



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 10, 2020 – 02:02 AM EST

PDB ID : 7KQI
Title : Antibodies that engage the hemagglutinin receptor-binding site of influenza B viruses
Authors : Bajic, G.; Harrison, S.C.
Deposited on : 2020-11-16
Resolution : 4.20 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	:	2.15.1
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)	:	2.15.1

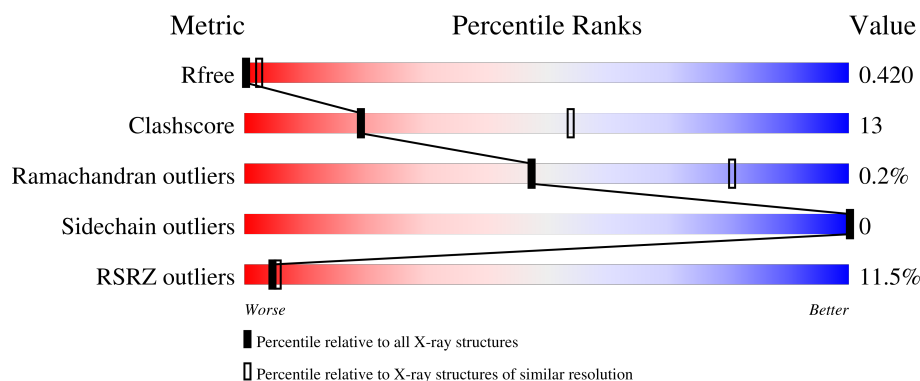
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.20 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	1005 (4.62-3.78)
Clashscore	141614	1044 (4.60-3.80)
Ramachandran outliers	138981	1000 (4.60-3.80)
Sidechain outliers	138945	1007 (4.62-3.78)
RSRZ outliers	127900	1063 (4.70-3.70)

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

Mol	Chain	Length	Quality of chain
1	A	240	<div> <div>15%</div> <div>64%</div> <div>25%</div> <div>10%</div> </div>
2	C	216	<div> <div>10%</div> <div>72%</div> <div>26%</div> <div>.</div> </div>
3	B	298	<div> <div>6%</div> <div>55%</div> <div>20%</div> <div>24%</div> </div>
4	D	3	<div>100%</div>
5	E	3	<div>100%</div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	BMA	E	3	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5070 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 1209 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	0	0	0
			1644	1045	279	312	8			

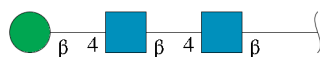
- Molecule 2 is a protein called 1209 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	211	Total	C	N	O	S	0	0	0
			1624	1016	276	326	6			

- Molecule 3 is a protein called Hemagglutinin.

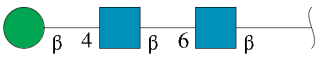
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	225	Total	C	N	O	S	0	0	0
			1724	1078	311	322	13			

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	3	Total	C	N	O		0	0	0
			39	22	2	15				

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.

