



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:09 PM UTC

PDB ID : 4RBP / pdb_00004rbp
Title : Crystal structure of HIV neutralizing antibody 2G12 in complex with a bacterial oligosaccharide analog of mammalian oligomanose
Authors : Stanfield, R.L.; Wilson, I.A.; De Castro, C.; Marzaioli, A.M.; Pantophlet, R.
Deposited on : 2014-09-12
Resolution : 1.85 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

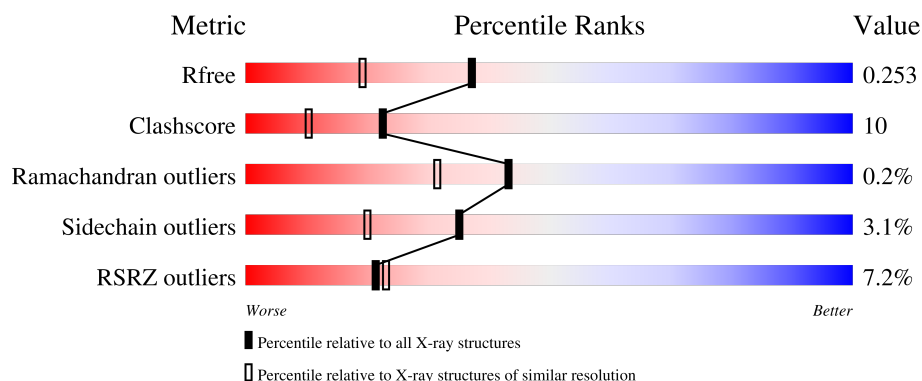
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	K	213	4% 86% 14%
1	L	213	4% 81% 19%
2	H	224	12% 78% 18% ••
2	M	224	8% 78% 20% •
3	A	6	67% 33%

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Mol	Chain	Length	Quality of chain
3	B	6	 50%50%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7363 atoms, of which 64 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.

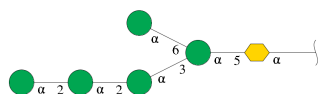
- Molecule 1 is a protein called Fab 2G12 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	213	Total	C	N	O	S	0	1	0
			1635	1028	274	327	6			
1	K	213	Total	C	N	O	S	0	3	0
			1651	1041	277	327	6			

- Molecule 2 is a protein called Fab 2G12 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	220	Total	C	N	O	S	0	1	0
			1650	1039	281	322	8			
2	M	224	Total	C	N	O	S	0	1	0
			1678	1055	286	329	8			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-5)-3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	A	6	Total	C	O	0	0	0
			71	38	33			
3	B	6	Total	C	O	0	0	0
			71	38	33			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	L	1	Total	C	H	O	0	0
			14	3	8	3		
4	L	1	Total	C	H	O	0	0
			14	3	8	3		
4	H	1	Total	C	H	O	0	0
			14	3	8	3		
4	H	1	Total	C	H	O	0	0
			14	3	8	3		
4	H	1	Total	C	H	O	0	0
			14	3	8	3		
4	K	1	Total	C	H	O	0	0
			14	3	8	3		
4	K	1	Total	C	H	O	0	0
			14	3	8	3		
4	K	1	Total	C	H	O	0	0
			14	3	8	3		

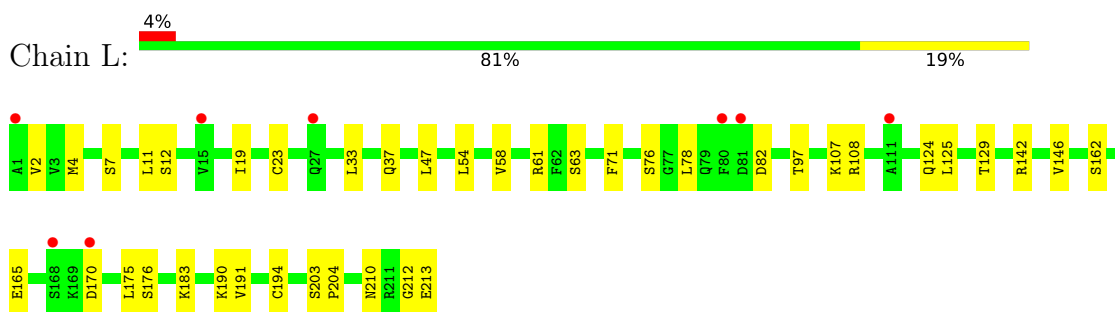
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	120	Total	O	0	0
			120	120		
5	H	114	Total	O	0	0
			114	114		
5	K	137	Total	O	0	0
			137	137		
5	M	124	Total	O	0	0
			124	124		

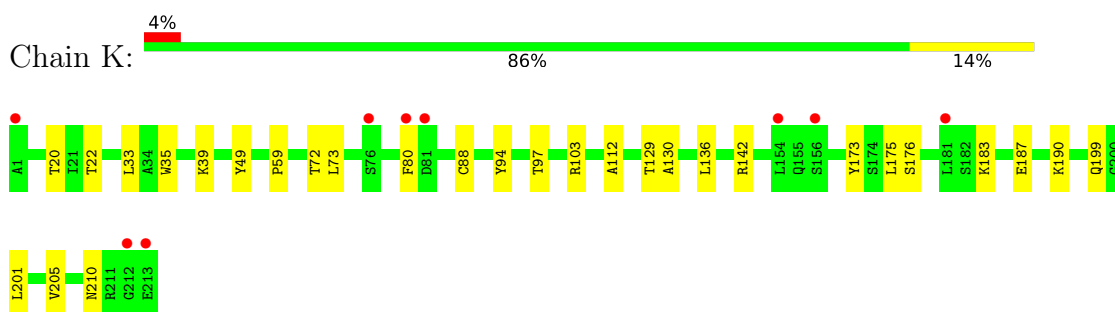
3 Residue-property plots

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.

