



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 10:47 AM BST

PDB ID : 4P2N
Title : Structure of the P domain from a GI.7 Norovirus variant in complex with LeX HBGA
Authors : Shanker, S.; Czako, R.; Sankaran, B.; Atmar, R.; Estes, M.; Prasad, B.V.V.
Deposited on : 2014-03-04
Resolution : 1.70 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

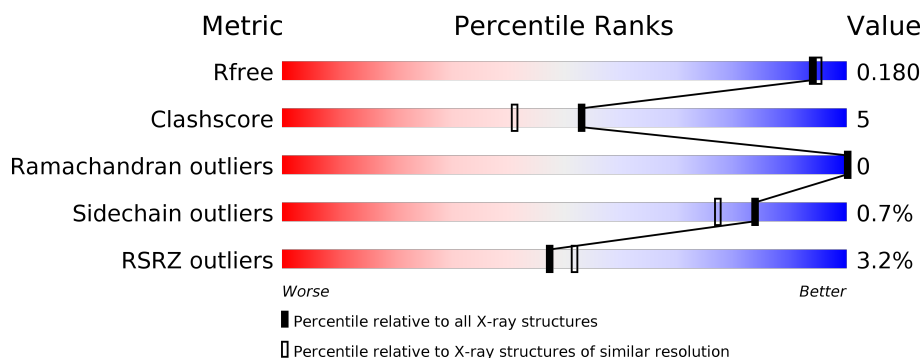
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




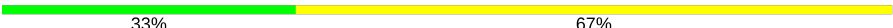
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 on 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	301	<div> <div>4%</div> <div> <div></div> <div>84%</div> <div>11%</div> <div>5%</div> </div> </div>
1	B	301	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>8%</div> <div>•</div> </div> </div>
1	C	301	<div> <div>4%</div> <div> <div></div> <div>86%</div> <div>9%</div> <div>• •</div> </div> </div>
1	D	301	<div> <div>3%</div> <div> <div></div> <div>90%</div> <div>5%</div> <div>5%</div> </div> </div>
2	E	3	<div> <div></div> <div> <div>33%</div> <div>33%</div> <div>33%</div> </div> </div>
2	F	3	<div> <div></div> <div> <div>33%</div> <div>67%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	G	3	 67% 33%
2	H	3	 33% 67%

2 Entry composition [i](#)

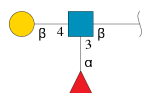
There are 3 unique types of molecules in this entry. The entry contains 10062 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Major capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	0	0	0
			2155	1378	363	406	8			
1	B	289	Total	C	N	O	S	0	0	0
			2199	1402	368	421	8			
1	C	288	Total	C	N	O	S	0	0	0
			2189	1398	366	417	8			
1	D	286	Total	C	N	O	S	0	0	0
			2188	1395	372	413	8			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	3	Total	C	N	O	0	0	0
			36	20	1	15			
2	F	3	Total	C	N	O	0	0	0
			36	20	1	15			
2	G	3	Total	C	N	O	0	0	0
			36	20	1	15			
2	H	3	Total	C	N	O	0	0	0
			36	20	1	15			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	300	Total	O	0	0
			300	300		

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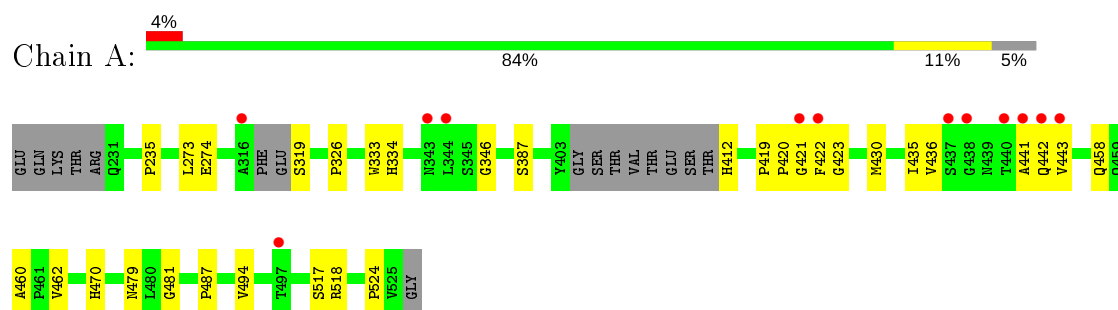
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	311	Total 311	O 311	0	0
3	C	290	Total 290	O 290	0	0
3	D	286	Total 286	O 286	0	0

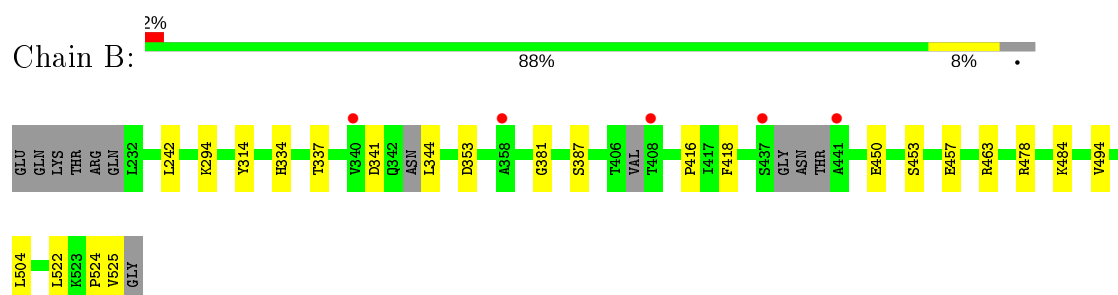
3 Residue-property plots [i](#)