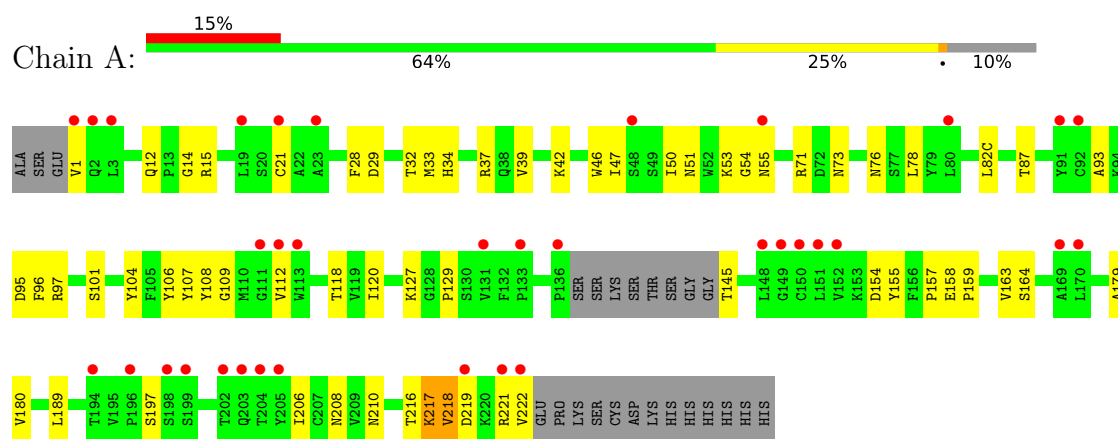


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	E	3	39	22	2	15	0	0	0

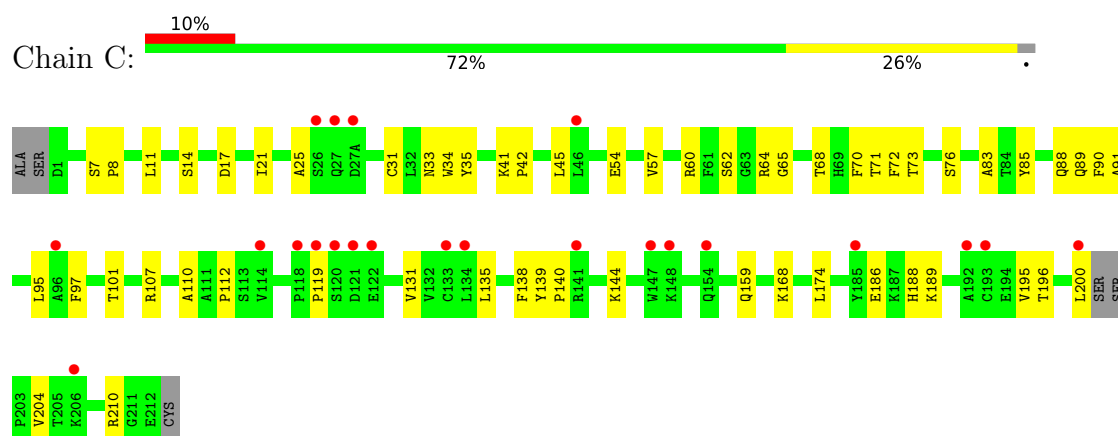
3 Residue-property plots [i](#)

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.

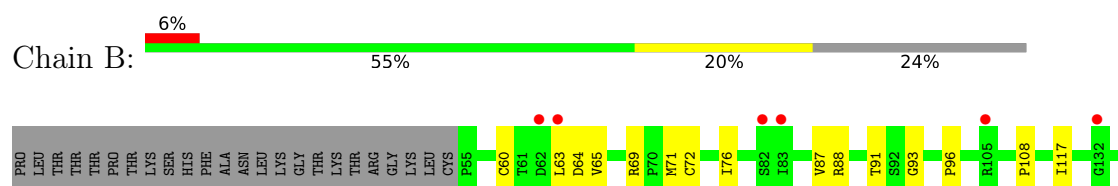
- Molecule 1: 1209 Fab heavy chain

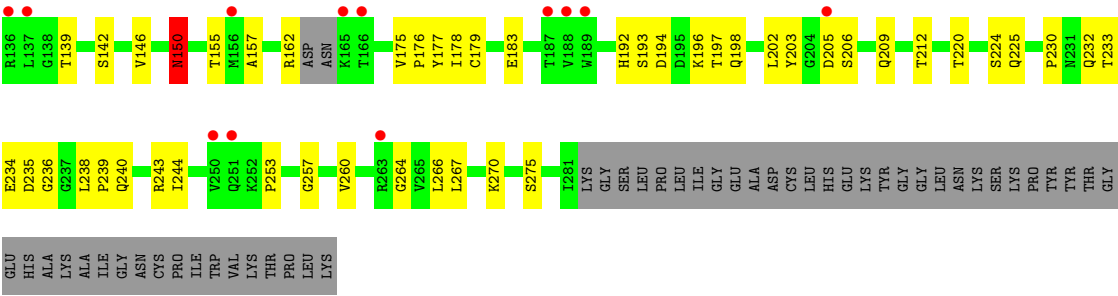


- Molecule 2: 1209 Fab light chain



- Molecule 3: Hemagglutinin





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



• Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	128.10Å 128.10Å 235.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.61 – 4.20 49.61 – 4.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.61-4.20) 99.9 (49.61-4.20)	Depositor EDS
R_{merge}	0.74	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 4.14Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.372 , 0.420 0.372 , 0.420	Depositor DCC
R_{free} test set	851 reflections (9.60%)	wwPDB-VP
Wilson B-factor (Å ²)	202.7	Xtriage
Anisotropy	0.178	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 217.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.36$, $\langle L^2 \rangle = 0.18$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	5070	wwPDB-VP
Average B, all atoms (Å ²)	234.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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 [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.27	0/1685	0.49	0/2291
2	C	0.28	0/1657	0.58	1/2247 (0.0%)
3	B	0.33	1/1763 (0.1%)	0.57	1/2395 (0.0%)
All	All	0.30	1/5105 (0.0%)	0.55	2/6933 (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	A	0	1
3	B	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	150	ASN	CG-OD1	5.24	1.35	1.24

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	150	ASN	C-N-CA	5.66	134.18	122.30
2	C	45	LEU	CB-CG-CD2	-5.64	101.41	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	217	LYS	Peptide
3	B	150	ASN	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1644	0	1605	48	0
2	C	1624	0	1584	38	1
3	B	1724	0	1710	50	0
4	D	39	0	34	3	0
5	E	39	0	34	3	0
All	All	5070	0	4967	129	1

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 13.

