



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 30, 2023 – 10:29 AM JST

PDB ID : 5AVR  
Title : Kinetics by X-ray crystallography: Tl<sup>+</sup>-substitution of bound K<sup>+</sup> in the E2.MgF42-.2K<sup>+</sup> crystal after 1.5 min  
Authors : Ogawa, H.; Cornelius, F.; Hirata, A.; Toyoshima, C.  
Deposited on : 2015-07-01  
Resolution : 2.70 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](mailto: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>.

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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)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
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) : 2.36

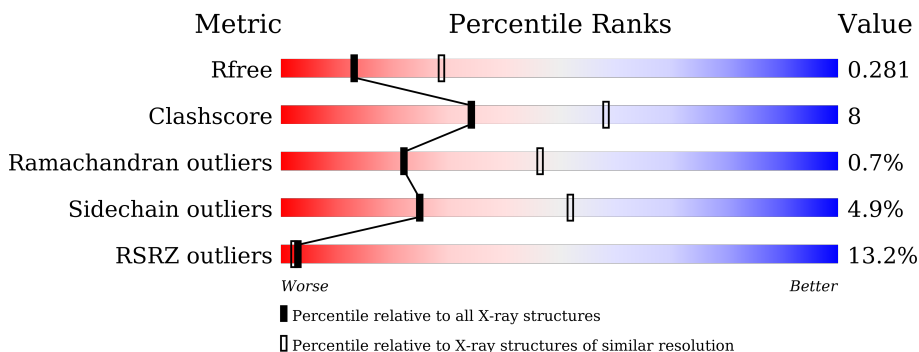
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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  $\geq 3$ , 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	1028	
2	B	305	
3	G	74	
4	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 crite-

ria:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
10	NAG	B	4021	-	-	-	X
4	NAG	C	2	-	-	-	X

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 10237 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 Na, K-ATPase alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	992	7675	4886	1290	1453	46	0	0	0

- Molecule 2 is a protein called Na<sup>+</sup>,K<sup>+</sup>-ATPase beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	268	2174	1409	358	396	11	0	0	0

- Molecule 3 is a protein called Phospholemman-like protein.

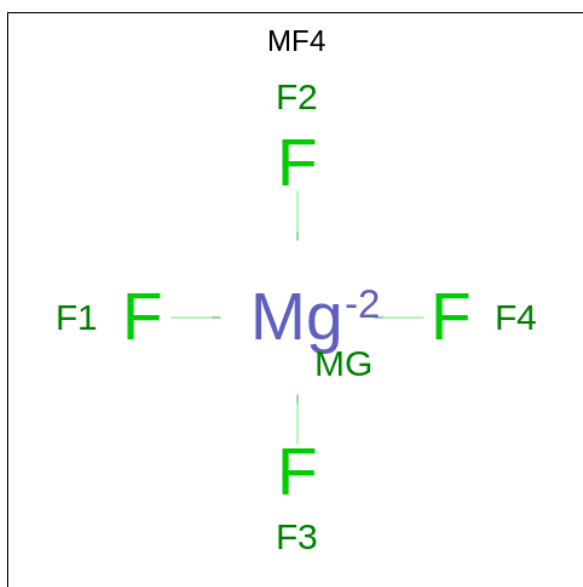
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	G	39	305	200	50	54	1	0	0	0

- Molecule 4 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			
4	C	2	28	16	2	10	0	0	0

- Molecule 5 is TETRAFLUOROMAGNESATE(2-) (three-letter code: MF4) (formula: F<sub>4</sub>Mg).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	F	Mg	0	0
			5	4	1		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		

- Molecule 7 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	3	Total	K	0	3
			3	3		

- Molecule 8 is THALLIUM (I) ION (three-letter code: TL) (formula: Tl).

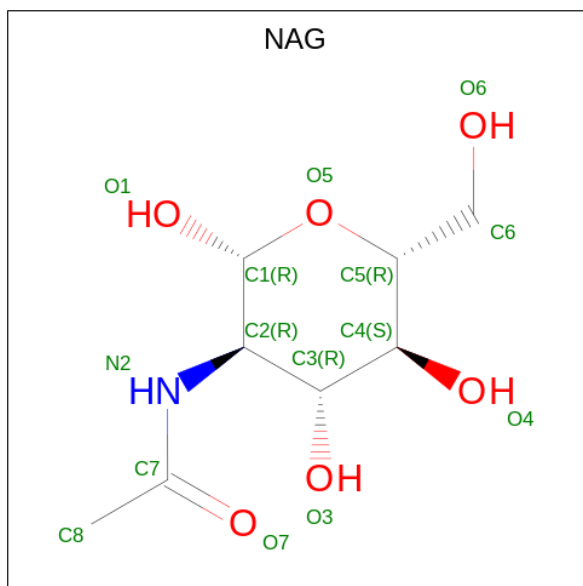
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	3	Total	Tl	0	3
			3	3		

- Molecule 9 is CHOLESTEROL (three-letter code: CLR) (formula: C<sub>27</sub>H<sub>46</sub>O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			28	27	1		

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	B	1	Total	C	N	O	0	0
			14	8	1	5		

