



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 07:43 PM UTC

PDB ID : 2CYF / pdb_00002cyf
Title : The Crystal Structure of Canavalia Maritima Lectin (ConM) in Complex with Trehalose and Maltose
Authors : Delatorre, P.; Rocha, B.A.M.; Sousa, E.P.; Gadelha, C.A.A.; Azevedo Jr., W.F.; Cavada, B.S.
Deposited on : 2005-07-06
Resolution : 1.80 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

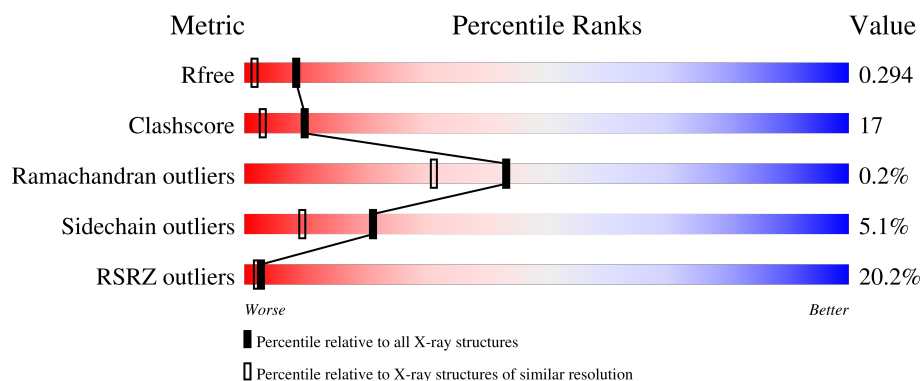
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	237	5% 76% 19% ...
1	C	237	34% 72% 22% ...
2	B	2	50% 50%
2	D	2	50% 50%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3877 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 Lectin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1747	1104	292	350	1			
1	C	231	Total	C	N	O	S	0	0	0
			1755	1110	293	351	1			

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	B	2	Total	C	O	0	0	0
			22	12	10			
2	D	2	Total	C	O	0	0	0
			22	12	10			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		
3	C	1	Total	Ca	0	0
			1	1		

- Molecule 4 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

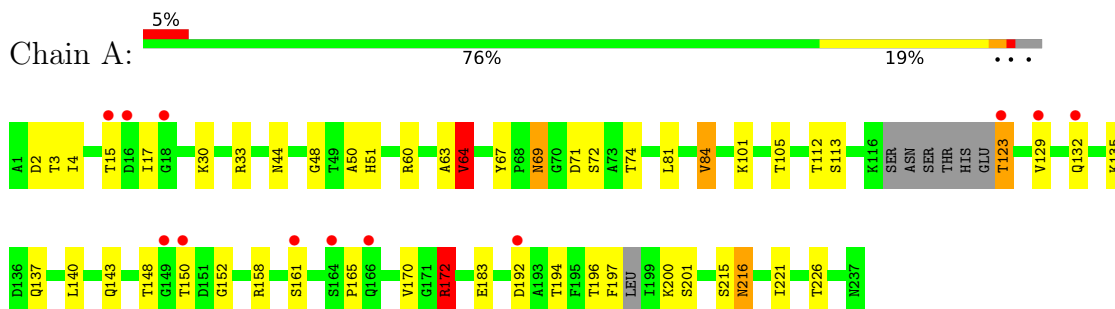
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	165	Total 165	O 165	0	0
5	C	162	Total 162	O 162	0	0

