



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 08:11 PM BST

PDB ID : 1Q25
Title : Crystal structure of N-terminal 3 domains of CI-MPR
Authors : Olson, L.J.; Dahms, N.M.; Kim, J.-J.P.
Deposited on : 2003-07-23
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 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

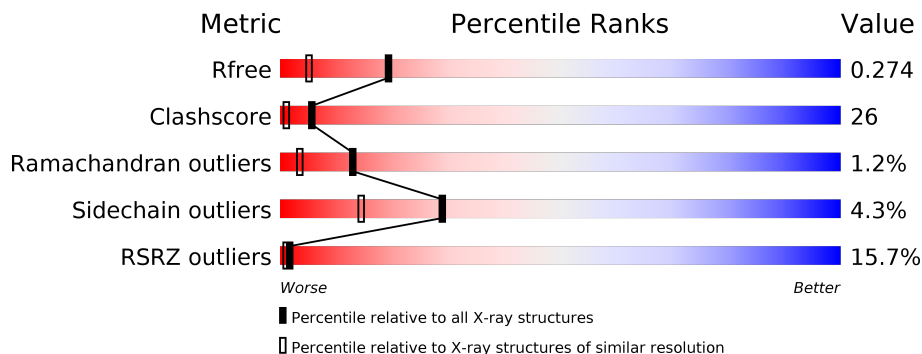
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (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 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	432	
2	B	5	
3	C	2	

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
3	NAG	C	2	-	-	-	X
4	GOL	A	4005	-	X	-	-

2 Entry composition i

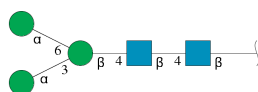
There are 5 unique types of molecules in this entry. The entry contains 3763 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 cation-independent mannose 6-phosphate receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	428	3303	2060	564	651	28	0	0	0

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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
			Total	C	N	O			
2	B	5	61	34	2	25	0	0	0

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	2	28	16	2	10	0	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

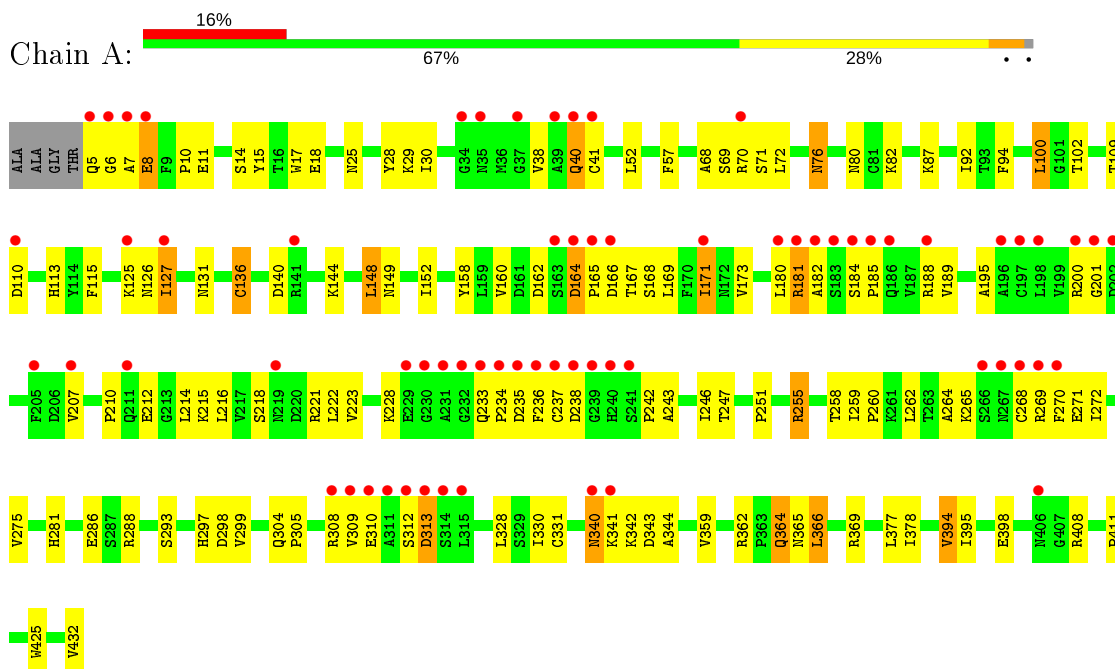
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	365	Total	O	0	0
			365	365		

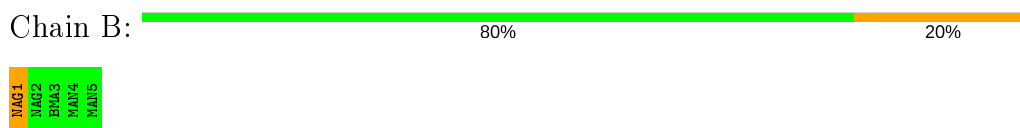
3 Residue-property plots [i](#)

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: cation-independent mannose 6-phosphate receptor



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



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.16Å 84.75Å 96.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.94 – 1.80 19.94 – 1.75	Depositor EDS
% Data completeness (in resolution range)	87.1 (19.94-1.80) 81.9 (19.94-1.75)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.03 (at 1.76Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.235 , 0.283 0.229 , 0.274	Depositor DCC
R_{free} test set	2820 reflections (6.72%)	wwPDB-VP
Wilson B-factor (Å ²)	21.9	Xtrriage
Anisotropy	0.257	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3763	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.19% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: GOL, BMA, NAG, MAN

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	0.36	1/3371 (0.0%)	0.67	1/4570 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	212	GLU	CD-OE2	7.52	1.33	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	76	ASN	CB-CA-C	-6.43	97.54	110.40

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	3303	0	3159	170	0
2	B	61	0	52	1	0
3	C	28	0	25	2	0
4	A	6	0	4	0	0
5	A	365	0	0	11	0
All	All	3763	0	3240	170	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 26.