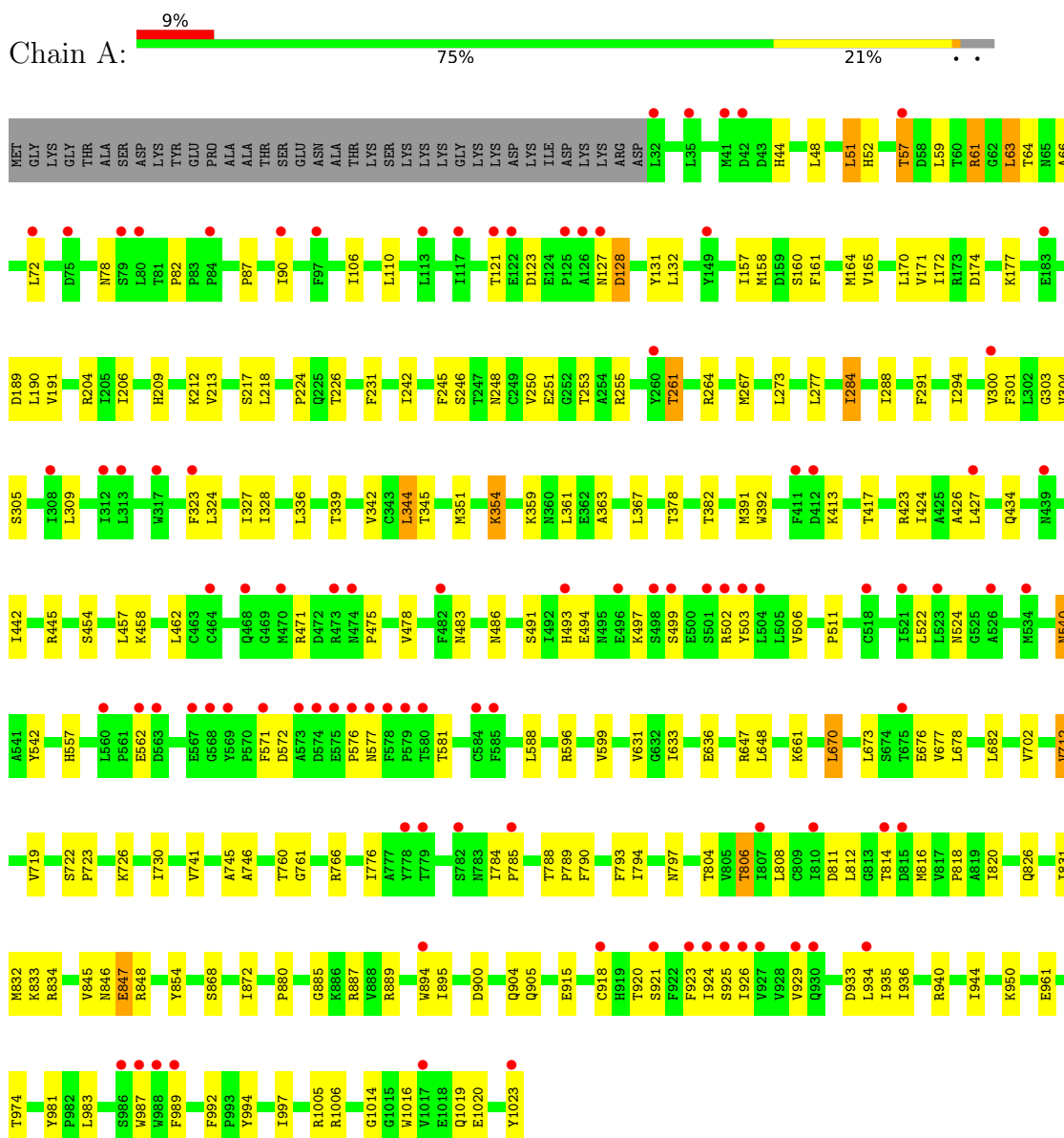
- Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	1	Total O 1 1	0	0

### 3 Residue-property plots

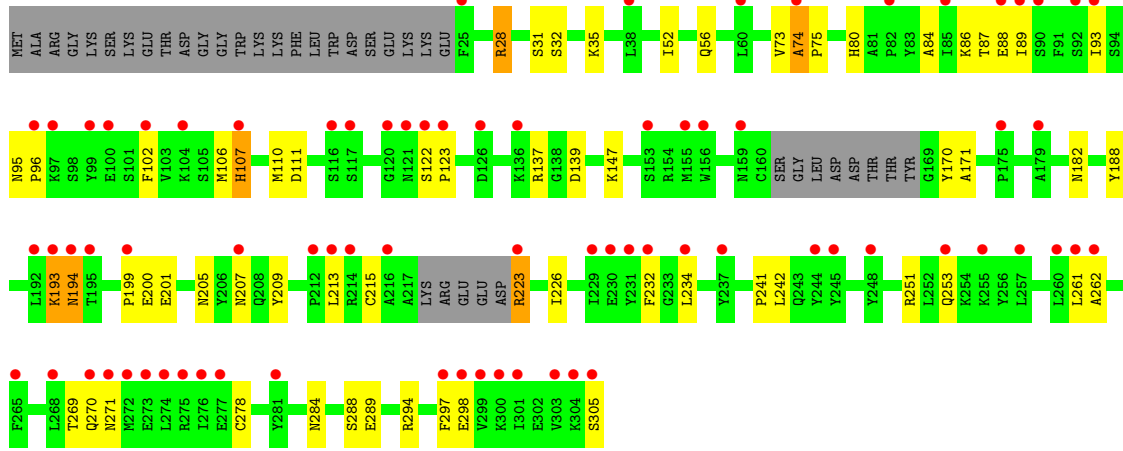
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Na, K-ATPase alpha subunit

