



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2026 – 07:14 PM UTC

PDB ID : 4HJ1 / pdb_00004hj1
Title : Crystal structure of glycoprotein C from Rift Valley Fever Virus (glycosylated)
Authors : Dessau, M.; Modis, Y.
Deposited on : 2012-10-12
Resolution : 1.90 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 ⓘ 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

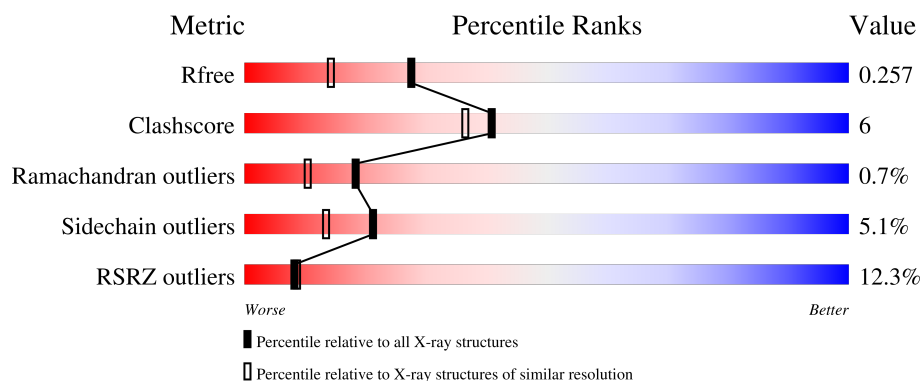
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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 $\leq 5\%$. 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	432	4% 87% 12% .
1	B	432	30% 82% 13% ..
1	C	432	10% 84% 14% .
1	D	432	5% 84% 14% .
2	E	4	75% 25%

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Mol	Chain	Length	Quality of chain
3	F	3	 100%
4	G	5	 100%
4	H	5	 60%  40%

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
7	GOL	D	1210	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14382 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 ENVELOPE GLYCOPROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	2	0
			3279	2036	561	653	29			
1	B	427	Total	C	N	O	S	0	0	0
			3242	2011	557	645	29			
1	C	430	Total	C	N	O	S	0	1	0
			3271	2031	561	649	30			
1	D	431	Total	C	N	O	S	0	5	0
			3296	2046	562	658	30			

There are 12 discrepancies between the modelled and reference sequences:

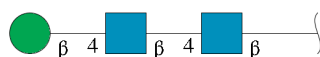
Chain	Residue	Modelled	Actual	Comment	Reference
A	688	ASP	-	expression tag	UNP A2T075
A	689	PRO	-	expression tag	UNP A2T075
A	690	GLY	-	expression tag	UNP A2T075
B	688	ASP	-	expression tag	UNP A2T075
B	689	PRO	-	expression tag	UNP A2T075
B	690	GLY	-	expression tag	UNP A2T075
C	688	ASP	-	expression tag	UNP A2T075
C	689	PRO	-	expression tag	UNP A2T075
C	690	GLY	-	expression tag	UNP A2T075
D	688	ASP	-	expression tag	UNP A2T075
D	689	PRO	-	expression tag	UNP A2T075
D	690	GLY	-	expression tag	UNP A2T075

- Molecule 2 is an oligosaccharide called beta-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.



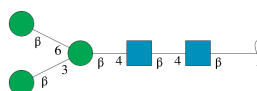
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 3 is an oligosaccharide called 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	F	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-3)-[beta-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.



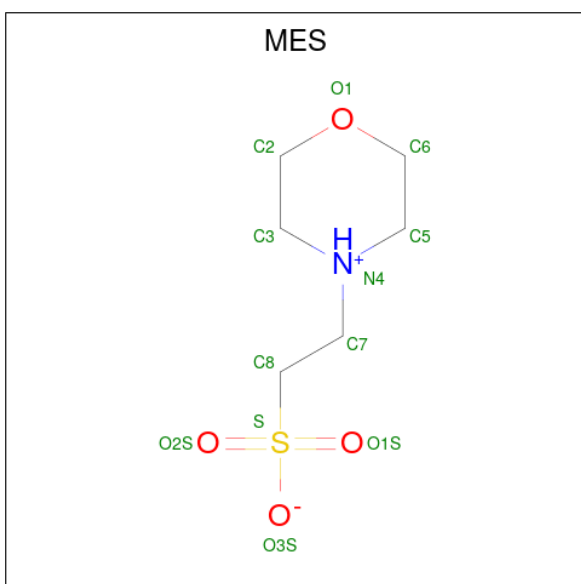
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	5	Total	C	N	O	0	0	0
			61	34	2	25			
4	H	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



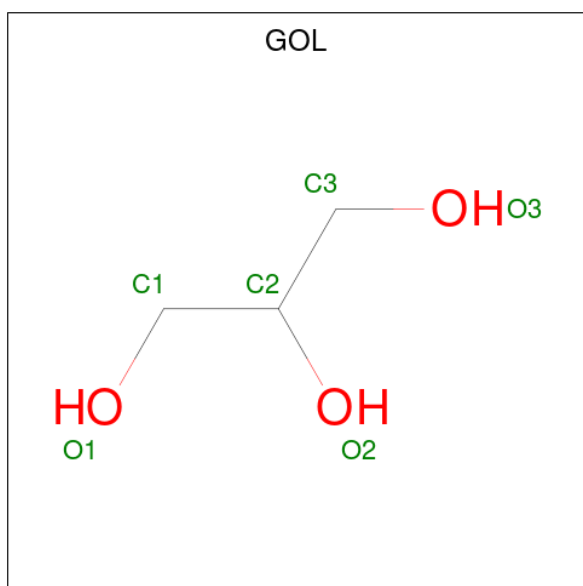
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	C	1	Total	C	N	O	0	0
			14	8	1	5		
5	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- 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	B	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		
7	D	1	Total	C	O	0	0
			6	3	3		
7	D	1	Total	C	O	0	0
			6	3	3		

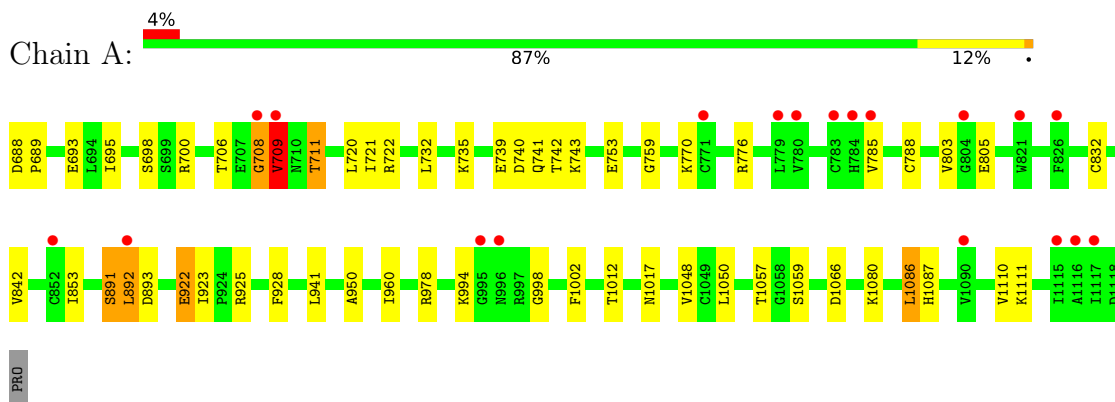
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	332	Total 332	O 332	0	0
8	B	111	Total 111	O 111	0	0
8	C	170	Total 170	O 170	0	0
8	D	324	Total 324	O 324	0	0

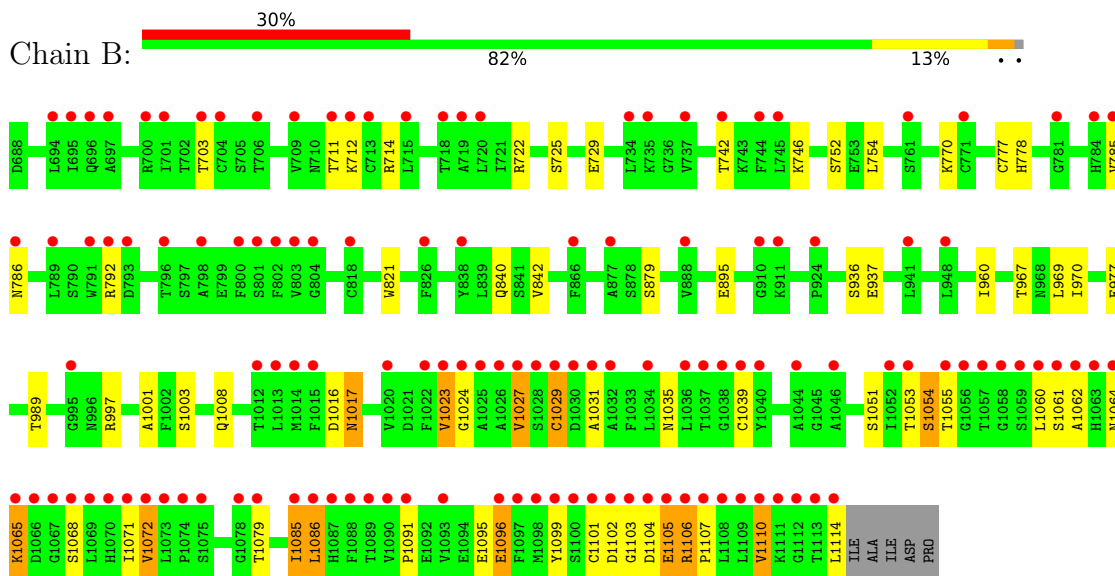
3 Residue-property plots

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.