All (129) 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:B:232:GLN:NE2	3:B:235:ASP:OD2	1.93	1.01
1:A:29:ASP:OD2	3:B:162:ARG:NH1	2.09	0.84
1:A:29:ASP:OD2	3:B:162:ARG:HD2	1.78	0.83
1:A:155:TYR:OH	1:A:158:GLU:OE2	2.02	0.76
3:B:212:THR:OG1	3:B:220:THR:O	2.04	0.74
1:A:101:SER:OG	1:A:104:TYR:O	2.06	0.73
2:C:119:PRO:HD3	2:C:131:VAL:HG22	1.69	0.73
1:A:109:GLY:HA2	2:C:33:ASN:ND2	2.04	0.73
3:B:142:SER:OG	3:B:240:GLN:NE2	2.25	0.70
3:B:63:LEU:HD13	3:B:108:PRO:HD3	1.75	0.67
4:D:1:NAG:H3	4:D:1:NAG:H83	1.76	0.67
1:A:127:LYS:NZ	1:A:154:ASP:O	2.24	0.67
3:B:232:GLN:HB2	5:E:1:NAG:H82	1.78	0.66
1:A:51:ASN:ND2	1:A:55:ASN:OD1	2.26	0.66
3:B:177:TYR:CZ	3:B:253:PRO:HA	2.31	0.65
1:A:33:MET:HB3	1:A:78:LEU:HD22	1.80	0.64
1:A:51:ASN:O	1:A:71:ARG:NH1	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:THR:HG21	1:A:106:TYR:HB2	1.83	0.61
1:A:97:ARG:HA	1:A:97:ARG:NH1	2.15	0.61
2:C:112:PRO:HB3	2:C:138:PHE:HB3	1.83	0.61
2:C:25:ALA:O	2:C:68:THR:OG1	2.19	0.60
1:A:164:SER:HB3	1:A:208:ASN:HB2	1.84	0.60
3:B:93:GLY:O	3:B:236:GLY:N	2.34	0.60
1:A:206:ILE:HG13	1:A:221:ARG:HA	1.84	0.60
1:A:34:HIS:HB2	1:A:93:ALA:HB3	1.83	0.60
2:C:135:LEU:HD11	2:C:195:VAL:HG11	1.84	0.60
1:A:180:VAL:HG11	2:C:159:GLN:HB3	1.84	0.59
1:A:53:LYS:NZ	3:B:202:LEU:O	2.35	0.59
3:B:65:VAL:HG22	3:B:72:CYS:HB3	1.84	0.59
3:B:177:TYR:O	3:B:179:CYS:N	2.36	0.59
2:C:62:SER:OG	2:C:73:THR:OG1	2.21	0.58
3:B:177:TYR:CG	3:B:177:TYR:O	2.56	0.58
2:C:144:LYS:HB2	2:C:196:THR:HB	1.87	0.57
1:A:87:THR:HG23	1:A:120:ILE:HA	1.86	0.56
1:A:101:SER:HB3	1:A:106:TYR:HB3	1.87	0.56
3:B:244:ILE:HD12	3:B:266:LEU:HD11	1.87	0.56
2:C:88:GLN:HG3	2:C:97:PHE:CE2	2.41	0.56
1:A:34:HIS:NE2	1:A:95:ASP:HB2	2.21	0.56
1:A:109:GLY:HA2	2:C:33:ASN:HD22	1.73	0.54
1:A:37:ARG:HB3	1:A:47:ILE:HD11	1.90	0.54
2:C:188:HIS:O	2:C:210:ARG:HD2	2.07	0.54
2:C:88:GLN:HG3	2:C:97:PHE:CZ	2.42	0.54
3:B:233:THR:HG22	3:B:234:GLU:HG3	1.88	0.54
3:B:197:THR:HG23	3:B:198:GLN:OE1	2.08	0.53
3:B:232:GLN:HB2	5:E:1:NAG:C8	2.37	0.53
1:A:97:ARG:HA	1:A:97:ARG:HH11	1.74	0.52
3:B:71:MET:HE1	3:B:146:VAL:HG12	1.92	0.52
3:B:69:ARG:CZ	3:B:93:GLY:HA3	2.40	0.52
3:B:232:GLN:CD	3:B:235:ASP:OD2	2.48	0.51
3:B:60:CYS:SG	3:B:64:ASP:HB3	2.51	0.51
2:C:189:LYS:HA	2:C:210:ARG:HD3	1.91	0.51
3:B:157:ALA:N	3:B:267:LEU:O	2.42	0.51
2:C:34:TRP:CE2	2:C:72:PHE:HB2	2.45	0.51
3:B:196:LYS:HG3	3:B:206:SER:HB3	1.93	0.50
3:B:232:GLN:CG	3:B:235:ASP:OD2	2.60	0.50
1:A:120:ILE:HD12	1:A:157:PRO:HB2	1.93	0.50
1:A:32:THR:HG22	1:A:51:ASN:HA	1.92	0.50
3:B:139:THR:OG1	3:B:150:ASN:ND2	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:139:THR:HB	3:B:150:ASN:HB2	1.93	0.50
1:A:21:CYS:HB3	1:A:78:LEU:HB3	1.94	0.50
1:A:29:ASP:HB3	1:A:73:ASN:HB3	1.93	0.49
3:B:212:THR:CG2	3:B:260:VAL:HB	2.42	0.49
3:B:183:GLU:HG2	3:B:275:SER:HB3	1.95	0.48
2:C:31:CYS:HB2	2:C:91:ALA:HB2	1.95	0.48
