



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 06:59 PM BST

PDB ID : 1BXH
Title : CONCANAVALIN A COMPLEXED TO METHYL ALPHA1-2 MANNOBIO-SIDE
Authors : Moothoo, D.N.; Canaan, B.; Field, R.A.; Naismith, J.H.
Deposited on : 1998-10-02
Resolution : 2.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

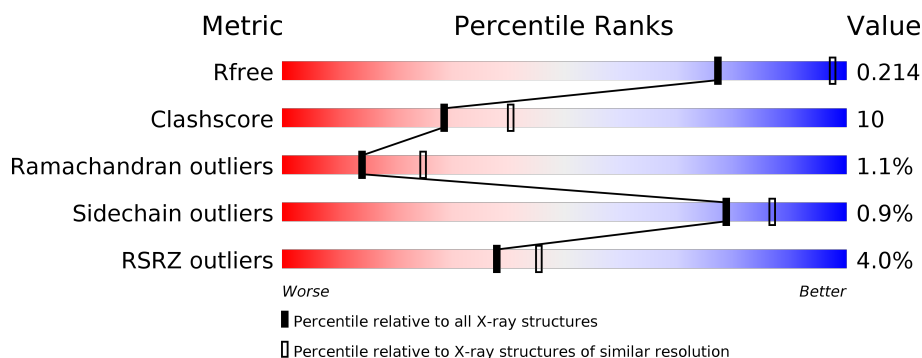
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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

Mol	Chain	Length	Quality of chain
1	A	237	<div> <div>3%</div> <div>81%</div> <div>18%</div> </div>
1	B	237	<div> <div>2%</div> <div>79%</div> <div>19%</div> </div>
1	C	237	<div> <div>6%</div> <div>78%</div> <div>21%</div> </div>
1	D	237	<div> <div>5%</div> <div>77%</div> <div>22%</div> </div>
2	E	2	<div> <div>100%</div> </div>
3	F	2	<div> <div>50%</div> <div>50%</div> </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
2	AMG	E	2	X	-	-	-
3	AMG	F	1	X	-	-	-
3	AMG	F	2	X	-	-	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7391 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 Concanavalin-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	37	0	0
			1809	1141	302	364	2			
1	B	237	Total	C	N	O	S	48	0	0
			1809	1141	302	364	2			
1	C	237	Total	C	N	O	S	57	0	0
			1809	1141	302	364	2			
1	D	237	Total	C	N	O	S	60	0	0
			1809	1141	302	364	2			

- Molecule 2 is an oligosaccharide called methyl alpha-D-galactopyranoside-(1-2)-methyl alpha-D-mannopyranoside.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	0	0	0
			24	13	11			

- Molecule 3 is an oligosaccharide called methyl alpha-D-galactopyranoside-(1-2)-methyl alpha-D-galactopyranoside.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	F	2	Total	C	O	0	0	0
			24	13	11			

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mn	0	0
			1	1		
4	A	1	Total	Mn	0	0
			1	1		
4	D	1	Total	Mn	0	0
			1	1		

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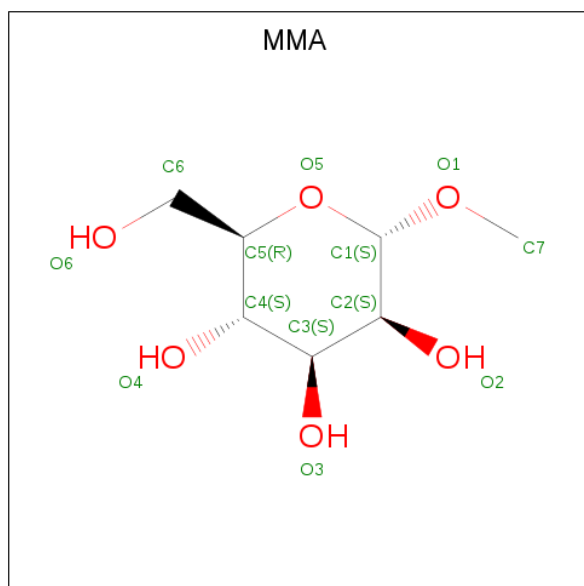
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total	Mn	0	0
			1	1		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Ca	0	0
			1	1		
5	A	1	Total	Ca	0	0
			1	1		
5	D	1	Total	Ca	0	0
			1	1		
5	C	1	Total	Ca	0	0
			1	1		

- Molecule 6 is methyl alpha-D-mannopyranoside (three-letter code: MMA) (formula: C₇H₁₄O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			13	7	6		
6	C	1	Total	C	O	0	0
			13	7	6		