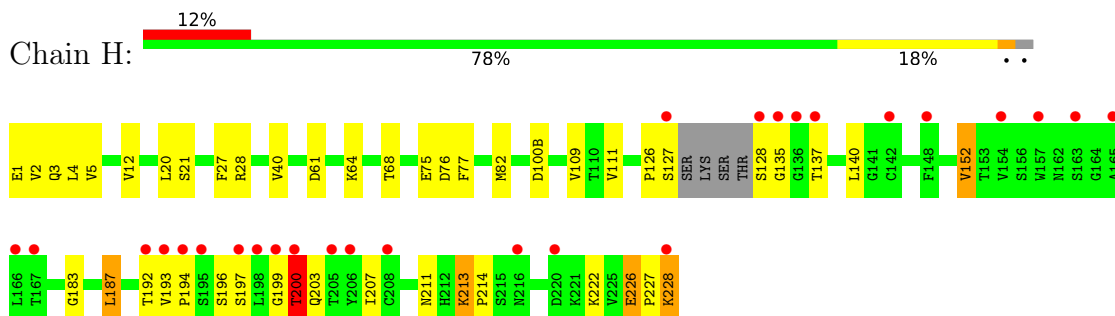
- Molecule 1: Fab 2G12 light chain



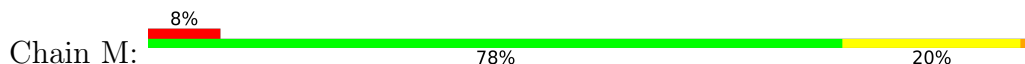
- Molecule 1: Fab 2G12 light chain

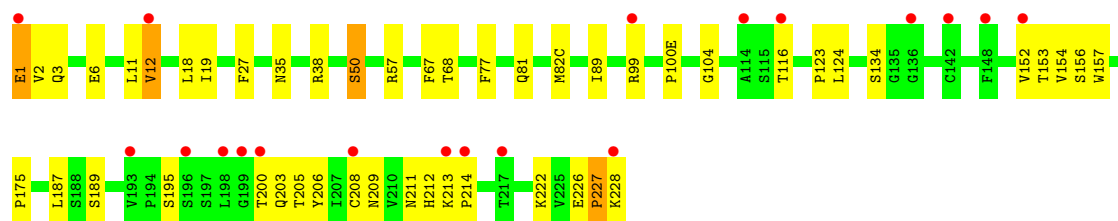


- Molecule 2: Fab 2G12 heavy chain



- Molecule 2: Fab 2G12 heavy chain





- Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-5)-3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid

Chain A:



- Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-5)-3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	45.30Å 130.88Å 170.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.77 – 1.85 43.77 – 1.85	Depositor EDS
% Data completeness (in resolution range)	87.9 (43.77-1.85) 88.0 (43.77-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 1.86Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.208 , 0.252 0.210 , 0.253	Depositor DCC
R_{free} test set	2000 reflections (2.28%)	wwPDB-VP
Wilson B-factor (Å ²)	22.8	Xtriage
Anisotropy	0.622	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 36.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7363	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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: MAN, GOL, KDO

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	K	0.46	0/1697	0.78	0/2303
1	L	0.44	0/1674	0.78	0/2273
2	H	0.52	0/1691	0.87	2/2302 (0.1%)
2	M	0.55	2/1720 (0.1%)	0.85	1/2342 (0.0%)
All	All	0.49	2/6782 (0.0%)	0.82	3/9220 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	226	GLU	C-N	5.51	1.41	1.33
2	M	227	PRO	N-CD	5.37	1.55	1.47

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	226	GLU	CA-C-N	-5.93	113.67	119.78
2	H	226	GLU	C-N-CA	-5.93	113.67	119.78
2	M	227	PRO	CB-CA-C	-5.59	104.24	111.39

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	K	1651	0	1620	24	0
1	L	1635	0	1598	26	0
2	H	1650	0	1621	44	0
2	M	1678	0	1652	48	0
3	A	71	0	58	7	0
3	B	71	0	58	2	0
4	H	18	24	24	2	0
4	K	18	24	24	2	0
4	L	12	16	16	2	0
5	H	114	0	0	4	0
5	K	137	0	0	6	0
5	L	120	0	0	4	0
5	M	124	0	0	2	0
All	All	7299	64	6671	141	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 10.

