



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 01:03 PM UTC

PDB ID : 4MA1 / pdb_00004ma1
Title : Unliganded 3 crystal structure of S25-26 Fab
Authors : Haji-Ghassemi, O.; Evans, S.V.
Deposited on : 2013-08-15
Resolution : 2.32 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

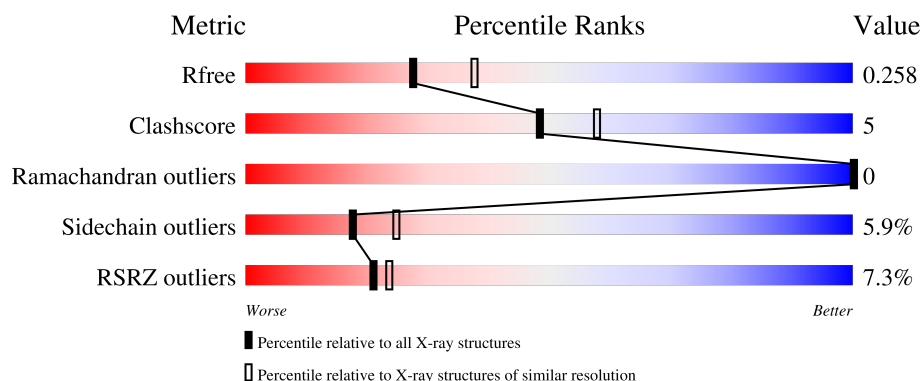
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.32 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	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	219	4% 86% 11% .
1	E	219	29% 77% 17% 5% .
1	H	219	4% 86% 11% .
2	C	219	2% 88% 11% .
2	F	219	3% 88% 10% .

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Mol	Chain	Length	Quality of chain
2	L	219	% 89% 10%
3	A	5	20% 60% 20%
4	D	5	20% 60% 20%
5	G	9	33% 67%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 10552 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.

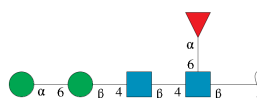
- Molecule 1 is a protein called S25-26 Fab (IgG1k) heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	218	Total	C	N	O	S	0	0	0
			1647	1050	273	317	7			
1	E	216	Total	C	N	O	S	0	0	0
			1631	1039	270	315	7			
1	H	218	Total	C	N	O	S	0	1	0
			1653	1053	274	318	8			

- Molecule 2 is a protein called S25-26 Fab (IgG1k) light chain.

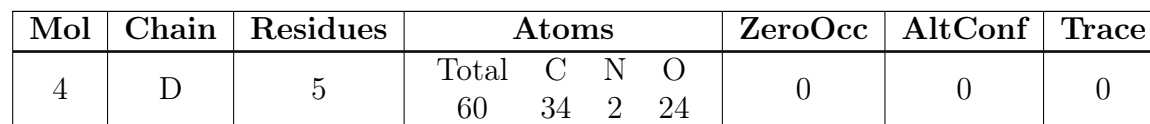
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	219	Total	C	N	O	S	0	0	0
			1712	1072	291	342	7			
2	F	219	Total	C	N	O	S	0	0	0
			1712	1072	291	342	7			
2	L	219	Total	C	N	O	S	0	0	0
			1712	1072	291	342	7			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	A	5	Total	C	N	O	0	0	0
			60	34	2	24			

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



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- The diagram shows two horizontal paths. The upper path starts at a yellow circle labeled α , followed by a yellow circle labeled 3, a blue square labeled 4, and ends at a blue square labeled β . The lower path starts at a green circle labeled α , followed by a green circle labeled 6, a blue square labeled 4, and ends at a blue square labeled β . Above the lower path, there is another green circle labeled α connected to the green circle labeled 6. To the right of the lower path, there is a red triangle pointing downwards towards the blue square labeled 4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	G	9	Total	C	N	O	0	0	0
			107	60	3	44			

- PEG
-
- The diagram illustrates the chemical structure of PEG (polyethylene glycol). It shows a zigzag chain of carbon atoms (C1, C2, C3, C4) and oxygen atoms (O1, O2). The chain starts with a hydroxyl group (HO) attached to C1 and ends with a hydroxyl group (OH) attached to C4. The oxygen atoms are labeled O1 and O2.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			7	4	3		



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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	H	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	L	1	Total	K	0	0
			1	1		

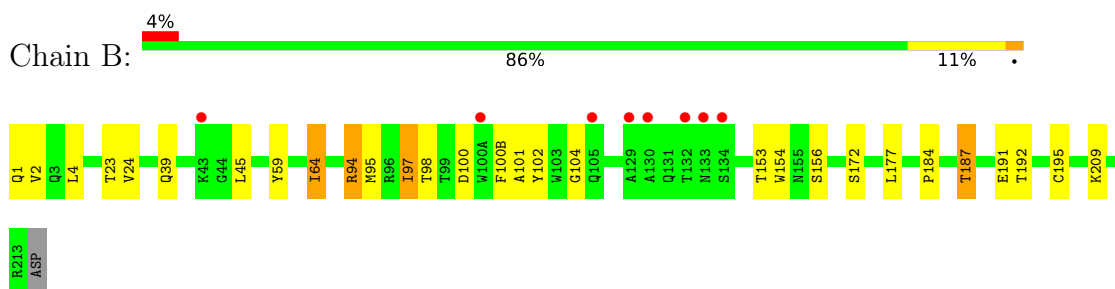
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	38	Total	O	0	0
			38	38		
8	E	16	Total	O	0	0
			16	16		
8	H	62	Total	O	0	0
			62	62		
8	C	34	Total	O	0	0
			34	34		
8	F	47	Total	O	0	0
			47	47		
8	L	46	Total	O	0	0
			46	46		

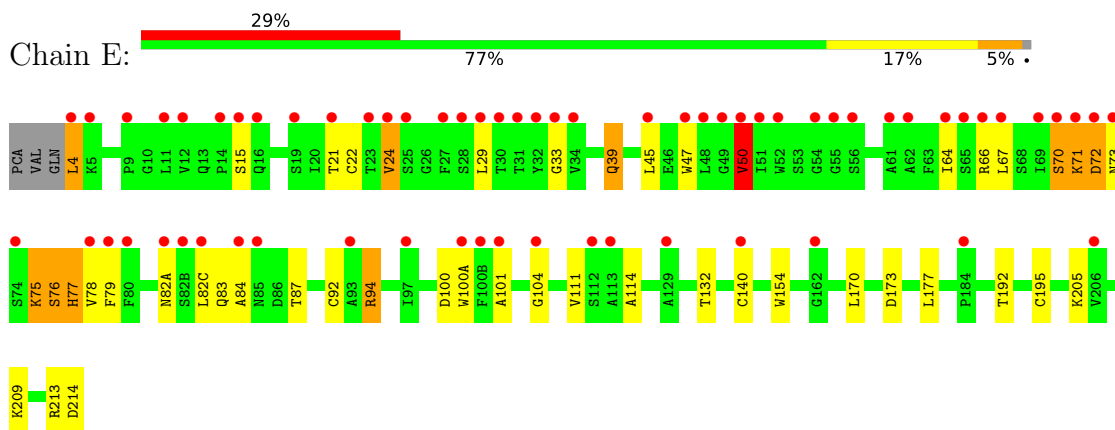
3 Residue-property plots [i](#)

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.