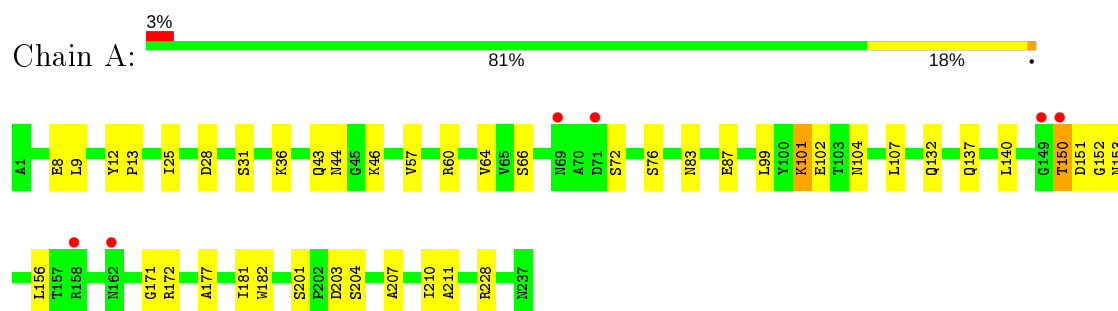
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	25	Total 25	O 25	0	0
7	B	24	Total 24	O 24	0	0
7	C	10	Total 10	O 10	0	0
7	D	14	Total 14	O 14	0	0

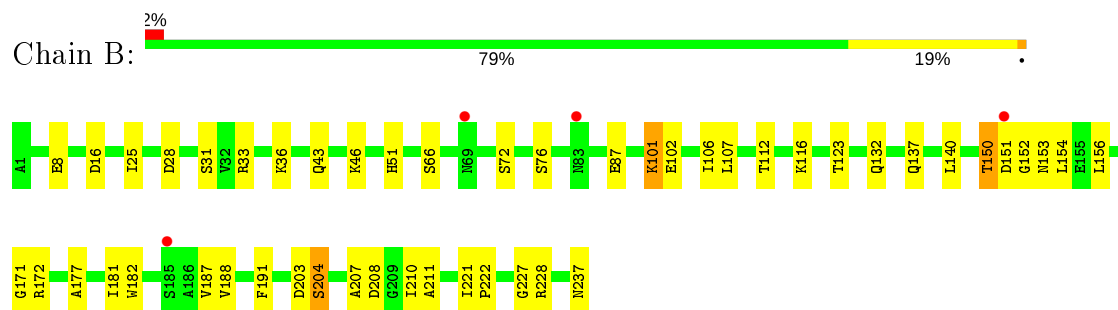
3 Residue-property plots [i](#)

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.

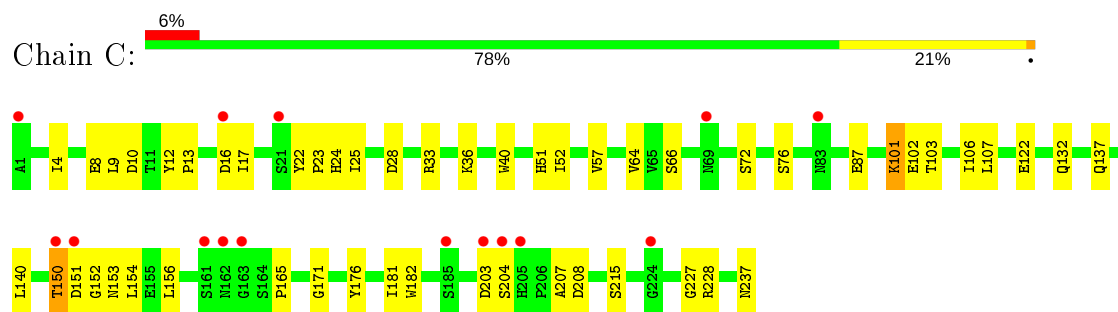
• Molecule 1: Concanavalin-A



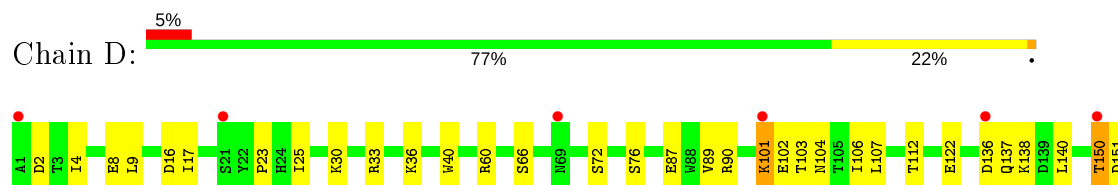
• Molecule 1: Concanavalin-A

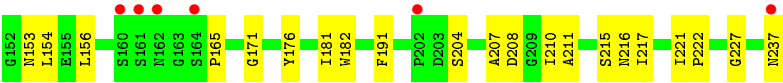


• Molecule 1: Concanavalin-A



• Molecule 1: Concanavalin-A





- Molecule 2: methyl alpha-D-galactopyranoside-(1-2)-methyl alpha-D-mannopyranoside

Chain E:

100%



- Molecule 3: methyl alpha-D-galactopyranoside-(1-2)-methyl alpha-D-galactopyranoside

Chain F:

50%50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	119.70 Å 119.70 Å 68.90 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.75 19.90 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.8 (25.00-2.75) 99.7 (19.90-2.75)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.52 (at 2.75 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.196 , 0.238 0.184 , 0.214	Depositor DCC
R_{free} test set	2641 reflections (10.02%)	wwPDB-VP
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.144	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.015 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7391	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.88% 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: CA, MN, MMA, AMG

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	0.44	0/1851	0.74	1/2522 (0.0%)
1	B	0.44	0/1851	0.73	0/2522
1	C	0.44	0/1851	0.74	1/2522 (0.0%)
1	D	0.43	0/1851	0.75	1/2522 (0.0%)
All	All	0.44	0/7404	0.74	3/10088 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	9	LEU	N-CA-C	-5.43	96.35	111.00
1	A	9	LEU	N-CA-C	-5.36	96.53	111.00
1	C	9	LEU	N-CA-C	-5.16	97.06	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1809	0	1755	35	1
1	B	1809	0	1755	35	0
1	C	1809	0	1755	36	0
1	D	1809	0	1755	35	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	24	0	23	2	0
3	F	24	0	23	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	B	13	0	14	0	0
6	C	13	0	14	0	0
7	A	25	0	0	2	0
7	B	24	0	0	3	0
7	C	10	0	0	1	0
7	D	14	0	0	1	0
All	All	7391	0	7094	136	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 10.