All (141) 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)
2:M:211:ASN:HD21	2:M:213:LYS:HE2	1.06	1.12
2:M:1:GLU:OE1	2:M:1:GLU:N	1.99	0.96
2:H:222:LYS:HE2	2:H:226:GLU:OE1	1.66	0.93
2:M:211:ASN:ND2	2:M:213:LYS:HE2	1.89	0.88
1:L:33:LEU:HD22	1:L:71:PHE:CG	2.08	0.88
1:L:142:ARG:NH1	5:L:434:HOH:O	2.06	0.87
2:M:12:VAL:HG11	2:M:82(C):MET:HE3	1.58	0.85
3:A:2:MAN:H61	3:A:6:MAN:H5	1.62	0.81
1:K:20:THR:HG23	1:K:72:THR:HG23	1.64	0.80
2:H:21:SER:HB3	2:M:19:ILE:HD13	1.65	0.78
2:H:61:ASP:OD1	2:H:64:LYS:NZ	2.18	0.77
2:H:199:GLY:O	2:H:200:THR:HG22	1.84	0.77
1:K:201:LEU:HD13	1:K:205:VAL:HG23	1.69	0.74
2:M:18:LEU:CB	2:M:82(C):MET:CE	2.69	0.71
1:L:165:GLU:HG3	5:L:487:HOH:O	1.91	0.71
2:M:18:LEU:CB	2:M:82(C):MET:HE1	2.21	0.71
2:H:199:GLY:C	2:H:200:THR:HG22	2.15	0.70
2:H:222:LYS:O	5:H:498:HOH:O	2.10	0.70
1:L:212:GLY:O	1:L:213:GLU:HB2	1.93	0.69
4:L:301:GOL:HO1	2:M:134:SER:HG	1.36	0.69
2:M:18:LEU:HB3	2:M:82(C):MET:CE	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:18:LEU:HB3	2:M:82(C):MET:HE1	1.76	0.68
1:K:112:ALA:O	5:K:496:HOH:O	2.10	0.68
3:A:1:KDO:O6	3:A:1:KDO:O8	2.10	0.68
1:L:2:VAL:O	1:L:97:THR:HG21	1.94	0.68
1:L:124:GLN:HG2	1:L:129:THR:O	1.95	0.67
1:K:20:THR:HG23	1:K:72:THR:CG2	2.25	0.66
1:L:203:SER:HB2	1:L:204:PRO:CD	2.26	0.66
1:L:190:LYS:NZ	5:L:505:HOH:O	2.27	0.65
2:H:1:GLU:OE2	5:H:505:HOH:O	2.15	0.65
2:H:227:PRO:O	2:H:228:LYS:HB2	1.96	0.64
1:L:37:GLN:HB2	1:L:47:LEU:HD11	1.80	0.64
1:L:33:LEU:HD22	1:L:71:PHE:CD2	2.33	0.63
1:L:175:LEU:HD23	1:L:176:SER:N	2.14	0.62
2:M:35:ASN:OD1	2:M:50:SER:HB2	1.99	0.62
2:H:3:GLN:C	2:H:4:LEU:HD12	2.23	0.62
2:M:18:LEU:HB2	2:M:82(C):MET:CE	2.30	0.61
2:H:197:SER:O	2:H:200:THR:HG23	2.00	0.61
2:M:205:THR:HG23	2:M:222:LYS:HD2	1.83	0.61
2:M:2:VAL:HG13	2:M:27:PHE:CD1	2.35	0.61
3:A:2:MAN:H61	3:A:6:MAN:C5	2.30	0.61
2:H:222:LYS:CE	2:H:226:GLU:OE1	2.45	0.60
1:L:175:LEU:HD23	1:L:175:LEU:C	2.26	0.60
2:M:187:LEU:C	2:M:187:LEU:HD12	2.26	0.59
2:H:4:LEU:HD12	2:H:4:LEU:N	2.17	0.59
2:M:153:THR:OG1	2:M:211:ASN:HB3	2.03	0.59
2:H:183:GLY:HA2	2:M:11:LEU:HD12	1.85	0.59
3:A:1:KDO:H7	3:A:2:MAN:C1	2.33	0.58
2:H:193:VAL:HB	2:H:194:PRO:CD	2.33	0.58
1:K:142:ARG:HG3	1:K:173:TYR:CD2	2.38	0.58
2:M:99:ARG:CZ	2:M:99:ARG:HB2	2.34	0.58
2:H:187:LEU:C	2:H:187:LEU:HD12	2.29	0.57
1:L:11:LEU:HD23	1:L:11:LEU:C	2.29	0.57
2:H:200:THR:HG23	2:H:203:GLN:H	1.70	0.56
2:H:222:LYS:HE2	2:H:226:GLU:CD	2.29	0.56
4:H:309:GOL:H12	5:H:447:HOH:O	2.06	0.56
1:K:199:GLN:HG3	5:K:478:HOH:O	2.06	0.56
2:M:156:SER:OG	2:M:209:ASN:HB2	2.06	0.55
3:A:2:MAN:C6	3:A:6:MAN:H5	2.35	0.55
2:H:77:PHE:CE2	2:M:68:THR:HG21	2.41	0.55
2:H:75:GLU:HG3	2:M:57:ARG:CZ	2.37	0.55
2:H:152:VAL:HG23	2:H:187:LEU:HD21	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:193:VAL:HB	2:H:194:PRO:HD2	1.88	0.54
2:H:126:PRO:O	2:H:127:SER:CB	2.55	0.54
2:M:18:LEU:HB2	2:M:82(C):MET:HE1	1.88	0.54
1:K:176:SER:OG	4:K:302:GOL:H11	2.07	0.53
2:M:99:ARG:HB2	2:M:99:ARG:NH1	2.23	0.53
4:L:301:GOL:O1	2:M:134:SER:OG	2.18	0.52
2:H:2:VAL:HG13	2:H:27:PHE:CD1	2.45	0.52
1:K:94:TYR:HB3	5:M:523:HOH:O	2.10	0.52
1:K:80[B]:PHE:HD2	5:K:447:HOH:O	1.93	0.52
2:H:183:GLY:HA2	2:M:11:LEU:CD1	2.40	0.51
2:M:153:THR:HG1	2:M:211:ASN:HB3	1.75	0.51
1:L:4:MET:HE3	1:L:23:CYS:SG	2.52	0.50