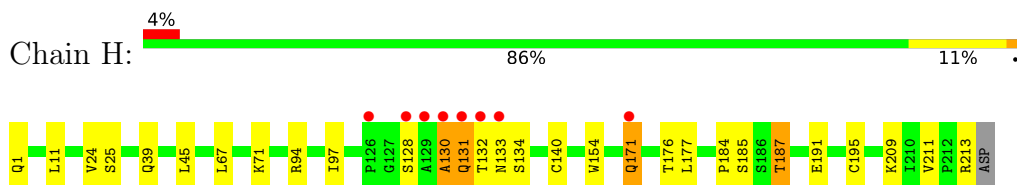
- Molecule 1: S25-26 Fab (IgG1k) heavy chain



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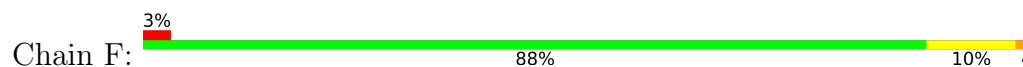


- Molecule 2: S25-26 Fab (IgG1k) light chain





- Molecule 2: S25-26 Fab (IgG1k) light chain



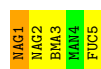
- Molecule 2: S25-26 Fab (IgG1k) light chain



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



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



- Molecule 5: alpha-D-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	196.26Å 66.51Å 122.08Å 90.00° 113.46° 90.00°	Depositor
Resolution (Å)	29.93 – 2.32 29.93 – 2.32	Depositor EDS
% Data completeness (in resolution range)	81.4 (29.93-2.32) 81.5 (29.93-2.32)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.12 (at 2.31Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.229 , 0.260 0.230 , 0.258	Depositor DCC
R_{free} test set	2621 reflections (4.17%)	wwPDB-VP
Wilson B-factor (Å ²)	33.7	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 33.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10552	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% 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: NAG, GAL, BMA, FUC, MAN, GLA, K, PCA, PEG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	B	0.62	0/1686	0.84	0/2311
1	E	0.55	0/1677	0.95	9/2297 (0.4%)
1	H	0.65	0/1692	0.89	3/2319 (0.1%)
2	C	0.59	0/1752	0.76	0/2376
2	F	0.67	0/1752	0.86	4/2376 (0.2%)
2	L	0.66	0/1752	0.81	1/2376 (0.0%)
All	All	0.63	0/10311	0.85	17/14055 (0.1%)

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 (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	82(A)	ASN	N-CA-C	12.90	127.14	111.40
1	E	71	LYS	N-CA-C	10.77	124.75	110.53
1	H	130	ALA	N-CA-C	9.72	121.47	111.07
1	E	70	SER	N-CA-C	9.34	122.87	108.96
2	F	108	ARG	CB-CA-C	-8.11	94.25	110.30
1	E	77	HIS	N-CA-C	7.15	120.55	108.90
2	F	4	MET	CA-C-N	-6.60	113.89	123.00
2	F	4	MET	C-N-CA	-6.60	113.89	123.00
1	E	64	ILE	N-CA-C	-6.51	100.58	109.37
2	L	2	ILE	CB-CA-C	6.42	119.40	111.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	50	VAL	CB-CA-C	-5.88	100.59	111.18
1	E	70	SER	CA-C-N	5.49	130.96	120.97
1	E	70	SER	C-N-CA	5.49	130.96	120.97
2	F	27(E)	ARG	CB-CG-CD	5.47	123.89	111.30
1	H	71	LYS	N-CA-C	5.27	116.29	108.60
1	H	25	SER	N-CA-C	5.09	118.76	111.02
1	E	101	ALA	N-CA-C	5.06	117.33	107.71