All (136) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43:GLN:HE21	1:B:46:LYS:HD2	1.42	0.85
1:A:43:GLN:HE21	1:A:46:LYS:HD2	1.43	0.82
1:A:99:LEU:HD23	2:E:1:MMA:H72	1.60	0.82
1:B:43:GLN:NE2	1:B:46:LYS:HD2	1.96	0.80
1:A:43:GLN:NE2	1:A:46:LYS:HD2	1.98	0.78
1:D:16:ASP:OD1	1:D:17:ILE:HG23	1.94	0.67
1:D:150:THR:HA	7:D:248:HOH:O	1.96	0.65
1:C:102:GLU:HG2	1:C:207:ALA:O	1.97	0.64
1:D:102:GLU:HG2	1:D:207:ALA:O	1.97	0.64
1:C:16:ASP:OD2	1:C:228:ARG:NH2	2.31	0.64
1:C:51:HIS:HB3	7:C:245:HOH:O	1.98	0.63
1:A:102:GLU:HG2	1:A:207:ALA:O	1.98	0.62
1:B:102:GLU:HG2	1:B:207:ALA:O	1.99	0.62
1:A:181:ILE:HG23	1:A:182:TRP:HD1	1.65	0.61
1:C:101:LYS:N	1:C:101:LYS:HD3	2.15	0.61
1:C:101:LYS:HD3	1:C:101:LYS:H	1.67	0.60
1:B:181:ILE:HG23	1:B:182:TRP:HD1	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:ARG:NH2	7:B:264:HOH:O	2.35	0.58
1:D:101:LYS:N	1:D:101:LYS:HD3	2.18	0.58
1:D:103:THR:HG22	1:D:165:PRO:HG3	1.86	0.56
1:B:101:LYS:N	1:B:101:LYS:HD3	2.21	0.54
1:C:33:ARG:HD2	1:C:237:ASN:O	2.07	0.54
1:D:101:LYS:HD3	1:D:101:LYS:H	1.71	0.54
1:D:181:ILE:HG23	1:D:182:TRP:HD1	1.71	0.54
1:C:181:ILE:HG23	1:C:182:TRP:HD1	1.73	0.54
1:A:172:ARG:NH2	7:A:262:HOH:O	2.41	0.54
1:B:16:ASP:OD1	1:B:228:ARG:NH2	2.41	0.54
1:C:151:ASP:HB2	1:C:153:ASN:ND2	2.23	0.54
1:C:16:ASP:OD2	1:C:17:ILE:HG23	2.08	0.54
1:D:103:THR:CG2	1:D:165:PRO:HG3	2.39	0.53
1:B:132:GLN:NE2	1:B:152:GLY:HA3	2.25	0.52
1:D:107:LEU:N	1:D:107:LEU:HD12	2.24	0.52
1:A:151:ASP:HB2	1:A:153:ASN:ND2	2.24	0.52
1:C:36:LYS:HD3	1:C:76:SER:O	2.10	0.52
1:B:101:LYS:HD3	1:B:101:LYS:H	1.73	0.52
1:B:181:ILE:HG23	1:B:182:TRP:CD1	2.46	0.51
1:A:101:LYS:HD3	1:A:101:LYS:H	1.76	0.51
1:A:181:ILE:HG23	1:A:182:TRP:CD1	2.44	0.51
1:A:150:THR:O	1:A:151:ASP:HB2	2.11	0.51
1:A:60:ARG:NH1	1:A:76:SER:HB3	2.26	0.51
1:B:36:LYS:HD3	1:B:76:SER:O	2.11	0.51
1:B:137:GLN:HG2	1:B:140:LEU:HD12	1.93	0.50
1:D:102:GLU:OE2	1:D:104:ASN:ND2	2.42	0.50
1:D:137:GLN:HG2	1:D:140:LEU:HD12	1.92	0.50
1:B:87:GLU:HG3	1:B:182:TRP:O	2.10	0.50
1:A:64:VAL:HG21	1:C:57:VAL:HG22	1.94	0.50
1:C:106:ILE:HB	1:C:154:LEU:HB3	1.94	0.50
1:A:101:LYS:N	1:A:101:LYS:HD3	2.26	0.50
1:A:36:LYS:HD3	1:A:76:SER:O	2.12	0.50
1:D:208:ASP:OD2	1:D:227:GLY:HA2	2.12	0.50
1:B:208:ASP:OD2	1:B:227:GLY:HA2	2.12	0.50
1:A:66:SER:HB3	1:A:72:SER:HB3	1.94	0.49
1:B:151:ASP:HB2	1:B:153:ASN:ND2	2.27	0.49
1:D:150:THR:O	1:D:151:ASP:HB2	2.12	0.49
1:B:33:ARG:HD2	1:B:237:ASN:O	2.13	0.49
1:A:182:TRP:HB2	7:A:265:HOH:O	2.13	0.49
1:C:150:THR:O	1:C:151:ASP:HB2	2.12	0.49
1:B:156:LEU:O	1:B:171:GLY:HA3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:137:GLN:HG2	1:C:140:LEU:HD12	1.94	0.48
1:D:66:SER:HB3	1:D:72:SER:HB3	1.94	0.48
1:C:87:GLU:HG3	1:C:182:TRP:O	2.13	0.48
1:D:151:ASP:HB2	1:D:153:ASN:ND2	2.29	0.48
1:D:156:LEU:O	1:D:171:GLY:HA3	2.14	0.48
1:A:102:GLU:OE2	1:A:104:ASN:ND2	2.44	0.48
1:B:8:GLU:OE1	1:B:28:ASP:OD2	2.32	0.48
1:C:103:THR:CG2	1:C:165:PRO:HG3	2.44	0.47
1:D:87:GLU:HG3	1:D:182:TRP:O	2.13	0.47