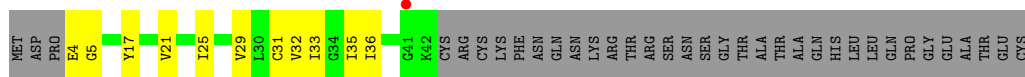
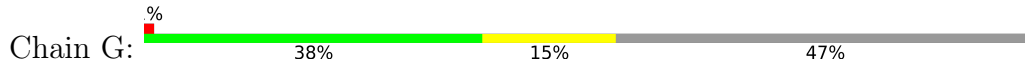


- Molecule 2: Na<sup>+</sup>,K<sup>+</sup>-ATPase beta subunit

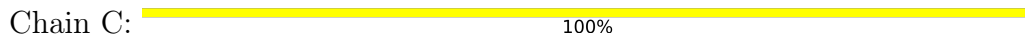




• Molecule 3: Phospholemman-like protein



• Molecule 4: 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	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	223.13Å 50.84Å 163.86Å 90.00° 104.73° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 43.71 – 2.60	Depositor EDS
% Data completeness (in resolution range)	80.7 (15.00-2.70) 94.3 (43.71-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.98 (at 2.61Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.265 , 0.281 0.272 , 0.281	Depositor DCC
$R_{free}$ test set	1588 reflections (2.87%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.1	Xtrriage
Anisotropy	0.309	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 60.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	10237	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	90.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MF4, K, NAG, CLR, TL, MG

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	0.38	0/7825	0.51	0/10616
2	B	0.36	0/2229	0.49	0/3002
3	G	0.36	0/309	0.46	0/419
All	All	0.38	0/10363	0.51	0/14037

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7675	0	7699	124	0
2	B	2174	0	2146	47	0
3	G	305	0	318	7	0
4	C	28	0	25	0	0
5	A	5	0	0	0	0
6	A	1	0	0	0	0
7	A	3	0	0	0	0
8	A	3	0	0	0	0
9	B	28	0	46	1	0
10	B	14	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	A	1	0	0	0	0
All	All	10237	0	10247	172	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 8.