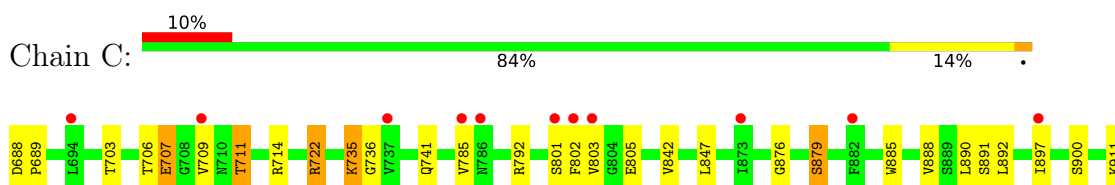
• Molecule 1: ENVELOPE GLYCOPROTEIN

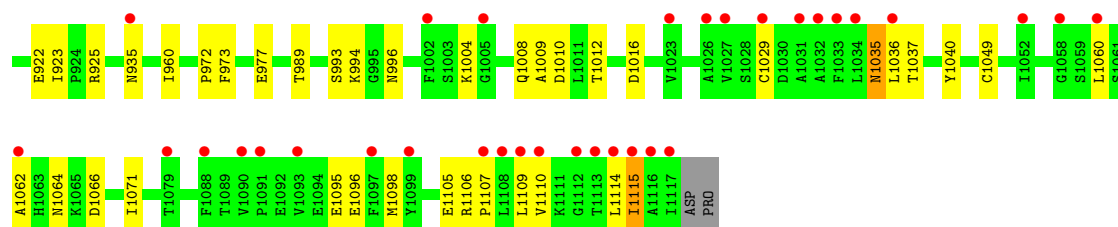


• Molecule 1: ENVELOPE GLYCOPROTEIN

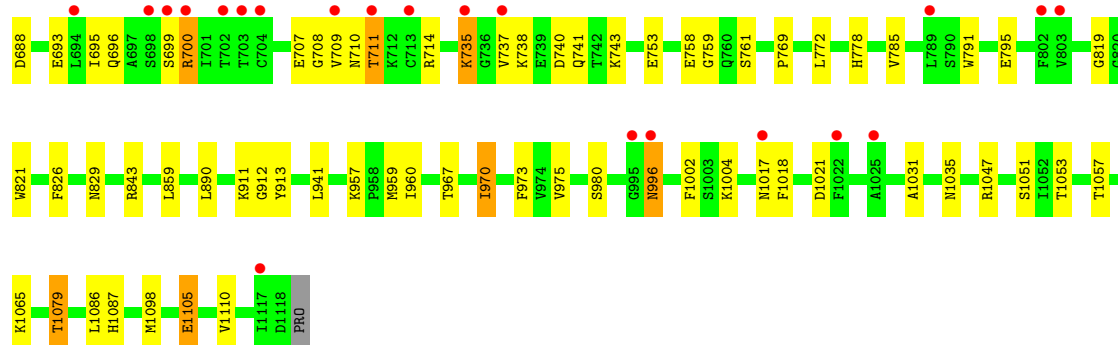
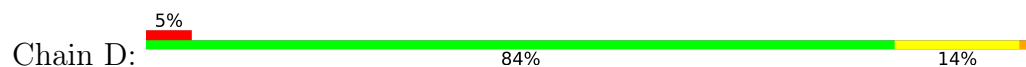


• Molecule 1: ENVELOPE GLYCOPROTEIN

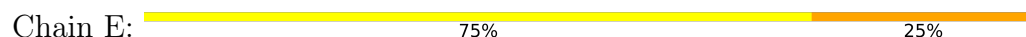




• Molecule 1: ENVELOPE GLYCOPROTEIN



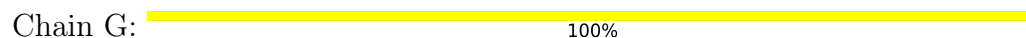
• Molecule 2: beta-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



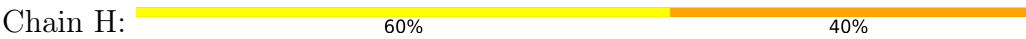
• Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 4: beta-D-mannopyranose-(1-3)-[beta-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



• Molecule 4: beta-D-mannopyranose-(1-3)-[beta-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



RMG1
RMG2
RMG3
RMG4
RMG5

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	128.68Å 56.37Å 140.19Å 90.00° 96.55° 90.00°	Depositor
Resolution (Å)	29.76 – 1.90 29.76 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.3 (29.76-1.90) 97.4 (29.76-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 1.91Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.214 , 0.255 0.215 , 0.257	Depositor DCC
R_{free} test set	7722 reflections (4.16%)	wwPDB-VP
Wilson B-factor (Å ²)	33.0	Xtrriage
Anisotropy	0.330	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14382	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.67 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.9715e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: NAG, GOL, MES, BMA

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	0/3345	0.84	3/4523 (0.1%)
1	B	0.50	0/3302	0.80	5/4463 (0.1%)
1	C	0.51	0/3331	0.78	1/4502 (0.0%)
1	D	0.64	0/3368	0.82	1/4553 (0.0%)
All	All	0.58	0/13346	0.81	10/18041 (0.1%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1106	ARG	N-CA-C	6.97	114.49	108.22
1	A	950	ALA	CA-C-N	-6.69	113.76	120.31
1	A	950	ALA	C-N-CA	-6.69	113.76	120.31
1	B	1035	ASN	N-CA-C	5.81	117.08	108.60
1	B	879	SER	N-CA-C	5.60	118.77	110.48
1	A	998	GLY	N-CA-C	-5.10	103.79	111.19
1	B	936	SER	N-CA-C	5.07	116.55	108.79
1	C	1035	ASN	N-CA-C	5.04	116.51	108.79
1	D	1105	GLU	N-CA-C	5.04	117.95	110.48
1	B	1054	SER	N-CA-C	5.04	114.94	108.34

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	3279	0	3155	39	0
1	B	3242	0	3111	40	0
1	C	3271	0	3145	38	0
1	D	3296	0	3168	54	0
2	E	50	0	43	1	0
3	F	39	0	34	0	0
4	G	61	0	52	0	0
4	H	61	0	52	2	0
5	A	14	0	13	0	0
5	B	14	0	13	0	0
5	C	14	0	13	0	0
5	D	14	0	13	0	0
6	A	12	0	13	1	0
6	B	12	0	13	0	0
6	C	12	0	13	0	0
6	D	24	0	26	3	0
7	A	6	0	8	0	0
7	B	6	0	8	0	0
7	C	6	0	8	0	0
7	D	12	0	16	10	0
8	A	332	0	0	12	0
8	B	111	0	0	1	0
8	C	170	0	0	7	0
8	D	324	0	0	11	0
All	All	14382	0	12917	171	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 6.