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

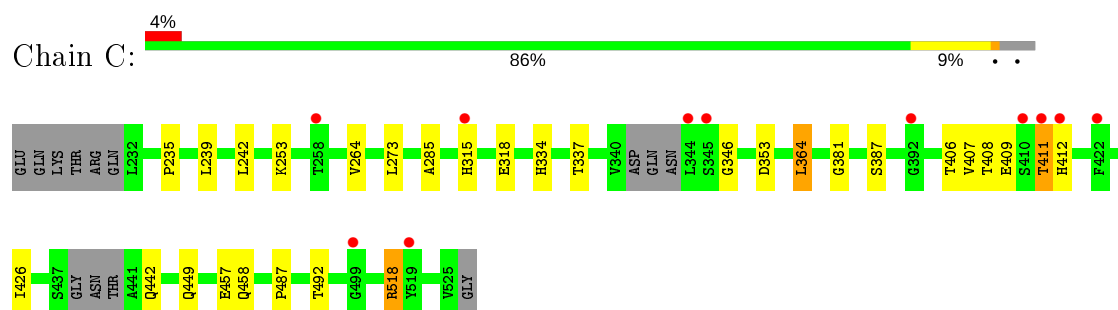
- Molecule 1: Major capsid protein



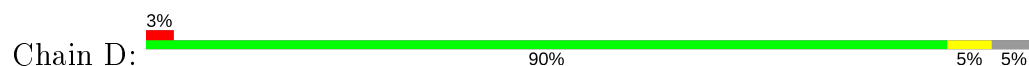
- Molecule 1: Major capsid protein

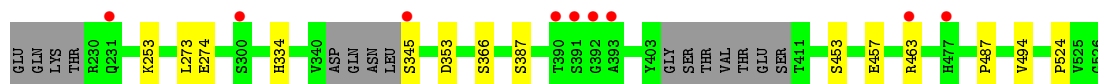


- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein





- Molecule 2: alpha-L-fucopyranose-(1-3)-[beta-D-galactopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: alpha-L-fucopyranose-(1-3)-[beta-D-galactopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: alpha-L-fucopyranose-(1-3)-[beta-D-galactopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: alpha-L-fucopyranose-(1-3)-[beta-D-galactopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	62.27Å 63.03Å 90.28Å 99.02° 98.16° 119.51°	Depositor
Resolution (Å)	45.95 – 1.70 45.95 – 1.70	Depositor EDS
% Data completeness (in resolution range)	96.9 (45.95-1.70) 96.9 (45.95-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 1.70Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.155 , 0.171 0.164 , 0.180	Depositor DCC
R_{free} test set	6140 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	13.7	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.006 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10062	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GAL, NAG, FUC

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	0.45	0/2219	0.59	0/3040
1	B	0.45	0/2263	0.58	0/3097
1	C	0.39	0/2254	0.59	1/3087 (0.0%)
1	D	0.36	0/2253	0.57	0/3081
All	All	0.41	0/8989	0.58	1/12305 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	364	LEU	CB-CG-CD2	-5.37	101.87	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	341	ASP	Peptide