All (172) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:74:ALA:HB3	2:B:75:PRO:HD3	1.47	0.94
1:A:478:VAL:HG21	1:A:571:PHE:HB2	1.64	0.79
1:A:905:GLN:NE2	2:B:182:ASN:HA	1.99	0.78
1:A:497:LYS:HE2	1:A:499:SER:HB2	1.69	0.75
1:A:868:SER:O	1:A:872:ILE:HG12	1.86	0.75
1:A:61:ARG:HH11	1:A:61:ARG:HB3	1.52	0.73
1:A:261:THR:HG22	1:A:264:ARG:NH2	2.02	0.73
1:A:51:LEU:HD13	1:A:204:ARG:HG3	1.69	0.71
2:B:270:GLN:HG2	2:B:271:ASN:HD22	1.58	0.68
1:A:766:ARG:HD2	1:A:832:MET:CE	2.24	0.68
1:A:339:THR:HG23	1:A:820:ILE:HD13	1.77	0.67
1:A:935:ILE:HG23	1:A:944:ILE:HD12	1.77	0.64
2:B:213:LEU:HD11	2:B:278:CYS:HB3	1.78	0.64
1:A:78:ASN:HA	1:A:261:THR:HG23	1.79	0.63
1:A:160:SER:HB3	1:A:741:VAL:HG22	1.80	0.63
1:A:816:MET:O	1:A:820:ILE:HG12	1.97	0.63
1:A:905:GLN:HE21	2:B:182:ASN:HA	1.60	0.63
2:B:74:ALA:CB	2:B:75:PRO:HD3	2.23	0.63
2:B:28:ARG:HB2	2:B:32:SER:HB3	1.81	0.63
1:A:52:HIS:HA	1:A:57:THR:HG23	1.80	0.63
1:A:673:LEU:HD22	1:A:677:VAL:HG11	1.80	0.62
2:B:193:LYS:HA	2:B:207:ASN:HD21	1.65	0.62
1:A:64:THR:HG22	1:A:66:ALA:H	1.65	0.61
1:A:323:PHE:O	1:A:327:ILE:HG12	2.01	0.61
3:G:29:VAL:O	3:G:33:ILE:HG12	2.00	0.60
1:A:363:ALA:HB1	1:A:730:ILE:HD12	1.83	0.60
1:A:483:ASN:HB2	1:A:486:ASN:HB2	1.82	0.60
2:B:31:SER:O	2:B:35:LYS:HG3	2.01	0.60
2:B:270:GLN:HG2	2:B:271:ASN:ND2	2.16	0.60
1:A:344:LEU:HB3	1:A:361:LEU:HG	1.85	0.59
1:A:392:TRP:HB3	1:A:588:LEU:HB2	1.84	0.59
2:B:84:ALA:HB1	2:B:88:GLU:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:ILE:O	1:A:110:LEU:HB2	2.03	0.59
3:G:21:VAL:O	3:G:25:ILE:HG12	2.02	0.59
1:A:212:LYS:HB2	1:A:251:GLU:HG2	1.85	0.58
2:B:106:MET:O	2:B:110:MET:HG2	2.03	0.58
1:A:345:THR:HA	1:A:361:LEU:HD11	1.84	0.57
2:B:75:PRO:HG2	2:B:294:ARG:HH21	1.68	0.57
2:B:74:ALA:HB3	2:B:75:PRO:CD	2.29	0.57
2:B:193:LYS:HA	2:B:207:ASN:ND2	2.20	0.57
1:A:491:SER:HB3	1:A:493:HIS:NE2	2.20	0.57
1:A:818:PRO:HB3	1:A:934:LEU:HD22	1.87	0.56
2:B:52:ILE:O	2:B:56:GLN:HG2	2.05	0.56
2:B:137:ARG:HD2	2:B:147:LYS:HB3	1.88	0.56
1:A:933:ASP:HA	1:A:936:ILE:HG12	1.86	0.56
1:A:172:ILE:HD13	1:A:177:LYS:HB3	1.87	0.55
1:A:190:LEU:HD11	1:A:206:ILE:HD11	1.88	0.55
1:A:994:TYR:O	1:A:997:ILE:HG22	2.06	0.55
1:A:351:MET:HA	1:A:354:LYS:HG2	1.88	0.55
1:A:157:ILE:HD11	1:A:745:ALA:HA	1.89	0.55
2:B:93:ILE:H	2:B:305:SER:HB2	1.72	0.55
1:A:596:ARG:HB2	1:A:599:VAL:HG23	1.89	0.55
1:A:261:THR:HG22	1:A:264:ARG:HH21	1.71	0.55
1:A:924:ILE:HD12	1:A:983:LEU:HD12	1.89	0.54
1:A:64:THR:HG22	1:A:66:ALA:N	2.23	0.54
1:A:994:TYR:HA	1:A:997:ILE:HG22	1.89	0.54
1:A:921:SER:HA	1:A:983:LEU:HD11	1.90	0.54
1:A:424:ILE:HG23	1:A:506:VAL:HB	1.90	0.53
2:B:213:LEU:HD23	2:B:261:LEU:HD13	1.89	0.53
1:A:51:LEU:CD1	1:A:204:ARG:HG3	2.36	0.53
1:A:161:PHE:HA	1:A:164:MET:HE3	1.90	0.53
1:A:324:LEU:O	1:A:328:ILE:HG12	2.09	0.53
1:A:161:PHE:HA	1:A:164:MET:CE	2.39	0.52
1:A:212:LYS:HD3	1:A:224:PRO:HB2	1.90	0.52
1:A:766:ARG:HD2	1:A:832:MET:HE2	1.91	0.52
1:A:808:LEU:O	1:A:812:LEU:HB2	2.10	0.52
2:B:75:PRO:HG2	2:B:294:ARG:NH2	2.25	0.52
3:G:32:VAL:O	3:G:36:ILE:HG12	2.09	0.52
1:A:1016:TRP:HE1	2:B:35:LYS:HE3	1.75	0.52
1:A:82:PRO:HA	1:A:158:MET:HG2	1.92	0.51
1:A:572:ASP:HB3	1:A:577:ASN:HB2	1.92	0.51
3:G:25:ILE:O	3:G:29:VAL:HG23	2.11	0.51
1:A:788:THR:N	1:A:789:PRO:HD2	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:THR:HA	1:A:522:LEU:HD22	1.93	0.51
2:B:288:SER:HB2	2:B:294:ARG:HH11	1.76	0.50
1:A:571:PHE:HA	1:A:577:ASN:HD22	1.76	0.50
1:A:359:LYS:HE2	1:A:746:ALA:O	2.12	0.49
2:B:232:PHE:HB2	2:B:262:ALA:HB3	1.93	0.49
1:A:826:GLN:HE22	1:A:950:LYS:HE3	1.78	0.49
1:A:1005:ARG:NH1	1:A:1006:ARG:HG3	2.28	0.49
2:B:209:TYR:HA	2:B:242:LEU:HD22	1.95	0.48
1:A:502:ARG:CG	1:A:503:TYR:H	2.27	0.48
1:A:442:ILE:O	1:A:445:ARG:HG2	2.14	0.48
1:A:323:PHE:CE1	1:A:793:PHE:HE2	2.32	0.47
1:A:171:VAL:HG12	1:A:191:VAL:HG22	1.97	0.47
1:A:1020:GLU:OE2	2:B:28:ARG:NH2	2.41	0.47
1:A:797:ASN:HD22	1:A:887:ARG:HD3	1.79	0.47
1:A:132:LEU:HD21	1:A:804:THR:HG21	1.97	0.47