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	100	ASP	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1647	0	1618	13	0
1	E	1631	0	1598	40	0
1	H	1653	0	1621	12	0
2	C	1712	0	1649	16	0
2	F	1712	0	1649	13	0
2	L	1712	0	1648	16	0
3	A	60	0	52	3	0
4	D	60	0	52	4	0
5	G	107	0	91	0	0
6	B	7	0	10	0	0
6	H	7	0	10	0	0
7	L	1	0	0	0	0
8	B	38	0	0	1	0
8	C	34	0	0	2	0
8	E	16	0	0	0	0
8	F	47	0	0	0	0
8	H	62	0	0	0	0
8	L	46	0	0	1	0
All	All	10552	0	9998	111	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 (111) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2:NAG:H82	3:A:5:FUC:O2	1.45	1.15
4:D:1:NAG:H62	4:D:5:FUC:H5	1.27	1.08
3:A:2:NAG:H82	3:A:5:FUC:HO2	1.33	0.91
4:D:1:NAG:H62	4:D:5:FUC:C5	2.07	0.82
1:E:71:LYS:HE3	1:E:73:ASN:OD1	1.82	0.80
1:E:47:TRP:HZ2	1:E:50:VAL:CG2	1.98	0.76
1:E:78:VAL:C	1:E:79:PHE:HD1	1.95	0.75
1:E:4:LEU:CD2	1:E:22:CYS:SG	2.77	0.73
1:E:29:LEU:HD13	1:E:72:ASP:HB3	1.71	0.72
1:E:71:LYS:HE3	1:E:73:ASN:CG	2.16	0.71
1:E:77:HIS:HB3	1:E:79:PHE:HE1	1.54	0.71
1:H:39:GLN:OE1	2:L:38:GLN:NE2	2.20	0.70
1:E:71:LYS:HE3	1:E:73:ASN:ND2	2.06	0.70
2:C:2:ILE:HD13	2:C:93:HIS:HB2	1.76	0.68
3:A:2:NAG:C8	3:A:5:FUC:O2	2.33	0.67
1:E:4:LEU:HD22	1:E:92:CYS:SG	2.35	0.67
2:F:210:ASN:N	2:F:210:ASN:OD1	2.28	0.67
1:E:33:GLY:O	1:E:94:ARG:NH1	2.28	0.66
2:F:2:ILE:HD13	2:F:93:HIS:HB2	1.77	0.65
1:E:77:HIS:HB3	1:E:79:PHE:CE1	2.32	0.65
1:E:71:LYS:CE	1:E:73:ASN:HD21	2.09	0.65
2:C:164:THR:HG23	2:C:165:ASP:O	1.97	0.64
1:E:47:TRP:HZ2	1:E:50:VAL:HG23	1.62	0.64
1:E:71:LYS:HE3	1:E:73:ASN:HD21	1.61	0.64
2:L:164:THR:HG23	2:L:165:ASP:O	2.00	0.62
2:L:2:ILE:HD11	2:L:4:MET:SD	2.40	0.62
1:E:24:VAL:O	1:E:76:SER:HB2	2.00	0.60
2:L:77:ARG:O	2:L:77:ARG:HG2	2.02	0.59
2:C:60:ASP:N	2:C:60:ASP:OD1	2.36	0.59
1:E:71:LYS:NZ	1:E:73:ASN:HD21	2.00	0.58
2:C:30:ASN:OD1	2:C:50:LYS:HE3	2.03	0.58
1:E:4:LEU:HD21	1:E:22:CYS:SG	2.44	0.57
1:E:83:GLN:O	1:E:111:VAL:HG21	2.05	0.57
1:B:154:TRP:CZ3	1:B:195:CYS:HB3	2.40	0.56
1:B:97:ILE:HD11	2:C:49:TYR:CG	2.40	0.56
1:H:131:GLN:HE21	1:H:131:GLN:HA	1.70	0.56
1:E:154:TRP:CZ3	1:E:195:CYS:HB3	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:82(C):LEU:HB3	1:E:111:VAL:HG11	1.88	0.55
1:B:94:ARG:NH2	1:B:100(B):PHE:O	2.39	0.54
2:C:67:SER:HB3	8:C:308:HOH:O	2.07	0.54
1:E:213:ARG:NH1	2:F:120:PRO:O	2.36	0.54
1:H:128:SER:O	1:H:130:ALA:N	2.41	0.54
2:L:145:ASN:HB3	2:L:197:THR:CG2	2.37	0.54
2:F:164:THR:HG23	2:F:165:ASP:O	2.06	0.54
4:D:1:NAG:C6	4:D:5:FUC:H5	2.19	0.52
2:C:24:ARG:HG2	2:C:70:ASP:OD1	2.09	0.52
1:B:4:LEU:O	1:B:104:GLY:HA2	2.10	0.52
1:E:47:TRP:CZ2	1:E:50:VAL:HG23	2.42	0.52
1:H:154:TRP:CZ3	1:H:195:CYS:HB3	2.45	0.52
1:H:171:GLN:NE2	1:H:176:THR:OG1	2.43	0.51
2:L:77:ARG:O	2:L:77:ARG:CG	2.58	0.51
1:B:59:TYR:HB2	1:B:64:ILE:HG13	1.93	0.51
1:E:114:ALA:HB2	1:E:173:ASP:HB3	1.92	0.50
1:E:87:THR:OG1	1:E:111:VAL:HG22	2.11	0.50
1:H:133:ASN:O	1:H:185:SER:HB2	2.11	0.50
2:L:2:ILE:HG23	8:L:401:HOH:O	2.11	0.50
2:L:2:ILE:HD13	2:L:25:SER:HB2	1.94	0.50
1:H:39:GLN:HB2	1:H:45:LEU:HD23	1.93	0.50
2:L:150:ILE:HD11	2:L:179:LEU:HD21	1.94	0.49
1:E:75:LYS:HB2	1:E:77:HIS:CE1	2.48	0.49
1:B:39:GLN:HB2	1:B:45:LEU:HD23	1.95	0.48
1:E:78:VAL:C	1:E:79:PHE:CD1	2.85	0.48
1:B:177:LEU:C	1:B:177:LEU:HD12	2.38	0.48
1:E:84:ALA:HA	1:E:111:VAL:HG23	1.94	0.48
1:E:39:GLN:HB2	1:E:45:LEU:HD23	1.94	0.48
2:C:46:LEU:HD23	2:C:55:PHE:CD1	2.48	0.48
1:E:21:THR:HG23	1:E:79:PHE:CE1	2.49	0.48
2:F:46:LEU:HD23	2:F:55:PHE:CD1	2.49	0.47
1:E:24:VAL:O	1:E:76:SER:CB	2.61	0.47
2:C:49:TYR:O	2:C:53:ASN:HB2	2.15	0.47
2:F:150:ILE:HD11	2:F:179:LEU:HD21	1.96	0.47
1:E:71:LYS:CE	1:E:73:ASN:ND2	2.73	0.47
1:E:100:ASP:HB2	1:E:100(A):TRP:CE3	2.50	0.47
2:F:170:ASP:OD1	2:F:170:ASP:C	2.58	0.47
1:H:184:PRO:O	1:H:187:THR:HG22	2.15	0.46
1:B:95:MET:HE1	2:C:98:PHE:CZ	2.50	0.46
1:E:79:PHE:CD1	1:E:79:PHE:N	2.83	0.46
2:C:150:ILE:HD11	2:C:179:LEU:HD21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:177:LEU:C	1:H:177:LEU:HD12	2.41	0.45
2:F:16:GLY:HA2	2:F:77:ARG:HG2	1.96	0.45
1:H:133:ASN:CG	1:H:134:SER:N	2.75	0.45
1:E:47:TRP:HZ2	1:E:50:VAL:HG22	1.78	0.45
1:B:154:TRP:CH2	1:B:195:CYS:HB3	2.52	0.44
1:H:39:GLN:NE2	2:L:38:GLN:OE1	2.40	0.44
4:D:1:NAG:C6	4:D:5:FUC:C5	2.86	0.44
1:E:177:LEU:C	1:E:177:LEU:HD12	2.42	0.44
2:F:2:ILE:HD12	2:F:2:ILE:N	2.33	0.44
2:L:54:ARG:HD3	2:L:58:VAL:O	2.17	0.44
1:B:2:VAL:HG21	1:B:100(B):PHE:HA	1.98	0.44
8:B:511:HOH:O	2:F:212:ASN:HB3	2.18	0.44
2:L:46:LEU:HD23	2:L:55:PHE:CD1	2.52	0.44
1:B:153:THR:HB	1:B:156:SER:O	2.17	0.43
2:C:164:THR:HG22	2:C:174:SER:H	1.83	0.43
2:C:67:SER:CB	8:C:308:HOH:O	2.65	0.43
1:E:29:LEU:CD1	1:E:72:ASP:HB3	2.44	0.42
1:B:184:PRO:O	1:B:187:THR:HG22	2.19	0.42
2:F:164:THR:HG22	2:F:174:SER:H	1.85	0.42
1:B:101:ALA:HB3	2:C:55:PHE:CE1	2.54	0.42
1:E:154:TRP:CH2	1:E:195:CYS:HB3	2.55	0.42
1:E:4:LEU:HD22	1:E:22:CYS:SG	2.59	0.42
2:L:91:GLY:HA2	2:L:96:TYR:CD1	2.55	0.42
2:L:164:THR:HG22	2:L:174:SER:H	1.85	0.42
1:E:4:LEU:HB3	1:E:104:GLY:HA2	2.02	0.41
1:E:47:TRP:CZ2	1:E:50:VAL:CG2	2.89	0.41
2:C:2:ILE:HD12	2:C:2:ILE:N	2.34	0.41
2:C:4:MET:HE3	2:C:23:CYS:SG	2.61	0.41
2:L:4:MET:HE3	2:L:23:CYS:SG	2.61	0.41
2:F:4:MET:HE3	2:F:23:CYS:SG	2.61	0.41
1:H:187:THR:OG1	1:H:191:GLU:HG3	2.22	0.40
2:F:27(D):HIS:O	2:F:27(E):ARG:HD2	2.21	0.40
2:L:136:LEU:N	2:L:136:LEU:HD12	2.36	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	B	216/219 (99%)	212 (98%)	4 (2%)	0	100	100
1	E	214/219 (98%)	205 (96%)	9 (4%)	0	100	100
1	H	217/219 (99%)	213 (98%)	4 (2%)	0	100	100
2	C	217/219 (99%)	214 (99%)	3 (1%)	0	100	100
2	F	217/219 (99%)	214 (99%)	3 (1%)	0	100	100
2	L	217/219 (99%)	214 (99%)	3 (1%)	0	100	100
All	All	1298/1314 (99%)	1272 (98%)	26 (2%)	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	B	187/188 (100%)	175 (94%)	12 (6%)	16	22
1	E	186/188 (99%)	167 (90%)	19 (10%)	7	8
1	H	188/188 (100%)	174 (93%)	14 (7%)	13	16
2	C	196/196 (100%)	187 (95%)	9 (5%)	24	35
2	F	196/196 (100%)	188 (96%)	8 (4%)	27	40
2	L	196/196 (100%)	189 (96%)	7 (4%)	31	45
All	All	1149/1152 (100%)	1080 (94%)	69 (6%)	18	24