All (171) 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:D:912:GLY:HA3	7:D:1210:GOL:H11	1.41	1.02
1:B:1060:LEU:HA	1:B:1101:CYS:HB3	1.53	0.89
1:B:1104:ASP:HB3	1:B:1105:GLU:HA	1.53	0.89
1:B:1102:ASP:HB3	1:B:1104:ASP:N	1.90	0.83
1:A:753:GLU:HG2	1:A:1002:PHE:CE1	2.13	0.82
1:D:1004:LYS:HE3	4:H:5:BMA:O3	1.81	0.81
1:B:1039:CYS:HA	1:B:1114:LEU:HG	1.61	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1087:HIS:HD2	8:D:1422:HOH:O	1.66	0.78
1:D:753[A]:GLU:HG2	1:D:1002:PHE:CE1	2.20	0.77
1:B:1104:ASP:CB	1:B:1105:GLU:HA	2.12	0.73
1:D:711:THR:HG21	1:D:741:GLN:HE22	1.54	0.73
1:A:735:LYS:HD2	1:A:742[A]:THR:HG22	1.71	0.73
1:A:892:LEU:C	1:A:892:LEU:HD23	2.14	0.72
1:A:805:GLU:HG2	8:A:1516:HOH:O	1.89	0.72
1:B:1060:LEU:O	1:B:1072:VAL:HA	1.89	0.71
1:B:792:ARG:HH11	1:B:792:ARG:HG2	1.53	0.71
1:D:696:GLN:NE2	1:D:735:LYS:HD3	2.06	0.71
7:D:1210:GOL:O3	8:D:1621:HOH:O	2.09	0.71
1:B:1065:LYS:HD2	1:B:1068:SER:HB2	1.72	0.70
1:A:688:ASP:N	1:A:689:PRO:HD3	2.07	0.69
1:D:753[A]:GLU:HG2	1:D:1002:PHE:CD1	2.27	0.69
1:A:892:LEU:CD2	8:A:1632:HOH:O	2.41	0.69
1:A:891:SER:HB2	1:A:1012:THR:OG1	1.93	0.68
1:B:778:HIS:NE2	1:B:785:VAL:HG23	2.09	0.67
1:A:706:THR:HG22	1:A:711:THR:HB	1.77	0.67
1:B:1062:ALA:HA	1:B:1099:TYR:HA	1.75	0.67
1:D:707:GLU:HG3	1:D:708:GLY:N	2.10	0.67
1:D:700:ARG:HG3	1:D:700:ARG:HH11	1.59	0.66
1:C:722:ARG:HD2	8:C:1366:HOH:O	1.94	0.66
1:D:778:HIS:CE1	6:D:1208:MES:H72	2.30	0.66
1:B:1104:ASP:HB3	1:B:1105:GLU:CA	2.23	0.65
1:A:803:VAL:HG12	8:A:1542:HOH:O	1.97	0.64
1:A:695:ILE:HG12	1:A:721:ILE:HD12	1.80	0.64
1:B:754:LEU:HD11	1:B:895:GLU:O	1.98	0.63
1:C:805:GLU:HG2	8:C:1444:HOH:O	2.00	0.62
1:D:970:ILE:HD11	1:D:975:VAL:HG21	1.82	0.61
1:A:695:ILE:HG13	1:A:732:LEU:HD12	1.81	0.61
1:D:912:GLY:CA	7:D:1210:GOL:H11	2.25	0.61
1:C:897:ILE:HB	1:C:900:SER:HB3	1.82	0.61
1:B:1029:CYS:HB3	1:B:1054:SER:HB2	1.81	0.60
1:D:707:GLU:HG3	1:D:708:GLY:H	1.65	0.60
1:B:1029:CYS:HB3	1:B:1054:SER:CB	2.31	0.60
1:C:688:ASP:N	1:C:689:PRO:HD3	2.16	0.60
1:A:892:LEU:HD23	1:A:893:ASP:N	2.16	0.60
1:A:753:GLU:HG2	1:A:1002:PHE:HE1	1.67	0.60
1:D:970:ILE:CD1	1:D:975:VAL:HG21	2.33	0.59
1:A:688:ASP:N	1:A:689:PRO:CD	2.65	0.59
1:A:688:ASP:N	2:E:4:BMA:HO6	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:792:ARG:HG2	1:B:792:ARG:NH1	2.15	0.59
1:C:891:SER:HB2	1:C:1012:THR:OG1	2.03	0.59
1:D:700:ARG:HG3	1:D:700:ARG:NH1	2.16	0.59
1:C:973:PHE:O	1:C:977:GLU:HG2	2.02	0.58
1:D:980[B]:SER:OG	7:D:1210:GOL:H31	2.03	0.58
1:C:885:TRP:HH2	1:C:888:VAL:HG22	1.68	0.58
1:B:1060:LEU:HA	1:B:1101:CYS:CB	2.31	0.58
1:B:1031:ALA:HA	1:B:1051:SER:O	2.04	0.58
1:A:892:LEU:CD1	8:A:1632:HOH:O	2.51	0.58
1:D:912:GLY:HA3	7:D:1210:GOL:C1	2.27	0.58
1:D:980[A]:SER:HB2	7:D:1210:GOL:H31	1.86	0.57
1:C:1098:MET:HE3	1:C:1105:GLU:HB3	1.85	0.57
1:D:913:TYR:O	7:D:1210:GOL:H32	2.04	0.57
1:A:892:LEU:HD22	8:A:1632:HOH:O	2.02	0.57
1:A:892:LEU:C	1:A:892:LEU:CD2	2.78	0.56
1:C:935:ASN:HB2	8:C:1334:HOH:O	2.05	0.56
1:D:1087:HIS:CD2	8:D:1422:HOH:O	2.49	0.55
1:C:703:THR:HG23	8:C:1352:HOH:O	2.05	0.55
1:A:698:SER:OG	1:A:700:ARG:HG2	2.07	0.55
1:C:1008:GLN:NE2	8:C:1470:HOH:O	2.38	0.55
1:A:1048:VAL:HG11	1:A:1086:LEU:HD22	1.88	0.55
1:A:708:GLY:O	1:A:709:VAL:HG22	2.07	0.54
1:C:892:LEU:HB3	1:C:1010:ASP:HB2	1.90	0.54
1:D:970:ILE:CD1	1:D:975:VAL:CG2	2.87	0.53
1:D:758[B]:GLU:HG3	1:D:759:GLY:N	2.20	0.53
1:D:1053:THR:HG23	1:D:1079:THR:HG22	1.91	0.52
1:C:1062:ALA:HB3	1:C:1071:ILE:HB	1.92	0.52
1:A:776:ARG:HD3	6:A:1206:MES:O1S	2.09	0.52
1:D:1098:MET:HE3	1:D:1105:GLU:HB3	1.92	0.52
1:C:735:LYS:O	1:C:735:LYS:HE2	2.11	0.51
1:C:1035:ASN:OD1	1:C:1049:CYS:HB2	2.11	0.51
1:D:769:PRO:HG3	1:D:967:THR:HG23	1.91	0.51
1:D:911:LYS:HE2	8:D:1621:HOH:O	2.11	0.51
1:B:1102:ASP:HB3	1:B:1103:GLY:C	2.35	0.50
1:B:1103:GLY:O	1:B:1104:ASP:HB2	2.09	0.50
1:D:821:TRP:CZ2	1:D:826:PHE:HA	2.46	0.50
1:D:913:TYR:H	7:D:1210:GOL:C1	2.25	0.50
1:A:1087:HIS:HD2	8:A:1449:HOH:O	1.95	0.49
1:C:688:ASP:N	1:C:689:PRO:CD	2.75	0.49
1:D:707:GLU:HG2	1:D:709:VAL:HG12	1.95	0.49
1:A:753:GLU:HG2	1:A:1002:PHE:CD1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1053:THR:HG22	1:B:1079:THR:HA	1.95	0.49
1:C:707:GLU:O	1:C:707:GLU:HG3	2.12	0.49
1:D:778:HIS:HE1	6:D:1208:MES:H72	1.75	0.48
1:B:785:VAL:HA	1:B:786:ASN:HA	1.67	0.48
1:C:892:LEU:O	1:C:1009:ALA:HA	2.14	0.48
1:B:1095:GLU:HB3	1:B:1110:VAL:HG22	1.96	0.47
1:C:1106:ARG:HB2	1:C:1107:PRO:HD2	1.96	0.47
1:C:923:ILE:O	1:C:925:ARG:HG3	2.14	0.47
1:D:859:LEU:HD23	1:D:890:LEU:HD21	1.96	0.47
1:A:711:THR:HG21	1:A:741:GLN:HE22	1.79	0.47
1:B:1064:ASN:ND2	1:B:1096:GLU:O	2.47	0.47
1:D:699:SER:HA	8:D:1435:HOH:O	2.13	0.47
1:A:759:GLY:HA3	1:A:853:ILE:HG23	1.95	0.47
1:C:736:GLY:HA3	1:C:741:GLN:HE21	1.80	0.47
1:D:711:THR:HG21	1:D:741:GLN:NE2	2.25	0.46
1:C:989:THR:OG1	1:C:1004:LYS:HD2	2.15	0.46
1:B:729:GLU:OE2	1:B:746:LYS:HB3	2.16	0.46
1:B:1061:SER:HA	1:B:1071:ILE:O	2.15	0.46
1:D:913:TYR:O	7:D:1210:GOL:C3	2.63	0.46
1:C:801:SER:C	1:C:803:VAL:H	2.24	0.46
1:A:693:GLU:HG2	8:A:1395:HOH:O	2.16	0.46
1:A:770:LYS:HD3	8:A:1618:HOH:O	2.16	0.46
1:C:847:LEU:HD12	1:C:972:PRO:HB2	1.98	0.46
1:B:1023:VAL:HA	1:B:1024:GLY:HA2	1.72	0.45
1:A:925:ARG:HG2	1:A:928:PHE:CD1	2.52	0.45
1:A:978:ARG:HD3	8:A:1350:HOH:O	2.15	0.45
1:D:711:THR:CG2	1:D:741:GLN:NE2	2.80	0.45
1:B:1105:GLU:O	1:B:1106:ARG:HG2	2.16	0.45
1:A:922:GLU:H	1:A:922:GLU:HG2	1.53	0.44
1:A:742[B]:THR:HB	1:A:1059:SER:HG	1.80	0.44
1:B:1085:ILE:O	1:B:1086:LEU:HD12	2.18	0.44
1:C:1040:TYR:HB3	1:C:1114:LEU:HD23	1.99	0.44
1:B:1062:ALA:C	1:B:1064:ASN:H	2.26	0.44
1:C:876:GLY:H	1:C:879:SER:HB2	1.81	0.44
1:D:709:VAL:HG13	1:D:710:ASN:OD1	2.17	0.44
1:D:743:LYS:HD2	1:D:1021:ASP:O	2.18	0.44
1:A:788:CYS:HB2	1:A:832:CYS:SG	2.58	0.44
1:B:752:SER:HB3	1:B:1003:SER:HB2	2.00	0.44
1:C:1095:GLU:HB2	1:C:1110:VAL:CG2	2.47	0.44
1:B:770:LYS:HG3	1:B:840:GLN:OE1	2.17	0.44
1:B:777:CYS:HB3	8:B:1404:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1109:LEU:HG	8:C:1455:HOH:O	2.17	0.44
1:C:1095:GLU:HB2	1:C:1110:VAL:HG23	2.00	0.43
1:D:735:LYS:HG2	8:D:1496:HOH:O	2.18	0.43
1:D:785:VAL:HG11	6:D:1208:MES:H32	1.99	0.43
1:D:753[A]:GLU:HG2	1:D:1002:PHE:HE1	1.80	0.43
1:B:722:ARG:NH2	1:B:1008:GLN:HA	2.32	0.43
1:B:967:THR:HB	1:B:969:LEU:HG	1.99	0.43
1:D:1021:ASP:OD1	1:D:1021:ASP:C	2.62	0.43
1:D:688:ASP:N	8:D:1606:HOH:O	2.52	0.43
1:A:892:LEU:HD13	8:A:1632:HOH:O	2.18	0.43
1:C:706:THR:HG23	1:C:711:THR:HG22	2.01	0.43
1:C:1008:GLN:HE22	1:D:819:GLY:H	1.67	0.43
1:D:1035:ASN:HD22	4:H:1:NAG:H83	1.84	0.42
1:D:700:ARG:NH2	8:D:1430:HOH:O	2.52	0.42
1:C:1115:ILE:H	1:C:1115:ILE:HG13	1.74	0.42
1:A:722:ARG:NH1	8:A:1632:HOH:O	2.35	0.42
1:A:1057:THR:HG23	8:A:1310:HOH:O	2.20	0.42
1:B:989:THR:O	1:B:1001:ALA:HA	2.19	0.42
1:D:819:GLY:HA3	1:D:829:ASN:O	2.20	0.42
1:D:957:LYS:HB3	1:D:959:MET:HE3	2.02	0.42
1:A:693:GLU:OE2	1:B:821:TRP:HD1	2.02	0.42
1:A:735:LYS:NZ	1:A:739:GLU:O	2.53	0.42
1:D:714:ARG:HA	1:D:1018:PHE:O	2.20	0.41
1:B:1102:ASP:N	1:B:1103:GLY:HA2	2.35	0.41
1:C:885:TRP:CH2	1:C:888:VAL:HG22	2.52	0.41
1:C:1064:ASN:HA	1:C:1096:GLU:O	2.20	0.41
7:D:1210:GOL:H12	8:D:1577:HOH:O	2.20	0.41
1:D:1031:ALA:HA	1:D:1051:SER:O	2.20	0.41
1:B:1027:VAL:HG21	1:B:1055:THR:HB	2.02	0.41
1:C:1060:LEU:HD23	1:C:1060:LEU:C	2.46	0.41
1:D:693:GLU:HG2	8:D:1434:HOH:O	2.20	0.41
1:B:1017:ASN:HD22	1:B:1017:ASN:HA	1.59	0.41
1:B:1085:ILE:H	1:B:1085:ILE:HG13	1.69	0.41
1:C:714:ARG:NH2	8:C:1377:HOH:O	2.54	0.41
1:D:996:ASN:ND2	8:D:1577:HOH:O	2.53	0.41
1:D:753[A]:GLU:OE1	1:D:1002:PHE:HE1	2.04	0.40
1:A:1066:ASP:OD1	1:A:1066:ASP:N	2.55	0.40
1:D:791:TRP:CE2	1:D:795:GLU:HG3	2.57	0.40
1:C:890:LEU:CD2	1:C:1009:ALA:HB1	2.51	0.40
1:C:993:SER:HB3	1:C:996:ASN:HB3	2.03	0.40
1:D:843:ARG:HD2	1:D:973:PHE:CE1	2.57	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	431/432 (100%)	417 (97%)	10 (2%)	4 (1%)	14	6
1	B	425/432 (98%)	404 (95%)	17 (4%)	4 (1%)	14	6
1	C	429/432 (99%)	413 (96%)	13 (3%)	3 (1%)	18	10
1	D	434/432 (100%)	422 (97%)	11 (2%)	1 (0%)	43	36
All	All	1719/1728 (100%)	1656 (96%)	51 (3%)	12 (1%)	18	10

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	960	ILE
1	B	960	ILE
1	C	785	VAL
1	C	960	ILE
1	D	960	ILE
1	A	708	GLY
1	A	709	VAL
1	B	1091	PRO
1	C	802	PHE
1	B	1107	PRO
1	B	1027	VAL
1	A	785	VAL

5.3.2 Protein sidechains [i](#)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	373/372 (100%)	355 (95%)	18 (5%)	23	15
1	B	368/372 (99%)	346 (94%)	22 (6%)	17	9
1	C	371/372 (100%)	354 (95%)	17 (5%)	24	16
1	D	376/372 (101%)	357 (95%)	19 (5%)	21	13
All	All	1488/1488 (100%)	1412 (95%)	76 (5%)	21	13