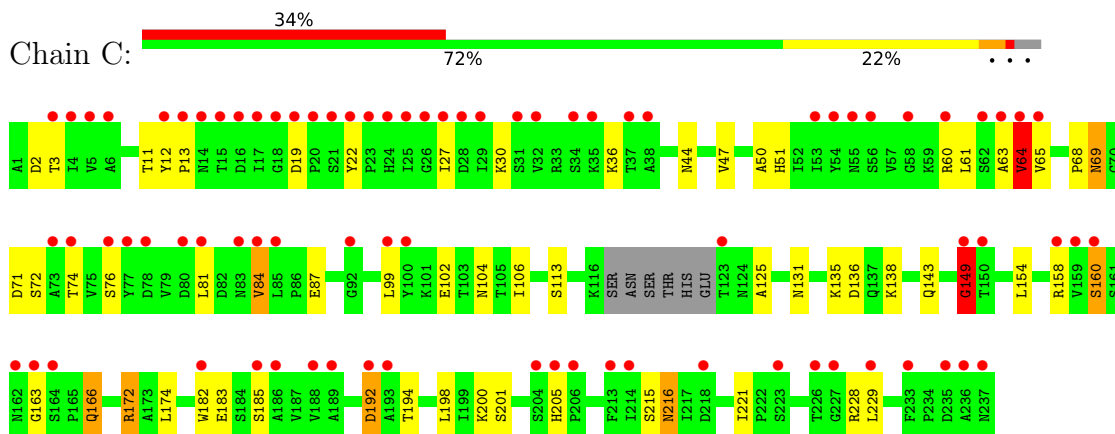
3 Residue-property plots

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: Lectin



- Molecule 1: Lectin



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	67.03Å 97.33Å 71.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	9.98 – 1.80 9.98 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (9.98-1.80) 98.7 (9.98-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.186 , 0.238 0.266 , 0.294	Depositor DCC
R_{free} test set	4360 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	17.8	Xtriage
Anisotropy	0.165	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.47 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3877	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 55.53 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.1202e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GLC, MN, CA

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	1.14	0/1785	1.05	2/2428 (0.1%)
1	C	1.20	4/1794 (0.2%)	1.06	1/2442 (0.0%)
All	All	1.17	4/3579 (0.1%)	1.05	3/4870 (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	A	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	125	ALA	CA-CB	-6.15	1.43	1.53
1	C	12	TYR	C-O	-5.88	1.20	1.25
1	C	19	ASP	CA-C	-5.57	1.47	1.53
1	C	149	GLY	N-CA	5.38	1.53	1.45

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	64	VAL	CB-CA-C	-9.44	95.97	110.50
1	C	64	VAL	CB-CA-C	-9.19	96.35	110.50
1	A	172	ARG	NE-CZ-NH2	-6.42	113.42	119.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	148	THR	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1747	0	1699	61	0
1	C	1755	0	1711	62	0
2	B	22	0	19	0	0
2	D	22	0	19	3	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	A	165	0	0	23	0
5	C	162	0	0	19	0
All	All	3877	0	3448	122	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 17.

All (122) 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:A:113:SER:HB2	5:A:497:HOH:O	1.19	1.29
1:A:172:ARG:HG2	5:A:515:HOH:O	1.34	1.26
1:A:170:VAL:HB	5:A:558:HOH:O	1.09	1.23
1:A:72:SER:HB3	5:A:505:HOH:O	1.19	1.23
1:A:113:SER:CB	5:A:497:HOH:O	1.77	1.15
1:C:192:ASP:HB3	5:C:531:HOH:O	1.48	1.11
1:A:72:SER:CB	5:A:505:HOH:O	1.72	1.10
1:C:143:GLN:OE1	1:C:172:ARG:HD2	1.57	1.04
1:C:113:SER:HB2	5:C:487:HOH:O	0.87	1.04
1:C:99:LEU:HD22	2:D:1:GLC:H4	1.41	1.02
1:C:143:GLN:OE1	1:C:172:ARG:CD	2.06	1.02
1:A:69:ASN:ND2	5:A:539:HOH:O	1.93	0.99
1:A:170:VAL:CG2	1:A:226:THR:HA	1.97	0.94