All (170) 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:92:ILE:HD13	1:A:115:PHE:HB2	1.37	1.04
1:A:246:ILE:HD13	1:A:272:ILE:HB	1.49	0.94
1:A:309:VAL:HG11	1:A:313:ASP:OD1	1.71	0.91
1:A:228:LYS:HZ2	1:A:228:LYS:HB3	1.33	0.90
1:A:164:ASP:HB3	1:A:167:THR:OG1	1.73	0.88
1:A:378:ILE:CD1	1:A:394:VAL:HB	2.04	0.88
1:A:80:ASN:HD21	1:A:87:LYS:HZ3	1.22	0.87
1:A:109:THR:HG22	1:A:110:ASP:H	1.43	0.84
1:A:195:ALA:HB2	1:A:210:PRO:HD3	1.57	0.84
1:A:293:SER:H	1:A:297:HIS:HD2	1.24	0.84
1:A:149:ASN:HA	1:A:152:ILE:HD13	1.59	0.84
1:A:309:VAL:HG13	1:A:408:ARG:NH2	1.94	0.81
1:A:76:ASN:OD1	5:A:774:HOH:O	1.99	0.79
1:A:80:ASN:HD21	1:A:87:LYS:NZ	1.81	0.77
1:A:207:VAL:HG23	1:A:242:PRO:HB3	1.67	0.76
1:A:299:VAL:HG23	1:A:432:VAL:HG13	1.68	0.75
1:A:92:ILE:HD13	1:A:115:PHE:CB	2.16	0.74
1:A:160:VAL:CG2	1:A:171:ILE:HD12	2.18	0.73
1:A:228:LYS:NZ	1:A:228:LYS:HB3	2.03	0.73
1:A:185:PRO:HA	1:A:188:ARG:HE	1.53	0.72
1:A:309:VAL:CG1	1:A:313:ASP:OD1	2.36	0.72
1:A:236:PHE:CE1	1:A:237:CYS:SG	2.82	0.72
1:A:6:GLY:HA2	1:A:10:PRO:CG	2.21	0.70
1:A:80:ASN:ND2	1:A:87:LYS:NZ	2.40	0.70
1:A:14:SER:HB2	1:A:15:TYR:CE1	2.27	0.69
1:A:330:ILE:HG23	1:A:331:CYS:SG	2.31	0.69
1:A:109:THR:HG22	1:A:110:ASP:N	2.07	0.69
1:A:242:PRO:HA	1:A:268:CYS:O	1.93	0.68
1:A:40:GLN:H	1:A:40:GLN:NE2	1.92	0.68
1:A:184:SER:O	1:A:188:ARG:HG3	1.94	0.68
1:A:246:ILE:CD1	1:A:272:ILE:HB	2.21	0.68
1:A:215:LYS:HE2	1:A:223:VAL:HG23	1.76	0.68
1:A:40:GLN:H	1:A:40:GLN:HE21	1.40	0.68
1:A:411:PRO:HG3	1:A:425:TRP:CZ3	2.29	0.67
1:A:340:ASN:CG	1:A:341:LYS:H	1.97	0.67
1:A:149:ASN:CA	1:A:152:ILE:HD13	2.25	0.66
1:A:25:ASN:ND2	1:A:52:LEU:HB2	2.12	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:GLN:H	1:A:364:GLN:HE21	1.44	0.65
1:A:364:GLN:H	1:A:364:GLN:NE2	1.94	0.65
1:A:233:GLN:HG3	1:A:242:PRO:HD3	1.79	0.64
1:A:160:VAL:HG23	1:A:171:ILE:HD12	1.77	0.64
1:A:251:PRO:HG3	1:A:275:VAL:CG1	2.28	0.63
1:A:136:CYS:SG	1:A:152:ILE:HD11	2.39	0.62
1:A:341:LYS:C	1:A:341:LYS:HD3	2.21	0.61
1:A:378:ILE:HD13	1:A:394:VAL:HB	1.80	0.61
1:A:242:PRO:HG3	1:A:268:CYS:SG	2.40	0.61
1:A:125:LYS:C	1:A:127:ILE:H	2.04	0.60
1:A:242:PRO:HA	1:A:268:CYS:HB3	1.84	0.60
1:A:233:GLN:HG3	1:A:242:PRO:CD	2.32	0.59
1:A:411:PRO:HG3	1:A:425:TRP:CE3	2.36	0.59
1:A:207:VAL:O	1:A:207:VAL:HG22	2.03	0.59
1:A:11:GLU:HG3	5:A:697:HOH:O	2.02	0.58
1:A:340:ASN:ND2	1:A:341:LYS:H	2.00	0.58
1:A:71:SER:HB2	1:A:94:PHE:O	2.04	0.58
1:A:207:VAL:HG21	1:A:270:PHE:CE1	2.39	0.58
1:A:341:LYS:HD3	1:A:341:LYS:O	2.04	0.57