1:A:95:ASP:OD1	1:A:108:TYR:N	2.40	0.48
2:C:135:LEU:HB2	2:C:174:LEU:HB3	1.95	0.48
2:C:54:GLU:O	2:C:57:VAL:HG22	2.14	0.47
1:A:96:PHE:CD2	1:A:97:ARG:HD2	2.49	0.47
3:B:232:GLN:HG2	3:B:235:ASP:OD2	2.14	0.47
2:C:83:ALA:HB3	2:C:85:TYR:CE1	2.49	0.47
3:B:177:TYR:CE1	3:B:253:PRO:HA	2.49	0.47
1:A:129:PRO:HD2	1:A:216:THR:HB	1.96	0.47
1:A:50:ILE:HD11	1:A:54:GLY:HA2	1.97	0.47
1:A:221:ARG:HG2	1:A:222:VAL:N	2.30	0.47
3:B:155:THR:HA	3:B:270:LYS:HB2	1.97	0.47
1:A:108:TYR:HA	2:C:90:PHE:CD1	2.50	0.47
1:A:39:VAL:HG13	1:A:42:LYS:HB2	1.97	0.47
2:C:14:SER:N	2:C:17:ASP:OD2	2.48	0.47
3:B:192:HIS:CE1	3:B:194:ASP:HB2	2.50	0.46
1:A:145:THR:N	1:A:197:SER:HG	2.12	0.46
3:B:87:VAL:HG23	3:B:88:ARG:HG3	1.98	0.46
3:B:205:ASP:OD2	3:B:209:GLN:NE2	2.37	0.46
2:C:168:LYS:HB3	2:C:168:LYS:HE2	1.68	0.46
1:A:179:ALA:HA	1:A:189:LEU:HB3	1.97	0.46
4:D:2:NAG:H3	4:D:3:BMA:O2	2.16	0.45
3:B:96:PRO:HB3	3:B:232:GLN:HG3	1.97	0.45
3:B:91:THR:O	3:B:234:GLU:HB3	2.17	0.45
3:B:232:GLN:HG2	3:B:235:ASP:CG	2.38	0.44
2:C:189:LYS:HA	2:C:210:ARG:CD	2.47	0.44
1:A:1:VAL:HG11	1:A:112:VAL:HG21	2.00	0.44
3:B:212:THR:HG22	3:B:260:VAL:HB	1.98	0.44
2:C:200:LEU:HD22	2:C:204:VAL:HG21	2.00	0.44
1:A:118:THR:HG21	1:A:159:PRO:HG3	2.00	0.44
3:B:230:PRO:O	3:B:243:ARG:NH2	2.50	0.44
2:C:21:ILE:HG12	2:C:101:THR:HG21	2.00	0.43
1:A:46:TRP:CD1	2:C:95:LEU:HD12	2.53	0.43
3:B:175:VAL:N	3:B:257:GLY:O	2.46	0.43
1:A:208:ASN:HA	1:A:219:ASP:HB2	2.01	0.43
2:C:31:CYS:O	2:C:89:GLN:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:LYS:O	1:A:218:VAL:C	2.56	0.43
2:C:8:PRO:HG3	2:C:11:LEU:HD23	2.01	0.43
1:A:109:GLY:HA2	2:C:33:ASN:HD21	1.83	0.43
3:B:76:ILE:HG12	3:B:117:ILE:HG13	2.00	0.43
2:C:60:ARG:HD2	2:C:76:SER:O	2.19	0.43
1:A:210:ASN:HB2	1:A:217:LYS:HG3	2.01	0.43
3:B:71:MET:SD	3:B:146:VAL:HB	2.58	0.43
2:C:65:GLY:HA3	2:C:70:PHE:HA	2.01	0.43
1:A:107:TYR:HD2	2:C:90:PHE:HB2	1.83	0.43
1:A:12:GLN:HB2	1:A:15:ARG:HG3	2.01	0.42
3:B:193:SER:OG	3:B:225:GLN:O	2.25	0.42
2:C:41:LYS:HB3	2:C:42:PRO:CD	2.49	0.42
2:C:64:ARG:O	2:C:71:THR:N	2.36	0.42
4:D:1:NAG:H3	4:D:1:NAG:C8	2.46	0.42
2:C:35:TYR:HE1	2:C:88:GLN:HB3	1.85	0.42
1:A:14:GLY:N	1:A:82(C):LEU:O	2.53	0.42
3:B:232:GLN:OE1	5:E:1:NAG:H82	2.20	0.42
3:B:232:GLN:NE2	3:B:238:LEU:O	2.42	0.41
1:A:163:VAL:HA	1:A:208:ASN:O	2.19	0.41
1:A:28:PHE:CD2	1:A:76:ASN:HA	2.55	0.41
3:B:193:SER:HB2	3:B:224:SER:HB2	2.02	0.41
3:B:192:HIS:HE1	3:B:194:ASP:HB2	1.84	0.41
2:C:186:GLU:HA	2:C:210:ARG:CZ	2.51	0.41
2:C:139:TYR:CG	2:C:140:PRO:HA	2.56	0.41
3:B:176:PRO:HB2	3:B:178:ILE:HG12	2.03	0.41
2:C:144:LYS:O	2:C:196:THR:N	2.54	0.41
3:B:238:LEU:HA	3:B:239:PRO:HD3	1.94	0.40
1:A:42:LYS:HB3	1:A:42:LYS:HE3	1.92	0.40
3:B:203:TYR:CZ	3:B:264:GLY:HA2	2.56	0.40
2:C:107:ARG:NH2	2:C:110:ALA:HB2	2.37	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:7:SER:OG	2:C:7:SER:OG[12_545]	1.98	0.22