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:44:ASN:HD21	1:C:201:SER:H	1.15	0.89
1:A:215:SER:HB2	5:A:506:HOH:O	1.70	0.89
1:A:44:ASN:HD21	1:A:201:SER:H	1.23	0.85
1:A:170:VAL:HG23	1:A:226:THR:HG22	1.57	0.85
1:C:87:GLU:OE2	5:C:546:HOH:O	1.96	0.83
1:C:143:GLN:OE1	1:C:172:ARG:HD3	1.79	0.83
1:A:143:GLN:OE1	1:A:172:ARG:CD	2.28	0.81
1:C:172:ARG:CG	5:C:474:HOH:O	2.27	0.79
1:C:192:ASP:CB	5:C:531:HOH:O	2.15	0.79
1:C:30:LYS:HE3	1:C:84:VAL:HG23	1.63	0.78
1:C:3:THR:H	1:C:216:ASN:ND2	1.82	0.77
1:A:143:GLN:OE1	1:A:172:ARG:HD2	1.86	0.76
1:C:205:HIS:HB2	5:C:502:HOH:O	1.85	0.76
1:C:172:ARG:HG2	5:C:474:HOH:O	1.83	0.74
1:C:192:ASP:CG	5:C:531:HOH:O	2.30	0.74
1:C:87:GLU:CD	5:C:546:HOH:O	2.33	0.71
1:A:67:TYR:HB3	5:A:539:HOH:O	1.91	0.71
1:A:143:GLN:OE1	1:A:172:ARG:HD3	1.91	0.70
1:A:170:VAL:HG21	1:A:226:THR:HA	1.73	0.69
1:C:172:ARG:NE	5:C:474:HOH:O	1.67	0.68
1:A:172:ARG:NE	5:A:515:HOH:O	1.80	0.67
1:A:64:VAL:HG13	1:A:74:THR:OG1	1.95	0.66
1:C:135:LYS:HA	1:C:149:GLY:HA3	1.76	0.66
1:C:3:THR:HG23	1:C:30:LYS:HE2	1.79	0.64
1:A:60:ARG:CZ	5:A:559:HOH:O	2.46	0.64
1:A:172:ARG:CG	5:A:515:HOH:O	2.06	0.64
1:C:44:ASN:HD21	1:C:201:SER:N	1.93	0.63
1:C:102:GLU:OE2	1:C:104:ASN:ND2	2.27	0.62
1:C:81:LEU:HA	1:C:84:VAL:HG13	1.84	0.60
1:C:160:SER:CB	5:C:554:HOH:O	2.50	0.60
1:A:123:THR:N	1:C:131:ASN:HD22	2.00	0.59
1:C:143:GLN:HB2	1:C:172:ARG:HG3	1.85	0.58
1:A:135:LYS:HB2	1:A:150:THR:HG22	1.86	0.58
1:A:170:VAL:HG22	1:A:226:THR:HA	1.83	0.58
1:C:163:GLY:N	5:C:554:HOH:O	2.35	0.58
1:C:228:ARG:HG2	2:D:2:GLC:O3	2.04	0.58
1:C:160:SER:C	5:C:554:HOH:O	2.46	0.57
1:A:3:THR:HG23	1:A:30:LYS:CE	2.36	0.56
1:A:60:ARG:NE	5:A:559:HOH:O	2.38	0.56
1:A:170:VAL:CG2	1:A:226:THR:CA	2.80	0.56
1:C:216:ASN:HD22	1:C:216:ASN:H	1.53	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:ASN:H	1:A:216:ASN:HD22	1.54	0.55
1:A:60:ARG:NH2	5:A:559:HOH:O	2.38	0.55
1:C:182:TRP:CZ3	5:C:546:HOH:O	2.61	0.54
1:C:158:ARG:HG2	1:C:166:GLN:HG3	1.89	0.53
1:C:135:LYS:CA	1:C:149:GLY:HA3	2.40	0.52
1:A:74:THR:HG22	5:A:532:HOH:O	2.09	0.52
1:A:3:THR:H	1:A:216:ASN:ND2	2.08	0.52
1:C:2:ASP:HB3	1:C:216:ASN:HD21	1.76	0.51
1:C:216:ASN:ND2	1:C:216:ASN:H	2.09	0.51
1:A:170:VAL:HG21	1:A:226:THR:CA	2.40	0.51
1:A:44:ASN:HD21	1:A:201:SER:N	2.01	0.51
1:C:172:ARG:HD2	1:C:221:ILE:HG13	1.92	0.50
1:A:3:THR:HG23	1:A:30:LYS:HE3	1.93	0.50
1:A:183:GLU:HB3	5:A:477:HOH:O	2.12	0.50
1:C:11:THR:O	1:C:205:HIS:HE1	1.96	0.49
1:A:69:ASN:ND2	1:A:71:ASP:H	2.09	0.49
1:A:216:ASN:HB3	5:A:504:HOH:O	2.12	0.49
1:A:81:LEU:HA	1:A:84:VAL:HG13	1.94	0.49
1:C:3:THR:HG23	1:C:30:LYS:CE	2.41	0.49
1:A:172:ARG:HD2	1:A:221:ILE:HG13	1.94	0.49
1:C:27:ILE:HG23	1:C:61:LEU:HD23	1.95	0.48
1:A:4:ILE:HD13	5:A:506:HOH:O	2.12	0.48
1:A:170:VAL:HG23	1:A:226:THR:CG2	2.37	0.48
1:A:170:VAL:CG2	1:A:226:THR:HG22	2.37	0.47
1:A:216:ASN:H	1:A:216:ASN:ND2	2.11	0.47
1:C:3:THR:H	1:C:216:ASN:HD22	1.59	0.47
1:A:3:THR:HG23	1:A:30:LYS:HE2	1.97	0.47
1:A:2:ASP:CB	1:A:216:ASN:HD21	2.26	0.47
1:A:105:THR:O	1:A:197:PHE:HA	2.14	0.47
1:C:182:TRP:CH2	5:C:546:HOH:O	2.55	0.47
1:A:112:THR:HB	1:A:192:ASP:OD1	2.15	0.47
1:A:113:SER:OG	5:A:497:HOH:O	1.93	0.46
1:A:101:LYS:HD3	1:A:165:PRO:O	2.16	0.46
1:C:158:ARG:HD3	5:C:555:HOH:O	2.17	0.45
1:A:67:TYR:CB	5:A:539:HOH:O	2.54	0.45
1:C:172:ARG:HD3	1:C:174:LEU:HD11	1.97	0.45
1:C:2:ASP:CB	1:C:216:ASN:HD21	2.29	0.45
1:C:183:GLU:OE2	1:C:185:SER:HB2	2.16	0.45
1:A:69:ASN:CG	5:A:539:HOH:O	2.44	0.45
1:A:3:THR:O	5:A:506:HOH:O	2.21	0.44
1:A:215:SER:CB	5:A:506:HOH:O	2.45	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:64:VAL:HG13	1:C:74:THR:OG1	2.18	0.44
1:C:113:SER:CB	5:C:487:HOH:O	1.75	0.44
1:C:30:LYS:HA	5:C:492:HOH:O	2.18	0.43
1:C:60:ARG:HD3	1:C:76:SER:HB3	2.00	0.43
1:A:30:LYS:HE3	1:A:84:VAL:HG23	1.99	0.43
1:C:44:ASN:ND2	1:C:200:LYS:HA	2.33	0.43
1:C:99:LEU:HB2	2:D:2:GLC:O5	2.17	0.43
1:C:3:THR:O	1:C:215:SER:HA	2.19	0.43
1:A:17:ILE:O	1:A:33:ARG:HG2	2.19	0.43
1:A:51:HIS:O	1:A:63:ALA:HA	2.19	0.42
1:A:2:ASP:HB3	1:A:216:ASN:HD21	1.84	0.42
1:A:48:GLY:O	1:A:196:THR:HA	2.20	0.42
1:A:132:GLN:HG3	1:A:152:GLY:HA2	2.00	0.42
1:C:106:ILE:HB	1:C:154:LEU:HB3	2.02	0.42
1:C:50:ALA:O	1:C:194:THR:HA	2.19	0.42
1:C:13:PRO:HG3	1:C:22:TYR:C	2.45	0.42
1:C:69:ASN:ND2	1:C:71:ASP:H	2.16	0.42
1:A:44:ASN:ND2	1:A:200:LYS:HA	2.34	0.41
1:C:47:VAL:O	1:C:68:PRO:HD3	2.20	0.41
1:C:51:HIS:O	1:C:63:ALA:HA	2.19	0.41
1:C:65:VAL:O	1:C:72:SER:HA	2.21	0.41
1:C:228:ARG:HG3	1:C:229:LEU:HG	2.03	0.41
1:A:50:ALA:O	1:A:194:THR:HA	2.21	0.41
1:A:137:GLN:HG2	1:A:140:LEU:HD12	2.02	0.40
1:C:136:ASP:OD2	1:C:138:LYS:NZ	2.43	0.40
1:C:87:GLU:HG3	1:C:182:TRP:O	2.20	0.40
1:C:172:ARG:HB3	5:C:474:HOH:O	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	224/237 (94%)	218 (97%)	6 (3%)	0	100	100
1	C	227/237 (96%)	217 (96%)	9 (4%)	1 (0%)	30	19
All	All	451/474 (95%)	435 (96%)	15 (3%)	1 (0%)	43	31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	149	GLY