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	23	THR
1	B	24	VAL
1	B	64	ILE
1	B	94	ARG
1	B	97	ILE
1	B	98	THR
1	B	102	TYR
1	B	172	SER
1	B	187	THR
1	B	191	GLU
1	B	192	THR
1	B	209	LYS
1	E	4	LEU
1	E	15	SER
1	E	24	VAL
1	E	39	GLN
1	E	50	VAL
1	E	66	ARG
1	E	67	LEU
1	E	70	SER
1	E	72	ASP
1	E	75	LYS
1	E	76	SER
1	E	94	ARG
1	E	132	THR
1	E	140	CYS
1	E	170	LEU
1	E	192	THR
1	E	205	LYS
1	E	209	LYS
1	E	214	ASP
1	H	11	LEU
1	H	24	VAL
1	H	67	LEU
1	H	94	ARG
1	H	97	ILE
1	H	131	GLN
1	H	132	THR
1	H	140[A]	CYS
1	H	140[B]	CYS
1	H	171	GLN
1	H	187	THR

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Mol	Chain	Res	Type
1	H	209	LYS
1	H	211	VAL
1	H	213	ARG
2	C	31	THR
2	C	50	LYS
2	C	54	ARG
2	C	60	ASP
2	C	106	LEU
2	C	142	LYS
2	C	156	GLN
2	C	164	THR
2	C	168	SER
2	F	18	GLN
2	F	20	SER
2	F	31	THR
2	F	52	SER
2	F	106	LEU
2	F	164	THR
2	F	188	ARG
2	F	210	ASN
2	L	2	ILE
2	L	3	LEU
2	L	33	LEU
2	L	77	ARG
2	L	105	GLU
2	L	142	LYS
2	L	164	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	13	GLN
1	B	164	HIS
1	E	13	GLN
1	E	73	ASN
1	H	39	GLN
1	H	131	GLN
1	H	171	GLN
2	C	157	ASN
2	F	189	HIS
2	L	38	GLN
2	L	157	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	PCA	H	1	1	7,8,9	0.53	0	9,10,12	1.45	1 (11%)
1	PCA	B	1	1	7,8,9	0.54	0	9,10,12	1.12	1 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PCA	H	1	1	-	0/0/11/13	0/1/1/1
1	PCA	B	1	1	-	0/0/11/13	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	1	PCA	CB-CA-C	-3.17	108.31	112.66
1	B	1	PCA	OE-CD-CG	-2.15	122.89	126.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

19 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	$\# Z > 2$
3	NAG	A	1	3,1	14,14,15	0.70	0	17,19,21	1.40	3 (17%)
3	NAG	A	2	3	14,14,15	0.64	0	17,19,21	2.69	3 (17%)
3	BMA	A	3	3	11,11,12	0.40	0	15,15,17	0.80	0
3	MAN	A	4	3	11,11,12	0.46	0	15,15,17	2.50	2 (13%)
3	FUC	A	5	3	10,10,11	0.30	0	14,14,16	0.58	0
4	NAG	D	1	4,1	14,14,15	0.55	0	17,19,21	1.63	3 (17%)
4	NAG	D	2	4	14,14,15	0.48	0	17,19,21	2.24	3 (17%)
4	BMA	D	3	4	11,11,12	0.30	0	15,15,17	1.70	2 (13%)
4	MAN	D	4	4	11,11,12	0.58	0	15,15,17	0.98	0
4	FUC	D	5	4	10,10,11	0.31	0	14,14,16	0.77	0
5	NAG	G	1	5,1	14,14,15	0.28	0	17,19,21	0.56	0
5	NAG	G	2	5	14,14,15	1.33	1 (7%)	17,19,21	2.21	3 (17%)
5	BMA	G	3	5	11,11,12	0.44	0	15,15,17	2.16	2 (13%)
5	MAN	G	4	5	11,11,12	0.49	0	15,15,17	1.34	1 (6%)
5	NAG	G	5	5	14,14,15	0.48	0	17,19,21	0.83	0
5	GAL	G	6	5	11,11,12	0.69	0	15,15,17	2.08	3 (20%)
5	GLA	G	7	5	11,11,12	0.40	0	15,15,17	0.94	1 (6%)
5	MAN	G	8	5	11,11,12	0.25	0	15,15,17	0.52	0
5	FUC	G	9	5	10,10,11	0.43	0	14,14,16	1.15	2 (14%)

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
3	NAG	A	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	A	2	3	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	A	3	3	-	2/2/19/22	0/1/1/1
3	MAN	A	4	3	-	2/2/19/22	0/1/1/1
3	FUC	A	5	3	-	-	0/1/1/1
4	NAG	D	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
4	BMA	D	3	4	-	0/2/19/22	0/1/1/1
4	MAN	D	4	4	-	2/2/19/22	0/1/1/1
4	FUC	D	5	4	-	-	0/1/1/1
5	NAG	G	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	5/6/23/26	0/1/1/1
5	BMA	G	3	5	-	2/2/19/22	0/1/1/1
5	MAN	G	4	5	-	1/2/19/22	0/1/1/1
5	NAG	G	5	5	-	2/6/23/26	0/1/1/1
5	GAL	G	6	5	-	0/2/19/22	0/1/1/1
5	GLA	G	7	5	-	1/2/19/22	0/1/1/1
5	MAN	G	8	5	-	2/2/19/22	0/1/1/1
5	FUC	G	9	5	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	2	NAG	O4-C4	-4.24	1.32	1.43