2:M:18:LEU:CB	2:M:82(C):MET:HE2	2.41	0.50
2:H:100(B):ASP:OD1	3:A:4:MAN:O6	2.29	0.50
2:H:40:VAL:HB	5:H:481:HOH:O	2.12	0.49
2:H:126:PRO:O	2:H:127:SER:HB3	2.12	0.49
2:M:152:VAL:HG12	2:M:212:HIS:CD2	2.48	0.48
1:L:78:LEU:HD12	1:L:82:ASP:HB2	1.95	0.48
2:M:6:GLU:OE1	2:M:104:GLY:HA3	2.14	0.48
2:M:203:GLN:HG2	2:M:206:TYR:CZ	2.49	0.47
2:H:194:PRO:C	2:H:196:SER:H	2.22	0.47
2:H:194:PRO:C	2:H:196:SER:N	2.72	0.47
1:L:203:SER:HB2	1:L:204:PRO:HD3	1.96	0.47
1:L:162:SER:OG	2:M:175:PRO:HD2	2.14	0.47
2:M:18:LEU:N	2:M:82(C):MET:HE2	2.29	0.47
3:B:1:KDO:O6	3:B:1:KDO:O8	2.20	0.47
1:K:97:THR:HG23	5:K:533:HOH:O	2.15	0.46
3:A:2:MAN:C6	3:A:6:MAN:C5	2.94	0.46
1:K:136:LEU:N	1:K:136:LEU:HD12	2.30	0.46
2:H:207:ILE:HG12	2:H:222:LYS:HG3	1.97	0.46
3:B:2:MAN:H61	3:B:6:MAN:H5	1.98	0.46
2:M:18:LEU:HB3	2:M:82(C):MET:HE2	1.95	0.46
2:M:38:ARG:HA	2:M:89:ILE:O	2.16	0.46
2:M:2:VAL:HG13	2:M:27:PHE:CE1	2.52	0.45
1:K:59:PRO:HG3	4:K:303:GOL:H12	1.99	0.45
1:K:20:THR:CG2	5:K:503:HOH:O	2.66	0.44
1:L:61:ARG:HB2	1:L:76:SER:O	2.16	0.44
1:K:35:TRP:CE2	1:K:73:LEU:HB2	2.52	0.44
1:L:33:LEU:HD22	1:L:71:PHE:CB	2.48	0.43
1:K:175:LEU:C	1:K:175:LEU:HD23	2.42	0.43
1:L:146:VAL:HG13	1:L:194[A]:CYS:SG	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:211:ASN:HD21	2:H:213:LYS:NZ	2.16	0.43
2:H:21:SER:CB	2:M:19:ILE:HD13	2.43	0.43
1:L:191:VAL:HG22	1:L:210:ASN:OD1	2.19	0.43
1:K:35:TRP:CZ3	1:K:88:CYS:HB3	2.54	0.43
1:K:183:LYS:NZ	1:K:187:GLU:OE2	2.41	0.43
2:H:75:GLU:CG	2:M:57:ARG:CZ	2.96	0.43
1:K:129:THR:HG22	1:K:130:ALA:N	2.34	0.42
2:M:67:PHE:HA	2:M:81:GLN:O	2.19	0.42
1:L:125:LEU:HD12	1:L:125:LEU:HA	1.78	0.42
2:M:124:LEU:HD23	5:M:501:HOH:O	2.18	0.42
2:M:157:TRP:CH2	2:M:208:CYS:HB3	2.55	0.42
1:K:136:LEU:N	1:K:136:LEU:CD1	2.83	0.42
2:H:213:LYS:N	2:H:214:PRO:CD	2.83	0.42
2:M:213:LYS:HD3	2:M:213:LYS:HA	1.84	0.42
2:H:68:THR:HG21	2:M:77:PHE:CE2	2.55	0.42
1:K:103[A]:ARG:NH1	5:K:464:HOH:O	2.27	0.42
1:L:108:ARG:HD2	1:L:170:ASP:O	2.20	0.41
1:K:49:TYR:CB	2:M:100(E):PRO:HG3	2.49	0.41
5:L:494:HOH:O	2:M:123:PRO:CD	2.67	0.41
2:H:82:MET:HE1	2:H:109:VAL:HG21	2.02	0.41
2:H:128:SER:O	2:H:137:THR:O	2.37	0.41
1:L:125:LEU:O	1:L:183:LYS:HD2	2.21	0.41
2:H:20:LEU:HG	2:H:82:MET:HE2	2.02	0.41
1:K:129:THR:CG2	1:K:130:ALA:N	2.84	0.41
2:M:187:LEU:C	2:M:187:LEU:CD1	2.93	0.41
2:H:152:VAL:CG2	2:H:187:LEU:HD21	2.50	0.41
2:M:154:VAL:HG11	2:M:189:SER:CB	2.50	0.41
1:L:12:SER:CB	1:L:107:LYS:HD3	2.51	0.41
2:H:12:VAL:O	2:H:111:VAL:HA	2.21	0.41
2:H:75:GLU:OE1	4:H:308:GOL:O1	2.25	0.41
2:H:222:LYS:CE	2:H:226:GLU:CD	2.91	0.41
2:H:12:VAL:HG13	2:H:111:VAL:HG22	2.03	0.41
2:H:28:ARG:NE	2:H:76:ASP:OD2	2.54	0.40
2:M:213:LYS:N	2:M:214:PRO:CD	2.85	0.40
1:L:54:LEU:HD11	1:L:58:VAL:CG1	2.51	0.40
1:K:190:LYS:O	1:K:210:ASN:HA	2.21	0.40
2:M:12:VAL:HG21	2:M:82(C):MET:HE1	2.03	0.40
1:K:190:LYS:HE3	1:K:210:ASN:HB3	2.02	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	K	214/213 (100%)	206 (96%)	8 (4%)	0	100	100
1	L	212/213 (100%)	205 (97%)	7 (3%)	0	100	100
2	H	217/224 (97%)	202 (93%)	13 (6%)	2 (1%)	14	4
2	M	223/224 (100%)	218 (98%)	5 (2%)	0	100	100
All	All	866/874 (99%)	831 (96%)	33 (4%)	2 (0%)	43	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	200	THR
2	H	135	GLY