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	A	2155	0	2074	32	0
1	B	2199	0	2111	15	0
1	C	2189	0	2109	36	0
1	D	2188	0	2116	9	0
2	E	36	0	33	1	0
2	F	36	0	33	4	0
2	G	36	0	33	0	0
2	H	36	0	33	1	0
3	A	300	0	0	13	0
3	B	311	0	0	5	0
3	C	290	0	0	4	0
3	D	286	0	0	2	0
All	All	10062	0	8542	94	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (94) 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:C:408:THR:O	1:C:411:THR:HG23	1.57	1.02
1:A:441:ALA:O	1:A:442:GLN:HG2	1.62	1.00
1:A:518:ARG:HD3	3:A:740:HOH:O	1.66	0.95
1:A:518:ARG:NH1	3:A:701:HOH:O	2.02	0.92
1:C:364:LEU:HD21	1:C:406:THR:HG21	1.53	0.91
1:C:318:GLU:O	1:C:412:HIS:HB2	1.75	0.87
1:A:518:ARG:CD	3:A:740:HOH:O	2.20	0.84
1:C:518:ARG:HH11	1:C:518:ARG:HG3	1.45	0.79
1:C:315:HIS:CE1	3:C:968:HOH:O	2.37	0.77
1:C:407:VAL:HG13	1:C:411:THR:HG21	1.66	0.77
1:C:408:THR:H	1:C:411:THR:CG2	1.99	0.76
1:A:436:VAL:O	1:A:436:VAL:HG12	1.90	0.70
1:C:273:LEU:HG	1:C:487:PRO:HA	1.74	0.69
1:C:334:HIS:HE1	1:C:387:SER:OG	1.76	0.69
1:C:264:VAL:HG22	3:C:943:HOH:O	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:334:HIS:HE1	1:D:387:SER:OG	1.78	0.67
1:A:334:HIS:HE1	1:A:387:SER:OG	1.79	0.65
1:B:334:HIS:HE1	1:B:387:SER:OG	1.80	0.64
1:C:318:GLU:O	1:C:412:HIS:N	2.30	0.63
1:A:422:PHE:C	3:A:933:HOH:O	2.37	0.63
1:C:253:LYS:HE3	1:C:442:GLN:HE22	1.64	0.62
1:B:344:LEU:N	3:B:988:HOH:O	2.31	0.62
1:A:235:PRO:HA	1:B:457:GLU:OE2	1.99	0.61
1:B:504:LEU:HD11	1:B:525:VAL:HG21	1.81	0.61
1:A:422:PHE:CA	3:A:933:HOH:O	2.50	0.59
1:A:274:GLU:HG3	1:A:462:VAL:HG23	1.84	0.59
1:C:457:GLU:OE1	1:C:458:GLN:NE2	2.24	0.59
1:C:408:THR:N	1:C:411:THR:CG2	2.66	0.58
1:A:479:ASN:OD1	1:A:481:GLY:N	2.37	0.58
1:C:407:VAL:CG1	1:C:411:THR:HG21	2.36	0.56
2:F:1:NAG:H61	2:F:3:GAL:O2	2.06	0.55
1:C:239:LEU:HD12	1:C:242:LEU:HD12	1.88	0.55
1:C:518:ARG:NH1	1:C:518:ARG:HG3	2.19	0.55
1:C:346:GLY:HA2	2:H:2:FUC:O5	2.07	0.55
1:A:319:SER:N	3:A:965:HOH:O	2.38	0.55
1:A:435:ILE:HD11	1:A:442:GLN:O	2.06	0.54
1:C:318:GLU:HB3	1:C:412:HIS:CD2	2.44	0.53
1:A:346:GLY:HA2	2:F:2:FUC:O5	2.09	0.53
1:C:518:ARG:HH11	1:C:518:ARG:CG	2.18	0.52
1:C:337:THR:HG22	1:C:381:GLY:HA3	1.93	0.51
1:C:318:GLU:HG2	3:C:935:HOH:O	2.11	0.51
1:C:408:THR:H	1:C:411:THR:HG22	1.76	0.50
1:C:518:ARG:NH1	1:C:518:ARG:CG	2.76	0.49
1:D:273:LEU:HG	1:D:487:PRO:HA	1.93	0.49
1:A:423:GLY:N	3:A:933:HOH:O	2.46	0.48
1:C:318:GLU:O	1:C:412:HIS:CB	2.55	0.48
1:A:412:HIS:N	3:A:885:HOH:O	2.46	0.47
1:C:364:LEU:HD21	1:C:406:THR:CG2	2.36	0.47
1:D:494:VAL:O	1:D:524:PRO:HA	2.15	0.47
1:B:494:VAL:O	1:B:524:PRO:HA	2.15	0.47
1:A:435:ILE:CD1	1:A:442:GLN:O	2.62	0.47
2:F:1:NAG:H61	2:F:3:GAL:C1	2.45	0.47
1:D:453:SER:O	1:D:457:GLU:HG3	2.14	0.47
1:B:463:ARG:NH2	3:B:1009:HOH:O	2.48	0.46
1:A:494:VAL:O	1:A:524:PRO:HA	2.15	0.46
1:A:479:ASN:OD1	1:A:479:ASN:C	2.53	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:504:LEU:HD11	1:B:525:VAL:CG2	2.46	0.45
1:A:470:HIS:CD2	1:A:479:ASN:ND2	2.84	0.45
1:A:458:GLN:HG2	1:A:460:ALA:HB2	1.99	0.45
1:B:334:HIS:HD2	1:B:353:ASP:OD1	2.00	0.44
1:C:442:GLN:NE2	3:C:923:HOH:O	2.46	0.44
1:C:407:VAL:HA	1:C:411:THR:HG21	2.00	0.44
1:D:334:HIS:CE1	1:D:387:SER:OG	2.66	0.44
1:A:273:LEU:HG	1:A:487:PRO:HA	1.99	0.44
1:B:294:LYS:HE3	3:B:730:HOH:O	2.18	0.44
1:A:422:PHE:N	3:A:933:HOH:O	2.49	0.43
1:A:419:PRO:HA	1:A:420:PRO:HD3	1.88	0.43
1:D:253:LYS:HD2	3:D:917:HOH:O	2.19	0.43
1:A:518:ARG:O	1:A:518:ARG:HG2	2.17	0.43
1:C:364:LEU:HD23	1:C:364:LEU:HA	1.69	0.43
1:B:242:LEU:HD22	1:B:450:GLU:HB2	2.01	0.43
1:A:326:PRO:HB2	1:A:333:TRP:CH2	2.53	0.43
1:A:430:MET:HA	1:A:443:VAL:O	2.18	0.43
1:C:334:HIS:CE1	1:C:387:SER:OG	2.64	0.42
1:C:364:LEU:CD2	1:C:406:THR:HG21	2.37	0.42
3:B:717:HOH:O	2:F:1:NAG:H81	2.19	0.42
1:C:409:GLU:H	1:C:409:GLU:CD	2.22	0.42
2:E:1:NAG:H61	2:E:3:GAL:C1	2.50	0.42
1:A:319:SER:CA	3:A:965:HOH:O	2.67	0.42
1:A:435:ILE:HD12	1:A:442:GLN:H	1.85	0.42
1:B:478:ARG:NH1	3:B:704:HOH:O	2.53	0.42
1:B:453:SER:O	1:B:457:GLU:HB2	2.20	0.41
1:A:421:GLY:C	3:A:933:HOH:O	2.58	0.41
1:C:334:HIS:HD2	1:C:353:ASP:OD1	2.03	0.41
1:C:285:ALA:HA	1:C:449:GLN:HG2	2.01	0.41
1:A:518:ARG:CG	3:A:740:HOH:O	2.62	0.41
1:B:484:LYS:HG3	1:B:522:LEU:HD21	2.03	0.41
1:D:274:GLU:HG3	3:D:902:HOH:O	2.20	0.41
1:B:337:THR:HG22	1:B:381:GLY:HA3	2.03	0.41
1:B:416:PRO:HB2	1:B:418:PHE:CE2	2.56	0.41
1:C:426:ILE:HD13	1:C:492:THR:HG22	2.03	0.41
1:D:334:HIS:HD2	1:D:353:ASP:OD1	2.03	0.41
1:A:441:ALA:HB2	3:A:955:HOH:O	2.22	0.40
1:C:235:PRO:HA	1:D:457:GLU:OE1	2.21	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	
1	A	279/301 (93%)	267 (96%)	12 (4%)	0	100	100
1	B	281/301 (93%)	274 (98%)	7 (2%)	0	100	100
1	C	282/301 (94%)	269 (95%)	13 (5%)	0	100	100
1	D	280/301 (93%)	268 (96%)	12 (4%)	0	100	100
All	All	1122/1204 (93%)	1078 (96%)	44 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	237/257 (92%)	236 (100%)	1 (0%)	91	87
1	B	245/257 (95%)	244 (100%)	1 (0%)	91	87
1	C	244/257 (95%)	242 (99%)	2 (1%)	81	74
1	D	243/257 (95%)	240 (99%)	3 (1%)	71	59
All	All	969/1028 (94%)	962 (99%)	7 (1%)	84	77