1:A:814:THR:HB	1:A:961:GLU:HG3	1.96	0.47
2:B:87:THR:HB	2:B:298:GLU:O	2.14	0.47
3:G:31:CYS:O	3:G:35:ILE:HG12	2.14	0.47
1:A:336:LEU:HD11	1:A:776:ILE:HG12	1.96	0.47
2:B:80:HIS:HB3	2:B:297:PHE:CZ	2.50	0.47
2:B:215:CYS:HA	2:B:278:CYS:HA	1.96	0.46
1:A:127:ASN:HB3	1:A:131:TYR:CD1	2.50	0.46
1:A:924:ILE:HD12	1:A:983:LEU:CD1	2.45	0.46
1:A:63:LEU:HD22	1:A:189:ASP:HB3	1.96	0.46
1:A:631:VAL:HG23	1:A:633:ILE:HG12	1.96	0.46
2:B:226:ILE:HG22	2:B:269:THR:HB	1.96	0.46
1:A:303:GLY:HA2	1:A:327:ILE:HG21	1.97	0.46
2:B:122:SER:HA	2:B:123:PRO:HA	1.75	0.46
1:A:670:LEU:HD23	1:A:678:LEU:HD21	1.96	0.46
1:A:784:ILE:HD11	1:A:854:TYR:CG	2.51	0.46
1:A:889:ARG:HD2	1:A:895:ILE:CD1	2.45	0.46
1:A:209:HIS:HB3	1:A:253:THR:HG22	1.98	0.45
1:A:475:PRO:HD2	1:A:494:GLU:HB2	1.99	0.45
1:A:676:GLU:H	1:A:676:GLU:CD	2.20	0.45
1:A:722:SER:OG	1:A:723:PRO:HD3	2.17	0.45
1:A:847:GLU:CD	1:A:847:GLU:H	2.20	0.45
1:A:631:VAL:CG2	1:A:633:ILE:HG12	2.46	0.45
2:B:84:ALA:HB1	2:B:88:GLU:N	2.32	0.45
1:A:915:GLU:O	1:A:918:CYS:HB2	2.17	0.44
1:A:52:HIS:HE2	1:A:59:LEU:HD12	1.82	0.44
2:B:194:ASN:HD22	2:B:194:ASN:N	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:806:THR:HG22	1:A:923:PHE:HB2	2.00	0.44
2:B:234:LEU:HG	2:B:241:PRO:HG3	1.99	0.44
1:A:246:SER:OG	1:A:267:MET:HG3	2.18	0.44
1:A:354:LYS:HZ2	1:A:354:LYS:HB2	1.81	0.44
2:B:107:HIS:O	2:B:111:ASP:HB2	2.18	0.43
2:B:107:HIS:ND1	2:B:170:TYR:HE1	2.17	0.43
1:A:273:LEU:O	1:A:277:LEU:HG	2.19	0.43
1:A:110:LEU:HD22	1:A:324:LEU:HD12	1.99	0.43
1:A:790:PHE:O	1:A:794:ILE:HG12	2.19	0.43
1:A:87:PRO:HD2	1:A:90:ILE:HD12	1.99	0.43
1:A:511:PRO:HG2	1:A:542:TYR:CE1	2.53	0.43
2:B:147:LYS:HB2	2:B:253:GLN:HG3	1.99	0.43
3:G:4:GLU:CD	3:G:5:GLY:H	2.23	0.43
1:A:64:THR:HA	1:A:174:ASP:OD1	2.19	0.42
2:B:28:ARG:NH1	9:B:3001:CLR:H22	2.34	0.42
1:A:661:LYS:HE2	1:A:661:LYS:HA	2.00	0.42
1:A:300:VAL:O	1:A:304:VAL:HG22	2.19	0.42
1:A:940:ARG:HE	1:A:1023:TYR:HB2	1.84	0.42
2:B:95:ASN:HA	2:B:96:PRO:HD3	1.86	0.42
1:A:291:PHE:HA	1:A:294:ILE:HD12	2.01	0.42
1:A:797:ASN:HB3	1:A:885:GLY:HA2	2.01	0.42
2:B:89:ILE:HG22	2:B:102:PHE:CE2	2.55	0.42
2:B:188:TYR:O	2:B:284:ASN:ND2	2.53	0.42
2:B:223:ARG:HB2	2:B:223:ARG:HH11	1.84	0.42
1:A:170:LEU:HD21	1:A:177:LYS:HD3	2.00	0.42
1:A:291:PHE:HB3	1:A:845:VAL:HB	2.02	0.42
2:B:74:ALA:CB	2:B:75:PRO:CD	2.92	0.42
1:A:48:LEU:HD23	1:A:59:LEU:HD11	2.01	0.42
1:A:367:LEU:HD23	1:A:761:GLY:HA3	2.01	0.42
1:A:784:ILE:N	1:A:785:PRO:HD2	2.35	0.42
2:B:194:ASN:HB3	2:B:205:ASN:OD1	2.20	0.42
1:A:110:LEU:CD2	1:A:324:LEU:HD12	2.50	0.41
1:A:378:THR:HA	1:A:382:THR:OG1	2.20	0.41
2:B:137:ARG:HB3	2:B:147:LYS:HD2	2.01	0.41
2:B:271:ASN:HD21	2:B:305:SER:N	2.18	0.41
1:A:846:ASN:ND2	1:A:848:ARG:HB2	2.35	0.41
1:A:785:PRO:HB2	1:A:926:ILE:CD1	2.51	0.41
1:A:920:THR:HG21	1:A:981:TYR:O	2.20	0.41
1:A:44:HIS:HB3	1:A:242:ILE:HD11	2.03	0.41
1:A:426:ALA:O	1:A:471:ARG:HD2	2.20	0.41
1:A:502:ARG:HE	1:A:562:GLU:HG2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:17:TYR:O	3:G:21:VAL:HG23	2.21	0.41
1:A:342:VAL:HB	1:A:820:ILE:HD12	2.03	0.41
1:A:502:ARG:HG3	1:A:562:GLU:HG2	2.02	0.41
1:A:540:ASN:HD22	1:A:540:ASN:N	2.18	0.41
1:A:647:ARG:HH21	1:A:648:LEU:HD11	1.86	0.41
1:A:284:ILE:O	1:A:288:ILE:HG12	2.21	0.41
1:A:423:ARG:O	1:A:427:LEU:HB2	2.21	0.41
1:A:458:LYS:O	1:A:462:LEU:HB2	2.21	0.41
1:A:1020:GLU:OE1	2:B:28:ARG:NH2	2.54	0.41
1:A:301:PHE:O	1:A:305:SER:HB2	2.20	0.41
1:A:702:VAL:HG13	1:A:712:VAL:HG21	2.03	0.41
1:A:894:TRP:CH2	2:B:86:LYS:HG2	2.56	0.41
1:A:831:ILE:O	1:A:834:ARG:HG2	2.22	0.40
1:A:900:ASP:OD1	1:A:904:GLN:HB2	2.21	0.40
1:A:989:PHE:HA	1:A:992:PHE:CD2	2.56	0.40
1:A:354:LYS:HE2	1:A:760:THR:HB	2.02	0.40
1:A:925:SER:O	1:A:929:VAL:HG22	2.22	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	990/1028 (96%)	942 (95%)	43 (4%)	5 (0%)	29 54
2	B	262/305 (86%)	223 (85%)	35 (13%)	4 (2%)	10 26
3	G	37/74 (50%)	33 (89%)	4 (11%)	0	100 100
All	All	1289/1407 (92%)	1198 (93%)	82 (6%)	9 (1%)	22 46