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2	NAG	O5-C1-C2	8.84	124.97	111.29
3	A	4	MAN	C1-O5-C5	8.71	123.86	112.19
4	D	2	NAG	C1-O5-C5	7.78	122.61	112.19
5	G	2	NAG	C4-C3-C2	-6.99	100.77	111.02
5	G	3	BMA	C1-O5-C5	6.81	121.31	112.19
5	G	6	GAL	C1-O5-C5	5.52	119.59	112.19
4	D	3	BMA	C1-C2-C3	4.91	116.79	109.64
5	G	4	MAN	C1-O5-C5	4.54	118.27	112.19
5	G	2	NAG	C1-O5-C5	4.52	118.25	112.19
3	A	2	NAG	C4-C3-C2	4.21	117.19	111.02
5	G	6	GAL	O3-C3-C2	-3.98	101.93	110.05
3	A	2	NAG	C3-C4-C5	3.87	117.25	110.23
4	D	1	NAG	O5-C1-C2	-3.70	105.57	111.29
5	G	3	BMA	C2-C3-C4	-3.33	105.00	110.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	2	NAG	O5-C5-C4	3.28	118.81	110.83
4	D	1	NAG	C1-O5-C5	3.28	116.58	112.19
3	A	1	NAG	O6-C6-C5	-3.08	100.86	111.33
3	A	4	MAN	O5-C5-C4	3.03	118.19	110.83
5	G	6	GAL	C2-C3-C4	-2.95	105.67	110.86
3	A	1	NAG	O5-C5-C4	-2.57	104.58	110.83
4	D	1	NAG	O7-C7-C8	-2.49	117.63	122.05
3	A	1	NAG	C3-C4-C5	-2.41	105.86	110.23
5	G	9	FUC	C2-C3-C4	-2.28	106.85	110.86
4	D	2	NAG	C3-C4-C5	2.24	114.29	110.23
5	G	7	GLA	O2-C2-C1	-2.21	104.16	109.22
4	D	3	BMA	O3-C3-C2	-2.14	105.69	110.05
5	G	9	FUC	O2-C2-C1	2.13	114.11	109.22
5	G	2	NAG	O4-C4-C3	2.11	115.34	110.38

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1	NAG	C4-C5-C6-O6
3	A	3	BMA	O5-C5-C6-O6
3	A	4	MAN	O5-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6
3	A	3	BMA	C4-C5-C6-O6
4	D	1	NAG	O5-C5-C6-O6
5	G	5	NAG	O5-C5-C6-O6
5	G	5	NAG	C4-C5-C6-O6
5	G	3	BMA	C4-C5-C6-O6
5	G	2	NAG	C8-C7-N2-C2
4	D	2	NAG	C4-C5-C6-O6
5	G	4	MAN	O5-C5-C6-O6
5	G	8	MAN	C4-C5-C6-O6
5	G	2	NAG	O5-C5-C6-O6
5	G	7	GLA	O5-C5-C6-O6
5	G	2	NAG	O7-C7-N2-C2
5	G	3	BMA	O5-C5-C6-O6
5	G	8	MAN	O5-C5-C6-O6
3	A	4	MAN	C4-C5-C6-O6
4	D	4	MAN	O5-C5-C6-O6
5	G	2	NAG	C4-C5-C6-O6
5	G	2	NAG	C3-C2-N2-C7
4	D	4	MAN	C4-C5-C6-O6

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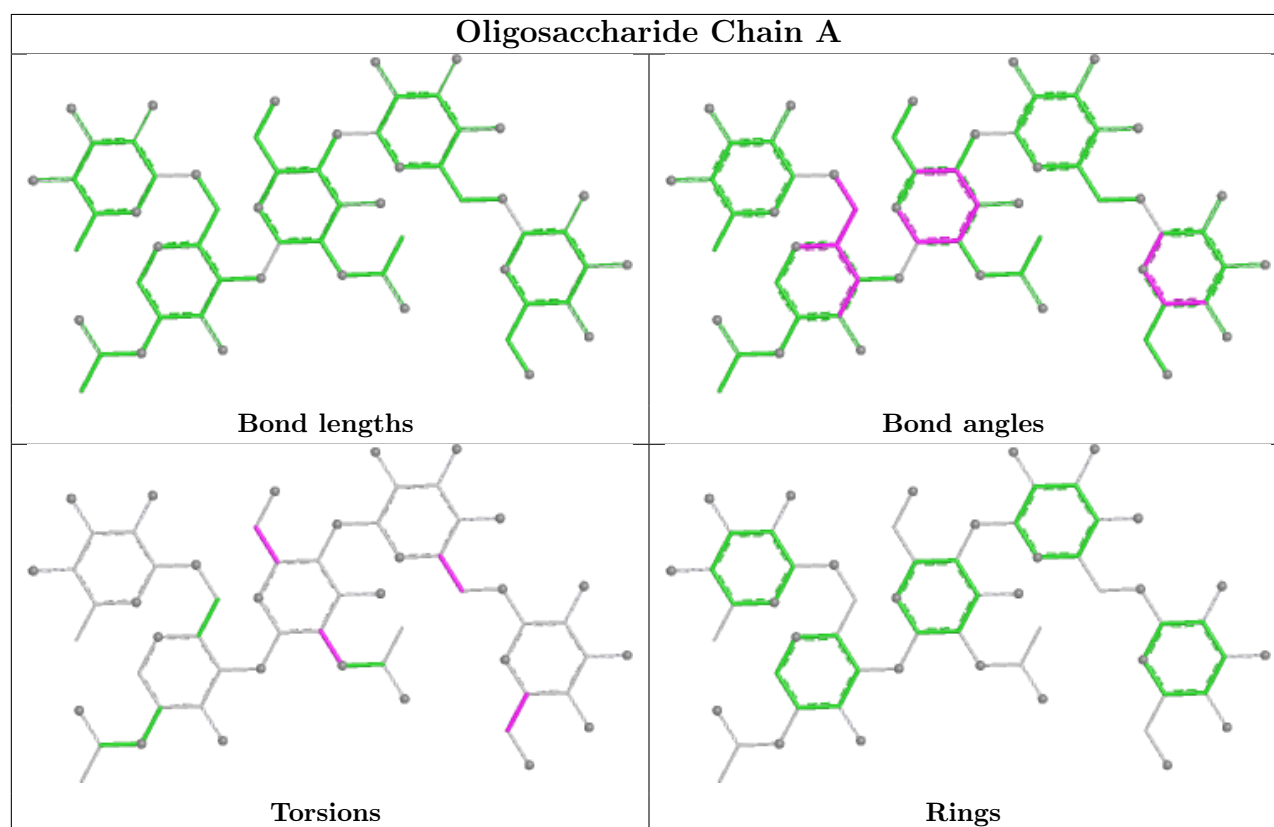
Mol	Chain	Res	Type	Atoms
3	A	2	NAG	C4-C5-C6-O6
3	A	2	NAG	C1-C2-N2-C7