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	517	SER
1	B	314	TYR

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Mol	Chain	Res	Type
1	C	411	THR
1	C	518	ARG
1	D	345	SER
1	D	366	SER
1	D	463	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	334	HIS
1	B	334	HIS
1	C	315	HIS
1	C	334	HIS
1	C	412	HIS
1	D	334	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 ⓘ

12 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	2	15,15,15	0.67	0	21,21,21	0.85	1 (4%)
2	FUC	E	2	2	10,10,11	0.34	0	14,14,16	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GAL	E	3	2	11,11,12	0.28	0	15,15,17	0.64	0
2	NAG	F	1	2	15,15,15	0.64	0	21,21,21	0.82	1 (4%)
2	FUC	F	2	2	10,10,11	0.33	0	14,14,16	0.79	0
2	GAL	F	3	2	11,11,12	0.29	0	15,15,17	0.85	1 (6%)
2	NAG	G	1	2	15,15,15	0.64	0	21,21,21	0.82	1 (4%)
2	FUC	G	2	2	10,10,11	0.34	0	14,14,16	0.79	0
2	GAL	G	3	2	11,11,12	0.29	0	15,15,17	0.85	0
2	NAG	H	1	2	15,15,15	0.63	0	21,21,21	0.82	1 (4%)
2	FUC	H	2	2	10,10,11	0.33	0	14,14,16	0.79	0
2	GAL	H	3	2	11,11,12	0.28	0	15,15,17	0.85	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	2	-	2/6/26/26	0/1/1/1
2	FUC	E	2	2	-	-	0/1/1/1
2	GAL	E	3	2	-	2/2/19/22	0/1/1/1
2	NAG	F	1	2	-	0/6/26/26	0/1/1/1
2	FUC	F	2	2	-	-	0/1/1/1
2	GAL	F	3	2	-	2/2/19/22	0/1/1/1
2	NAG	G	1	2	-	2/6/26/26	0/1/1/1
2	FUC	G	2	2	-	-	0/1/1/1
2	GAL	G	3	2	-	0/2/19/22	0/1/1/1
2	NAG	H	1	2	-	2/6/26/26	0/1/1/1
2	FUC	H	2	2	-	-	0/1/1/1
2	GAL	H	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1	NAG	C1-O5-C5	-2.24	109.44	113.66
2	E	1	NAG	C1-O5-C5	-2.22	109.48	113.66
2	H	1	NAG	C1-O5-C5	-2.21	109.48	113.66
2	F	1	NAG	C1-O5-C5	-2.20	109.50	113.66
2	F	3	GAL	C1-O5-C5	-2.00	109.48	112.19

There are no chirality outliers.

All (10) torsion outliers are listed below:

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

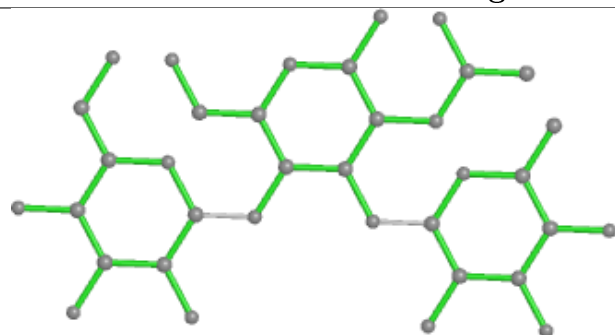
There are no ring outliers.

6 monomers are involved in 6 short contacts:

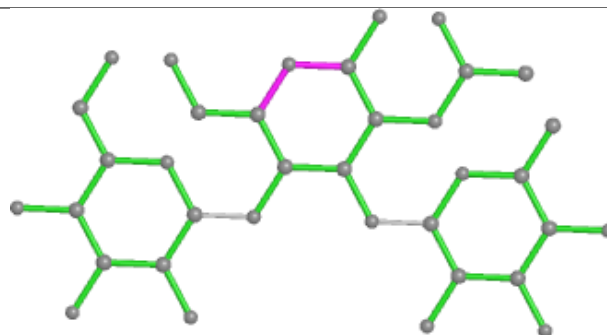
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	3	GAL	1	0
2	F	1	NAG	3	0
2	E	1	NAG	1	0
2	F	2	FUC	1	0
2	H	2	FUC	1	0
2	F	3	GAL	2	0