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	709	VAL
1	A	711	THR
1	A	720	LEU
1	A	740	ASP
1	A	743	LYS
1	A	842	VAL
1	A	891	SER
1	A	892	LEU
1	A	922	GLU
1	A	923	ILE
1	A	941	LEU
1	A	994	LYS
1	A	1017	ASN
1	A	1050	LEU
1	A	1080	LYS
1	A	1086	LEU
1	A	1110	VAL
1	A	1111	LYS
1	B	703	THR
1	B	711	THR
1	B	712	LYS
1	B	714	ARG
1	B	725	SER
1	B	742	THR
1	B	842	VAL
1	B	937	GLU
1	B	970	ILE
1	B	977	GLU
1	B	997	ARG
1	B	1016	ASP
1	B	1017	ASN

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Mol	Chain	Res	Type
1	B	1023	VAL
1	B	1029	CYS
1	B	1065	LYS
1	B	1072	VAL
1	B	1085	ILE
1	B	1086	LEU
1	B	1096	GLU
1	B	1105	GLU
1	B	1110	VAL
1	C	707	GLU
1	C	709	VAL
1	C	711	THR
1	C	722	ARG
1	C	735	LYS
1	C	792	ARG
1	C	842	VAL
1	C	879	SER
1	C	911	LYS
1	C	922	GLU
1	C	994	LYS
1	C	1016	ASP
1	C	1029	CYS
1	C	1036	LEU
1	C	1037	THR
1	C	1066	ASP
1	C	1115	ILE
1	D	695	ILE
1	D	700	ARG
1	D	711	THR
1	D	735	LYS
1	D	737	VAL
1	D	738	LYS
1	D	740	ASP
1	D	761	SER
1	D	772	LEU
1	D	941	LEU
1	D	970	ILE
1	D	996	ASN
1	D	1017	ASN
1	D	1047	ARG
1	D	1057	THR
1	D	1065	LYS

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Mol	Chain	Res	Type
1	D	1079	THR
1	D	1086	LEU
1	D	1110	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	710	ASN
1	A	996	ASN
1	A	1000	GLN
1	A	1043	ASN
1	B	996	ASN
1	B	1000	GLN
1	B	1017	ASN
1	B	1063	HIS
1	B	1064	ASN
1	C	741	GLN
1	C	760	GLN
1	C	1008	GLN
1	C	1077	ASN
1	D	696	GLN
1	D	760	GLN
1	D	778	HIS
1	D	784	HIS
1	D	996	ASN
1	D	1000	GLN
1	D	1017	ASN

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 ⓘ

17 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	E	1	1,2	14,14,15	0.62	0	17,19,21	1.30	3 (17%)
2	NAG	E	2	2	14,14,15	0.73	0	17,19,21	1.26	1 (5%)
2	BMA	E	3	2	11,11,12	0.81	0	15,15,17	1.30	2 (13%)
2	BMA	E	4	2	11,11,12	0.73	0	15,15,17	1.65	3 (20%)
3	NAG	F	1	1,3	14,14,15	0.56	0	17,19,21	1.38	2 (11%)
3	NAG	F	2	3	14,14,15	0.41	0	17,19,21	1.71	6 (35%)
3	BMA	F	3	3	11,11,12	1.05	1 (9%)	15,15,17	1.07	1 (6%)
4	NAG	G	1	4,1	14,14,15	0.47	0	17,19,21	1.48	5 (29%)
4	NAG	G	2	4	14,14,15	0.57	0	17,19,21	1.26	1 (5%)
4	BMA	G	3	4	11,11,12	0.50	0	15,15,17	0.92	1 (6%)
4	BMA	G	4	4	11,11,12	0.48	0	15,15,17	1.29	1 (6%)
4	BMA	G	5	4	11,11,12	0.52	0	15,15,17	2.07	3 (20%)
4	NAG	H	1	4,1	14,14,15	0.52	0	17,19,21	1.23	3 (17%)
4	NAG	H	2	4	14,14,15	0.78	0	17,19,21	1.37	1 (5%)
4	BMA	H	3	4	11,11,12	0.89	1 (9%)	15,15,17	2.87	6 (40%)
4	BMA	H	4	4	11,11,12	0.66	0	15,15,17	2.43	6 (40%)
4	BMA	H	5	4	11,11,12	0.51	0	15,15,17	1.84	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	E	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	BMA	E	3	2	-	2/2/19/22	0/1/1/1
2	BMA	E	4	2	-	2/2/19/22	0/1/1/1
3	NAG	F	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	F	2	3	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	F	3	3	-	2/2/19/22	0/1/1/1
4	NAG	G	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	G	2	4	-	2/6/23/26	0/1/1/1
4	BMA	G	3	4	-	0/2/19/22	0/1/1/1
4	BMA	G	4	4	-	2/2/19/22	1/1/1/1
4	BMA	G	5	4	-	2/2/19/22	0/1/1/1
4	NAG	H	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	BMA	H	3	4	-	2/2/19/22	0/1/1/1
4	BMA	H	4	4	-	2/2/19/22	0/1/1/1
4	BMA	H	5	4	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	3	BMA	O5-C1	3.03	1.48	1.43
4	H	3	BMA	O5-C1	2.22	1.47	1.43

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	5	BMA	C1-O5-C5	5.87	120.05	112.19
4	H	5	BMA	C1-O5-C5	-5.80	104.42	112.19
4	H	4	BMA	C1-O5-C5	5.76	119.90	112.19
4	H	3	BMA	C3-C4-C5	-5.53	100.21	110.23
4	H	3	BMA	O5-C5-C6	4.81	117.03	107.66
4	H	3	BMA	O3-C3-C4	4.44	120.83	110.38
4	H	3	BMA	O5-C1-C2	4.32	121.10	110.79
4	H	4	BMA	C3-C4-C5	4.18	117.81	110.23
4	G	4	BMA	C1-O5-C5	4.11	117.69	112.19
4	H	2	NAG	O4-C4-C5	-3.91	99.70	109.32
4	H	3	BMA	O3-C3-C2	3.87	117.95	110.05
4	G	5	BMA	C3-C4-C5	3.67	116.89	110.23
3	F	2	NAG	C3-C4-C5	3.60	116.77	110.23
2	E	4	BMA	C1-O5-C5	3.47	116.84	112.19
4	H	4	BMA	O5-C1-C2	3.38	118.84	110.79
4	G	2	NAG	C4-C3-C2	3.36	115.95	111.02
4	G	1	NAG	C4-C3-C2	-3.34	106.12	111.02
2	E	4	BMA	C1-C2-C3	3.31	114.46	109.64
2	E	3	BMA	O5-C5-C6	-3.24	101.35	107.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	1	NAG	O5-C1-C2	-3.20	106.35	111.29
4	H	4	BMA	C1-C2-C3	3.17	114.26	109.64
4	G	5	BMA	O5-C5-C4	3.05	118.25	110.83
2	E	2	NAG	O4-C4-C5	-2.91	102.16	109.32
3	F	2	NAG	C1-O5-C5	2.86	116.02	112.19
2	E	1	NAG	O7-C7-C8	-2.66	117.31	122.05
4	H	3	BMA	C1-C2-C3	-2.60	105.85	109.64
4	H	1	NAG	C8-C7-N2	2.58	120.39	116.12
3	F	3	BMA	C1-C2-C3	-2.56	105.92	109.64
2	E	3	BMA	C6-C5-C4	2.49	119.12	113.02
4	H	5	BMA	O5-C5-C6	2.48	112.48	107.66
3	F	2	NAG	O5-C1-C2	-2.43	107.52	111.29
2	E	4	BMA	O5-C1-C2	2.38	116.47	110.79
2	E	1	NAG	C1-C2-N2	-2.38	106.69	110.43
4	H	1	NAG	O7-C7-C8	-2.37	117.83	122.05
4	G	1	NAG	C8-C7-N2	2.35	120.02	116.12
4	H	4	BMA	C2-C3-C4	2.33	114.97	110.86
4	G	1	NAG	O5-C1-C2	-2.31	107.72	111.29
2	E	1	NAG	C8-C7-N2	2.28	119.91	116.12
4	G	3	BMA	O5-C5-C6	2.28	112.10	107.66
3	F	2	NAG	C6-C5-C4	-2.23	107.53	113.02
4	G	1	NAG	C1-C2-N2	2.22	113.93	110.43
3	F	2	NAG	C4-C3-C2	2.21	114.25	111.02
4	H	1	NAG	O5-C1-C2	-2.17	107.94	111.29
3	F	1	NAG	C8-C7-N2	2.12	119.63	116.12
4	G	1	NAG	O7-C7-C8	-2.08	118.36	122.05
4	H	4	BMA	O5-C5-C4	2.01	115.72	110.83
3	F	2	NAG	O5-C5-C4	2.01	115.71	110.83

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	3	BMA	C4-C5-C6-O6
2	E	3	BMA	O5-C5-C6-O6
4	H	3	BMA	O5-C5-C6-O6
4	G	5	BMA	O5-C5-C6-O6
4	G	2	NAG	O5-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
4	G	4	BMA	O5-C5-C6-O6
2	E	4	BMA	O5-C5-C6-O6
4	G	2	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	G	4	BMA	C4-C5-C6-O6
4	H	3	BMA	C4-C5-C6-O6
4	H	4	BMA	O5-C5-C6-O6
4	G	5	BMA	C4-C5-C6-O6
2	E	4	BMA	C4-C5-C6-O6
2	E	1	NAG	C8-C7-N2-C2
2	E	1	NAG	O7-C7-N2-C2
3	F	1	NAG	C8-C7-N2-C2
3	F	1	NAG	O7-C7-N2-C2
4	G	1	NAG	C8-C7-N2-C2
4	G	1	NAG	O7-C7-N2-C2
4	H	1	NAG	C8-C7-N2-C2
4	H	1	NAG	O7-C7-N2-C2
3	F	1	NAG	C4-C5-C6-O6
3	F	3	BMA	C4-C5-C6-O6
3	F	3	BMA	O5-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
4	H	4	BMA	C4-C5-C6-O6