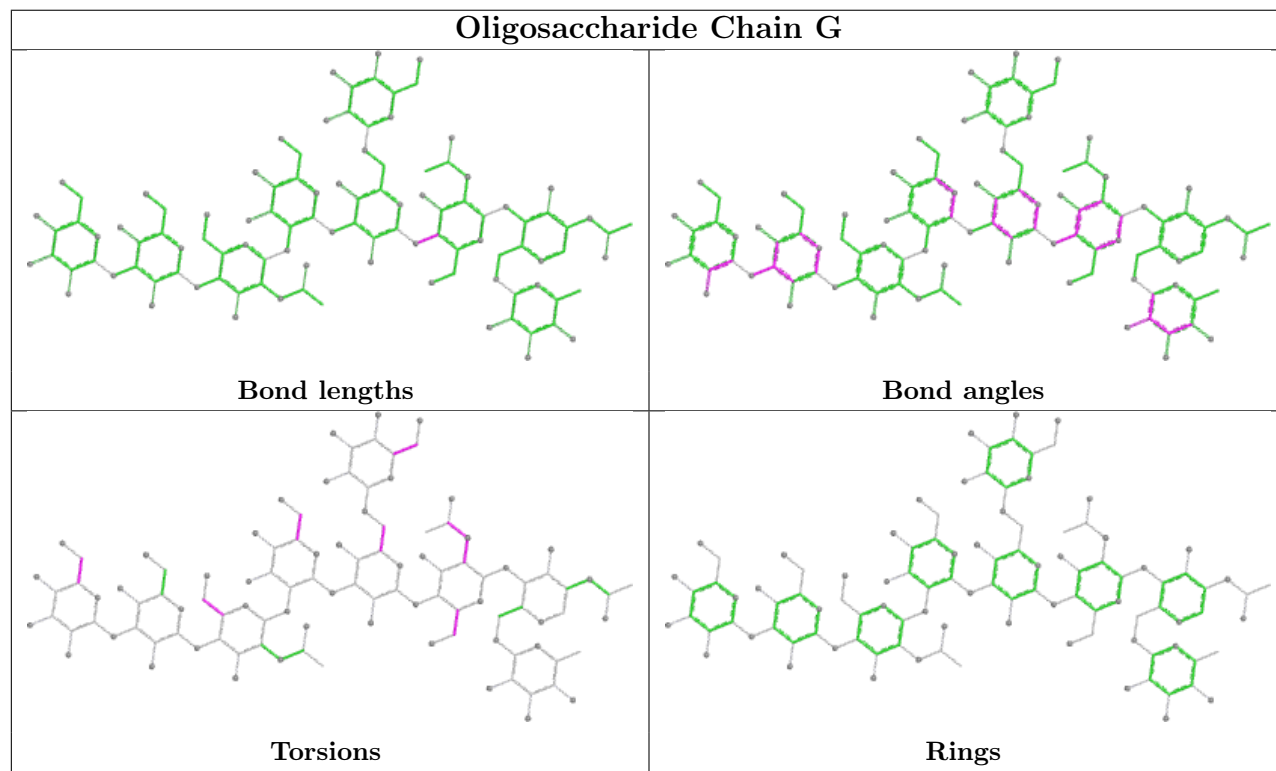
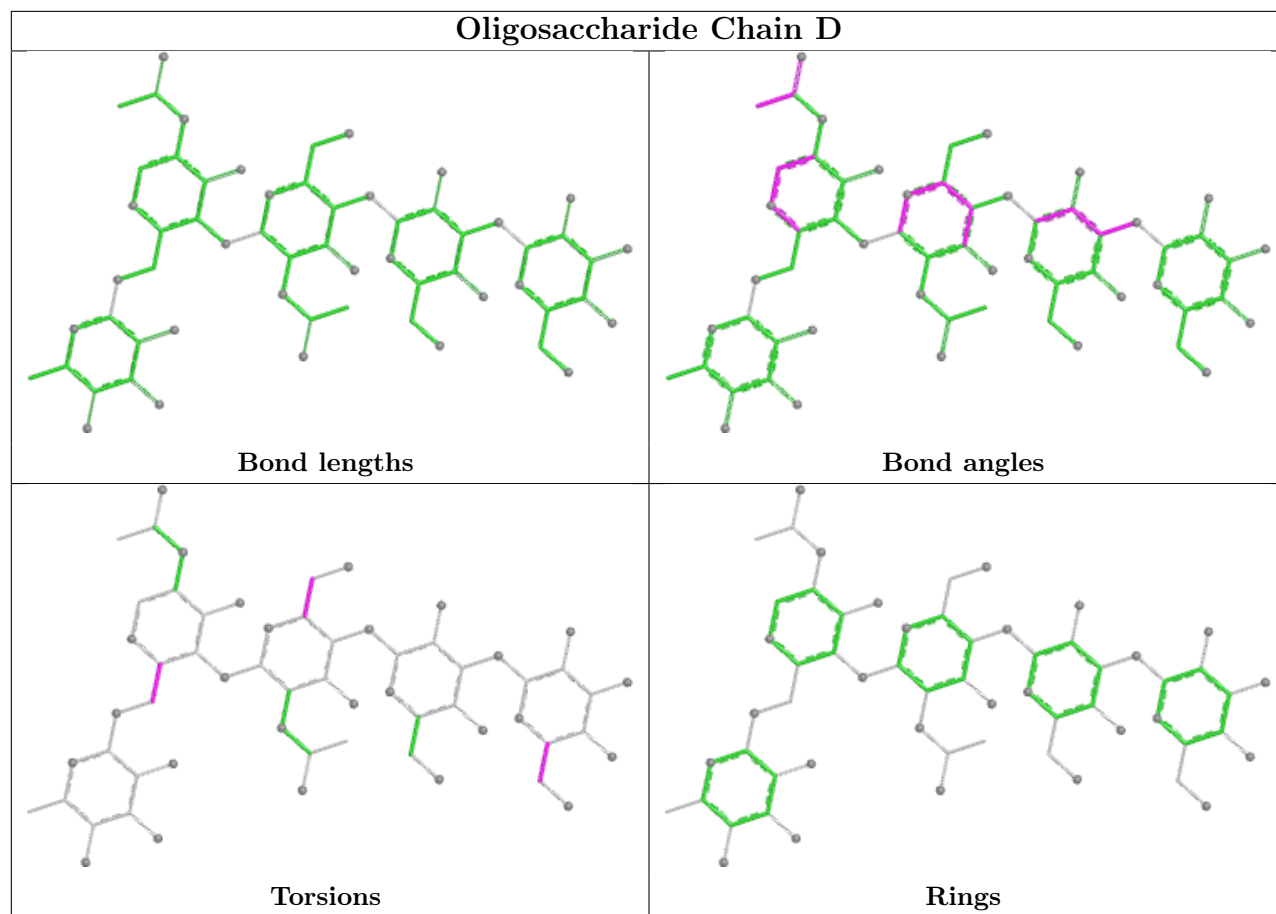
There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	5	FUC	3	0
3	A	2	NAG	3	0
4	D	1	NAG	4	0
4	D	5	FUC	4	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