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

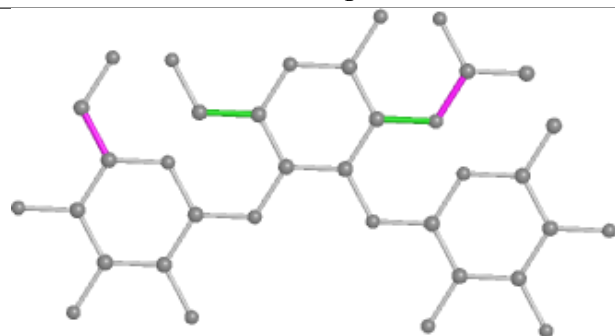
Oligosaccharide Chain E



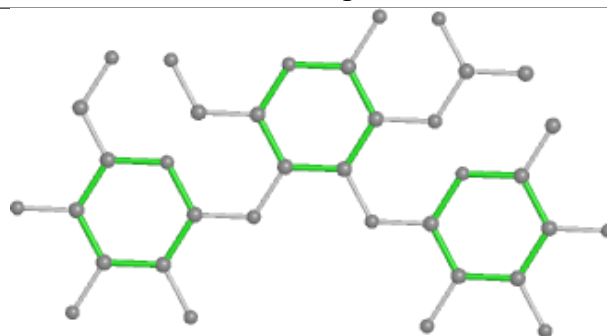
Bond lengths



Bond angles

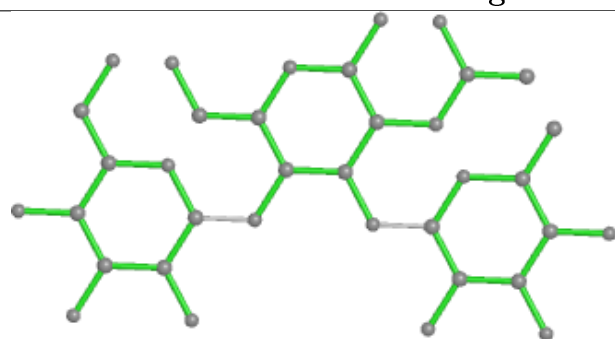


Torsions

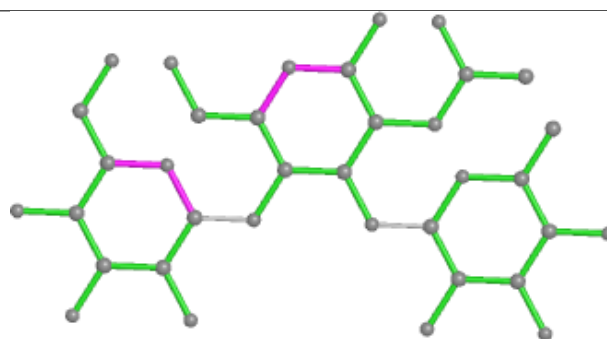


Rings

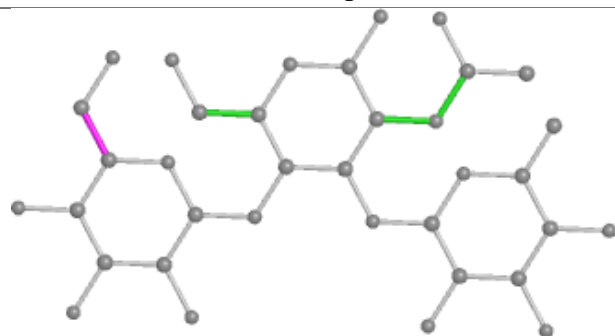
Oligosaccharide Chain F



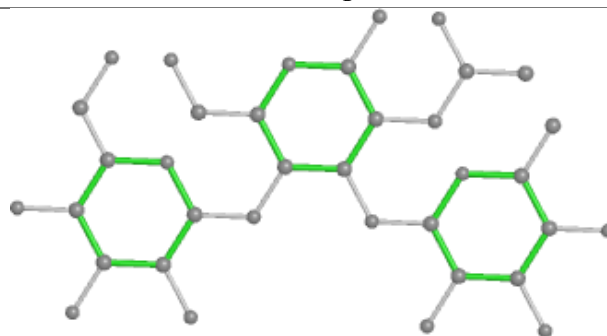
Bond lengths



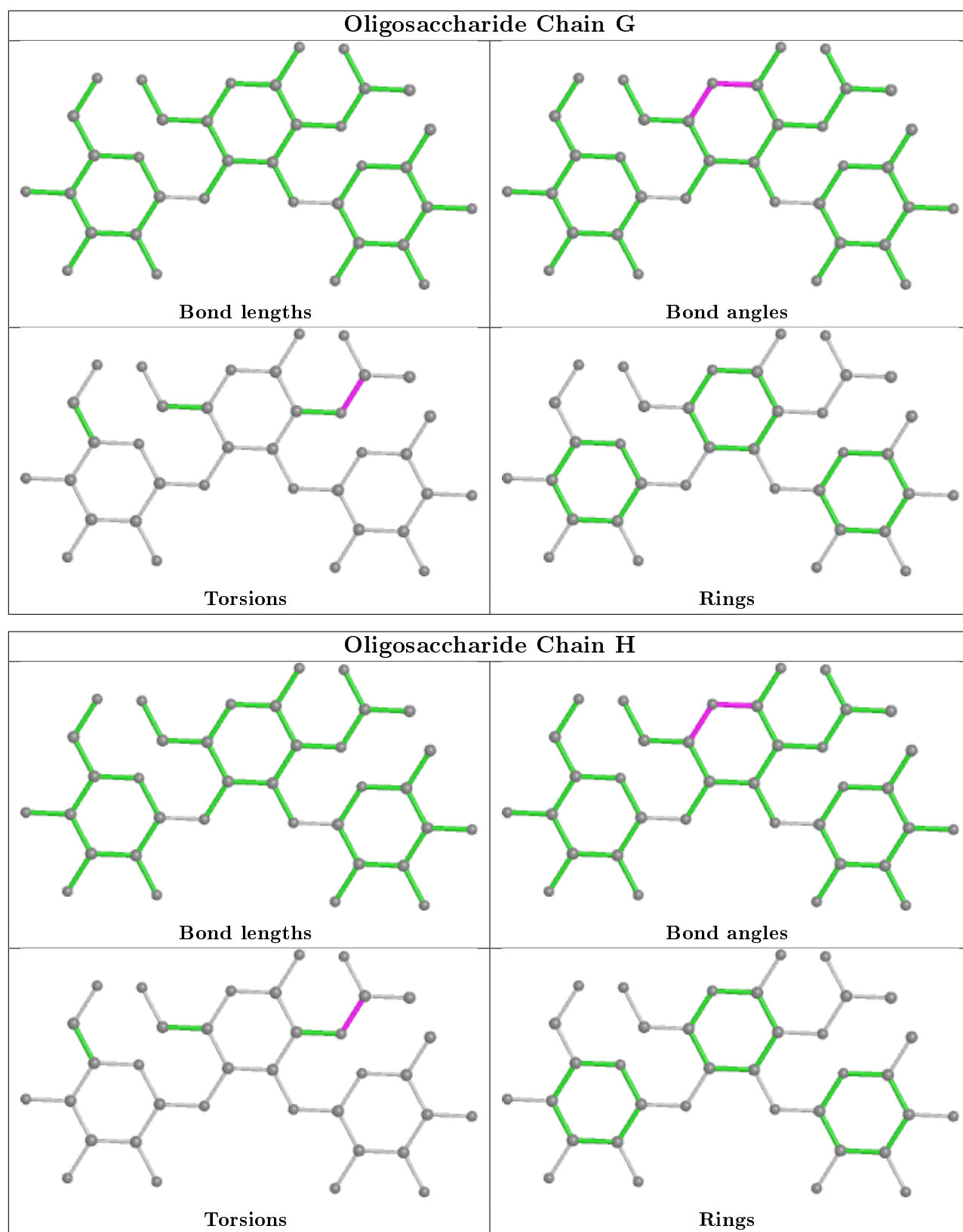
Bond angles



Torsions



Rings



5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 ⓘ

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	285/301 (94%)	-0.11	12 (4%) 36 40	8, 15, 36, 46	0
1	B	289/301 (96%)	-0.18	5 (1%) 70 74	8, 14, 33, 48	0
1	C	288/301 (95%)	-0.19	11 (3%) 40 45	8, 16, 32, 43	0
1	D	286/301 (95%)	-0.20	9 (3%) 49 53	8, 16, 32, 44	0
All	All	1148/1204 (95%)	-0.17	37 (3%) 47 52	8, 15, 34, 48	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	441	ALA	6.6