1:B:107:LEU:N	1:B:107:LEU:HD12	2.30	0.47
1:C:181:ILE:HG23	1:C:182:TRP:CD1	2.49	0.47
1:C:66:SER:HB3	1:C:72:SER:CB	2.44	0.47
1:D:106:ILE:HB	1:D:154:LEU:HB3	1.96	0.47
1:D:181:ILE:HG23	1:D:182:TRP:CD1	2.49	0.47
1:C:66:SER:HB3	1:C:72:SER:HB3	1.97	0.47
1:A:64:VAL:HG21	1:C:57:VAL:CG2	2.45	0.46
1:C:107:LEU:HD12	1:C:107:LEU:N	2.30	0.46
1:C:52:ILE:N	1:C:52:ILE:HD12	2.31	0.46
1:D:33:ARG:HD2	1:D:237:ASN:O	2.15	0.46
1:A:132:GLN:NE2	1:A:152:GLY:HA3	2.31	0.46
1:D:90:ARG:NH1	1:D:217:ILE:HG23	2.30	0.46
1:D:60:ARG:NH1	1:D:76:SER:HB3	2.30	0.46
1:A:228:ARG:HG2	2:E:2:AMG:O3	2.16	0.46
1:B:150:THR:O	1:B:151:ASP:HB2	2.15	0.46
1:B:51:HIS:HB3	7:B:260:HOH:O	2.16	0.45
1:C:8:GLU:O	1:C:25:ILE:HA	2.16	0.45
1:C:8:GLU:OE1	1:C:28:ASP:OD2	2.35	0.45
1:D:66:SER:HB3	1:D:72:SER:CB	2.47	0.45
1:D:89:VAL:HB	1:D:215:SER:O	2.17	0.45
1:A:156:LEU:O	1:A:171:GLY:HA3	2.17	0.45
1:D:36:LYS:HD3	1:D:76:SER:O	2.16	0.45
1:A:87:GLU:HG3	1:A:182:TRP:O	2.16	0.45
1:A:8:GLU:OE1	1:A:28:ASP:OD2	2.34	0.44
1:A:28:ASP:HB3	1:A:31:SER:O	2.18	0.44
1:B:28:ASP:HB3	1:B:31:SER:O	2.17	0.44
1:A:12:TYR:HA	1:A:13:PRO:HD3	1.88	0.44
1:D:8:GLU:O	1:D:25:ILE:HA	2.18	0.44
1:A:137:GLN:HG2	1:A:140:LEU:HD12	2.00	0.43
1:A:57:VAL:HG22	1:C:64:VAL:HG21	2.00	0.43
1:B:132:GLN:HE21	1:B:152:GLY:HA3	1.83	0.43
1:B:210:ILE:HG22	1:B:211:ALA:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:208:ASP:OD2	1:C:227:GLY:HA2	2.18	0.43
1:B:8:GLU:O	1:B:25:ILE:HA	2.18	0.43
1:A:8:GLU:O	1:A:25:ILE:HA	2.19	0.43
1:D:136:ASP:OD2	1:D:138:LYS:HE2	2.18	0.43
1:A:60:ARG:NH1	1:A:76:SER:CB	2.82	0.43
1:D:107:LEU:N	1:D:107:LEU:CD1	2.81	0.43
1:B:187:VAL:HG12	1:B:188:VAL:HG23	2.00	0.42
1:B:66:SER:HB3	1:B:72:SER:HB3	2.00	0.42
1:A:66:SER:HB3	1:A:72:SER:CB	2.49	0.42
1:C:101:LYS:CD	1:C:101:LYS:N	2.81	0.42
1:D:112:THR:O	1:D:191:PHE:HA	2.19	0.42
1:D:210:ILE:HG22	1:D:211:ALA:N	2.34	0.42
1:C:132:GLN:NE2	1:C:152:GLY:HA3	2.35	0.42
1:A:132:GLN:HE21	1:A:152:GLY:HA3	1.83	0.42
1:C:181:ILE:CG2	1:C:182:TRP:HD1	2.32	0.42
1:C:4:ILE:HD13	1:C:215:SER:HB3	2.00	0.42
1:B:116:LYS:HD3	1:B:123:THR:OG1	2.20	0.42
1:A:44:ASN:HD21	1:A:201:SER:HB3	1.85	0.42
1:D:2:ASP:HB3	1:D:216:ASN:OD1	2.20	0.42
1:C:103:THR:HG23	1:C:165:PRO:HG3	2.01	0.42
1:C:23:PRO:HB2	1:C:40:TRP:O	2.20	0.41
1:D:221:ILE:HA	1:D:222:PRO:HD3	1.91	0.41
1:C:12:TYR:HA	1:C:13:PRO:HD3	1.88	0.41
1:D:4:ILE:HD13	1:D:215:SER:HB3	2.02	0.41
1:B:203:ASP:O	1:B:204:SER:O	2.39	0.41
1:B:106:ILE:HB	1:B:154:LEU:HB3	2.01	0.41
1:D:23:PRO:HB2	1:D:40:TRP:O	2.20	0.41
1:B:66:SER:HB3	1:B:72:SER:CB	2.51	0.41
1:A:107:LEU:HD12	1:A:107:LEU:N	2.36	0.41
1:B:221:ILE:HA	1:B:222:PRO:HD3	1.91	0.41
1:C:156:LEU:O	1:C:171:GLY:HA3	2.21	0.40
1:A:177:ALA:HB2	1:B:177:ALA:HB2	2.03	0.40
1:A:210:ILE:HG22	1:A:211:ALA:N	2.36	0.40
1:B:112:THR:O	1:B:191:PHE:HA	2.21	0.40
1:C:10:ASP:HB3	1:C:24:HIS:CE1	2.56	0.40
1:B:150:THR:N	7:B:250:HOH:O	2.44	0.40
1:C:176:TYR:CE2	1:D:176:TYR:CE2	3.09	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)
1:A:83:ASN:O	1:D:30:LYS:NZ[4_556]	2.19	0.01