1:A:28:TYR:OH	1:A:113:HIS:HD2	1.88	0.57
1:A:341:LYS:O	1:A:343:ASP:N	2.36	0.57
1:A:265:LYS:NZ	1:A:265:LYS:HB3	2.20	0.57
1:A:127:ILE:O	1:A:127:ILE:HD13	2.05	0.56
1:A:6:GLY:HA2	1:A:10:PRO:HG2	1.87	0.56
1:A:182:ALA:HB3	1:A:188:ARG:HG2	1.87	0.56
1:A:246:ILE:HD11	1:A:272:ILE:HD12	1.88	0.56
1:A:299:VAL:HG23	1:A:432:VAL:CG1	2.36	0.55
1:A:378:ILE:HD12	1:A:394:VAL:HB	1.89	0.55
1:A:286:GLU:OE1	1:A:369:ARG:HD3	2.06	0.55
1:A:259:ILE:HG23	1:A:260:PRO:HD2	1.89	0.55
1:A:171:ILE:H	1:A:171:ILE:HD13	1.72	0.55
1:A:158:TYR:HB2	1:A:171:ILE:CD1	2.37	0.55
1:A:364:GLN:O	1:A:365:ASN:OD1	2.24	0.55
1:A:164:ASP:CB	1:A:167:THR:OG1	2.53	0.54
1:A:82:LYS:HD3	1:A:110:ASP:OD1	2.07	0.54
1:A:218:SER:OG	1:A:221:ARG:HB2	2.07	0.54
1:A:309:VAL:HG12	1:A:310:GLU:N	2.22	0.54
1:A:125:LYS:O	1:A:127:ILE:N	2.41	0.54
1:A:180:LEU:HB2	1:A:181:ARG:HD2	1.89	0.54
1:A:181:ARG:HD2	1:A:181:ARG:N	2.23	0.54
1:A:243:ALA:HB2	1:A:269:ARG:NH1	2.22	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:GLU:H	1:A:11:GLU:CD	2.12	0.53
1:A:166:ASP:O	1:A:200:ARG:HA	2.08	0.53
1:A:362:ARG:HD3	5:A:844:HOH:O	2.08	0.53
1:A:158:TYR:O	1:A:171:ILE:HD13	2.08	0.53
1:A:365:ASN:OD1	3:C:1:NAG:H2	2.09	0.53
1:A:125:LYS:C	1:A:127:ILE:N	2.61	0.53
1:A:288:ARG:HG2	5:A:672:HOH:O	2.09	0.53
1:A:5:GLN:HE21	1:A:5:GLN:HA	1.74	0.52
1:A:144:LYS:HG3	1:A:281:HIS:HD2	1.74	0.52
1:A:365:ASN:OD1	3:C:1:NAG:C2	2.57	0.52
1:A:140:ASP:OD2	1:A:144:LYS:HB2	2.10	0.51
1:A:6:GLY:HA2	1:A:10:PRO:HG3	1.91	0.51
1:A:243:ALA:N	1:A:268:CYS:O	2.43	0.51
1:A:264:ALA:HB3	1:A:271:GLU:HB2	1.92	0.51
1:A:304:GLN:N	1:A:305:PRO:HD2	2.26	0.51
1:A:251:PRO:HG2	1:A:255:ARG:HD2	1.92	0.51
1:A:148:LEU:O	1:A:152:ILE:CD1	2.59	0.50
1:A:5:GLN:NE2	1:A:5:GLN:HA	2.26	0.50
1:A:5:GLN:HG3	1:A:6:GLY:N	2.26	0.50
1:A:207:VAL:CG2	1:A:242:PRO:HB3	2.40	0.49
1:A:246:ILE:CD1	1:A:272:ILE:HD12	2.42	0.49
1:A:395:ILE:HD12	1:A:395:ILE:N	2.27	0.49
1:A:127:ILE:C	1:A:127:ILE:HD13	2.33	0.49
1:A:76:ASN:HB3	5:A:644:HOH:O	2.12	0.48
1:A:200:ARG:O	1:A:200:ARG:HG2	2.14	0.48
1:A:72:LEU:HD12	1:A:92:ILE:O	2.13	0.48
1:A:251:PRO:HG3	1:A:275:VAL:HG12	1.93	0.48
1:A:364:GLN:C	1:A:365:ASN:OD1	2.52	0.48
1:A:80:ASN:ND2	1:A:87:LYS:HZ2	2.12	0.48
1:A:343:ASP:HA	5:A:925:HOH:O	2.13	0.48
1:A:340:ASN:CG	1:A:341:LYS:N	2.67	0.48
1:A:125:LYS:HB2	1:A:127:ILE:HG22	1.96	0.48
1:A:309:VAL:HG13	1:A:408:ARG:HH21	1.76	0.48
1:A:215:LYS:HE2	1:A:223:VAL:CG2	2.44	0.47
1:A:40:GLN:HB3	1:A:57:PHE:HB2	1.96	0.47
1:A:237:CYS:O	1:A:238:ASP:HB2	2.14	0.47
1:A:234:PRO:O	1:A:235:ASP:HB2	2.13	0.47