1	A	440	THR	6.2
1	B	358	ALA	5.6
1	D	391	SER	4.8
1	D	392	GLY	4.6
1	A	422	PHE	4.2
1	C	344	LEU	4.1
1	A	343	ASN	4.0
1	A	344	LEU	3.9
1	A	421	GLY	3.8
1	A	442	GLN	3.6
1	B	340	VAL	3.2
1	C	422	PHE	3.2
1	C	345	SER	3.1
1	A	437	SER	2.8
1	C	411	THR	2.8
1	D	477	HIS	2.7
1	A	443	VAL	2.7
1	B	437	SER	2.7
1	D	345	SER	2.7
1	A	438	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	410	SER	2.6
1	B	441	ALA	2.5
1	C	519	TYR	2.4
1	B	408	THR	2.4
1	A	497	THR	2.4
1	D	463	ARG	2.4
1	D	390	THR	2.4
1	D	393	ALA	2.3
1	D	231	GLN	2.3
1	C	412	HIS	2.3
1	C	499	GLY	2.2
1	C	392	GLY	2.1
1	A	316	ALA	2.0
1	C	315	HIS	2.0
1	D	300	SER	2.0
1	C	258	THR	2.0

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

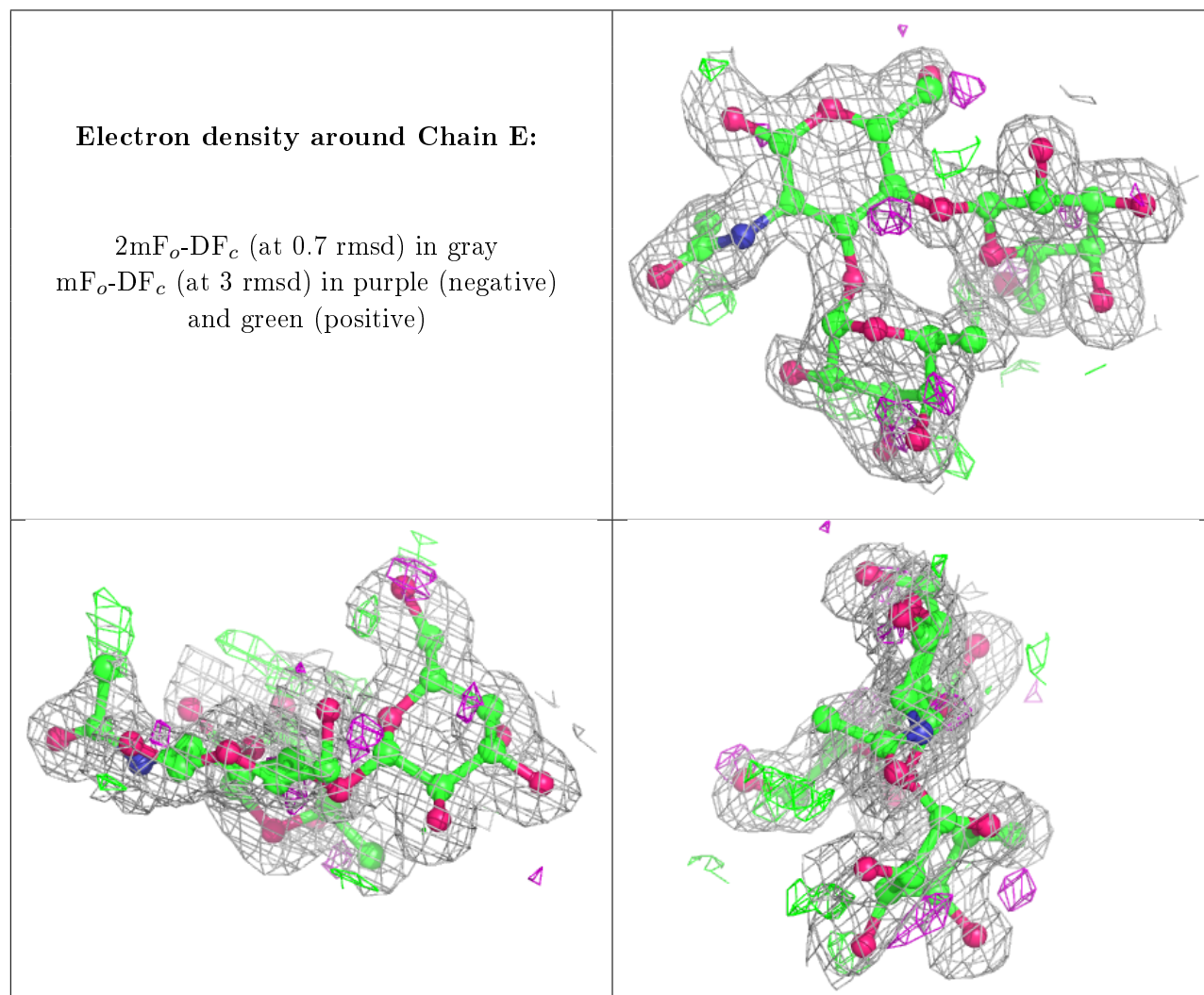
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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