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	212/240 (88%)	200 (94%)	11 (5%)	1 (0%)	29	68
2	C	207/216 (96%)	197 (95%)	10 (5%)	0	100	100
3	B	221/298 (74%)	209 (95%)	12 (5%)	0	100	100
All	All	640/754 (85%)	606 (95%)	33 (5%)	1 (0%)	47	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	218	VAL

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	181/202 (90%)	181 (100%)	0	100	100
2	C	184/188 (98%)	184 (100%)	0	100	100
3	B	193/254 (76%)	193 (100%)	0	100	100
All	All	558/644 (87%)	558 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	33	ASN
3	B	192	HIS
3	B	240	GLN

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 ⓘ

6 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	$\# Z > 2$
4	NAG	D	1	3,4	14,14,15	0.57	0	17,19,21	1.48	1 (5%)
4	NAG	D	2	4	14,14,15	1.80	2 (14%)	17,19,21	1.22	1 (5%)
4	BMA	D	3	4	11,11,12	1.36	2 (18%)	15,15,17	1.15	1 (6%)
5	NAG	E	1	3,5	14,14,15	0.58	0	17,19,21	0.52	0
5	NAG	E	2	5	14,14,15	0.50	0	17,19,21	0.81	1 (5%)
5	BMA	E	3	5	11,11,12	0.66	0	15,15,17	1.53	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	D	1	3,4	-	3/6/23/26	0/1/1/1
4	NAG	D	2	4	-	3/6/23/26	0/1/1/1

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

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	2	NAG	O5-C1	-5.64	1.34	1.43
4	D	3	BMA	C1-C2	3.60	1.60	1.52
4	D	2	NAG	C1-C2	2.96	1.56	1.52
4	D	3	BMA	O5-C1	2.53	1.47	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1	NAG	C2-N2-C7	4.59	129.44	122.90
5	E	3	BMA	C1-O5-C5	4.30	118.01	112.19
4	D	2	NAG	C4-C3-C2	4.18	117.15	111.02
4	D	3	BMA	C1-C2-C3	2.73	113.02	109.67
5	E	3	BMA	O5-C1-C2	2.69	114.92	110.77
5	E	2	NAG	C3-C4-C5	2.39	114.50	110.24

There are no chirality outliers.