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	195/202 (96%)	185 (95%)	10 (5%)	21	9
1	C	196/202 (97%)	186 (95%)	10 (5%)	21	9
All	All	391/404 (97%)	371 (95%)	20 (5%)	21	9

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	THR
1	A	64	VAL
1	A	69	ASN
1	A	84	VAL
1	A	123	THR
1	A	129	VAL
1	A	158	ARG
1	A	161	SER
1	A	172	ARG
1	A	216	ASN
1	C	36	LYS
1	C	64	VAL
1	C	69	ASN
1	C	84	VAL
1	C	160	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	166	GLN
1	C	172	ARG
1	C	192	ASP
1	C	198	LEU
1	C	216	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	44	ASN
1	A	69	ASN
1	A	216	ASN
1	A	237	ASN
1	C	43	GLN
1	C	44	ASN
1	C	69	ASN
1	C	132	GLN
1	C	166	GLN
1	C	216	ASN
1	C	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	GLC	B	1	2	11,11,12	0.42	0	15,15,17	1.33	2 (13%)
2	GLC	B	2	2	11,11,12	0.45	0	15,15,17	1.04	0
2	GLC	D	1	2	11,11,12	0.42	0	15,15,17	0.95	0
2	GLC	D	2	2	11,11,12	0.97	0	15,15,17	2.82	7 (46%)

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	GLC	B	1	2	-	1/2/19/22	0/1/1/1
2	GLC	B	2	2	-	0/2/19/22	0/1/1/1
2	GLC	D	1	2	-	2/2/19/22	0/1/1/1
2	GLC	D	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	GLC	O3-C3-C4	6.39	125.45	110.38
2	D	2	GLC	C2-C3-C4	-5.05	101.99	110.86
2	D	2	GLC	C1-C2-C3	-3.87	104.01	109.64
2	D	2	GLC	O4-C4-C5	-3.24	101.34	109.32
2	D	2	GLC	O4-C4-C3	2.90	117.22	110.38
2	D	2	GLC	O2-C2-C1	2.71	115.43	109.22
2	B	1	GLC	O4-C4-C3	-2.60	104.25	110.38
2	D	2	GLC	O5-C1-C2	-2.41	105.03	110.79
2	B	1	GLC	C1-O5-C5	2.37	115.36	112.19

There are no chirality outliers.