All (9) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	121	THR
1	A	128	ASP
1	A	576	PRO
2	B	74	ALA
2	B	171	ALA
2	B	201	GLU
1	A	123	ASP
1	A	1014	GLY
2	B	199	PRO

### 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	840/869 (97%)	796 (95%)	44 (5%)	23	49
2	B	234/266 (88%)	224 (96%)	10 (4%)	29	57
3	G	32/62 (52%)	32 (100%)	0	100	100
All	All	1106/1197 (92%)	1052 (95%)	54 (5%)	25	52

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LEU
1	A	57	THR
1	A	61	ARG
1	A	63	LEU
1	A	72	LEU
1	A	128	ASP
1	A	165	VAL
1	A	213	VAL
1	A	217	SER
1	A	218	LEU
1	A	226	THR
1	A	231	PHE
1	A	245	PHE
1	A	248	ASN

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Mol	Chain	Res	Type
1	A	250	VAL
1	A	255	ARG
1	A	261	THR
1	A	284	ILE
1	A	309	LEU
1	A	344	LEU
1	A	354	LYS
1	A	391	MET
1	A	413	LYS
1	A	434	GLN
1	A	454	SER
1	A	457	LEU
1	A	524	ASN
1	A	540	ASN
1	A	557	HIS
1	A	581	THR
1	A	636	GLU
1	A	670	LEU
1	A	682	LEU
1	A	712	VAL
1	A	719	VAL
1	A	726	LYS
1	A	806	THR
1	A	811	ASP
1	A	833	LYS
1	A	847	GLU
1	A	880	PRO
1	A	974	THR
1	A	987	TRP
1	A	1019	GLN
2	B	28	ARG
2	B	73	VAL
2	B	107	HIS
2	B	139	ASP
2	B	193	LYS
2	B	194	ASN
2	B	200	GLU
2	B	223	ARG
2	B	251	ARG
2	B	289	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	118	GLN
1	A	129	ASN
1	A	163	ASN
1	A	225	GLN
1	A	290	HIS
1	A	434	GLN
1	A	524	ASN
1	A	540	ASN
1	A	557	HIS
1	A	577	ASN
1	A	754	ASN
1	A	797	ASN
1	A	826	GLN
1	A	905	GLN
1	A	1019	GLN
2	B	80	HIS
2	B	194	ASN
2	B	207	ASN
2	B	264	GLN
2	B	271	ASN
2	B	284	ASN

### 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](#)

2 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	C	1	2,4	14,14,15	0.49	0	17,19,21	0.91	1 (5%)
4	NAG	C	2	4	14,14,15	0.67	0	17,19,21	1.41	1 (5%)

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	C	1	2,4	-	1/6/23/26	0/1/1/1
4	NAG	C	2	4	-	3/6/23/26	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(°)
4	C	2	NAG	C2-N2-C7	3.98	128.57	122.90
4	C	1	NAG	C1-O5-C5	2.63	115.75	112.19

There are no chirality outliers.