All (10) torsion outliers are listed below:

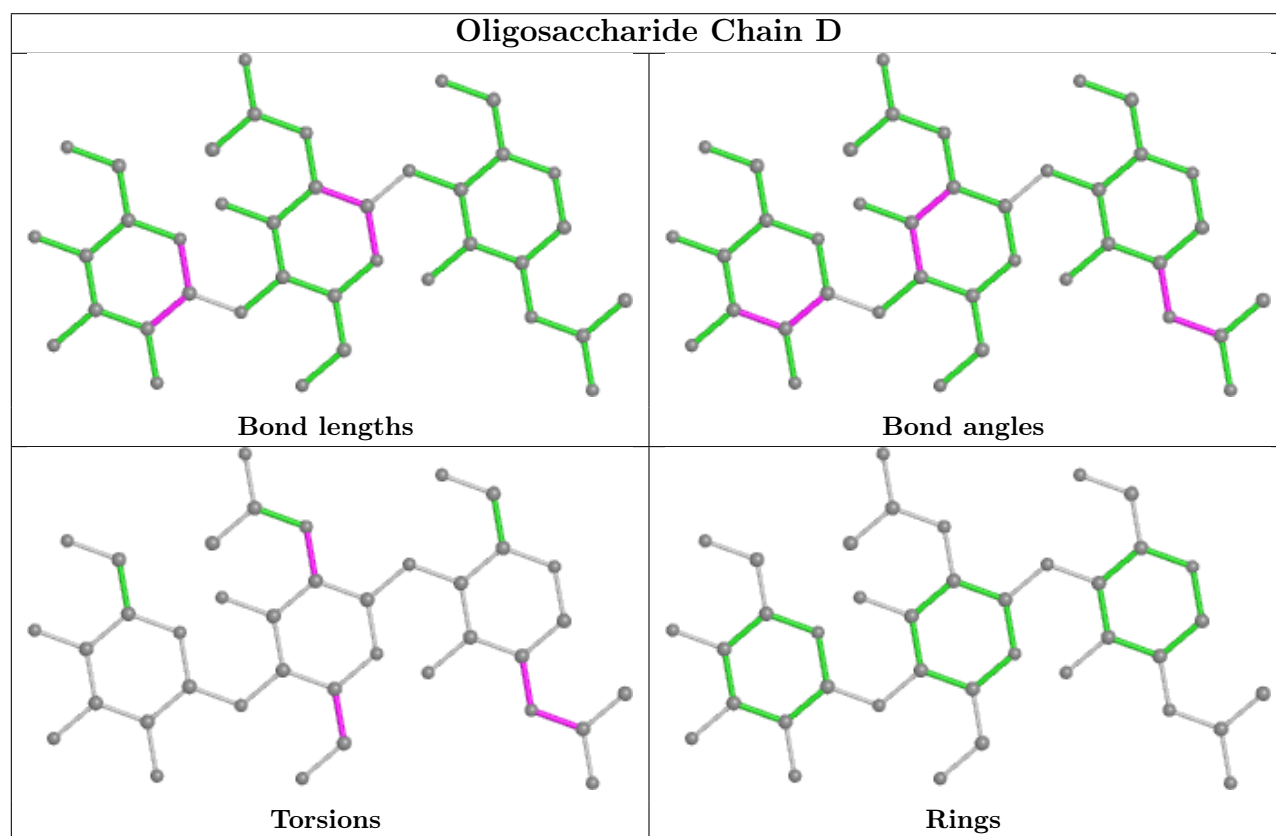
Mol	Chain	Res	Type	Atoms
5	E	2	NAG	O5-C5-C6-O6
4	D	1	NAG	C8-C7-N2-C2
4	D	1	NAG	O7-C7-N2-C2
5	E	2	NAG	C4-C5-C6-O6
4	D	2	NAG	C1-C2-N2-C7
5	E	1	NAG	C4-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6
5	E	1	NAG	O5-C5-C6-O6
4	D	1	NAG	C3-C2-N2-C7
4	D	2	NAG	C3-C2-N2-C7