All (3) torsion outliers are listed below:

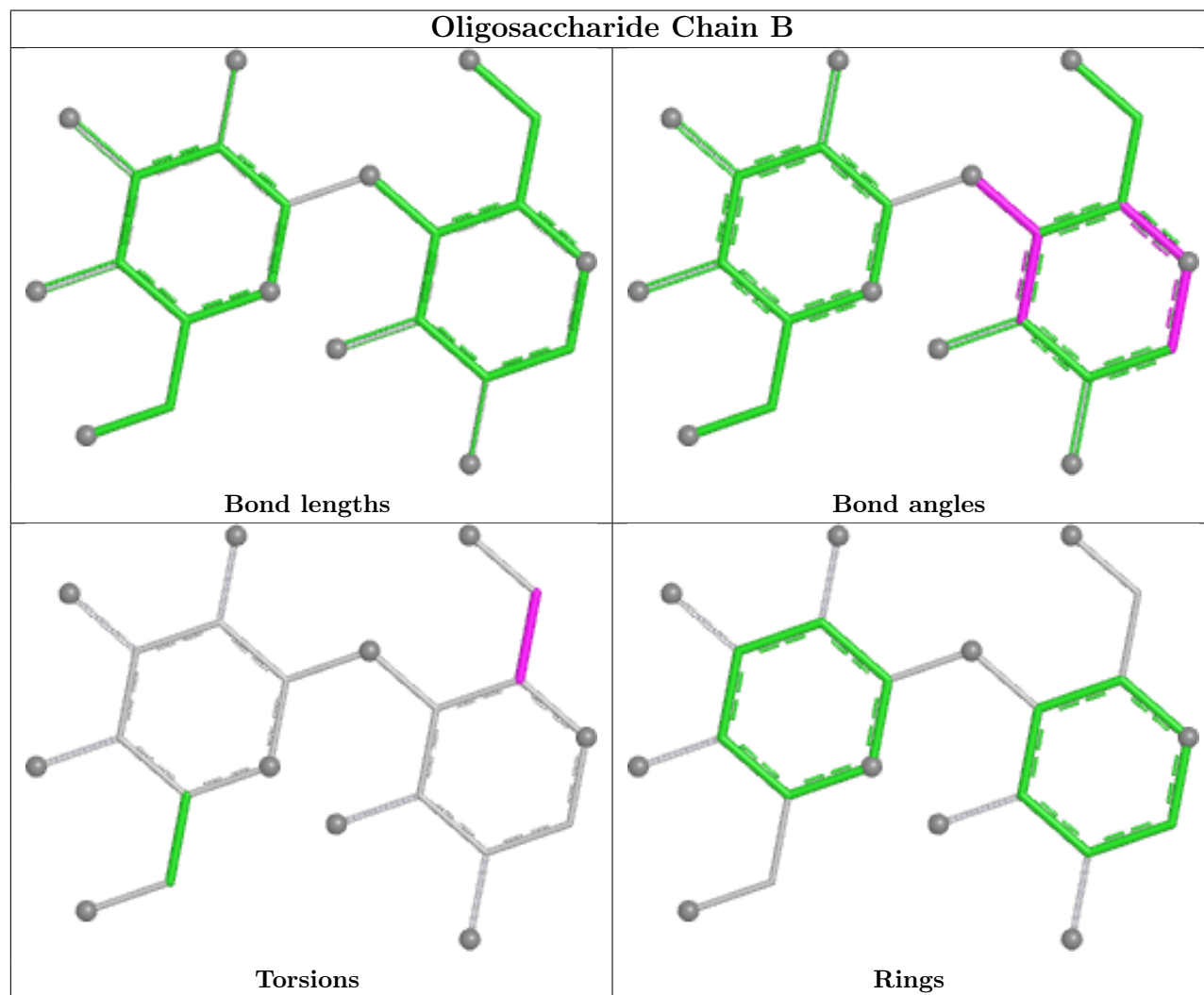
Mol	Chain	Res	Type	Atoms
2	D	1	GLC	O5-C5-C6-O6
2	D	1	GLC	C4-C5-C6-O6
2	B	1	GLC	C4-C5-C6-O6