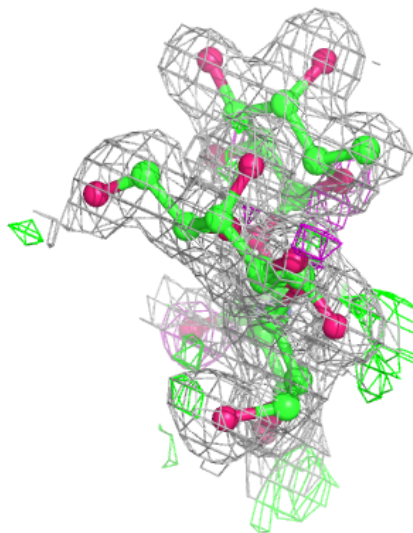
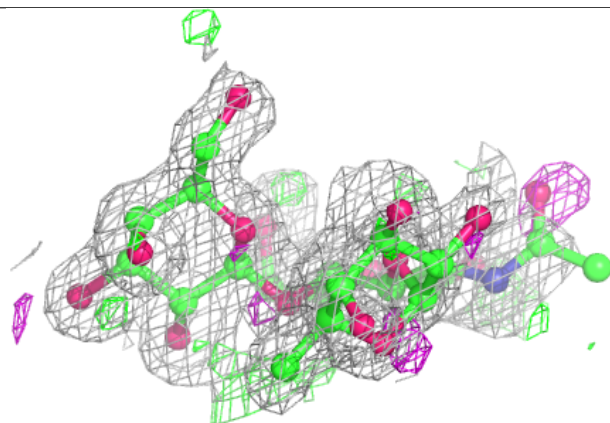
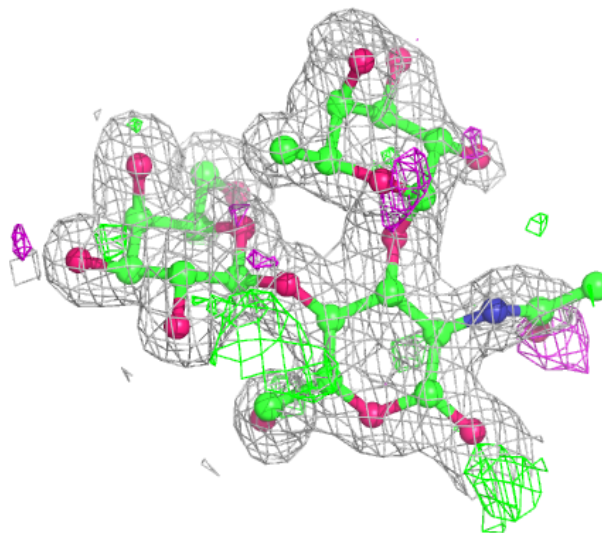
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FUC	G	2	10/11	0.69	0.25	30,39,42,45	0
2	FUC	E	2	10/11	0.74	0.19	24,29,35,35	0
2	NAG	G	1	15/15	0.79	0.23	30,38,51,55	0
2	FUC	F	2	10/11	0.80	0.19	18,30,33,37	0
2	NAG	F	1	15/15	0.83	0.25	25,35,48,50	0
2	FUC	H	2	10/11	0.84	0.23	22,31,34,37	0
2	NAG	E	1	15/15	0.86	0.18	23,33,39,41	0
2	NAG	H	1	15/15	0.88	0.23	25,32,39,41	0
2	GAL	G	3	11/12	0.89	0.20	18,21,32,37	0
2	GAL	F	3	11/12	0.90	0.12	14,19,27,32	0
2	GAL	E	3	11/12	0.92	0.11	13,17,22,25	0
2	GAL	H	3	11/12	0.92	0.15	15,19,24,28	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.



