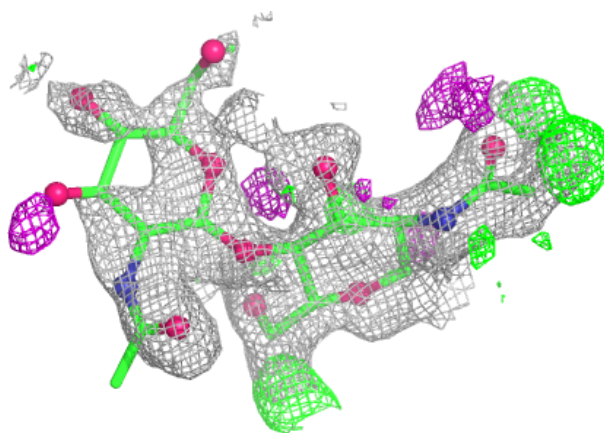
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MAN	F	5	11/12	0.32	0.18	120,127,131,135	0
3	MAN	D	5	11/12	0.41	0.19	92,103,109,111	0
2	NAG	E	2	14/15	0.47	0.18	82,107,112,113	0
2	NAG	C	2	14/15	0.57	0.17	65,97,101,101	0
3	MAN	F	4	11/12	0.59	0.16	78,92,97,98	0
3	MAN	D	4	11/12	0.68	0.18	68,83,93,96	0
2	NAG	C	1	14/15	0.69	0.16	42,54,75,83	0
2	NAG	E	1	14/15	0.80	0.15	56,63,71,95	0
3	BMA	F	3	11/12	0.80	0.13	45,65,83,98	0
3	NAG	F	2	14/15	0.92	0.10	27,36,46,48	0
3	BMA	D	3	11/12	0.92	0.10	30,45,58,74	0
3	NAG	D	2	14/15	0.94	0.09	24,31,47,50	0
3	NAG	F	1	14/15	0.95	0.07	19,24,30,38	0
3	NAG	D	1	14/15	0.96	0.07	22,27,32,39	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.

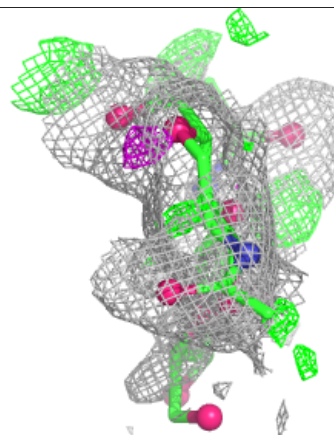
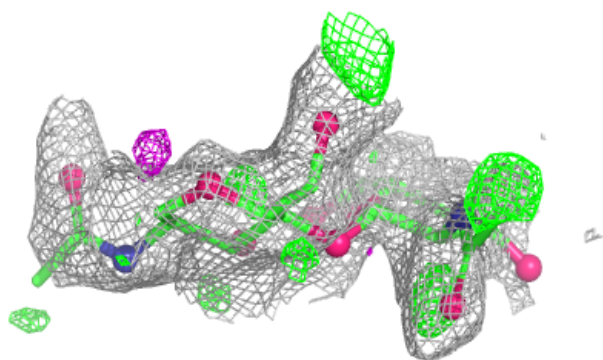
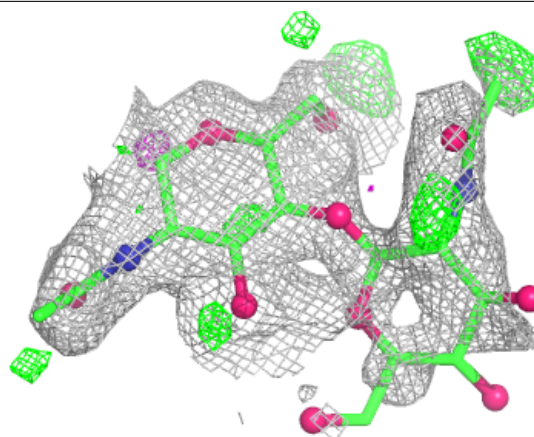
Electron density around Chain C:

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



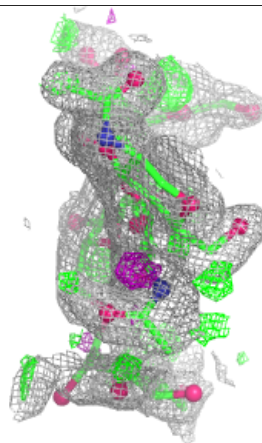
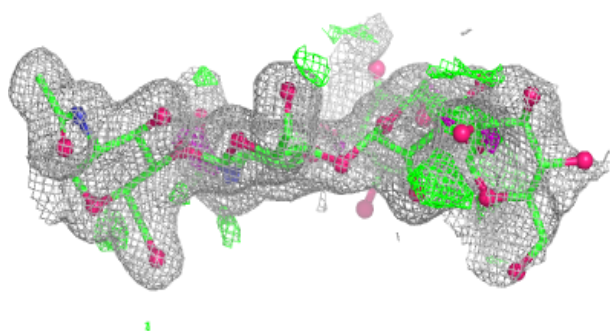
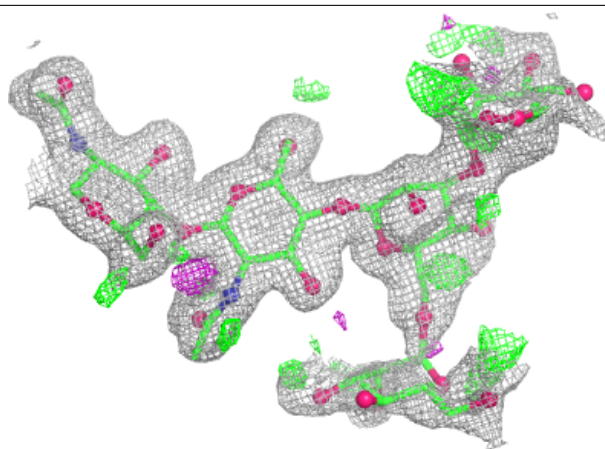
Electron density around Chain E:

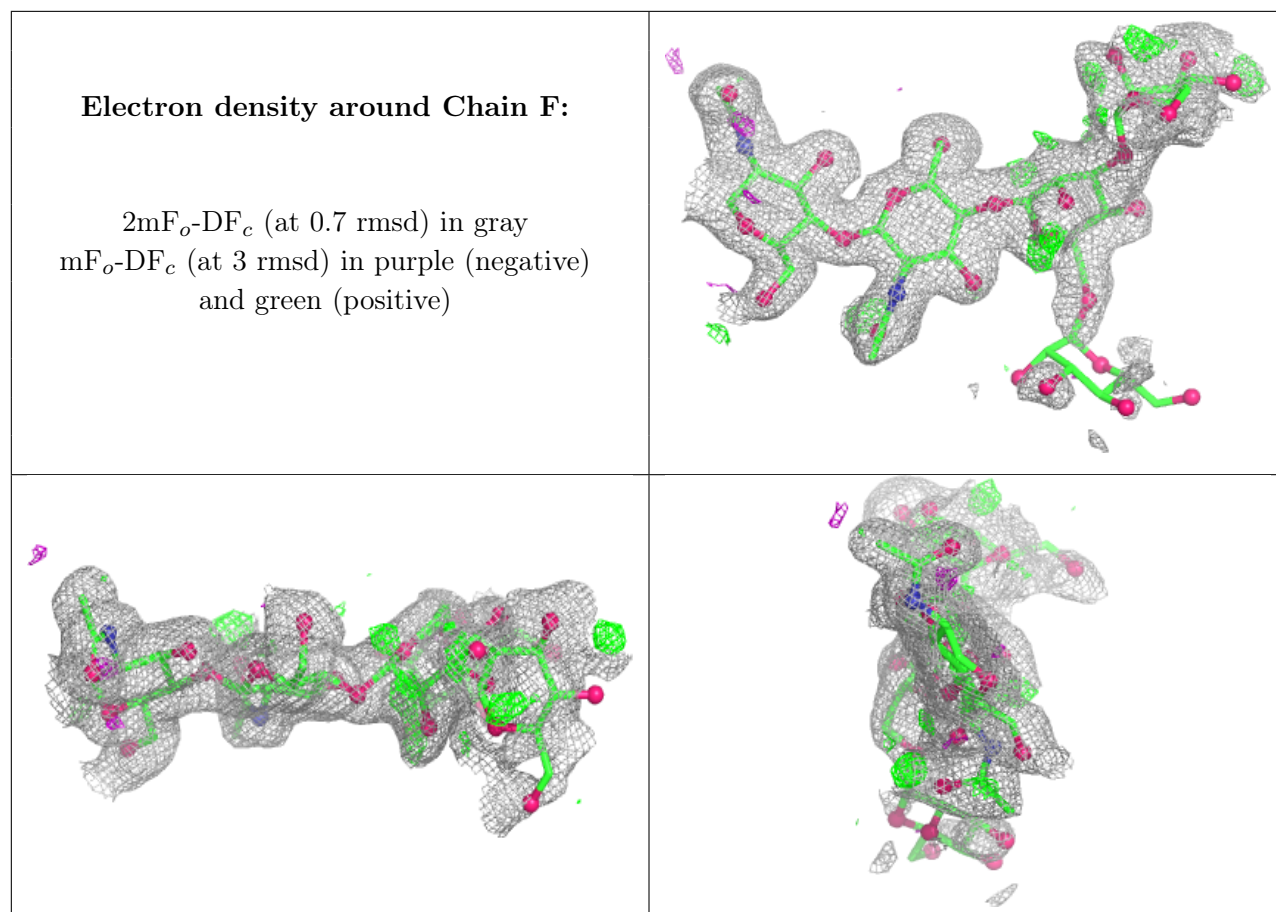
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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 [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	NAG	B	508	14/15	0.57	0.15	70,94,105,106	0
4	NAG	A	508	14/15	0.65	0.15	72,89,96,100	0
7	GOL	B	511	6/6	0.73	0.17	40,47,56,56	0
7	GOL	A	517	6/6	0.74	0.19	40,46,50,55	0
6	CIT	B	510	13/13	0.80	0.14	39,55,65,65	0
7	GOL	A	513	6/6	0.83	0.16	60,63,66,76	0
7	GOL	B	513	6/6	0.83	0.16	56,62,66,70	0
7	GOL	B	514	6/6	0.84	0.18	38,52,61,75	0
7	GOL	A	511	6/6	0.85	0.17	28,47,50,59	0
7	GOL	A	518	6/6	0.88	0.18	24,54,59,68	0
7	GOL	A	512	6/6	0.88	0.17	20,44,47,64	0
7	GOL	A	515	6/6	0.89	0.14	25,40,45,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	GOL	B	512	6/6	0.90	0.12	28,36,44,49	0
7	GOL	B	516	6/6	0.91	0.12	22,36,46,54	0
7	GOL	B	515	6/6	0.92	0.13	24,41,48,66	0
6	CIT	A	510	13/13	0.92	0.08	28,35,42,44	0
7	GOL	A	516	6/6	0.93	0.11	25,44,51,66	0
5	DGJ	B	509	11/11	0.96	0.06	17,21,22,23	0
7	GOL	A	514	6/6	0.96	0.09	20,28,36,41	0
5	DGJ	A	509	11/11	0.99	0.04	11,13,15,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.