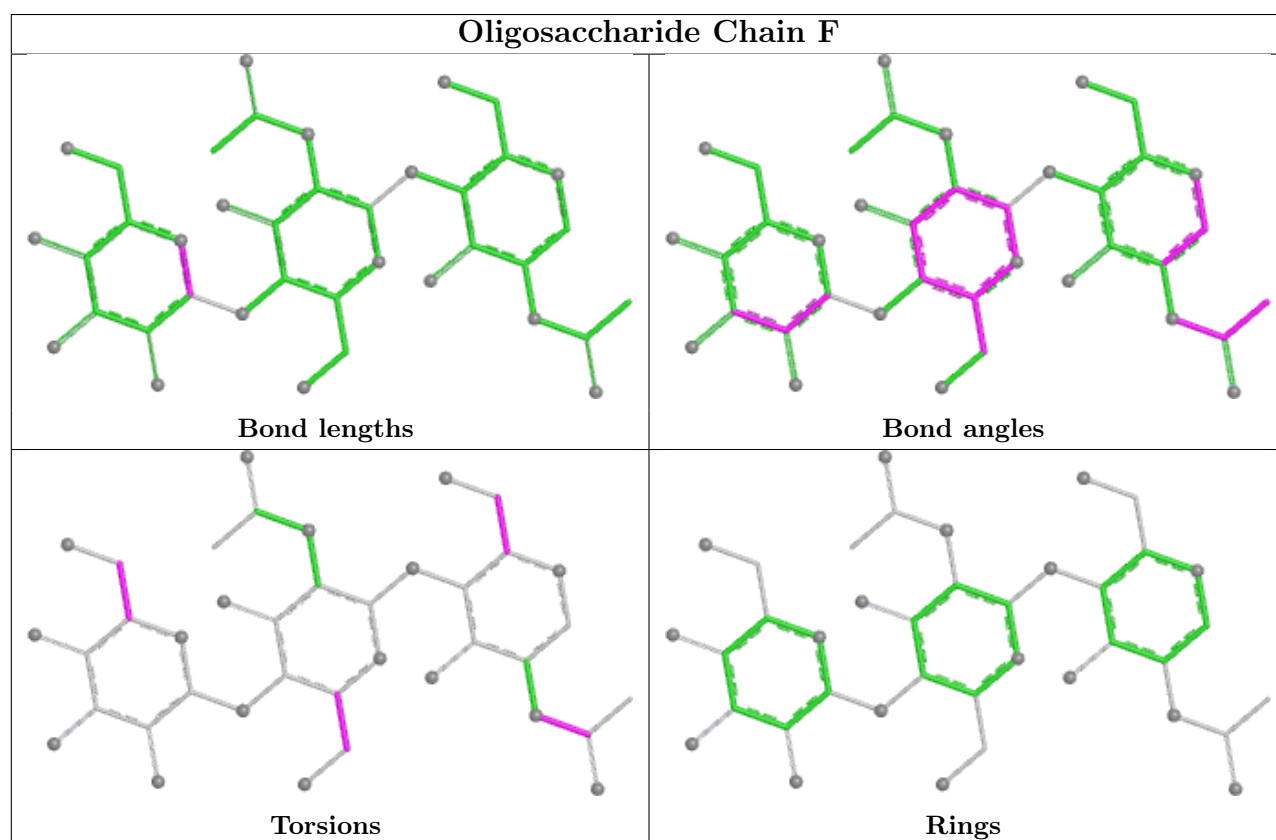
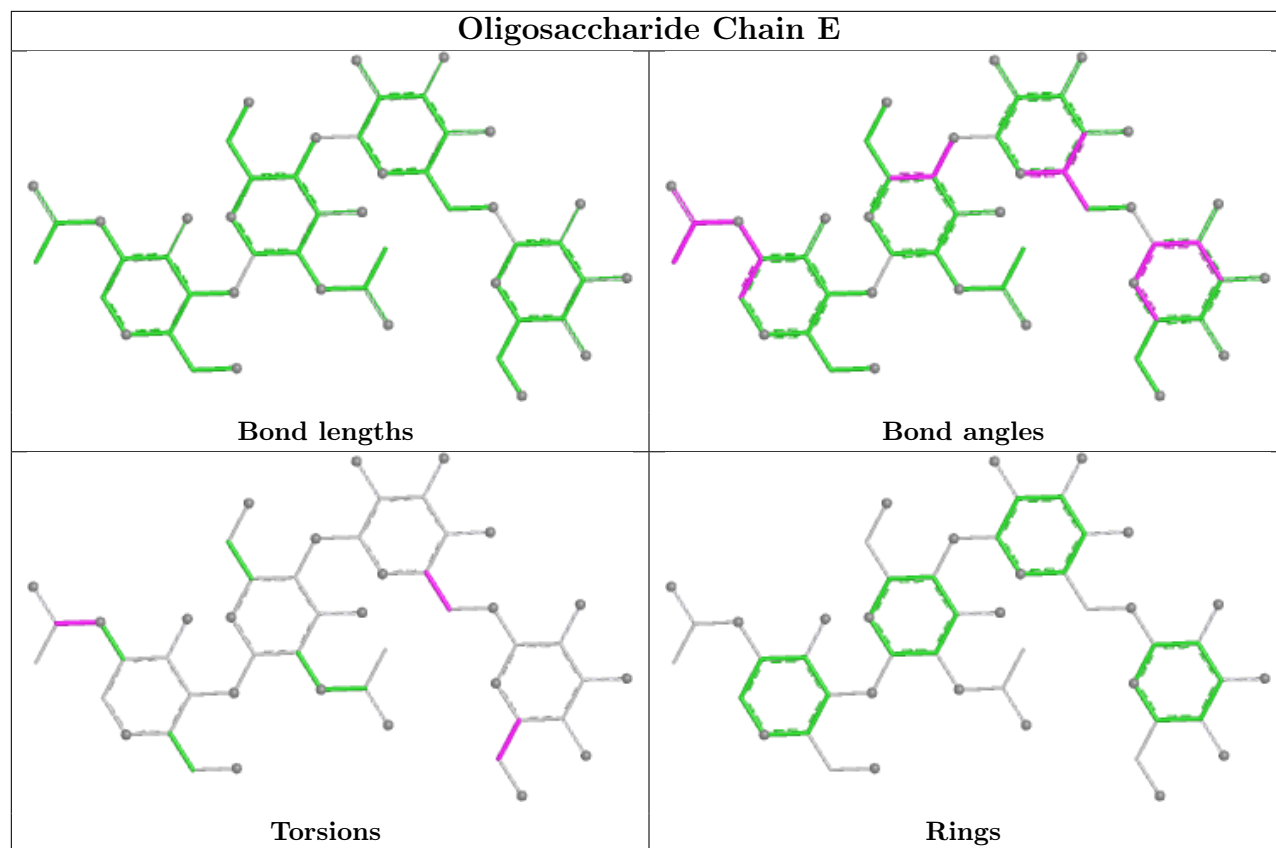
All (1) ring outliers are listed below:

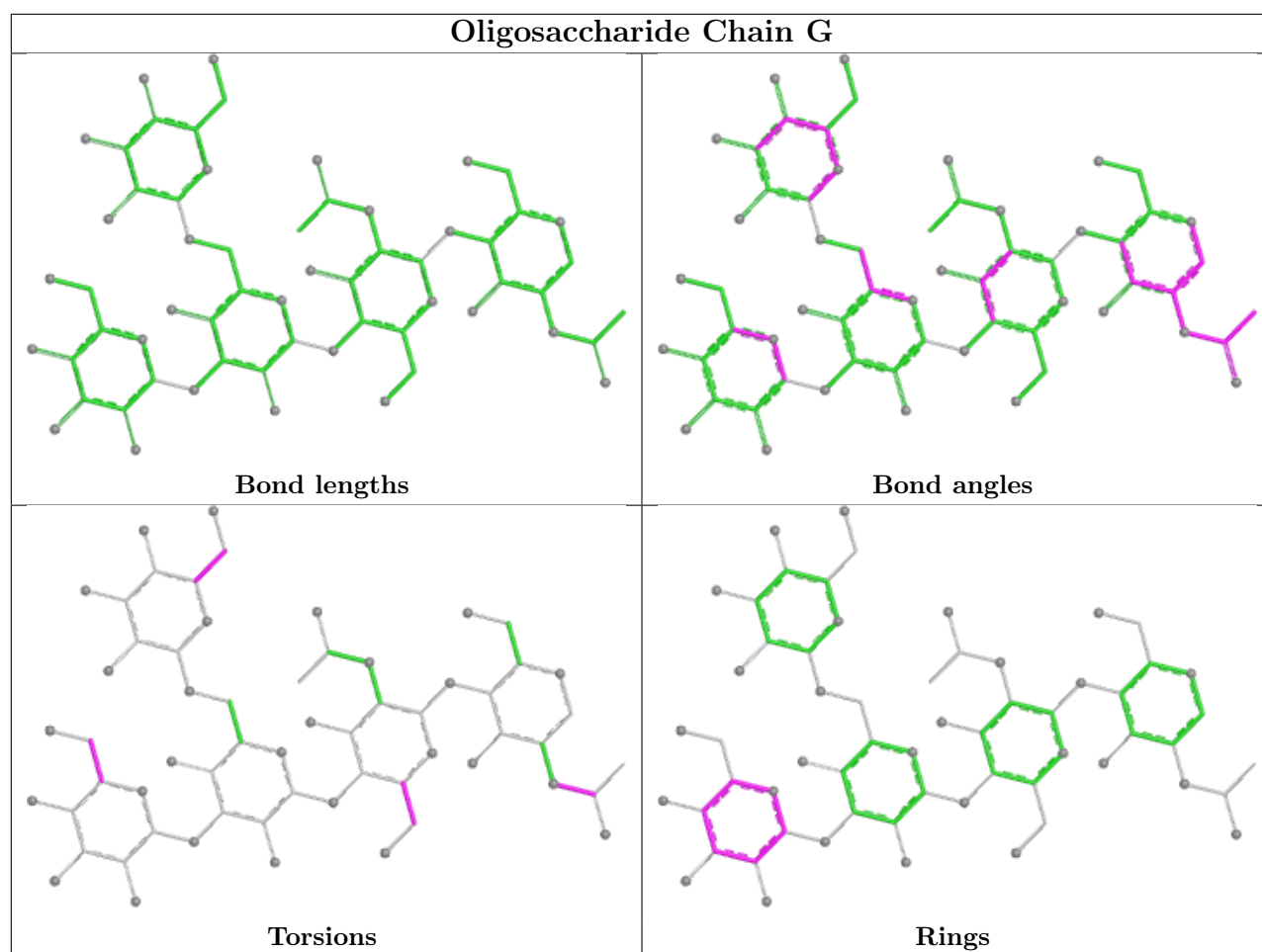
Mol	Chain	Res	Type	Atoms
4	G	4	BMA	C1-C2-C3-C4-C5-O5