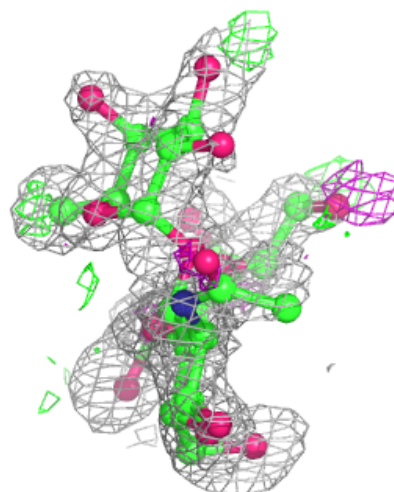
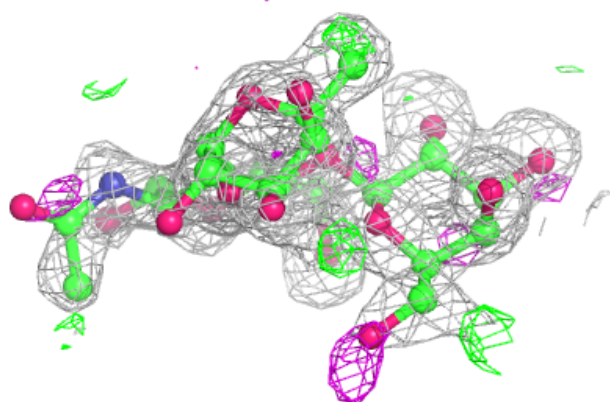
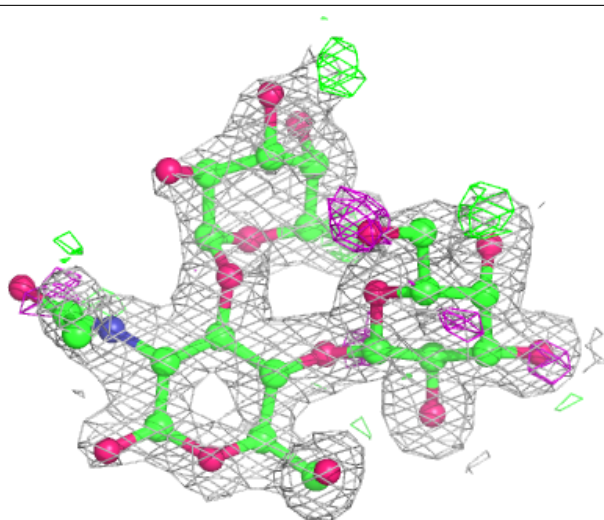
Electron density around Chain F:

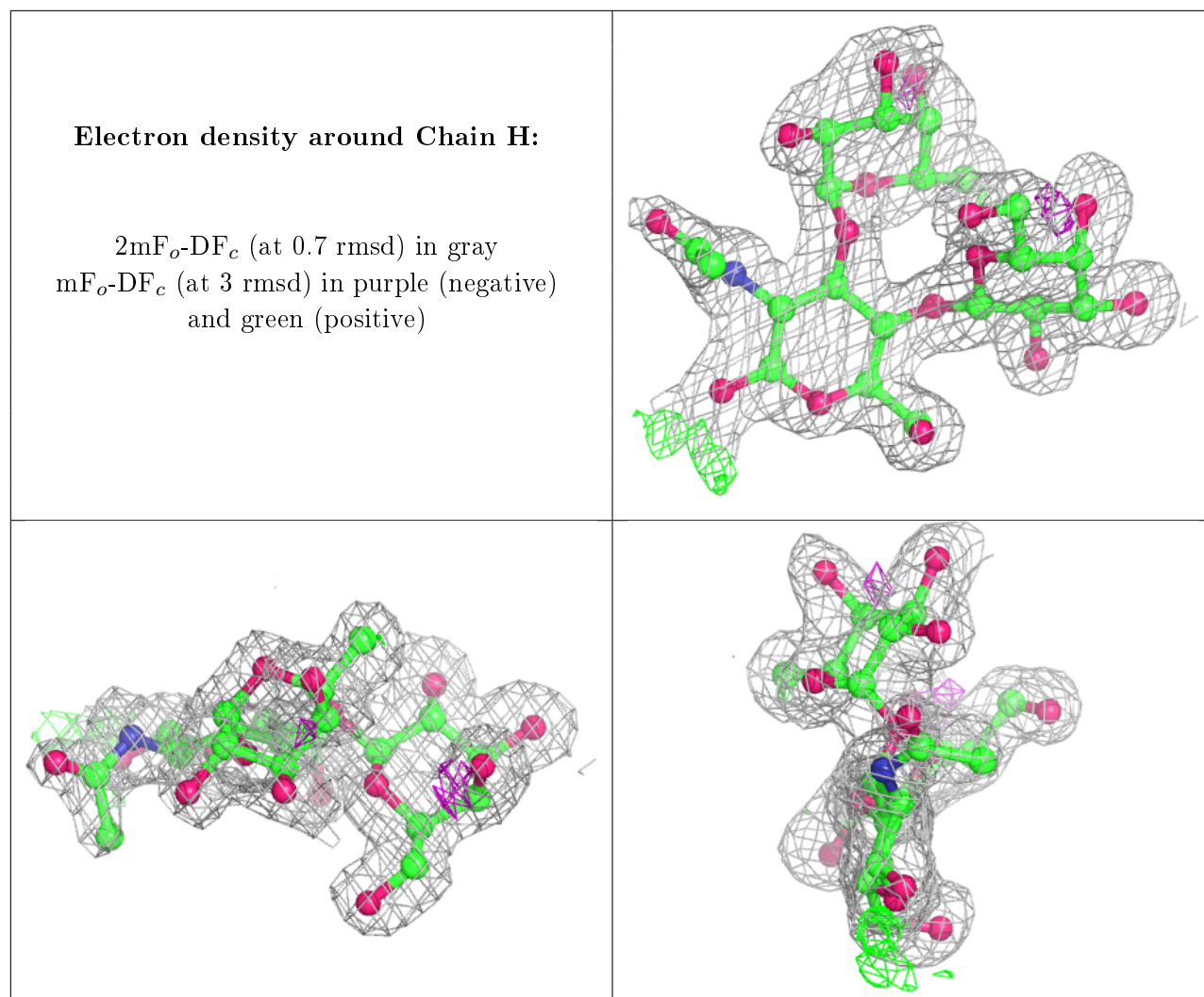
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.