1:A:152:ILE:N	1:A:152:ILE:HD12	2.30	0.47
1:A:432:VAL:HG12	1:A:432:VAL:OXT	2.14	0.47
1:A:366:LEU:C	1:A:366:LEU:HD12	2.35	0.47
1:A:259:ILE:CG2	1:A:260:PRO:HD2	2.45	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:GLU:OE2	1:A:68:ALA:CB	2.64	0.46
1:A:214:LEU:HD21	1:A:222:LEU:HD13	1.98	0.46
1:A:5:GLN:HG3	1:A:7:ALA:H	1.80	0.46
1:A:286:GLU:O	1:A:297:HIS:HE1	1.98	0.46
1:A:158:TYR:HB2	1:A:171:ILE:HD11	1.97	0.46
1:A:152:ILE:HG13	1:A:173:VAL:O	2.16	0.46
1:A:109:THR:CG2	1:A:110:ASP:N	2.78	0.45
1:A:233:GLN:CG	1:A:242:PRO:HD3	2.47	0.45
1:A:30:ILE:N	1:A:30:ILE:HD12	2.30	0.45
1:A:243:ALA:HB3	1:A:269:ARG:HD2	1.99	0.45
1:A:255:ARG:NH2	1:A:258:THR:OG1	2.50	0.45
1:A:18:GLU:HA	1:A:28:TYR:O	2.17	0.44
1:A:265:LYS:NZ	1:A:265:LYS:CB	2.80	0.44
1:A:131:ASN:HB2	5:A:762:HOH:O	2.16	0.44
1:A:6:GLY:CA	1:A:10:PRO:HG3	2.48	0.44
1:A:70:ARG:NH1	5:A:855:HOH:O	2.49	0.44
1:A:305:PRO:O	1:A:308:ARG:HG2	2.18	0.44
1:A:293:SER:H	1:A:297:HIS:CD2	2.16	0.44
1:A:181:ARG:CD	1:A:181:ARG:N	2.81	0.44
1:A:109:THR:CG2	1:A:110:ASP:H	2.22	0.43
1:A:158:TYR:HB2	1:A:171:ILE:HD13	2.00	0.43
1:A:265:LYS:HB3	1:A:265:LYS:HZ3	1.84	0.43
1:A:270:PHE:H	1:A:270:PHE:HD1	1.65	0.43
1:A:69:SER:HB2	1:A:72:LEU:HB3	1.99	0.43
1:A:432:VAL:CG1	1:A:432:VAL:OXT	2.67	0.43
1:A:76:ASN:OD1	2:B:1:NAG:C2	2.67	0.43
1:A:270:PHE:N	1:A:270:PHE:CD1	2.87	0.43
1:A:221:ARG:NH1	1:A:247:THR:HG21	2.33	0.42
1:A:185:PRO:HA	1:A:188:ARG:NE	2.29	0.42
1:A:17:TRP:HH2	1:A:100:LEU:HD13	1.85	0.42
1:A:6:GLY:C	1:A:10:PRO:HG3	2.39	0.42
1:A:293:SER:N	1:A:297:HIS:HD2	2.05	0.42
1:A:297:HIS:O	1:A:298:ASP:HB2	2.20	0.42
1:A:310:GLU:O	1:A:312:SER:N	2.47	0.42
1:A:160:VAL:HG22	1:A:171:ILE:HD12	1.97	0.42
1:A:366:LEU:HD13	1:A:377:LEU:HD11	2.01	0.42
1:A:340:ASN:CB	5:A:790:HOH:O	2.68	0.41
1:A:189:VAL:O	1:A:189:VAL:HG12	2.20	0.41
1:A:216:LEU:HD23	1:A:216:LEU:C	2.41	0.41
1:A:164:ASP:HA	1:A:165:PRO:HD3	1.88	0.41
1:A:10:PRO:HD2	1:A:11:GLU:OE2	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:ASP:HB3	1:A:262:LEU:HD12	2.02	0.41
1:A:343:ASP:N	5:A:925:HOH:O	2.53	0.41
1:A:344:ALA:HB2	1:A:359:VAL:HG22	2.03	0.41
1:A:38:VAL:HB	1:A:41:CYS:SG	2.60	0.41
1:A:92:ILE:HD13	1:A:115:PHE:CG	2.55	0.41
1:A:29:LYS:C	1:A:30:ILE:HD12	2.41	0.41
1:A:102:THR:HG23	5:A:635:HOH:O	2.20	0.41
1:A:182:ALA:O	1:A:188:ARG:HD3	2.21	0.40
1:A:378:ILE:HD13	1:A:394:VAL:HA	2.04	0.40
1:A:328:LEU:N	1:A:328:LEU:HD12	2.37	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	A	426/432 (99%)	392 (92%)	29 (7%)	5 (1%)	13 3