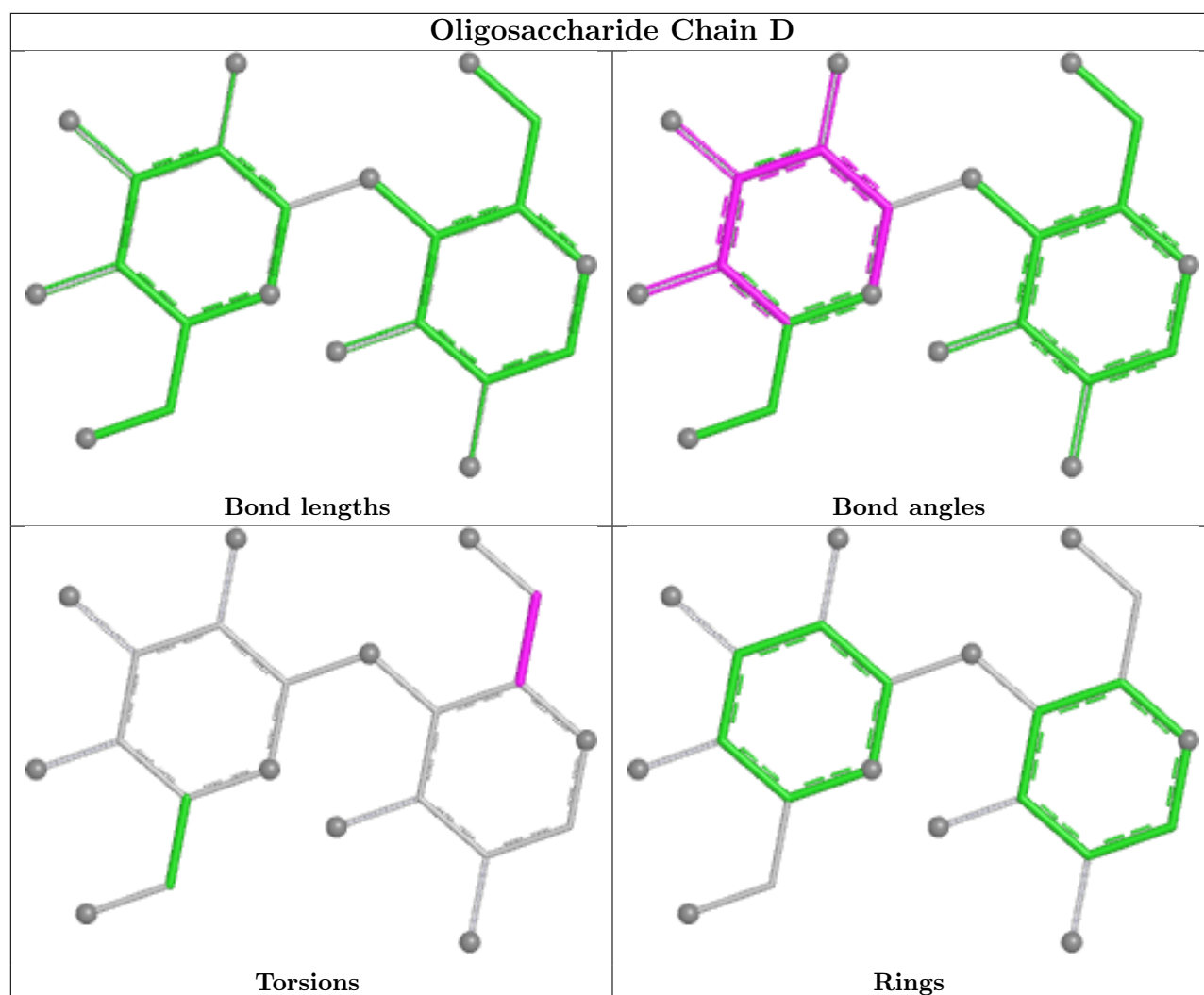
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	GLC	1	0
2	D	2	GLC	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.





5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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 [i](#)