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	PEG	B	406	-	6,6,6	0.55	0	5,5,5	0.28	0
6	PEG	H	410	-	6,6,6	0.45	0	5,5,5	0.34	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
6	PEG	B	406	-	-	3/4/4/4	-
6	PEG	H	410	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	406	PEG	O1-C1-C2-O2
6	H	410	PEG	O1-C1-C2-O2
6	H	410	PEG	O2-C3-C4-O4
6	B	406	PEG	O2-C3-C4-O4
6	B	406	PEG	C4-C3-O2-C2
6	H	410	PEG	C1-C2-O2-C3

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	B	217/219 (99%)	0.58	8 (3%)	45	48	25, 45, 68, 75	0
1	E	216/219 (98%)	1.53	64 (29%)	1	1	36, 70, 134, 182	0
1	H	217/219 (99%)	0.23	8 (3%)	45	48	12, 33, 58, 105	1 (0%)
2	C	219/219 (100%)	0.60	5 (2%)	61	63	30, 48, 71, 85	0
2	F	219/219 (100%)	0.39	7 (3%)	50	53	26, 39, 60, 79	0
2	L	219/219 (100%)	0.26	3 (1%)	73	75	14, 37, 58, 78	0
All	All	1307/1314 (99%)	0.60	95 (7%)	21	24	12, 43, 89, 182	1 (0%)

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	51	ILE	5.6
1	H	130	ALA	4.7
1	E	55	GLY	4.5
1	E	30	THR	4.4
1	E	29	LEU	4.4
1	H	132	THR	4.3
1	E	32	TYR	4.3
1	E	74	SER	4.1
2	F	210	ASN	4.0
1	E	33	GLY	4.0
1	E	79	PHE	4.0
1	H	129	ALA	4.0
2	F	212	ASN	3.9
1	E	65	SER	3.9
1	E	23	THR	3.9
1	E	71	LYS	3.8
2	F	214	CYS	3.6
1	B	105	GLN	3.6
1	E	100(B)	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
1	E	21	THR	3.5
1	H	131	GLN	3.5
1	E	28	SER	3.4
1	E	64	ILE	3.4
1	E	69	ILE	3.4
1	E	4	LEU	3.3
1	E	93	ALA	3.3
1	E	24	VAL	3.2
1	E	78	VAL	3.2
1	E	82(C)	LEU	3.2
1	E	84	ALA	3.1
1	B	132	THR	3.0
2	C	212	ASN	3.0
1	E	14	PRO	3.0
1	E	66	ARG	2.9
1	E	52	TRP	2.8
1	E	49	GLY	2.8
2	L	212	ASN	2.8
1	E	19	SER	2.8
1	B	129	ALA	2.8
1	B	133	ASN	2.7
1	E	31	THR	2.7
1	E	72	ASP	2.7
1	E	56	SER	2.7
1	E	67	LEU	2.7
2	F	3	LEU	2.7
1	E	27	PHE	2.7
1	E	9	PRO	2.7
1	H	126	PRO	2.6
1	H	171	GLN	2.6
1	E	34	VAL	2.6
1	H	128	SER	2.6
1	E	48	LEU	2.6
1	E	70	SER	2.6
2	F	2	ILE	2.6
1	E	50	VAL	2.5
1	E	82(B)	SER	2.4
1	B	100(A)	TRP	2.4
1	E	113	ALA	2.4
1	E	184	PRO	2.4
1	E	162	GLY	2.3
1	E	80	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	134	SER	2.3
1	E	11	LEU	2.3
1	E	5	LYS	2.3
1	E	85	ASN	2.3
2	C	203	SER	2.3
2	C	190	ASN	2.3
1	E	61	ALA	2.3
2	F	163	TRP	2.3
1	E	140	CYS	2.2
1	E	62	ALA	2.2
1	B	130	ALA	2.2
1	E	97	ILE	2.2
2	C	77	ARG	2.2
1	E	101	ALA	2.2
2	L	203	SER	2.2
1	E	100(A)	TRP	2.1
1	E	12	VAL	2.1
1	E	54	GLY	2.1
2	L	76	SER	2.1
1	H	133	ASN	2.1
1	E	206	VAL	2.1
1	E	129	ALA	2.1
1	E	73	ASN	2.1
2	C	194	CYS	2.1
1	B	43	LYS	2.1
2	F	213	GLU	2.1
1	E	82(A)	ASN	2.1
1	E	112	SER	2.0
1	E	104	GLY	2.0
1	E	47	TRP	2.0
1	E	15	SER	2.0
1	E	25	SER	2.0
1	E	16	GLN	2.0
1	E	45	LEU	2.0

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

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
1	PCA	B	1	8/9	0.80	0.18	58,69,74,78	0
1	PCA	H	1	8/9	0.89	0.11	47,50,52,54	0

6.3 Carbohydrates [i](#)

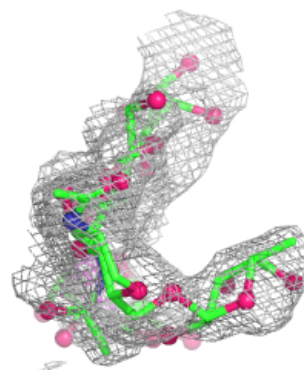
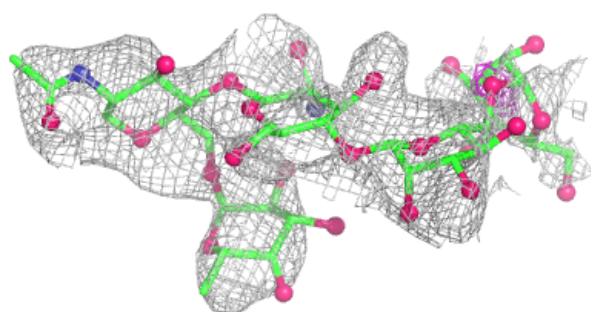
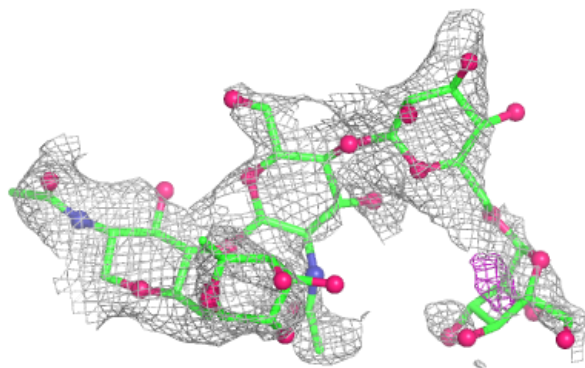
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	A	1	14/15	-	-	56,69,80,84	0
3	NAG	A	2	14/15	-	-	85,91,98,101	0
3	BMA	A	3	11/12	-	-	92,99,108,115	0
3	MAN	A	4	11/12	-	-	108,119,121,122	0
3	FUC	A	5	10/11	-	-	90,93,96,97	0
4	NAG	D	1	14/15	-	-	59,71,101,105	0
4	NAG	D	2	14/15	-	-	104,110,114,115	0
4	BMA	D	3	11/12	-	-	97,105,109,109	0
4	MAN	D	4	11/12	-	-	77,92,99,101	0
4	FUC	D	5	10/11	-	-	95,104,107,109	0
5	MAN	G	4	11/12	0.17	0.17	97,105,108,111	0
5	NAG	G	2	14/15	0.39	0.16	60,64,70,80	0
5	BMA	G	3	11/12	0.64	0.12	84,93,98,100	0
5	NAG	G	1	14/15	0.78	0.12	41,50,62,74	0
5	NAG	G	5	14/15	-	-	104,107,109,113	0
5	GAL	G	6	11/12	-	-	89,100,103,105	0
5	GLA	G	7	11/12	-	-	86,92,93,94	0
5	MAN	G	8	11/12	-	-	92,97,99,100	0
5	FUC	G	9	10/11	-	-	79,85,91,91	0