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	340	ASN
1	A	342	LYS
1	A	201	GLY
1	A	126	ASN
1	A	8	GLU

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	368/370 (100%)	352 (96%)	16 (4%)	29	14

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	GLN
1	A	100	LEU
1	A	127	ILE
1	A	136	CYS
1	A	148	LEU
1	A	164	ASP
1	A	168	SER
1	A	169	LEU
1	A	171	ILE
1	A	181	ARG
1	A	255	ARG
1	A	313	ASP
1	A	364	GLN
1	A	366	LEU
1	A	394	VAL
1	A	398	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	24	ASN
1	A	25	ASN
1	A	40	GLN
1	A	58	HIS
1	A	80	ASN
1	A	85	ASN
1	A	113	HIS
1	A	149	ASN
1	A	233	GLN
1	A	297	HIS
1	A	304	GLN
1	A	348	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	364	GLN
1	A	401	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

7 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	NAG	B	1	1,2	14,14,15	1.31	2 (14%)	17,19,21	1.35	1 (5%)
2	NAG	B	2	2	14,14,15	0.52	0	17,19,21	0.91	0
2	BMA	B	3	2	11,11,12	0.59	0	15,15,17	0.41	0
2	MAN	B	4	2	11,11,12	0.50	0	15,15,17	0.49	0
2	MAN	B	5	2	11,11,12	0.43	0	15,15,17	0.60	0
3	NAG	C	1	1,3	14,14,15	1.01	2 (14%)	17,19,21	1.20	2 (11%)
3	NAG	C	2	3	14,14,15	0.56	0	17,19,21	0.71	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	NAG	B	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

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

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NAG	C1-C2	3.23	1.57	1.52
2	B	1	NAG	C4-C3	2.43	1.58	1.52
3	C	1	NAG	C4-C5	2.06	1.57	1.53
3	C	1	NAG	C4-C3	2.03	1.57	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	NAG	O5-C1-C2	-3.31	106.06	111.29
3	C	1	NAG	O5-C1-C2	-2.95	106.63	111.29
3	C	1	NAG	C3-C4-C5	2.29	114.32	110.24

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2
2	B	5	MAN	O5-C5-C6-O6
3	C	1	NAG	C8-C7-N2-C2
3	C	1	NAG	O7-C7-N2-C2
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
3	C	1	NAG	O5-C5-C6-O6
2	B	5	MAN	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

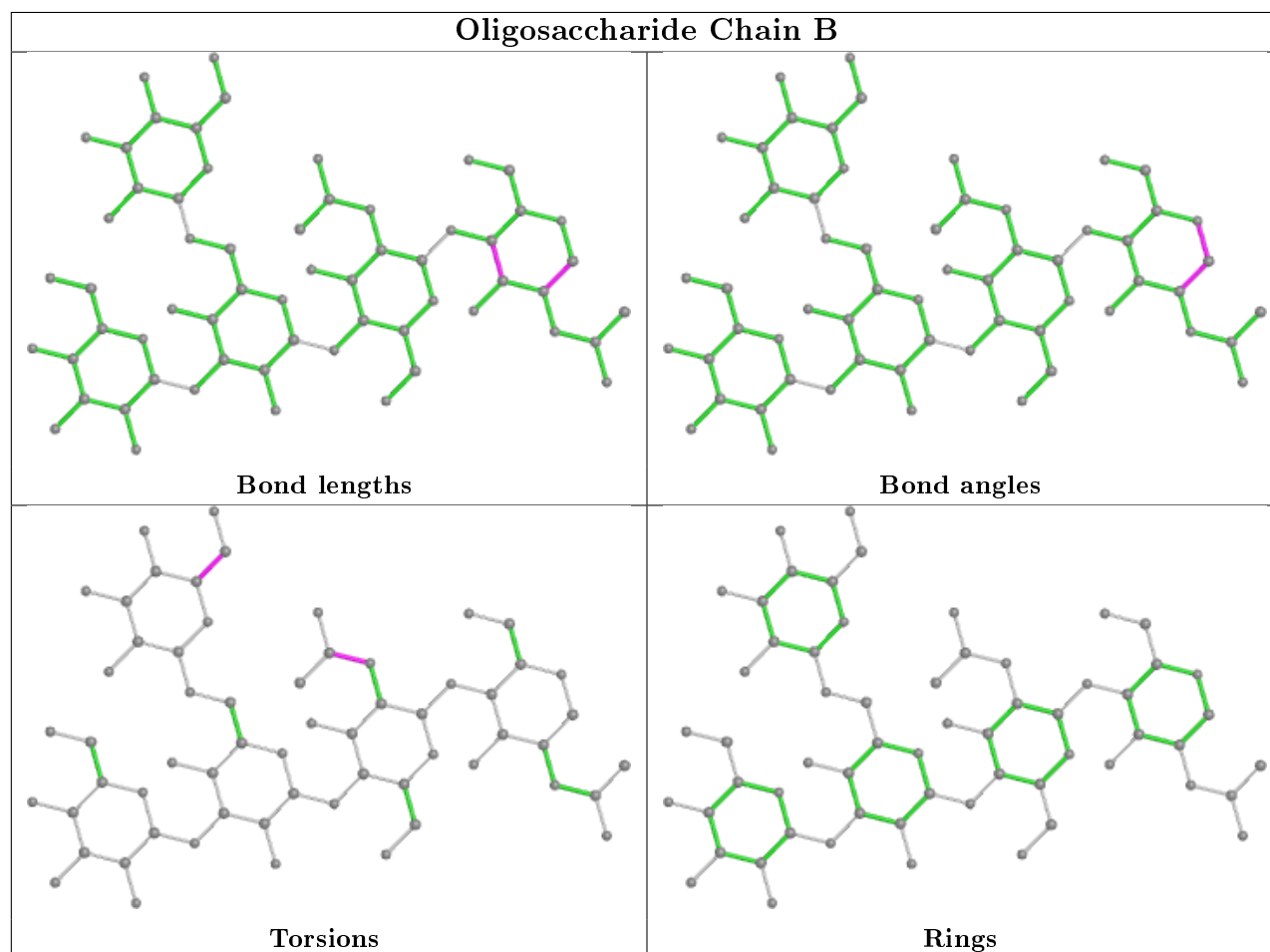
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	NAG	1	0