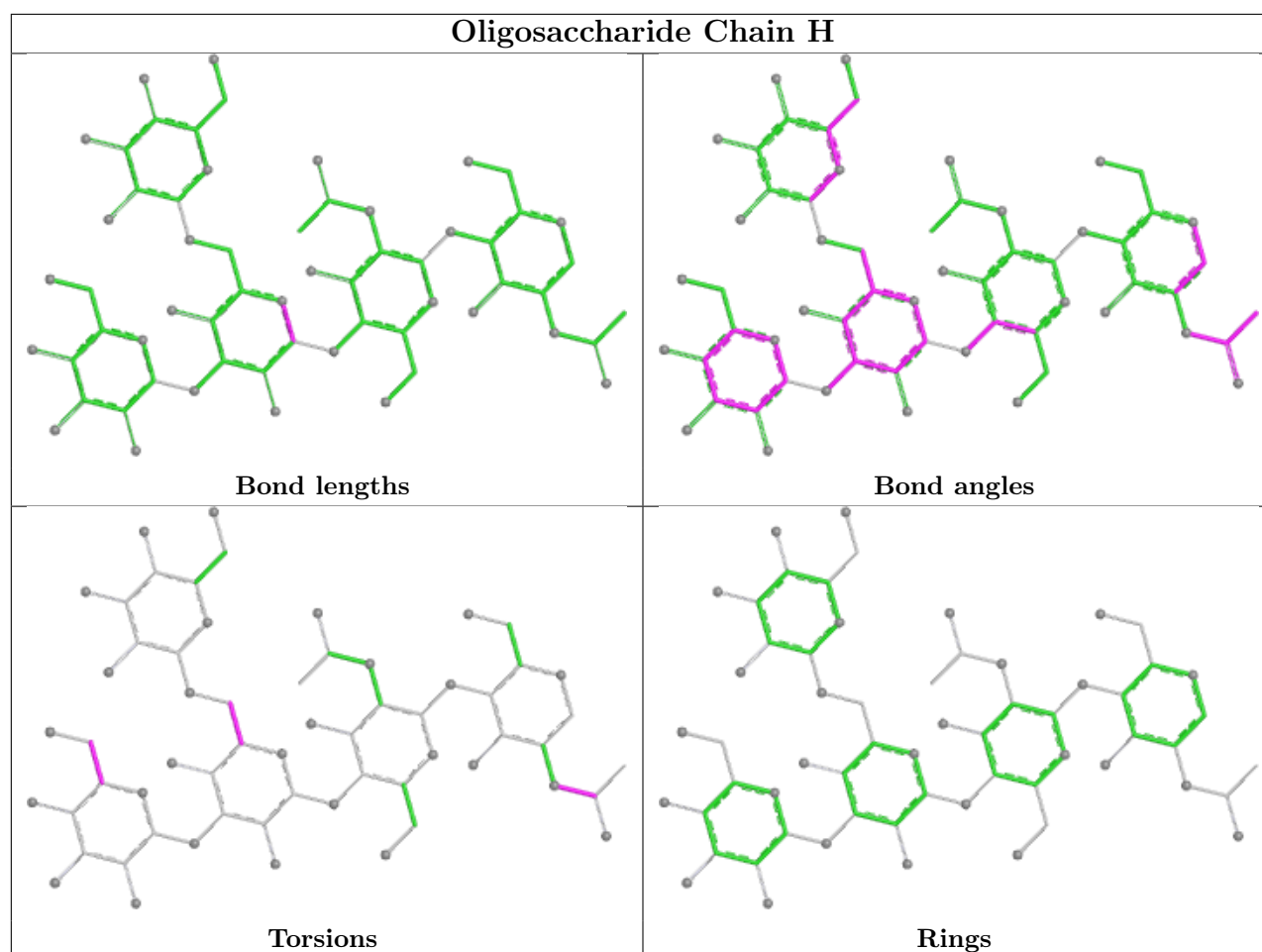
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	1	NAG	1	0
2	E	4	BMA	1	0
4	H	5	BMA	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](#)

14 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	$\# Z > 2$
5	NAG	D	1201	1	14,14,15	0.47	0	17,19,21	0.94	1 (5%)
6	MES	A	1206	-	12,12,12	2.31	1 (8%)	15,16,16	6.00	8 (53%)
5	NAG	C	1201	1	14,14,15	0.53	0	17,19,21	1.10	1 (5%)
5	NAG	A	1201	1	14,14,15	0.52	0	17,19,21	1.26	2 (11%)
6	MES	D	1207	-	12,12,12	2.45	1 (8%)	15,16,16	5.70	9 (60%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	MES	C	1207	-	12,12,12	2.45	1 (8%)	15,16,16	5.06	5 (33%)
7	GOL	C	1208	-	5,5,5	0.20	0	5,5,5	0.50	0
7	GOL	D	1210	-	5,5,5	0.09	0	5,5,5	0.60	0
5	NAG	B	1201	1	14,14,15	0.48	0	17,19,21	1.06	0
7	GOL	A	1207	-	5,5,5	0.21	0	5,5,5	0.68	0
7	GOL	B	1206	-	5,5,5	0.34	0	5,5,5	0.38	0
6	MES	D	1208	-	12,12,12	2.19	1 (8%)	15,16,16	6.06	5 (33%)
6	MES	B	1205	-	12,12,12	2.14	1 (8%)	15,16,16	1.45	1 (6%)
7	GOL	D	1209	-	5,5,5	0.39	0	5,5,5	0.55	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
5	NAG	D	1201	1	-	2/6/23/26	0/1/1/1
6	MES	A	1206	-	-	3/6/14/14	0/1/1/1
5	NAG	C	1201	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1201	1	-	2/6/23/26	0/1/1/1
6	MES	D	1207	-	-	5/6/14/14	0/1/1/1
6	MES	C	1207	-	-	2/6/14/14	0/1/1/1
7	GOL	C	1208	-	-	0/4/4/4	-
7	GOL	D	1210	-	-	2/4/4/4	-
5	NAG	B	1201	1	-	4/6/23/26	0/1/1/1
7	GOL	A	1207	-	-	0/4/4/4	-
7	GOL	B	1206	-	-	1/4/4/4	-
6	MES	D	1208	-	-	4/6/14/14	0/1/1/1
6	MES	B	1205	-	-	4/6/14/14	0/1/1/1
7	GOL	D	1209	-	-	0/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1207	MES	C8-S	-8.28	1.66	1.77
6	D	1207	MES	C8-S	-8.17	1.66	1.77
6	A	1206	MES	C8-S	-7.65	1.66	1.77
6	D	1208	MES	C8-S	-7.23	1.67	1.77
6	B	1205	MES	C8-S	-7.00	1.67	1.77

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	1207	MES	O3S-S-O1S	-11.76	81.97	111.40
6	D	1208	MES	O3S-S-O2S	-11.65	82.26	111.40
6	A	1206	MES	O3S-S-C8	-11.21	84.08	106.00
6	D	1208	MES	O3S-S-C8	-11.10	84.28	106.00
6	A	1206	MES	O3S-S-O2S	-10.89	84.17	111.40
6	C	1207	MES	O2S-S-C8	10.48	122.57	106.73
6	D	1208	MES	O2S-S-C8	10.28	122.27	106.73
6	D	1207	MES	O3S-S-O2S	-10.15	86.00	111.40
6	A	1206	MES	O3S-S-O1S	-10.12	86.08	111.40
6	D	1208	MES	O3S-S-O1S	-10.00	86.37	111.40
6	D	1207	MES	O3S-S-C8	-9.31	87.79	106.00
6	A	1206	MES	O1S-S-C8	9.30	120.78	106.73
6	C	1207	MES	O1S-S-C8	9.23	120.67	106.73
6	D	1208	MES	O1S-S-C8	8.60	119.72	106.73
6	C	1207	MES	O3S-S-O1S	-8.48	90.18	111.40
6	A	1206	MES	O2S-S-C8	8.31	119.29	106.73
6	C	1207	MES	O3S-S-C8	-8.13	90.10	106.00
6	D	1207	MES	O2S-S-C8	7.89	118.65	106.73
6	D	1207	MES	O1S-S-C8	7.52	118.09	106.73
6	C	1207	MES	O3S-S-O2S	-6.40	95.40	111.40
6	B	1205	MES	O3S-S-C8	4.16	114.15	106.00
6	D	1207	MES	C2-C3-N4	-3.73	104.44	110.12
6	A	1206	MES	C5-N4-C3	3.63	116.66	108.84
6	D	1207	MES	C6-C5-N4	-2.95	105.64	110.12
5	A	1201	NAG	C2-N2-C7	2.45	126.19	122.90
6	A	1206	MES	C6-C5-N4	2.45	113.84	110.12
6	D	1207	MES	C8-C7-N4	-2.30	103.65	112.36
6	D	1207	MES	O2S-S-O1S	2.27	121.20	113.82
6	A	1206	MES	C7-N4-C3	-2.24	105.26	111.24
5	D	1201	NAG	C8-C7-N2	2.14	119.67	116.12
5	A	1201	NAG	C8-C7-N2	2.08	119.57	116.12
5	C	1201	NAG	O7-C7-C8	-2.01	118.47	122.05

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1206	MES	C7-C8-S-O1S
6	B	1205	MES	C7-C8-S-O2S
6	B	1205	MES	C7-C8-S-O3S
6	C	1207	MES	C7-C8-S-O2S

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Mol	Chain	Res	Type	Atoms
7	D	1210	GOL	O1-C1-C2-C3
5	A	1201	NAG	C8-C7-N2-C2
5	A	1201	NAG	O7-C7-N2-C2
5	B	1201	NAG	C8-C7-N2-C2
5	B	1201	NAG	O7-C7-N2-C2
5	C	1201	NAG	C8-C7-N2-C2
5	C	1201	NAG	O7-C7-N2-C2
5	D	1201	NAG	C8-C7-N2-C2
5	D	1201	NAG	O7-C7-N2-C2
6	A	1206	MES	C7-C8-S-O3S
6	C	1207	MES	C7-C8-S-O3S
6	D	1207	MES	C7-C8-S-O3S
5	B	1201	NAG	O5-C5-C6-O6
5	B	1201	NAG	C4-C5-C6-O6
7	D	1210	GOL	O1-C1-C2-O2
6	D	1208	MES	C7-C8-S-O3S
6	B	1205	MES	N4-C7-C8-S
6	D	1208	MES	C8-C7-N4-C5
6	B	1205	MES	C7-C8-S-O1S
6	D	1207	MES	C7-C8-S-O2S
6	D	1208	MES	C7-C8-S-O2S
6	A	1206	MES	N4-C7-C8-S
6	D	1207	MES	N4-C7-C8-S
6	D	1207	MES	C8-C7-N4-C3
6	D	1207	MES	C8-C7-N4-C5
6	D	1208	MES	C8-C7-N4-C3
7	B	1206	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1206	MES	1	0
7	D	1210	GOL	10	0
6	D	1208	MES	3	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	431/432 (99%)	0.17	19 (4%) 39 41	20, 37, 68, 100	2 (0%)
1	B	427/432 (98%)	1.55	128 (29%) 1 1	35, 70, 169, 214	0
1	C	430/432 (99%)	0.85	44 (10%) 12 12	23, 52, 110, 139	1 (0%)
1	D	431/432 (99%)	0.32	21 (4%) 35 37	15, 39, 71, 128	5 (1%)
All	All	1719/1728 (99%)	0.72	212 (12%) 8 9	15, 49, 120, 214	8 (0%)