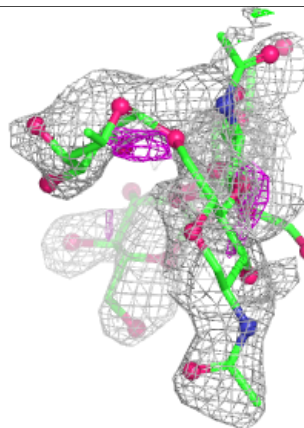
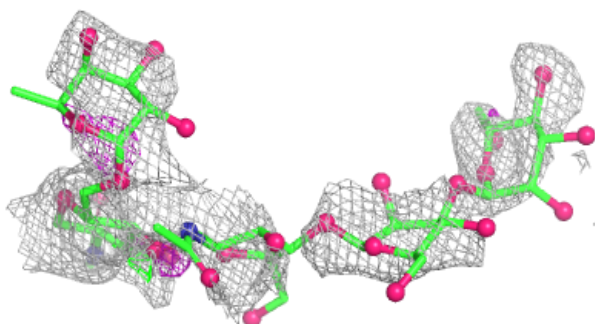
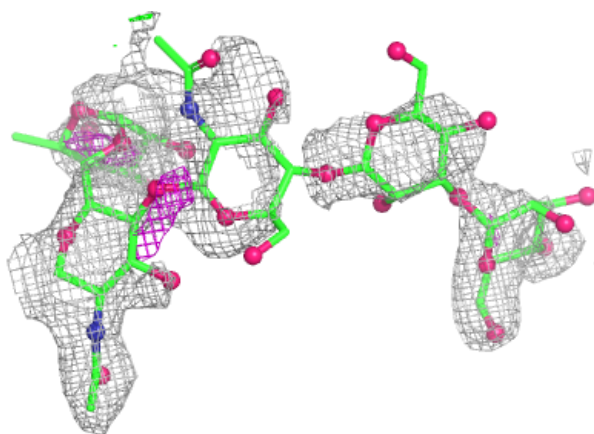
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

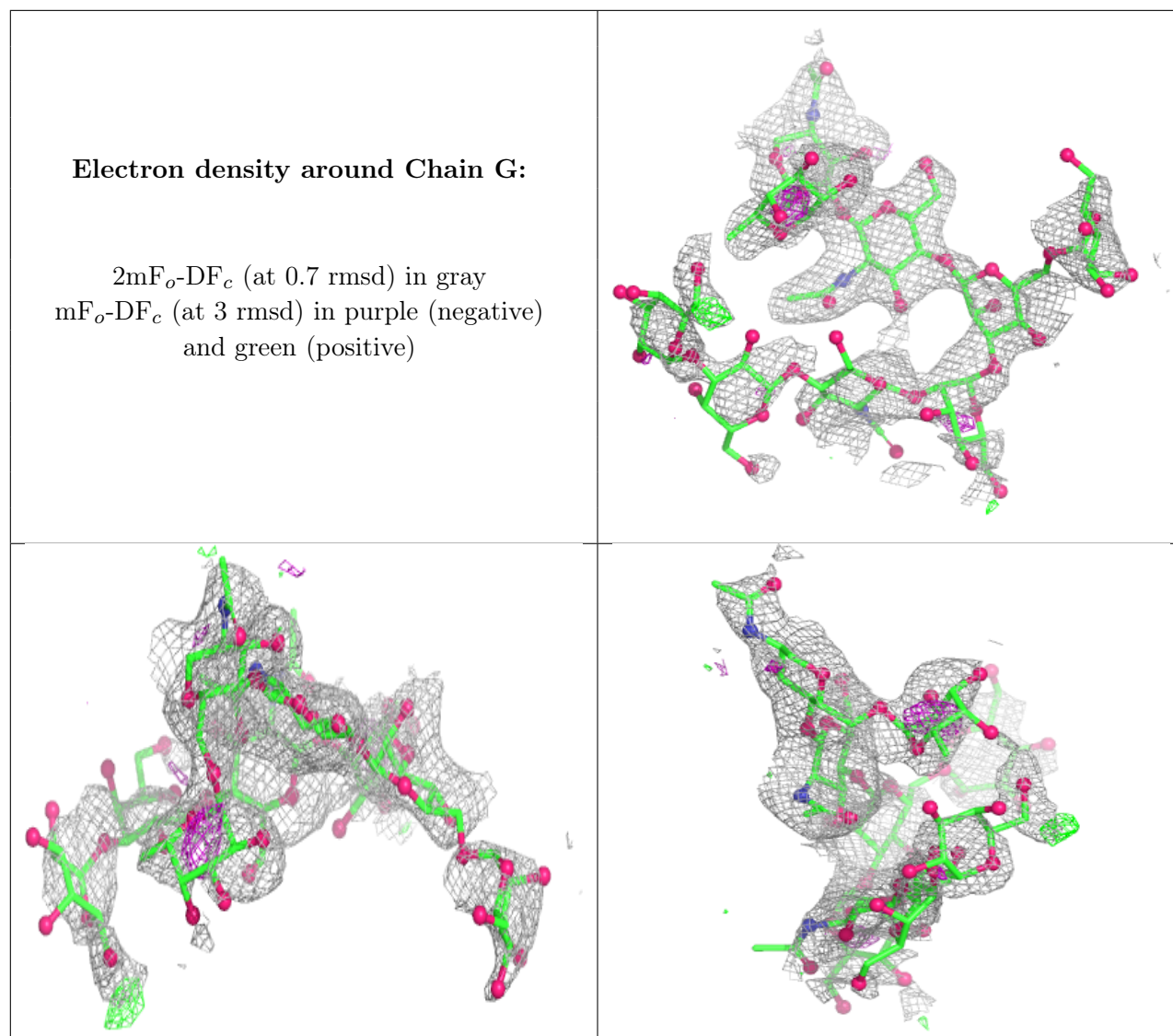
Electron density around Chain A:

$2mF_o-DF_c$ (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
6	PEG	H	410	7/7	0.73	0.15	54,56,59,61	0
6	PEG	B	406	7/7	0.87	0.12	44,46,48,48	0
7	K	L	301	1/1	0.97	0.09	39,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.