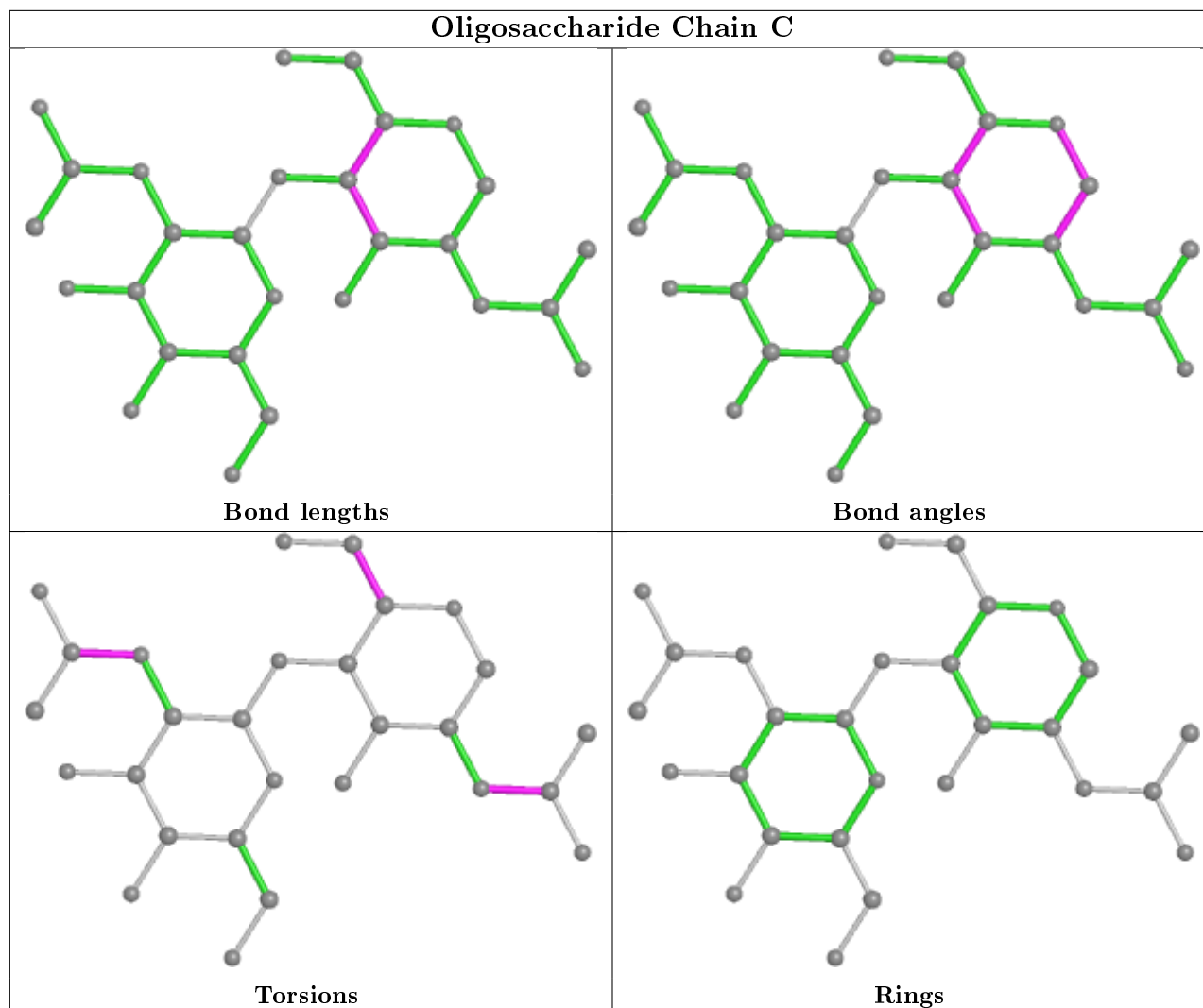
Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	NAG	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](#)

1 ligand is 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	A	4005	-	5,5,5	4.62	5 (100%)	5,5,5	5.74	3 (60%)

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	A	4005	-	-	2/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	4005	GOL	C3-C2	-7.56	1.20	1.51
4	A	4005	GOL	O1-C1	4.65	1.62	1.42
4	A	4005	GOL	O3-C3	3.43	1.56	1.42
4	A	4005	GOL	C1-C2	-2.87	1.39	1.51
4	A	4005	GOL	O2-C2	-2.82	1.35	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	4005	GOL	O3-C3-C2	10.42	160.18	110.20
4	A	4005	GOL	O2-C2-C3	6.75	138.86	109.12
4	A	4005	GOL	O1-C1-C2	3.21	125.59	110.20