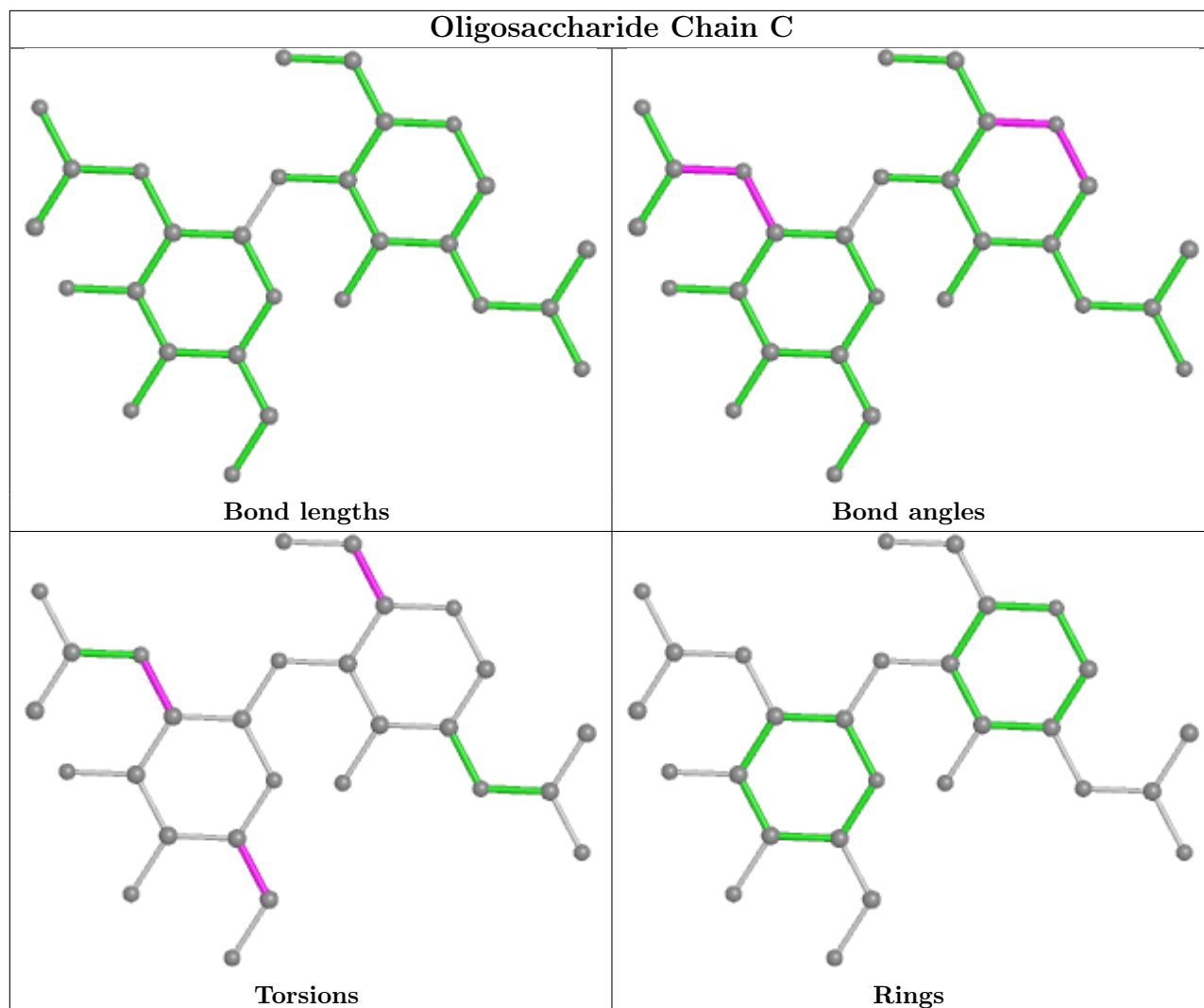
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	2	NAG	C4-C5-C6-O6
4	C	2	NAG	O5-C5-C6-O6
4	C	1	NAG	O5-C5-C6-O6
4	C	2	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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 10 ligands modelled in this entry, 7 are monoatomic - leaving 3 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	$\# Z  > 2$
9	CLR	B	3001	-	31,31,31	0.46	0	48,48,48	1.10	5 (10%)
10	NAG	B	4021	2	14,14,15	0.60	0	17,19,21	1.25	2 (11%)
5	MF4	A	2001	1	0,4,4	-	-	-		

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
9	CLR	B	3001	-	-	2/10/68/68	0/4/4/4
10	NAG	B	4021	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	3001	CLR	C15-C14-C13	2.94	107.38	103.84
10	B	4021	NAG	C1-O5-C5	2.66	115.80	112.19
9	B	3001	CLR	C1-C2-C3	2.58	113.78	110.47
9	B	3001	CLR	C4-C5-C6	-2.49	117.01	120.61
9	B	3001	CLR	C4-C5-C10	2.41	119.62	116.42
10	B	4021	NAG	C4-C3-C2	2.26	114.33	111.02
9	B	3001	CLR	C12-C11-C9	2.07	116.70	113.11

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	B	3001	CLR	C23-C24-C25-C26
9	B	3001	CLR	C23-C24-C25-C27

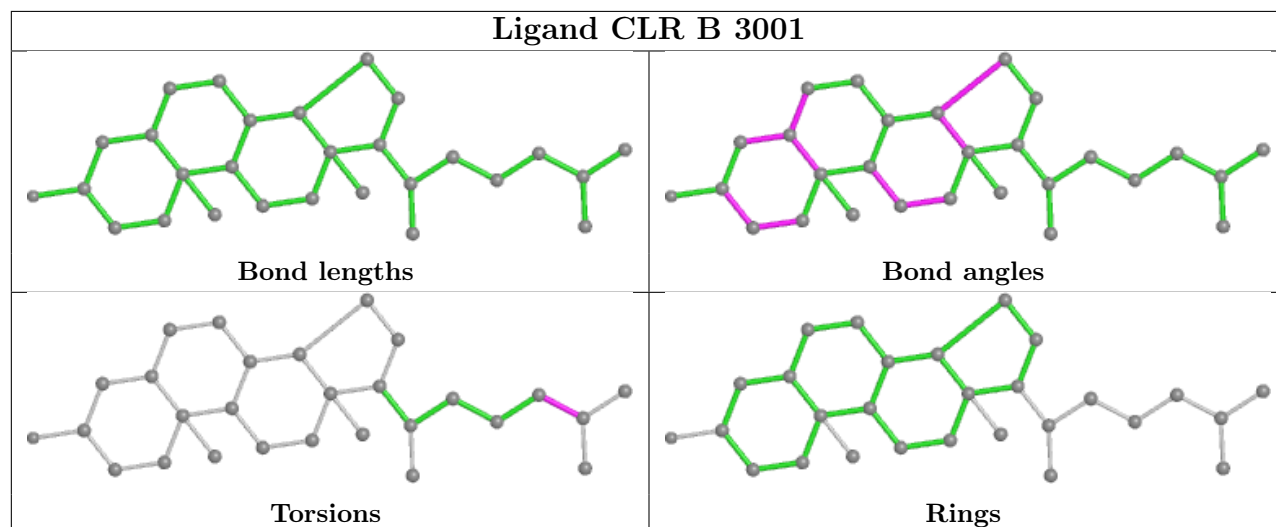
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	3001	CLR	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	992/1028 (96%)	0.74	94 (9%) 8 6	54, 76, 117, 142	0
2	B	268/305 (87%)	1.40	77 (28%) 0 0	75, 126, 150, 160	0
3	G	39/74 (52%)	0.43	1 (2%) 56 57	71, 80, 123, 127	0
All	All	1299/1407 (92%)	0.86	172 (13%) 3 2	54, 81, 138, 160	0