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	235/237 (99%)	213 (91%)	19 (8%)	3 (1%)	12	21
1	B	235/237 (99%)	214 (91%)	19 (8%)	2 (1%)	17	31
1	C	235/237 (99%)	214 (91%)	18 (8%)	3 (1%)	12	21
1	D	235/237 (99%)	216 (92%)	17 (7%)	2 (1%)	17	31
All	All	940/948 (99%)	857 (91%)	73 (8%)	10 (1%)	14	25

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	204	SER
1	B	204	SER
1	C	204	SER
1	D	204	SER
1	B	150	THR
1	C	203	ASP
1	D	150	THR
1	A	150	THR
1	A	203	ASP
1	C	150	THR

5.3.2 Protein sidechains [i](#)

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

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

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	203/203 (100%)	202 (100%)	1 (0%)	88	92
1	B	203/203 (100%)	202 (100%)	1 (0%)	88	92
1	C	203/203 (100%)	200 (98%)	3 (2%)	65	78
1	D	203/203 (100%)	201 (99%)	2 (1%)	76	85
All	All	812/812 (100%)	805 (99%)	7 (1%)	78	87

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

Mol	Chain	Res	Type
1	A	101	LYS
1	B	101	LYS
1	C	22	TYR
1	C	101	LYS
1	C	122	GLU
1	D	101	LYS
1	D	122	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	132	GLN
1	A	153	ASN
1	A	205	HIS
1	A	237	ASN
1	B	43	GLN
1	B	132	GLN
1	B	153	ASN
1	B	166	GLN
1	B	237	ASN
1	C	43	GLN
1	C	132	GLN
1	C	153	ASN
1	C	237	ASN
1	D	43	GLN
1	D	153	ASN
1	D	237	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 ⓘ

4 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MMA	E	1	2	13,13,13	0.47	0	18,18,18	0.84	1 (5%)
2	AMG	E	2	2	11,11,13	0.43	0	15,15,18	0.78	0
3	AMG	F	1	3	13,13,13	0.57	0	18,18,18	0.66	1 (5%)
3	AMG	F	2	3	11,11,13	0.65	0	15,15,18	0.50	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MMA	E	1	2	-	2/4/24/24	0/1/1/1
2	AMG	E	2	2	2/2/4/5	0/2/19/24	0/1/1/1
3	AMG	F	1	3	2/2/5/5	0/4/24/24	0/1/1/1
3	AMG	F	2	3	2/2/4/5	0/2/19/24	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(°)
2	E	1	MMA	C7-O1-C1	-2.46	109.48	113.27
3	F	1	AMG	C7-O1-C1	-2.02	110.16	113.27

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	F	1	AMG	C2
3	F	1	AMG	C4
2	E	2	AMG	C2
2	E	2	AMG	C4
3	F	2	AMG	C2
3	F	2	AMG	C4

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	1	MMA	C2-C1-O1-C7
2	E	1	MMA	O5-C1-O1-C7