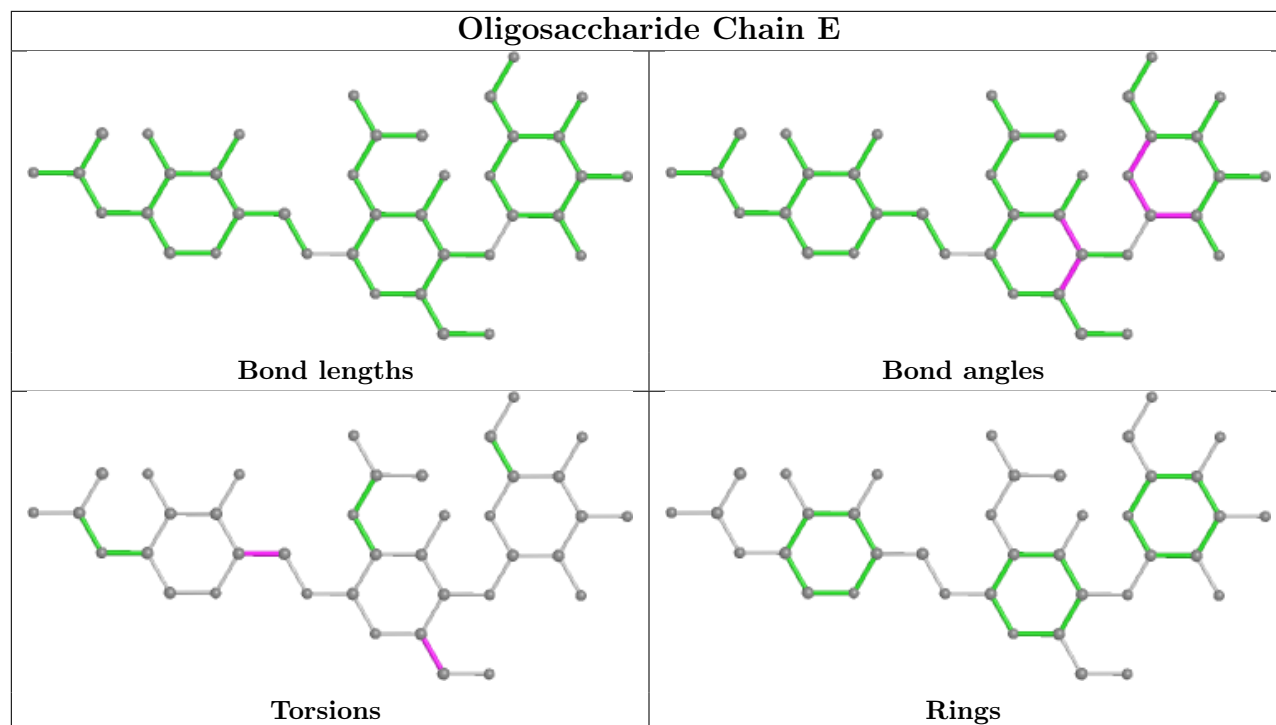
There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	3	BMA	1	0
4	D	1	NAG	2	0
5	E	1	NAG	3	0
4	D	2	NAG	1	0

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





5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	216/240 (90%)	0.73	35 (16%) 1 2	173, 214, 285, 333	0
2	C	211/216 (97%)	0.55	22 (10%) 6 6	161, 209, 269, 295	0
3	B	225/298 (75%)	0.36	18 (8%) 12 11	214, 261, 326, 412	0
All	All	652/754 (86%)	0.54	75 (11%) 4 5	161, 234, 301, 412	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	193	CYS	10.0
1	A	148	LEU	7.5
1	A	205	TYR	7.1
2	C	192	ALA	7.0
1	A	202	THR	6.9
1	A	112	VAL	5.9
2	C	27	GLN	5.5
1	A	203	GLN	5.2
2	C	148	LYS	4.9
3	B	263	ARG	4.9
1	A	221	ARG	4.9
3	B	166	THR	4.7
1	A	2	GLN	4.5
1	A	3	LEU	4.5
1	A	111	GLY	4.5
3	B	188	VAL	4.2
1	A	169	ALA	4.2
1	A	199	SER	4.1
1	A	136	PRO	4.0
2	C	122	GLU	4.0
1	A	198	SER	3.9
1	A	113	TRP	3.9
2	C	120	SER	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	92	CYS	3.8
1	A	204	THR	3.7
1	A	149	GLY	3.7
2	C	147	TRP	3.7
2	C	154	GLN	3.7
3	B	156	MET	3.6
3	B	132	GLY	3.6
3	B	136	ARG	3.4
1	A	152	VAL	3.4
2	C	206	LYS	3.2
3	B	62	ASP	3.2
1	A	151	LEU	3.1
1	A	170	LEU	3.1
3	B	251	GLN	3.1
2	C	133	CYS	3.0
1	A	131	VAL	3.0
3	B	165	LYS	3.0
1	A	219	ASP	2.9
2	C	119	PRO	2.9
2	C	96	ALA	2.8
1	A	133	PRO	2.8
3	B	189	TRP	2.8
3	B	187	THR	2.7
2	C	121	ASP	2.7
3	B	83	ILE	2.6
2	C	200	LEU	2.6
3	B	82	SER	2.6
3	B	63	LEU	2.6
1	A	23	ALA	2.5
1	A	222	VAL	2.5
2	C	114	VAL	2.5
1	A	19	LEU	2.5
2	C	118	PRO	2.5
1	A	150	CYS	2.5
2	C	185	TYR	2.4
2	C	26	SER	2.4
3	B	205	ASP	2.4
3	B	105	ARG	2.3
1	A	55	ASN	2.3
3	B	137	LEU	2.3
1	A	21	CYS	2.3
1	A	194	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	1	VAL	2.2
2	C	27(A)	ASP	2.2
3	B	250	VAL	2.2
1	A	48	SER	2.1
2	C	46	LEU	2.1
1	A	196	PRO	2.1
1	A	91	TYR	2.1
2	C	134	LEU	2.1
2	C	141	ARG	2.0
1	A	80	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