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	230/237 (97%)	0.67	12 (5%) 33 31	11, 18, 31, 40	0
1	C	231/237 (97%)	1.74	81 (35%) 1 1	11, 18, 28, 38	0
All	All	461/474 (97%)	1.20	93 (20%) 3 2	11, 18, 30, 40	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	149	GLY	5.9
1	A	15	THR	4.9
1	A	149	GLY	4.6
1	C	16	ASP	4.6
1	C	18	GLY	4.2
1	C	236	ALA	3.8
1	C	237	ASN	3.7
1	C	185	SER	3.6
1	A	123	THR	3.6
1	A	16	ASP	3.5
1	C	84	VAL	3.5
1	C	205	HIS	3.4
1	C	15	THR	3.2
1	C	54	TYR	3.2
1	C	34	SER	3.2
1	C	182	TRP	3.1
1	C	123	THR	3.1
1	C	20	PRO	3.1
1	C	233	PHE	3.1
1	A	150	THR	3.1
1	C	22	TYR	3.0
1	C	223	SER	3.0
1	C	65	VAL	2.9
1	C	159	VAL	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	6	ALA	2.9
1	C	12	TYR	2.9
1	C	23	PRO	2.9
1	C	19	ASP	2.8
1	C	164	SER	2.8
1	C	17	ILE	2.8
1	C	60	ARG	2.8
1	C	226	THR	2.8
1	C	53	ILE	2.8
1	C	99	LEU	2.7
1	C	204	SER	2.7
1	C	38	ALA	2.7
1	C	192	ASP	2.7
1	C	188	VAL	2.7
1	A	192	ASP	2.6
1	C	27	ILE	2.6
1	C	24	HIS	2.6
1	A	129	VAL	2.6
1	C	5	VAL	2.6
1	C	31	SER	2.6
1	C	37	THR	2.6
1	C	83	ASN	2.5
1	C	189	ALA	2.5
1	C	193	ALA	2.5
1	C	158	ARG	2.5
1	C	14	ASN	2.5
1	C	150	THR	2.5
1	C	81	LEU	2.5
1	C	3	THR	2.5
1	C	92	GLY	2.4
1	C	78	ASP	2.4
1	C	13	PRO	2.4
1	C	32	VAL	2.4
1	C	229	LEU	2.4
1	C	64	VAL	2.4
1	C	163	GLY	2.4
1	C	160	SER	2.4
1	C	100	TYR	2.3
1	C	74	THR	2.3
1	C	206	PRO	2.3
1	C	162	ASN	2.3
1	C	35	LYS	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	63	ALA	2.2
1	C	186	ALA	2.2
1	C	76	SER	2.2
1	C	214	ILE	2.2
1	A	161	SER	2.2
1	C	73	ALA	2.2
1	C	77	TYR	2.2
1	A	132	GLN	2.2
1	C	28	ASP	2.2
1	A	164	SER	2.2
1	C	227	GLY	2.2
1	C	25	ILE	2.1
1	C	4	ILE	2.1
1	C	85	LEU	2.1
1	C	80	ASP	2.1
1	C	235	ASP	2.1
1	C	56	SER	2.1
1	C	62	SER	2.1
1	A	18	GLY	2.1
1	C	213	PHE	2.0
1	C	21	SER	2.0
1	C	55	ASN	2.0
1	C	218	ASP	2.0
1	C	29	ILE	2.0
1	A	166	GLN	2.0
1	C	26	GLY	2.0
1	C	58	GLY	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($\text{\AA}^2$)	Q<0.9
2	GLC	B	1	11/12	-	-	26,30,33,36	0

Continued on next page...

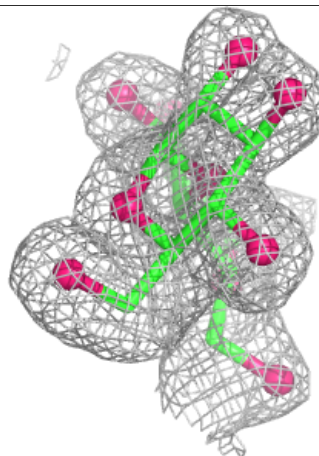
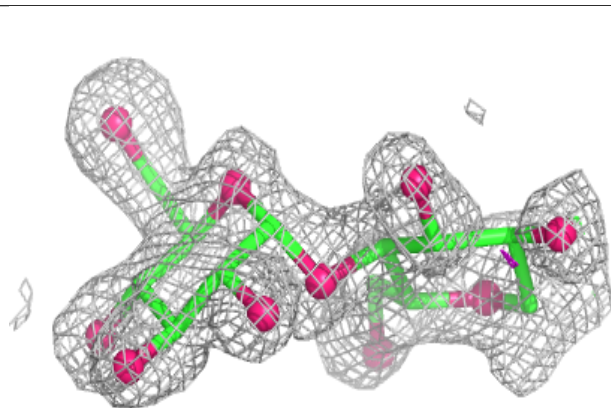
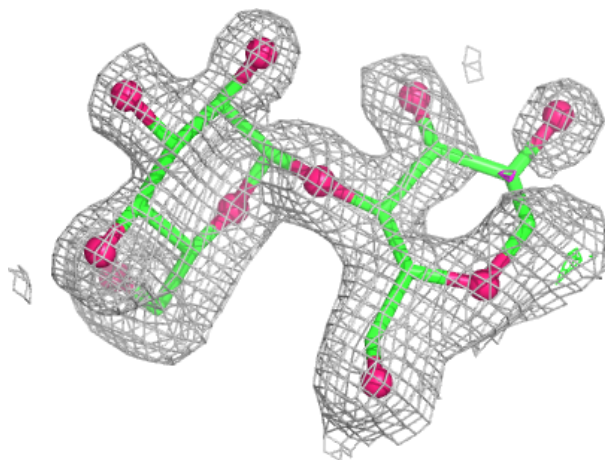
Continued from previous page...