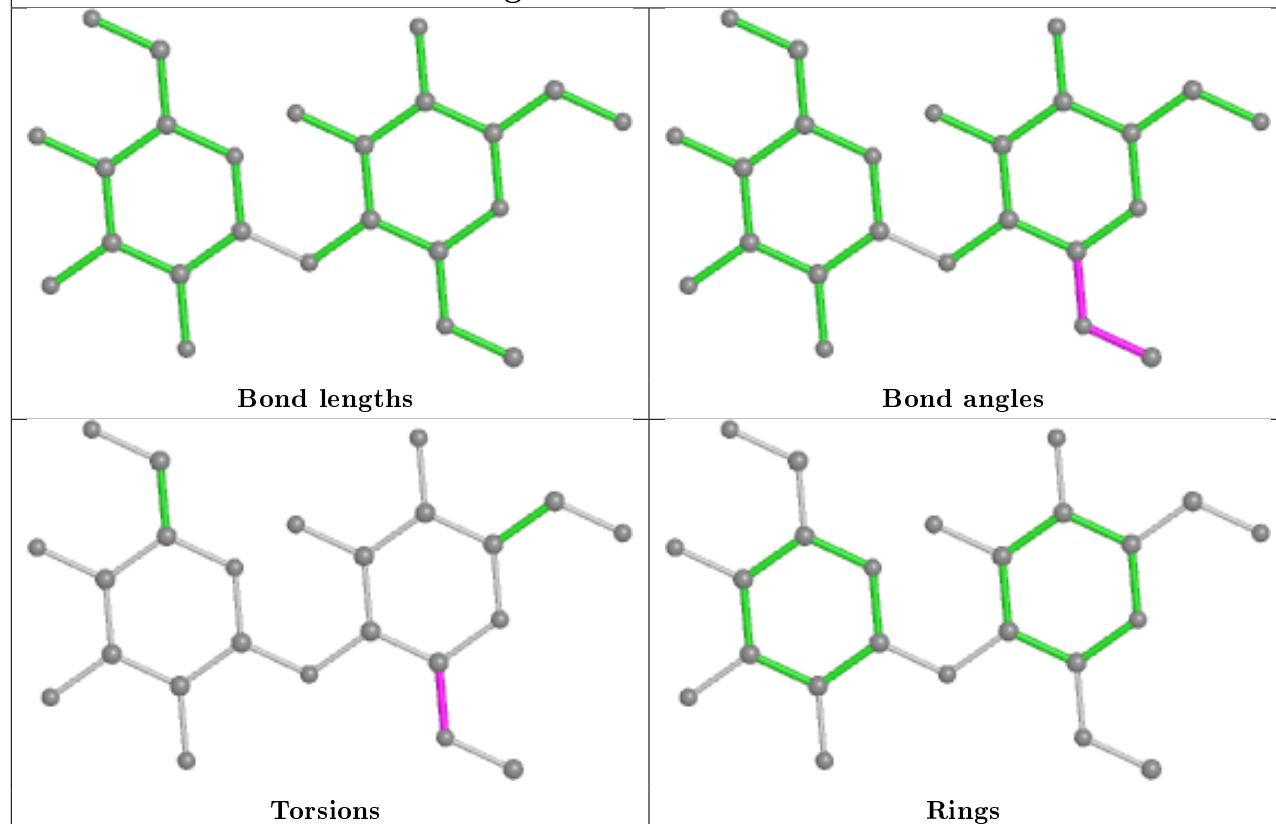
There are no ring outliers.

2 monomers are involved in 2 short contacts:

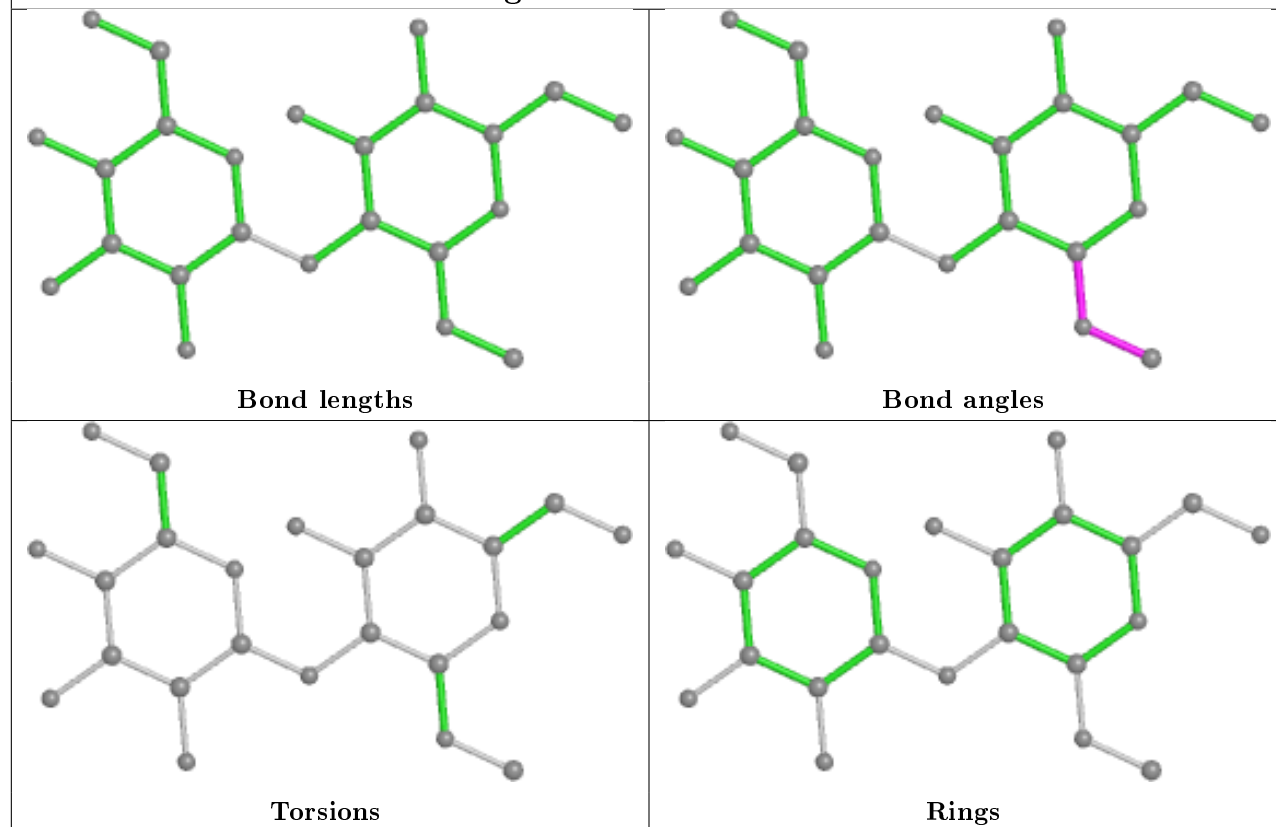
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	2	AMG	1	0
2	E	1	MMA	1	0