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	4005	GOL	O1-C1-C2-C3
4	A	4005	GOL	C1-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	428/432 (99%)	0.81	67 (15%) 2 1	13, 28, 68, 83	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	268	CYS	8.5
1	A	166	ASP	8.1
1	A	341	LYS	7.9
1	A	236	PHE	7.8
1	A	5	GLN	7.4
1	A	315	LEU	6.8
1	A	6	GLY	6.6
1	A	311	ALA	6.6
1	A	340	ASN	6.2
1	A	163	SER	6.1
1	A	237	CYS	6.1
1	A	309	VAL	6.0
1	A	312	SER	5.8
1	A	7	ALA	5.7
1	A	165	PRO	5.2
1	A	238	ASP	5.2
1	A	181	ARG	4.6
1	A	180	LEU	4.6
1	A	240	HIS	4.5
1	A	127	ILE	4.5
1	A	185	PRO	4.2
1	A	266	SER	4.2
1	A	269	ARG	4.1
1	A	310	GLU	4.1
1	A	183	SER	4.0
1	A	202	ASP	4.0
1	A	235	ASP	3.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	182	ALA	3.9
1	A	34	GLY	3.8
1	A	267	ASN	3.7
1	A	229	GLU	3.7
1	A	200	ARG	3.4
1	A	205	PHE	3.3
1	A	164	ASP	3.3
1	A	201	GLY	3.3
1	A	125	LYS	3.2
1	A	232	GLY	3.2
1	A	234	PRO	3.0
1	A	219	ASN	3.0
1	A	233	GLN	3.0
1	A	313	ASP	2.9
1	A	35	ASN	2.8
1	A	40	GLN	2.8
1	A	70	ARG	2.7
1	A	8	GLU	2.7
1	A	186	GLN	2.7
1	A	39	ALA	2.7
1	A	230	GLY	2.7
1	A	188	ARG	2.7
1	A	239	GLY	2.6
1	A	241	SER	2.6
1	A	231	ALA	2.6
1	A	308	ARG	2.5
1	A	314	SER	2.5
1	A	141	ARG	2.5
1	A	406	ASN	2.4
1	A	41	CYS	2.4
1	A	270	PHE	2.3
1	A	196	ALA	2.3
1	A	184	SER	2.3
1	A	207	VAL	2.3
1	A	197	CYS	2.2
1	A	198	LEU	2.2
1	A	110	ASP	2.1
1	A	171	ILE	2.1
1	A	37	GLY	2.1
1	A	211	GLN	2.0

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

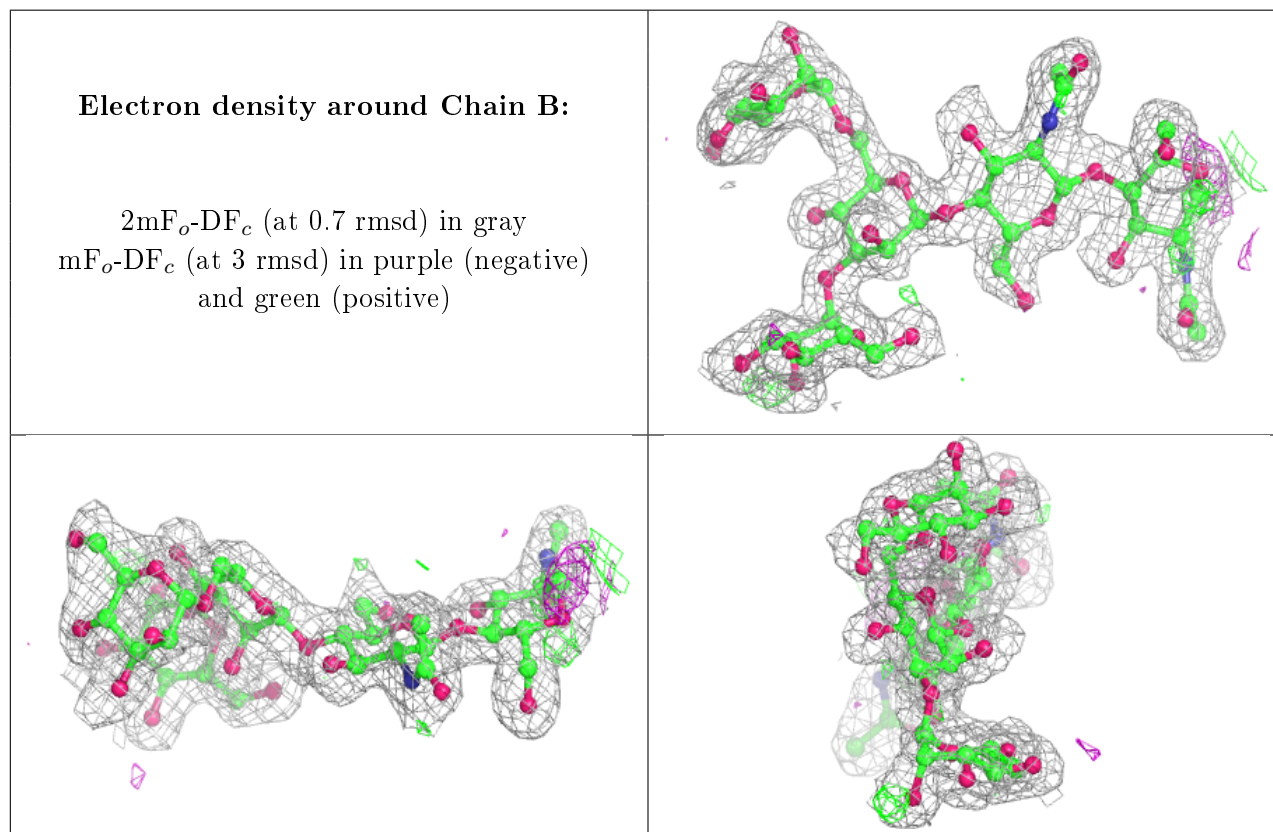
There are no non-standard protein/DNA/RNA residues in this entry.