All (212) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	789	LEU	5.7
1	B	1107	PRO	5.7
1	A	785	VAL	5.6
1	B	1114	LEU	5.5
1	C	1117	ILE	5.4
1	B	1098	MET	5.3
1	B	1097	PHE	5.2
1	B	1071	ILE	5.2
1	B	1031	ALA	5.2
1	B	1108	LEU	5.2
1	B	709	VAL	5.2
1	B	737	VAL	5.2
1	B	1099	TYR	5.2
1	B	1110	VAL	5.0
1	B	1069	LEU	4.8
1	B	1086	LEU	4.6
1	B	785	VAL	4.3
1	B	1088	PHE	4.3
1	B	1060	LEU	4.3
1	B	1101	CYS	4.3
1	C	1115	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
1	D	709	VAL	4.2
1	B	734	LEU	4.2
1	C	1031	ALA	4.1
1	B	1100	SER	4.1
1	B	1052	ILE	4.1
1	B	713	CYS	4.1
1	B	1109	LEU	4.1
1	B	1091	PRO	4.0
1	B	715	LEU	4.0
1	B	1023	VAL	4.0
1	B	1093	VAL	4.0
1	C	1109	LEU	3.9
1	B	1062	ALA	3.8
1	B	1106	ARG	3.8
1	B	803	VAL	3.8
1	B	1027	VAL	3.8
1	B	1072	VAL	3.7
1	B	1090	VAL	3.7
1	B	1020	VAL	3.7
1	B	1029	CYS	3.7
1	A	709	VAL	3.7
1	B	1070	HIS	3.6
1	C	1029	CYS	3.6
1	B	1044	ALA	3.5
1	B	1103	GLY	3.5
1	B	706	THR	3.5
1	B	1032	ALA	3.5
1	C	803	VAL	3.5
1	B	1026	ALA	3.5
1	B	1112	GLY	3.4
1	B	1025	ALA	3.4
1	C	1097	PHE	3.4
1	B	711	THR	3.4
1	B	694	LEU	3.4
1	B	1030	ASP	3.4
1	C	801	SER	3.3
1	C	709	VAL	3.3
1	B	1022	PHE	3.3
1	B	695	ILE	3.2
1	C	1032	ALA	3.2
1	D	996	ASN	3.2
1	C	1114	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	1040	TYR	3.1
1	B	995	GLY	3.1
1	B	1036	LEU	3.1
1	B	1064	ASN	3.1
1	B	1079	THR	3.1
1	B	1063	HIS	3.1
1	D	995	GLY	3.1
1	B	720	LEU	3.1
1	C	1027	VAL	3.1
1	B	1028	SER	3.1
1	B	1073	LEU	3.1
1	C	1093	VAL	3.1
1	D	699	SER	3.1
1	C	1090	VAL	3.0
1	A	1116	ALA	3.0
1	B	877	ALA	3.0
1	B	1104	ASP	3.0
1	B	1085	ILE	3.0
1	D	700	ARG	3.0
1	B	789	LEU	3.0
1	C	1099	TYR	3.0
1	B	1037	THR	3.0
1	C	1110	VAL	2.9
1	B	1024	GLY	2.9
1	B	802	PHE	2.9
1	B	745	LEU	2.9
1	B	1055	THR	2.9
1	D	1025	ALA	2.9
1	B	888	VAL	2.9
1	D	802	PHE	2.9
1	B	1111	LYS	2.9
1	A	821	TRP	2.9
1	B	1089	THR	2.8
1	B	696	GLN	2.8
1	B	697	ALA	2.8
1	B	798	ALA	2.8
1	D	704	CYS	2.8
1	C	1108	LEU	2.8
1	B	1053	THR	2.8
1	B	1057	THR	2.8
1	A	826	PHE	2.8
1	B	1105	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	1090	VAL	2.8
1	B	1068	SER	2.7
1	B	1039	CYS	2.7
1	B	796	THR	2.7
1	C	1034	LEU	2.7
1	D	1117	ILE	2.7
1	B	735	LYS	2.7
1	D	803	VAL	2.7
1	A	784	HIS	2.7
1	C	1088	PHE	2.7
1	A	779	LEU	2.7
1	C	802	PHE	2.6
1	D	703	THR	2.6
1	B	712	LYS	2.6
1	B	784	HIS	2.6
1	B	1102	ASP	2.6
1	D	702	THR	2.6
1	B	791	TRP	2.6
1	B	866	PHE	2.6
1	B	1059	SER	2.6
1	B	744	PHE	2.6
1	B	1015	PHE	2.6
1	C	1036	LEU	2.6
1	C	1060	LEU	2.6
1	D	694	LEU	2.6
1	B	804	GLY	2.6
1	B	1113	THR	2.6
1	B	948	LEU	2.5
1	C	1023	VAL	2.5
1	C	1113	THR	2.5
1	B	1066	ASP	2.5
1	A	892	LEU	2.5
1	B	941	LEU	2.5
1	B	1056	GLY	2.5
1	B	1075	SER	2.5
1	B	1058	GLY	2.4
1	B	1096	GLU	2.4
1	B	742	THR	2.4
1	C	1116	ALA	2.4
1	B	704	CYS	2.4
1	B	1014	MET	2.4
1	C	935	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	1115	ILE	2.4
1	C	1026	ALA	2.4
1	C	737	VAL	2.4
1	A	771	CYS	2.4
1	C	694	LEU	2.3
1	C	1002	PHE	2.3
1	D	737	VAL	2.3
1	B	1034	LEU	2.3
1	B	718	THR	2.3
1	B	826	PHE	2.3
1	B	1046	ALA	2.3
1	B	1038	GLY	2.3
1	B	1065	LYS	2.3
1	B	801	SER	2.3
1	B	1087	HIS	2.3
1	B	1074	PRO	2.3
1	C	1107	PRO	2.3
1	C	1052	ILE	2.3
1	B	838	TYR	2.2
1	B	1078	GLY	2.2
1	C	1091	PRO	2.2
1	C	882	PHE	2.2
1	B	701	ILE	2.2
1	D	735	LYS	2.2
1	A	780	VAL	2.2
1	B	761	SER	2.2
1	B	1061	SER	2.2
1	C	1005	GLY	2.2
1	C	785	VAL	2.2
1	B	771	CYS	2.2
1	D	713	CYS	2.2
1	A	804	GLY	2.2
1	C	1112	GLY	2.2
1	B	719	ALA	2.2
1	C	1062	ALA	2.2
1	B	911	LYS	2.2
1	A	996	ASN	2.1
1	B	703	THR	2.1
1	A	708	GLY	2.1
1	A	995	GLY	2.1
1	B	910	GLY	2.1
1	C	786	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	800	PHE	2.1
1	C	897	ILE	2.1
1	B	1067	GLY	2.1
1	A	783	CYS	2.1
1	A	852	CYS	2.1
1	D	1017	ASN	2.1
1	C	873	ILE	2.1
1	B	700	ARG	2.1
1	B	792	ARG	2.1
1	B	1012	THR	2.1
1	C	1079	THR	2.1
1	D	711	THR	2.1
1	C	1058	GLY	2.1
1	B	818	CYS	2.1
1	B	1013	LEU	2.1
1	B	793	ASP	2.1
1	C	1033	PHE	2.0
1	D	698	SER	2.0
1	B	786	ASN	2.0
1	A	1117	ILE	2.0
1	D	1022	PHE	2.0
1	B	781	GLY	2.0
1	B	924	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

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.

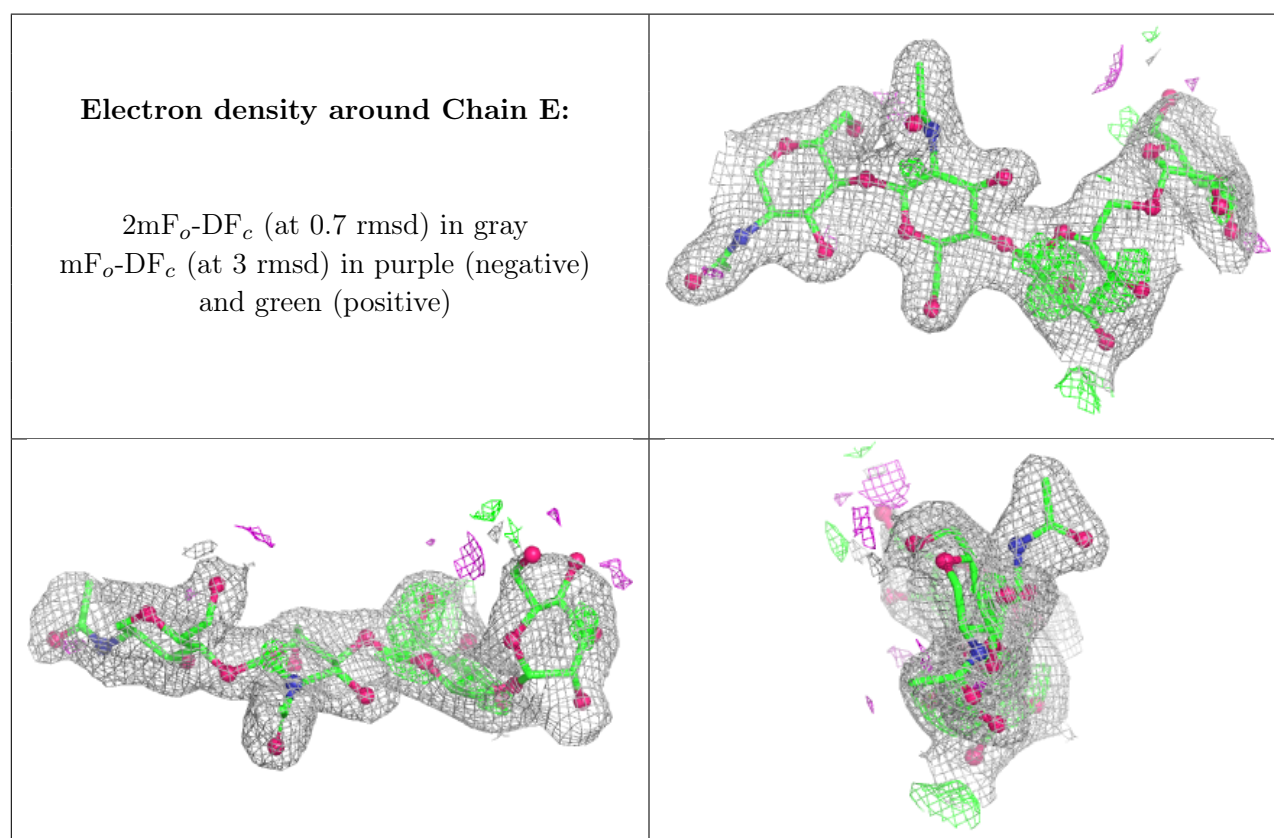
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BMA	G	3	11/12	0.53	0.14	98,102,107,109	0
4	BMA	G	5	11/12	0.56	0.12	108,113,115,116	0
4	BMA	H	5	11/12	0.58	0.17	94,103,107,109	0
3	BMA	F	3	11/12	0.64	0.14	88,93,96,99	0
4	BMA	H	3	11/12	0.69	0.17	51,64,73,84	0