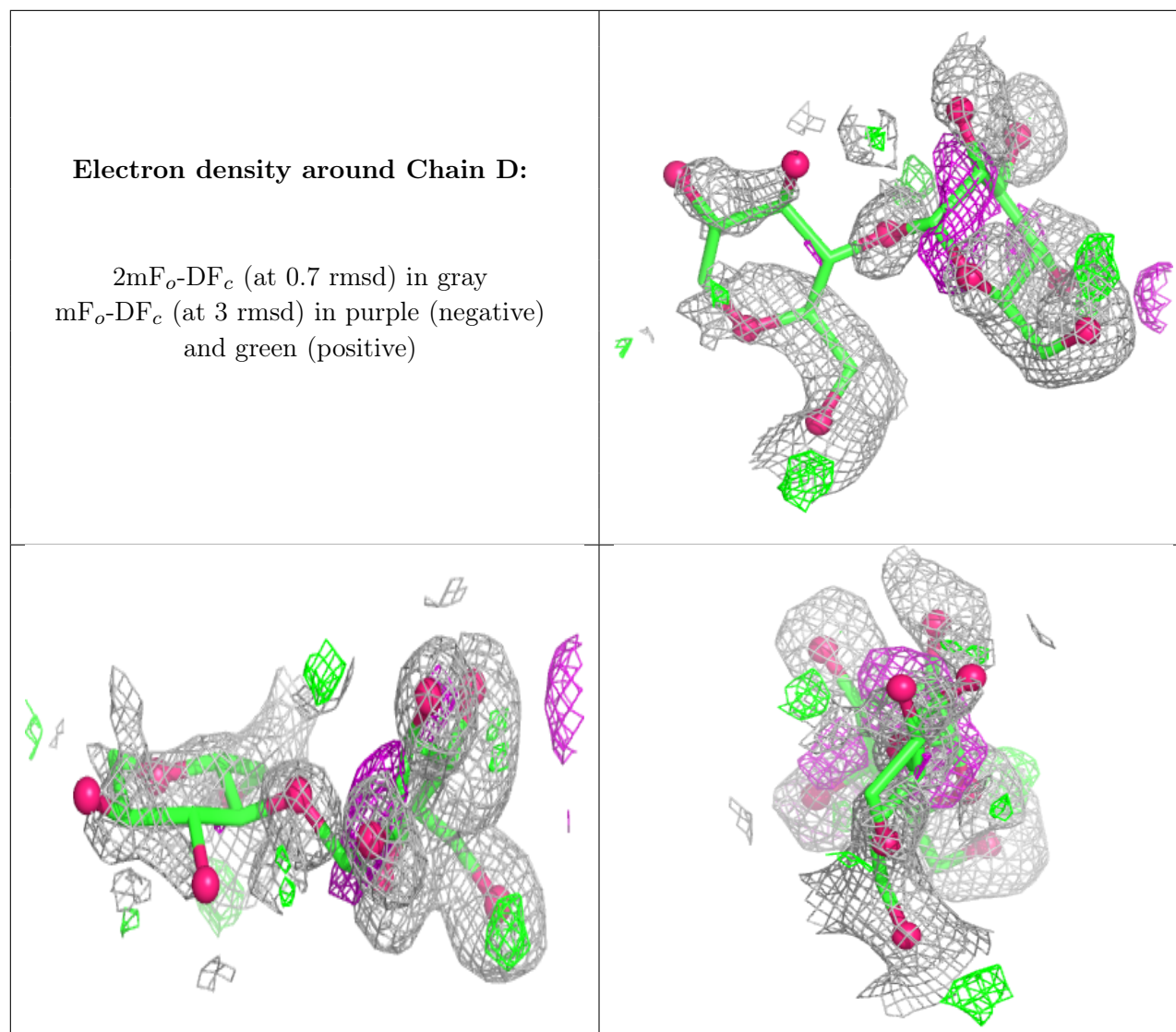
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GLC	B	2	11/12	-	-	16,22,24,26	0
2	GLC	D	1	11/12	0.53	0.15	42,49,51,53	0
2	GLC	D	2	11/12	0.61	0.21	18,27,34,37	0

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 B:

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	MN	C	239	1/1	0.52	0.14	18,18,18,18	0
3	CA	C	238	1/1	0.59	0.18	17,17,17,17	0
4	MN	A	239	1/1	0.94	0.04	18,18,18,18	0
3	CA	A	238	1/1	0.97	0.04	17,17,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.