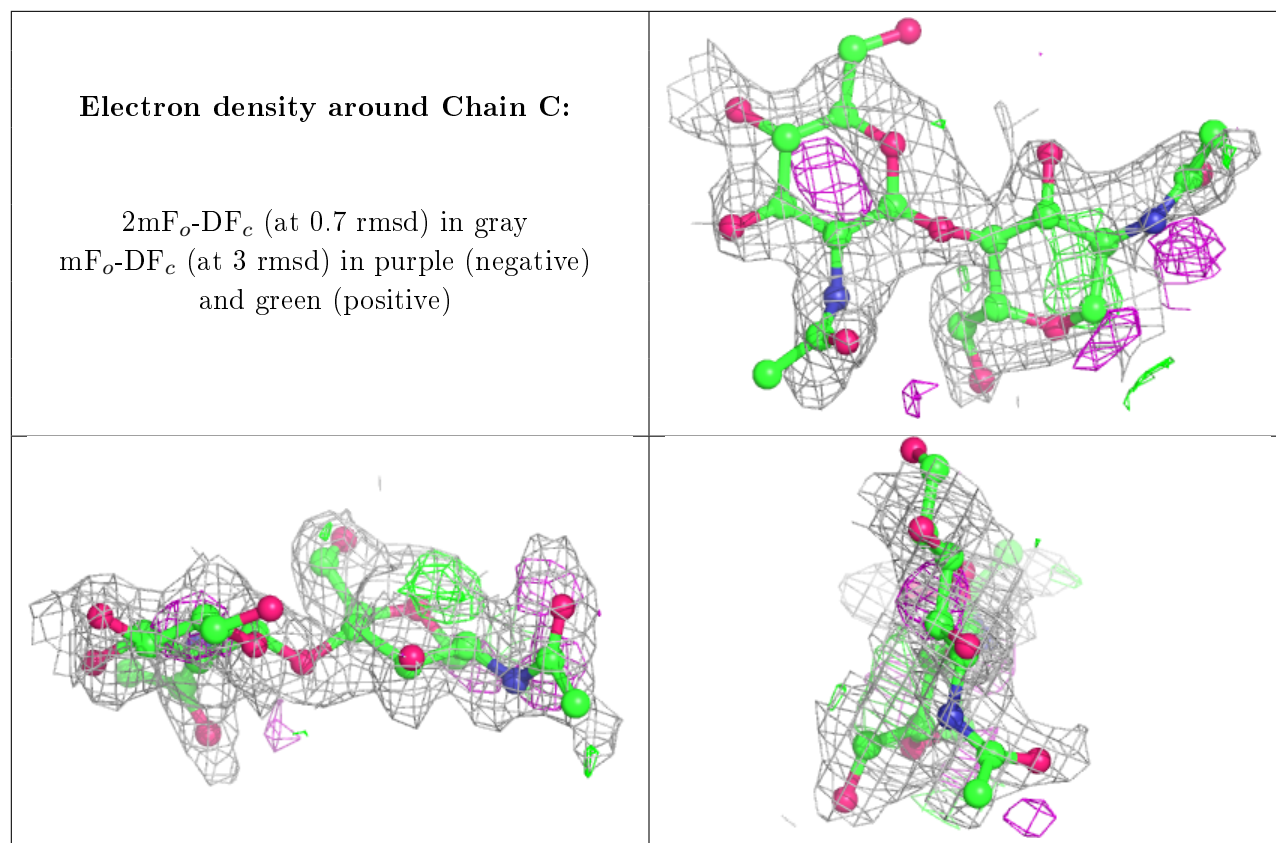
6.3 Carbohydrates [i](#)

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	NAG	C	2	14/15	0.56	0.44	60,62,63,64	0
3	NAG	C	1	14/15	0.73	0.29	47,51,55,57	0
2	MAN	B	5	11/12	0.82	0.23	40,42,45,47	0
2	NAG	B	1	14/15	0.84	0.15	27,30,32,33	0
2	NAG	B	2	14/15	0.86	0.15	30,33,37,39	0
2	MAN	B	4	11/12	0.86	0.13	19,21,25,31	0
2	BMA	B	3	11/12	0.91	0.12	22,27,31,36	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.





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(\AA^2)	Q<0.9
4	GOL	A	4005	6/6	0.84	0.16	36,39,41,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.