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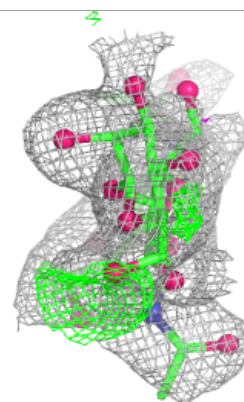
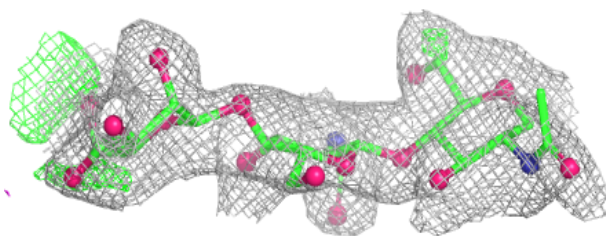
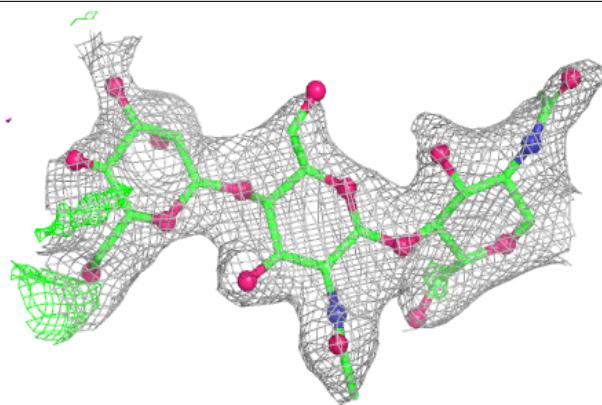
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	BMA	G	4	11/12	0.73	0.14	105,110,113,115	0
4	BMA	H	4	11/12	0.74	0.17	64,73,76,76	0
2	BMA	E	3	11/12	0.77	0.20	101,104,105,106	0
4	NAG	G	1	14/15	0.77	0.14	75,78,90,93	0
2	BMA	E	4	11/12	0.79	0.19	102,103,104,104	0
3	NAG	F	1	14/15	0.85	0.11	79,83,91,92	0
3	NAG	F	2	14/15	0.86	0.12	75,81,83,88	0
4	NAG	G	2	14/15	0.87	0.11	69,78,84,92	0
4	NAG	H	2	14/15	0.92	0.08	35,36,44,44	0
2	NAG	E	2	14/15	0.93	0.09	34,38,46,51	0
4	NAG	H	1	14/15	0.93	0.08	37,38,48,53	0
2	NAG	E	1	14/15	0.94	0.09	37,39,52,57	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.



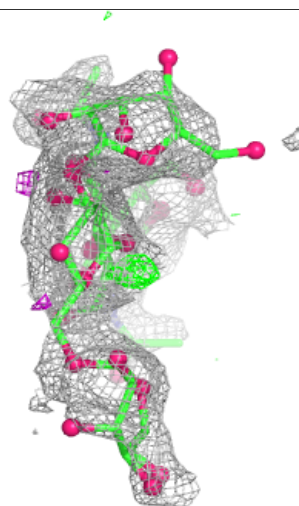
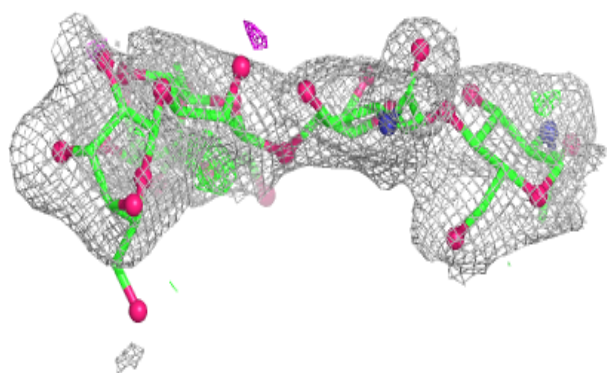
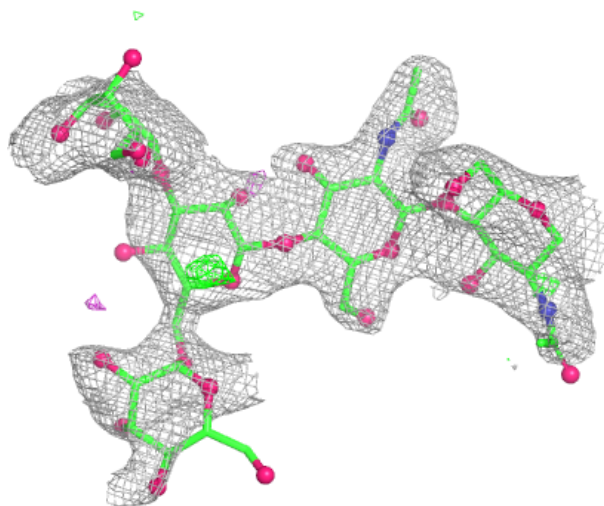
Electron density around Chain F:

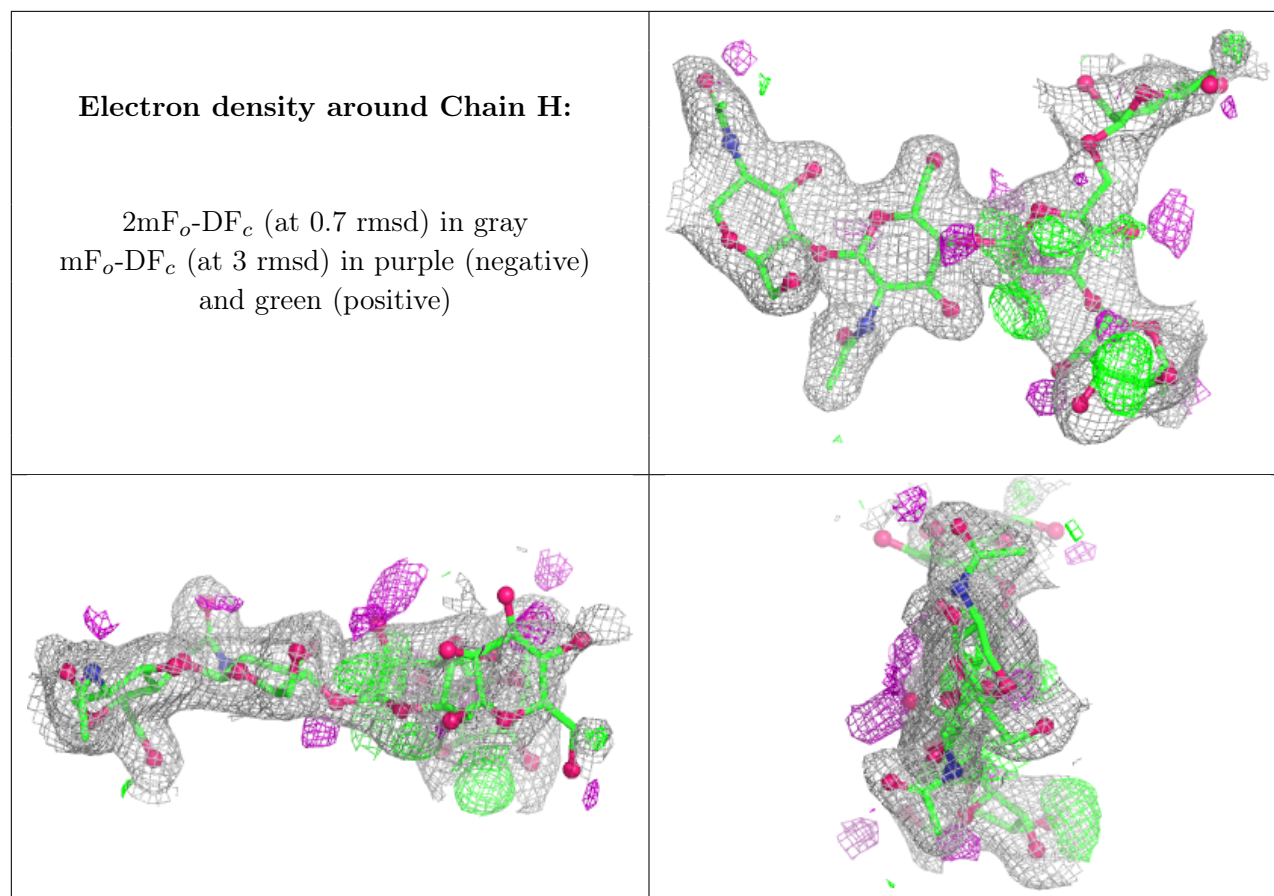
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain G:

$2mF_o-DF_c$ (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	NAG	B	1201	14/15	0.54	0.14	129,141,158,160	0
5	NAG	D	1201	14/15	0.64	0.14	79,89,94,95	0
5	NAG	C	1201	14/15	0.69	0.12	103,110,114,115	0
5	NAG	A	1201	14/15	0.72	0.12	82,96,99,100	0
6	MES	D	1208	12/12	0.81	0.21	55,63,70,71	12
7	GOL	D	1210	6/6	0.81	0.25	33,39,47,47	0
6	MES	A	1206	12/12	0.89	0.16	52,57,60,60	12
6	MES	D	1207	12/12	0.89	0.14	69,76,81,81	0
7	GOL	B	1206	6/6	0.91	0.10	69,70,71,71	0
7	GOL	A	1207	6/6	0.91	0.10	35,36,39,41	0
6	MES	B	1205	12/12	0.92	0.11	59,67,74,75	0
7	GOL	C	1208	6/6	0.93	0.08	47,54,57,62	0
7	GOL	D	1209	6/6	0.93	0.10	35,39,40,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	MES	C	1207	12/12	0.93	0.14	33,40,49,49	12

6.5 Other polymers [i](#)

There are no such residues in this entry.