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	K	186/183 (102%)	183 (98%)	3 (2%)	55	44
1	L	184/183 (100%)	181 (98%)	3 (2%)	55	44
2	H	186/189 (98%)	178 (96%)	8 (4%)	26	11
2	M	190/189 (100%)	181 (95%)	9 (5%)	23	9
All	All	746/744 (100%)	723 (97%)	23 (3%)	35	20

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	7	SER
1	L	19	ILE
1	L	63	SER
2	H	5	VAL
2	H	140	LEU
2	H	152	VAL
2	H	187	LEU
2	H	192	THR
2	H	200	THR
2	H	213	LYS
2	H	228	LYS
1	K	22	THR
1	K	33	LEU
1	K	39	LYS
2	M	1	GLU
2	M	3	GLN
2	M	12	VAL
2	M	50	SER
2	M	116	THR
2	M	195	SER
2	M	200	THR
2	M	227	PRO
2	M	228	LYS

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

Mol	Chain	Res	Type
1	L	137	ASN
1	L	189	HIS
2	H	211	ASN
1	K	38	GLN
2	M	211	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 ⓘ

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$
3	KDO	A	1	3	16,16,16	2.14	6 (37%)	17,24,24	1.08	1 (5%)
3	MAN	A	2	3	11,11,12	0.76	0	15,15,17	0.83	0
3	MAN	A	3	3	11,11,12	0.53	0	15,15,17	0.96	1 (6%)
3	MAN	A	4	3	11,11,12	0.55	0	15,15,17	0.92	1 (6%)
3	MAN	A	5	3	11,11,12	0.58	0	15,15,17	1.18	1 (6%)
3	MAN	A	6	3	11,11,12	0.48	0	15,15,17	0.81	0
3	KDO	B	1	3	16,16,16	2.34	6 (37%)	17,24,24	1.04	2 (11%)
3	MAN	B	2	3	11,11,12	0.54	0	15,15,17	0.89	1 (6%)
3	MAN	B	3	3	11,11,12	0.56	0	15,15,17	0.98	1 (6%)
3	MAN	B	4	3	11,11,12	0.50	0	15,15,17	1.17	1 (6%)
3	MAN	B	5	3	11,11,12	0.40	0	15,15,17	1.02	1 (6%)
3	MAN	B	6	3	11,11,12	0.46	0	15,15,17	1.04	1 (6%)

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	KDO	A	1	3	-	7/12/30/30	0/1/1/1
3	MAN	A	2	3	-	2/2/19/22	0/1/1/1
3	MAN	A	3	3	-	0/2/19/22	0/1/1/1
3	MAN	A	4	3	-	0/2/19/22	0/1/1/1
3	MAN	A	5	3	-	0/2/19/22	0/1/1/1
3	MAN	A	6	3	-	0/2/19/22	0/1/1/1
3	KDO	B	1	3	-	6/12/30/30	0/1/1/1
3	MAN	B	2	3	-	0/2/19/22	0/1/1/1
3	MAN	B	3	3	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	B	4	3	-	0/2/19/22	0/1/1/1
3	MAN	B	5	3	-	0/2/19/22	0/1/1/1
3	MAN	B	6	3	-	2/2/19/22	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1	KDO	O6-C2	-5.47	1.37	1.43
3	A	1	KDO	O6-C2	-4.72	1.38	1.43
3	B	1	KDO	O6-C6	-4.05	1.37	1.44
3	A	1	KDO	O6-C6	-3.44	1.38	1.44
3	A	1	KDO	C2-C1	-2.69	1.49	1.53
3	B	1	KDO	C2-C1	-2.58	1.50	1.53
3	B	1	KDO	O7-C7	-2.48	1.38	1.43
3	A	1	KDO	O7-C7	-2.47	1.38	1.43
3	B	1	KDO	C3-C4	-2.44	1.49	1.53
3	B	1	KDO	O4-C4	-2.34	1.38	1.43
3	A	1	KDO	O4-C4	-2.21	1.38	1.43
3	A	1	KDO	C3-C4	-2.19	1.49	1.53

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	5	MAN	C1-O5-C5	3.18	116.45	112.19
3	B	3	MAN	C2-C3-C4	-2.68	106.14	110.86
3	B	6	MAN	C2-C3-C4	-2.38	106.67	110.86
3	B	4	MAN	C1-O5-C5	2.37	115.37	112.19
3	A	4	MAN	C1-O5-C5	2.34	115.33	112.19
3	A	3	MAN	C2-C3-C4	-2.33	106.76	110.86
3	B	1	KDO	C3-C4-C5	-2.25	108.65	110.84
3	A	1	KDO	O1A-C1-C2	-2.22	120.15	123.85
3	B	1	KDO	O1A-C1-C2	-2.17	120.23	123.85
3	B	2	MAN	C1-O5-C5	2.15	115.06	112.19
3	B	5	MAN	C2-C3-C4	-2.05	107.26	110.86

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1	KDO	O1A-C1-C2-O6
3	A	1	KDO	C6-C7-C8-O8

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Mol	Chain	Res	Type	Atoms
3	A	1	KDO	O7-C7-C8-O8
3	B	1	KDO	C6-C7-C8-O8
3	B	6	MAN	C4-C5-C6-O6
3	B	1	KDO	O7-C7-C8-O8
3	B	6	MAN	O5-C5-C6-O6
3	A	2	MAN	O5-C5-C6-O6
3	A	2	MAN	C4-C5-C6-O6
3	A	1	KDO	C5-C6-C7-O7
3	B	1	KDO	O1A-C1-C2-C3
3	B	1	KDO	O1B-C1-C2-C3
3	B	1	KDO	O1A-C1-C2-O6
3	A	1	KDO	O1B-C1-C2-O6
3	B	1	KDO	O1B-C1-C2-O2
3	A	1	KDO	C5-C6-C7-C8
3	A	1	KDO	O6-C6-C7-O7

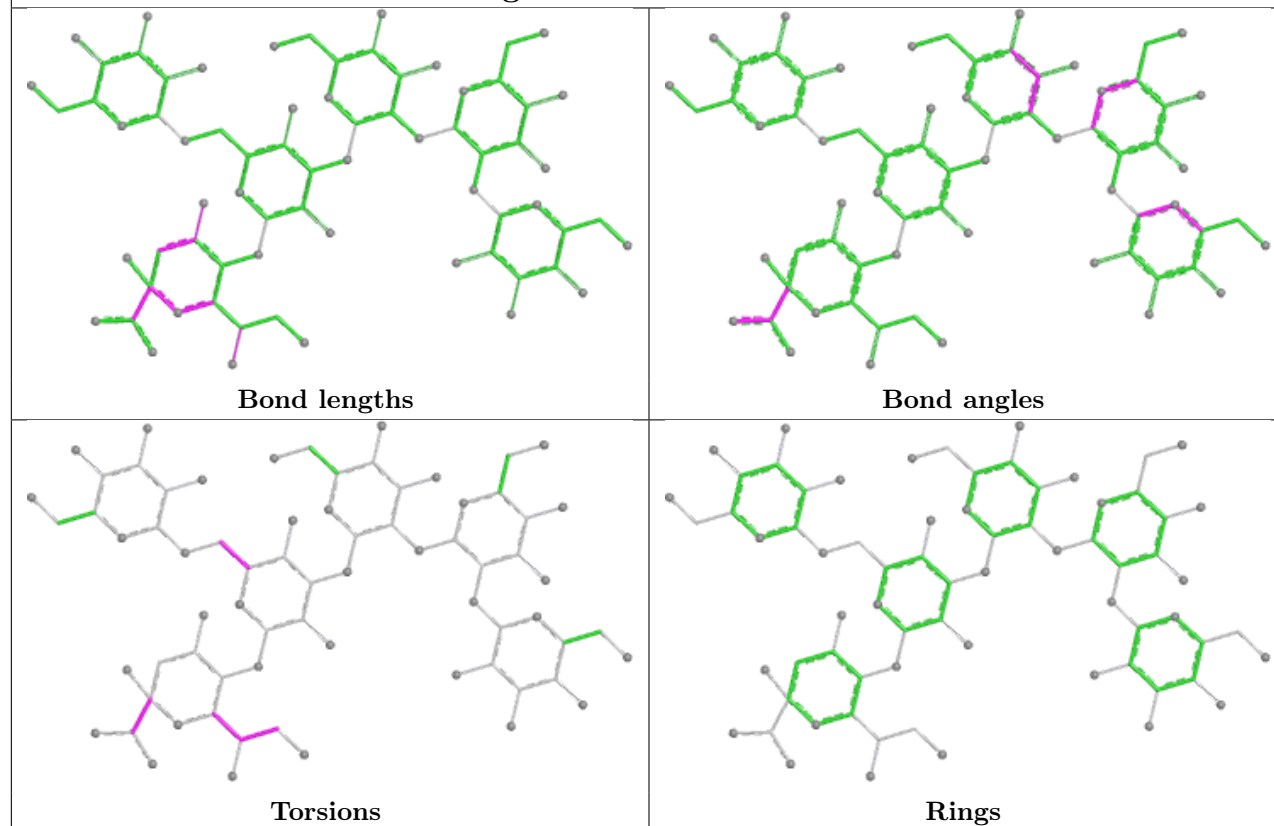
There are no ring outliers.