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

Oligosaccharide Chain E



Oligosaccharide Chain F



5.6 Ligand geometry

Of 10 ligands modelled in this entry, 8 are 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	MMA	C	241	-	13,13,13	0.60	0	18,18,18	0.62	0
6	MMA	B	241	-	13,13,13	0.50	0	18,18,18	0.58	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	MMA	C	241	-	-	0/4/24/24	0/1/1/1
6	MMA	B	241	-	-	0/4/24/24	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	233/237 (98%)	-0.10	6 (2%)	56	65	9, 23, 46, 60	2 (0%)
1	B	233/237 (98%)	-0.06	4 (1%)	70	78	10, 24, 48, 59	5 (2%)
1	C	233/237 (98%)	0.11	15 (6%)	19	23	10, 27, 50, 61	8 (3%)
1	D	233/237 (98%)	-0.06	12 (5%)	27	33	11, 26, 48, 62	11 (4%)
All	All	932/948 (98%)	-0.03	37 (3%)	38	45	9, 25, 49, 62	26 (2%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	204	SER	8.7
1	C	1	ALA	5.8
1	C	203	ASP	5.0
1	C	69	ASN	4.2
1	C	16	ASP	4.1
1	D	21	SER	3.9
1	C	205	HIS	3.6
1	D	162	ASN	3.6
1	A	69	ASN	3.3
1	A	150	THR	3.2
1	C	151	ASP	3.1
1	C	185	SER	3.1
1	D	160	SER	3.1
1	D	202	PRO	3.0
1	C	162	ASN	3.0
1	D	69	ASN	2.9
1	C	161	SER	2.9
1	D	150	THR	2.9
1	A	162	ASN	2.8
1	B	151	ASP	2.8
1	D	161	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	164	SER	2.7
1	C	163	GLY	2.6
1	C	150	THR	2.6
1	D	1	ALA	2.6
1	C	83	ASN	2.5
1	A	149	GLY	2.4
1	D	101	LYS	2.3
1	A	158	ARG	2.3
1	D	237	ASN	2.3
1	B	185	SER	2.3
1	C	224	GLY	2.2
1	C	21	SER	2.1
1	D	136	ASP	2.1
1	A	71	ASP	2.1
1	B	83	ASN	2.0
1	B	69	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

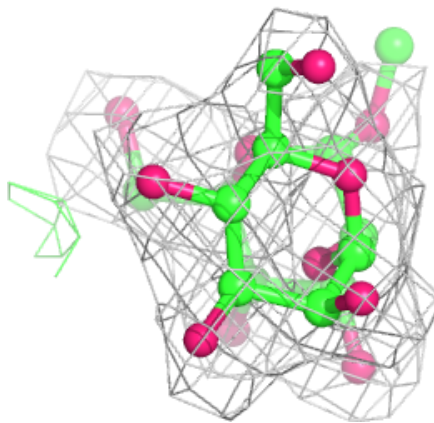
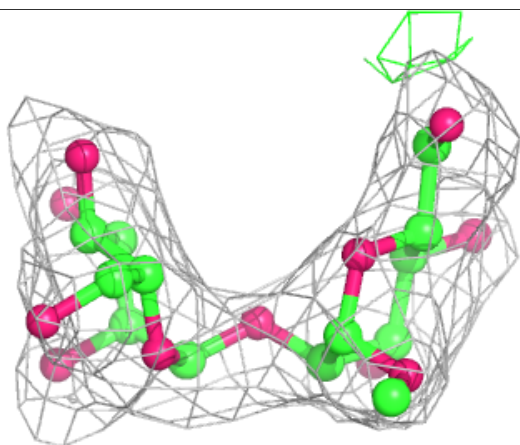
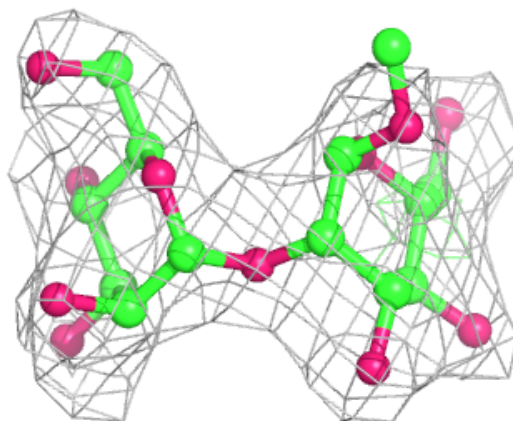
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