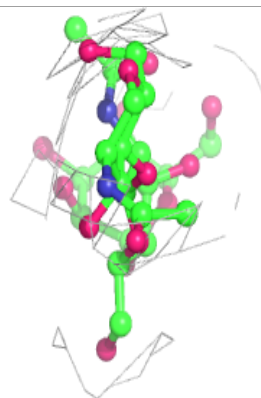
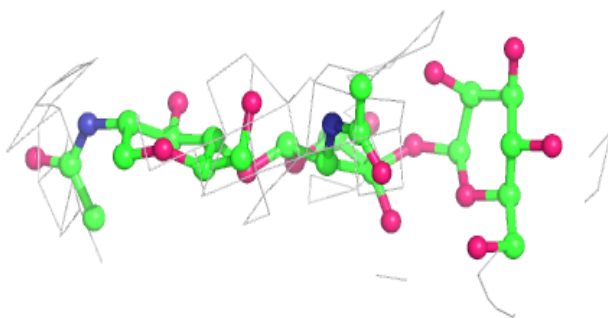
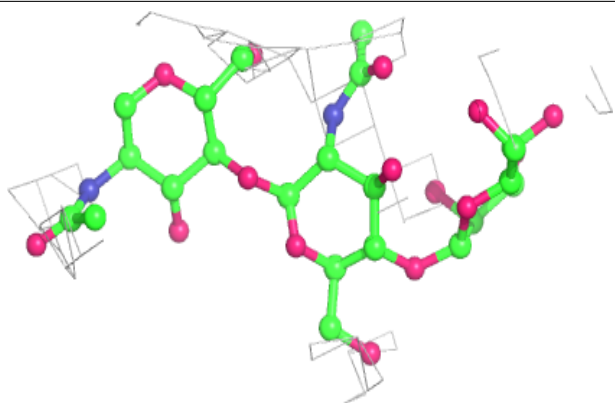
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	BMA	D	3	11/12	0.63	0.31	266,275,281,282	0
4	NAG	D	2	14/15	0.71	0.21	258,272,278,281	0
5	BMA	E	3	11/12	0.72	0.88	259,273,280,281	0
4	NAG	D	1	14/15	0.75	0.30	266,278,287,288	0
5	NAG	E	2	14/15	0.78	0.27	243,263,269,270	0
5	NAG	E	1	14/15	0.78	0.20	245,264,279,280	0

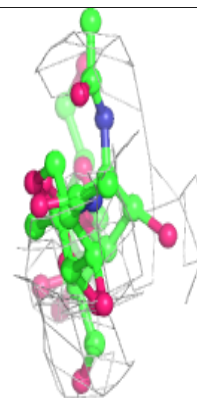
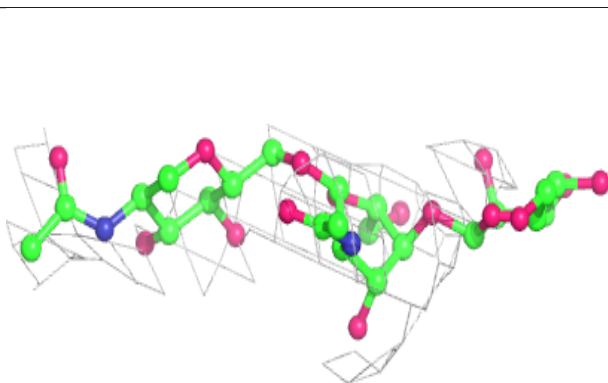
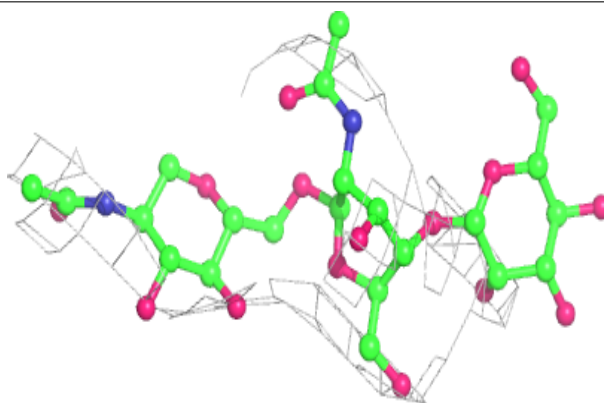
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain D:

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

**Electron density around Chain E:**

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



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.