7 monomers are involved in 9 short contacts:

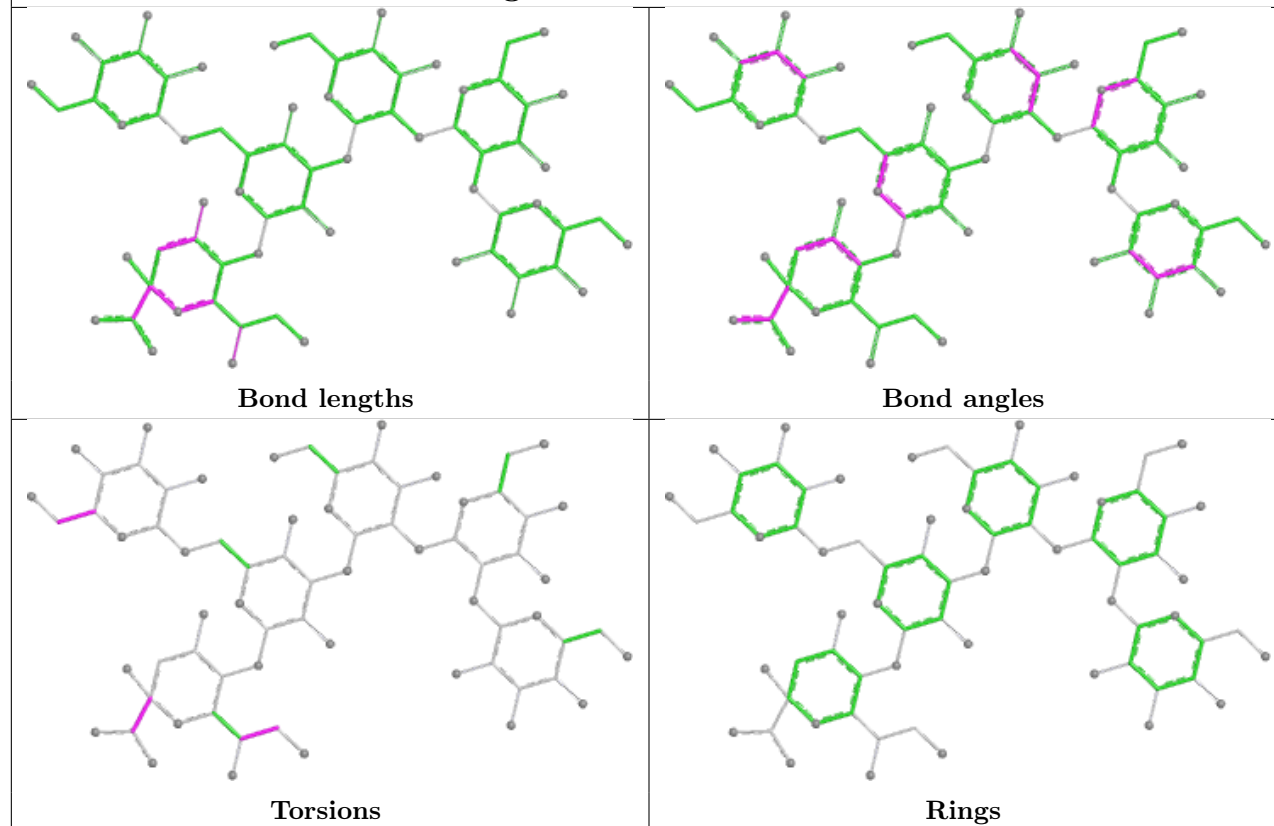
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	6	MAN	1	0
3	A	2	MAN	5	0
3	B	1	KDO	1	0
3	B	2	MAN	1	0
3	A	6	MAN	4	0
3	A	4	MAN	1	0
3	A	1	KDO	2	0