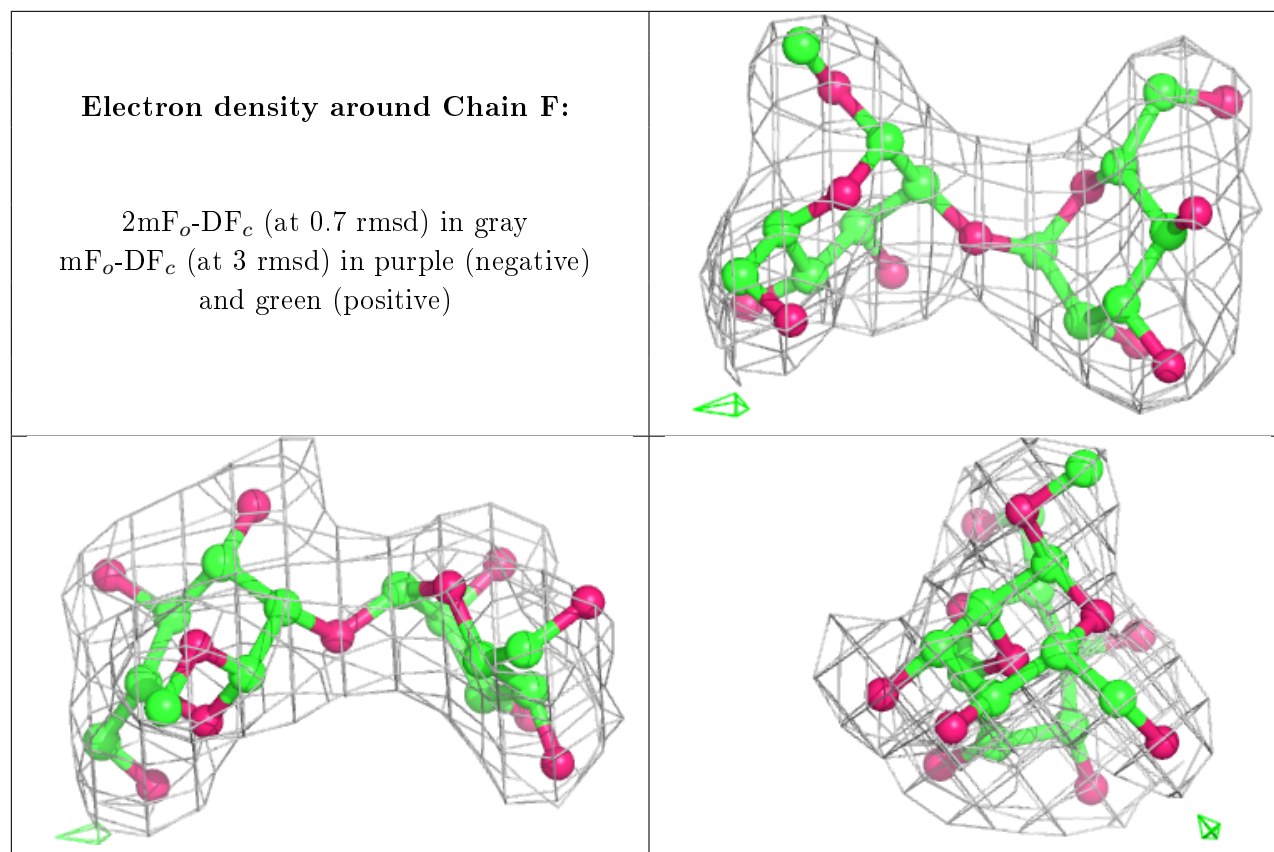
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	AMG	F	2	11/13	0.91	0.18	41,44,46,46	0
2	MMA	E	1	13/13	0.94	0.17	31,37,41,41	0
3	AMG	F	1	13/13	0.95	0.12	39,42,42,42	0
2	AMG	E	2	11/13	0.97	0.12	19,23,25,26	0

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 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 ⓘ

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
6	MMA	C	241	13/13	0.78	0.25	35,37,39,40	0
5	CA	C	239	1/1	0.89	0.10	33,33,33,33	0
5	CA	D	239	1/1	0.90	0.14	34,34,34,34	0
6	MMA	B	241	13/13	0.92	0.15	19,25,27,27	0
4	MN	B	238	1/1	0.96	0.06	34,34,34,34	0
4	MN	C	238	1/1	0.98	0.05	49,49,49,49	0
5	CA	B	239	1/1	0.98	0.15	24,24,24,24	0
5	CA	A	239	1/1	0.98	0.08	15,15,15,15	0
4	MN	A	238	1/1	0.99	0.03	33,33,33,33	0
4	MN	D	238	1/1	0.99	0.02	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.