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 A



Oligosaccharide Chain B



5.6 Ligand geometry

8 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	$\# Z > 2$
4	GOL	H	308	-	5,5,5	0.41	0	5,5,5	0.27	0
4	GOL	H	307	-	5,5,5	0.36	0	5,5,5	0.15	0
4	GOL	K	301	-	5,5,5	0.31	0	5,5,5	0.72	0
4	GOL	K	302	-	5,5,5	0.42	0	5,5,5	0.49	0
4	GOL	L	301	-	5,5,5	0.46	0	5,5,5	0.98	0
4	GOL	K	303	-	5,5,5	0.44	0	5,5,5	0.50	0
4	GOL	H	309	-	5,5,5	0.32	0	5,5,5	0.36	0
4	GOL	L	302	-	5,5,5	0.36	0	5,5,5	0.17	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	H	308	-	-	0/4/4/4	-
4	GOL	H	307	-	-	2/4/4/4	-
4	GOL	K	301	-	-	3/4/4/4	-
4	GOL	K	302	-	-	2/4/4/4	-
4	GOL	L	301	-	-	0/4/4/4	-
4	GOL	K	303	-	-	1/4/4/4	-
4	GOL	H	309	-	-	3/4/4/4	-
4	GOL	L	302	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L	302	GOL	O1-C1-C2-C3
4	H	307	GOL	C1-C2-C3-O3
4	H	307	GOL	O2-C2-C3-O3
4	H	309	GOL	O1-C1-C2-C3
4	K	301	GOL	O1-C1-C2-C3
4	K	302	GOL	O1-C1-C2-C3
4	L	302	GOL	C1-C2-C3-O3
4	K	301	GOL	O1-C1-C2-O2
4	K	302	GOL	O1-C1-C2-O2
4	L	302	GOL	O1-C1-C2-O2
4	H	309	GOL	O1-C1-C2-O2
4	L	302	GOL	O2-C2-C3-O3
4	H	309	GOL	O2-C2-C3-O3
4	K	301	GOL	O2-C2-C3-O3
4	K	303	GOL	C1-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	308	GOL	1	0
4	K	302	GOL	1	0
4	L	301	GOL	2	0
4	K	303	GOL	1	0
4	H	309	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	K	213/213 (100%)	0.58	9 (4%) 40 44	18, 33, 47, 63	3 (1%)
1	L	213/213 (100%)	0.78	8 (3%) 44 48	18, 36, 48, 59	1 (0%)
2	H	220/224 (98%)	0.84	27 (12%) 8 8	19, 36, 60, 73	1 (0%)
2	M	224/224 (100%)	0.82	19 (8%) 16 17	18, 34, 51, 61	1 (0%)
All	All	870/874 (99%)	0.76	63 (7%) 21 23	18, 35, 53, 73	6 (0%)

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	135	GLY	5.2
1	K	1	ALA	4.9
2	H	128	SER	4.3
1	K	80[A]	PHE	4.3
2	M	199	GLY	4.1
2	M	214	PRO	3.9
1	L	1	ALA	3.7
2	H	136	GLY	3.5
2	M	116	THR	3.4
1	L	81	ASP	3.2
2	H	228	LYS	3.2
2	M	200	THR	3.2
2	H	167	THR	3.1
2	H	137	THR	3.1
2	M	198	LEU	3.0
2	M	213	LYS	3.0
1	L	80	PHE	2.9
2	H	148	PHE	2.9
2	M	114	ALA	2.8
1	L	111	ALA	2.8
2	H	163	SER	2.8

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Mol	Chain	Res	Type	RSRZ
2	H	197	SER	2.8
2	M	217	THR	2.8
1	K	76	SER	2.7
1	K	154	LEU	2.7
2	H	205	THR	2.7
1	K	156	SER	2.6
2	M	193	VAL	2.6
2	H	166	LEU	2.6
2	H	165	ALA	2.6
2	M	148	PHE	2.6
2	M	1	GLU	2.6
1	K	212	GLY	2.6
2	M	142	CYS	2.5
2	H	198	LEU	2.5
2	M	228	LYS	2.5
2	M	136	GLY	2.5
1	L	168	SER	2.5
2	H	194	PRO	2.5
2	H	199	GLY	2.4
2	H	195	SER	2.4
2	H	193	VAL	2.3
1	K	81	ASP	2.3
2	H	142	CYS	2.3
1	L	27	GLN	2.3
1	K	213	GLU	2.2
2	M	196	SER	2.2
2	H	216	ASN	2.2
1	L	170	ASP	2.2
2	H	154	VAL	2.2
2	H	192	THR	2.2
2	H	200	THR	2.2
2	H	206	TYR	2.2
1	L	15	VAL	2.2
2	H	127	SER	2.1
2	M	152	VAL	2.1
1	K	181	LEU	2.1
2	H	220	ASP	2.1
2	M	99	ARG	2.1
2	M	12	VAL	2.1
2	M	208	CYS	2.1
2	H	157	TRP	2.0
2	H	208	CYS	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 ⓘ

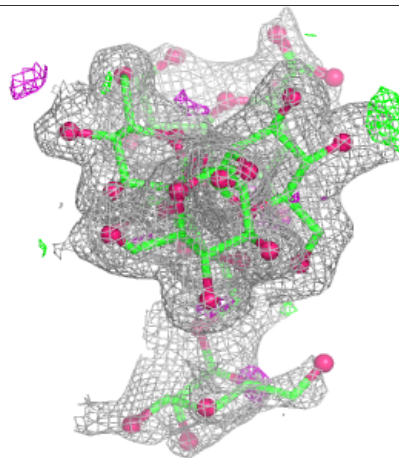
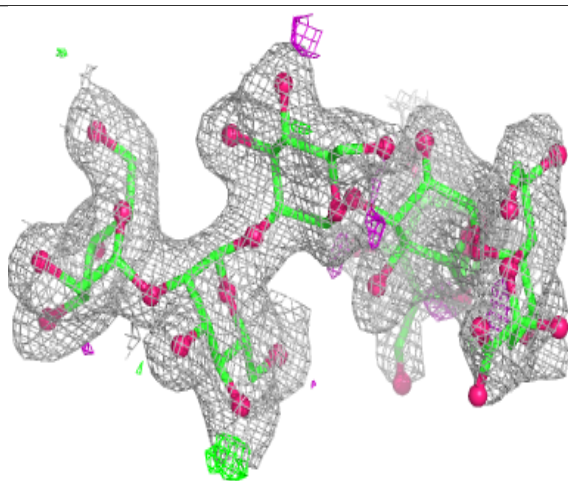
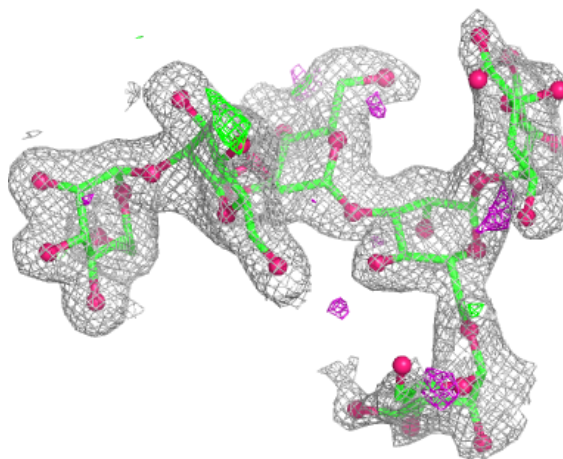
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

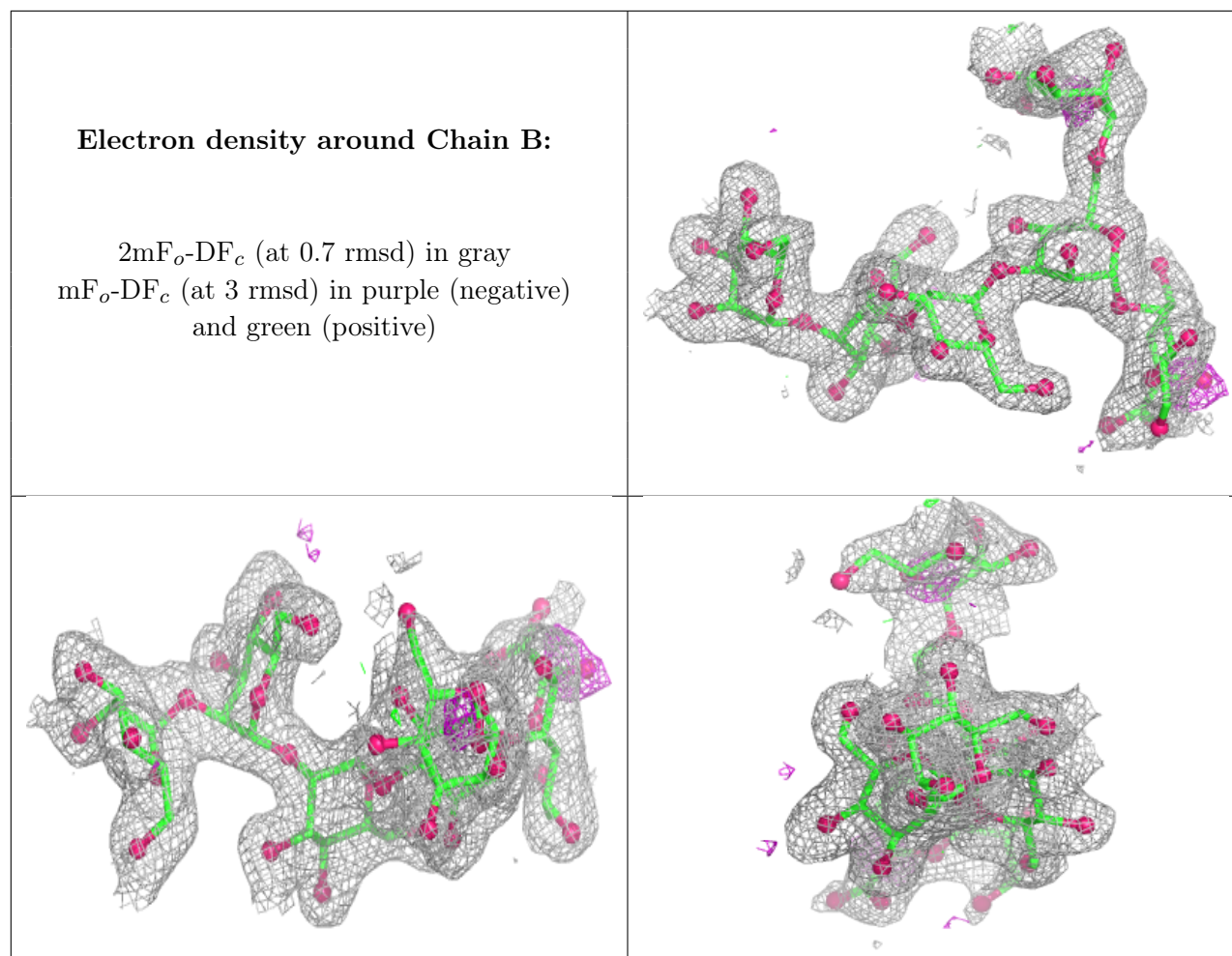
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	KDO	A	1	16/16	-	-	50,58,66,67	0
3	MAN	A	2	11/12	-	-	32,41,54,57	0
3	MAN	A	3	11/12	-	-	30,33,36,46	0
3	MAN	A	4	11/12	-	-	27,32,34,34	0
3	MAN	A	5	11/12	-	-	23,26,29,30	0
3	MAN	A	6	11/12	-	-	60,63,67,68	0
3	KDO	B	1	16/16	-	-	41,54,69,70	0
3	MAN	B	2	11/12	-	-	32,34,42,47	0
3	MAN	B	3	11/12	-	-	28,32,40,47	0
3	MAN	B	4	11/12	-	-	26,30,33,35	0
3	MAN	B	5	11/12	-	-	22,25,28,30	0
3	MAN	B	6	11/12	-	-	55,57,60,62	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)





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	H	307	6/6	0.58	0.17	64,76,86,89	0
4	GOL	K	303	6/6	0.58	0.22	48,59,72,75	0
4	GOL	L	302	6/6	0.69	0.17	55,66,71,73	0
4	GOL	H	308	6/6	0.77	0.16	30,52,62,65	0
4	GOL	H	309	6/6	0.78	0.15	41,51,56,61	0
4	GOL	K	302	6/6	0.78	0.15	37,45,53,58	0
4	GOL	L	301	6/6	0.78	0.15	38,46,49,50	0
4	GOL	K	301	6/6	0.82	0.14	48,59,66,75	0

6.5 Other polymers [i](#)

There are no such residues in this entry.