All (172) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	93	ILE	9.3
1	A	573	ALA	8.1
2	B	214	ARG	7.3
1	A	562	GLU	7.1
1	A	317	TRP	6.0
1	A	498	SER	6.0
1	A	563	ASP	5.7
2	B	231	TYR	5.7
2	B	216	ALA	5.6
2	B	298	GLU	5.4
1	A	534	MET	5.2
1	A	72	LEU	5.1
1	A	504	LEU	4.9
2	B	121	ASN	4.8
2	B	230	GLU	4.7
2	B	304	LYS	4.6
2	B	234	LEU	4.5
1	A	578	PHE	4.4
2	B	195	THR	4.4
2	B	268	LEU	4.3
2	B	229	ILE	4.2
2	B	274	LEU	4.2
1	A	894	TRP	4.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	585	PHE	4.1
2	B	192	LEU	4.1
2	B	120	GLY	4.0
2	B	89	ILE	4.0
1	A	79	SER	4.0
2	B	232	PHE	4.0
1	A	568	GLY	3.9
1	A	986	SER	3.8
2	B	199	PRO	3.8
2	B	85	ILE	3.8
2	B	25	PHE	3.8
1	A	496	GLU	3.8
2	B	273	GLU	3.7
1	A	503	TYR	3.6
2	B	276	ILE	3.6
2	B	194	ASN	3.6
1	A	412	ASP	3.5
1	A	574	ASP	3.5
1	A	502	ARG	3.5
1	A	439	ASN	3.5
1	A	32	LEU	3.5
1	A	84	PRO	3.5
2	B	257	LEU	3.4
2	B	99	TYR	3.4
1	A	579	PRO	3.4
1	A	42	ASP	3.4
2	B	212	PRO	3.3
1	A	127	ASN	3.3
1	A	464	CYS	3.3
1	A	260	TYR	3.3
1	A	121	THR	3.2
2	B	271	ASN	3.2
2	B	156	TRP	3.2
1	A	924	ILE	3.1
2	B	96	PRO	3.1
2	B	272	MET	3.1
1	A	927	VAL	3.1
2	B	100	GLU	3.0
1	A	675	THR	3.0
2	B	90	SER	3.0
1	A	779	THR	3.0
1	A	1017	VAL	3.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	B	122	SER	3.0
2	B	303	VAL	3.0
1	A	313	LEU	3.0
2	B	305	SER	3.0
2	B	97	LYS	3.0
1	A	41	MET	3.0
2	B	155	MET	2.9
1	A	97	PHE	2.9
2	B	92	SER	2.9
1	A	117	ILE	2.9
1	A	499	SER	2.9
2	B	102	PHE	2.9
1	A	427	LEU	2.9
1	A	300	VAL	2.9
1	A	815	ASP	2.9
2	B	299	VAL	2.8
2	B	117	SER	2.8
2	B	270	GLN	2.8
1	A	149	TYR	2.8
2	B	60	LEU	2.8
2	B	207	ASN	2.7
1	A	567	GLU	2.7
1	A	183	GLU	2.7
2	B	88	GLU	2.7
1	A	926	ILE	2.7
2	B	255	LYS	2.7
1	A	125	PRO	2.7
1	A	989	PHE	2.7
2	B	123	PRO	2.6
1	A	521	ILE	2.6
1	A	571	PHE	2.6
1	A	411	PHE	2.6
1	A	501	SER	2.6
1	A	575	GLU	2.6
1	A	126	ALA	2.6
2	B	300	LYS	2.6
1	A	308	ILE	2.6
2	B	74	ALA	2.6
1	A	810	ILE	2.5
1	A	987	TRP	2.5
2	B	82	PRO	2.5
2	B	104	LYS	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	B	175	PRO	2.5
2	B	301	ILE	2.5
1	A	122	GLU	2.5
1	A	1023	TYR	2.5
1	A	90	ILE	2.5
2	B	244	TYR	2.5
3	G	41	GLY	2.5
2	B	253	GLN	2.5
1	A	930	GLN	2.4
1	A	80	LEU	2.4
1	A	782	SER	2.4
2	B	213	LEU	2.4
2	B	223	ARG	2.4
2	B	126	ASP	2.4
2	B	245	TYR	2.4
1	A	474	ASN	2.4
1	A	934	LEU	2.4
1	A	468	GLN	2.3
2	B	179	ALA	2.3
1	A	577	ASN	2.3
1	A	57	THR	2.3
1	A	925	SER	2.3
1	A	35	LEU	2.3
2	B	281	TYR	2.3
1	A	75	ASP	2.3
1	A	470	MET	2.3
1	A	929	VAL	2.3
1	A	518	CYS	2.3
2	B	297	PHE	2.2
2	B	277	GLU	2.2
2	B	237	TYR	2.2
1	A	523	LEU	2.2
1	A	482	PHE	2.2
2	B	248	TYR	2.2
1	A	785	PRO	2.2
1	A	312	ILE	2.2
2	B	262	ALA	2.2
1	A	814	THR	2.2
1	A	323	PHE	2.2
2	B	260	LEU	2.1
1	A	923	PHE	2.1
1	A	576	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	275	ARG	2.1
1	A	526	ALA	2.1
2	B	159	ASN	2.1
1	A	584	CYS	2.1
1	A	918	CYS	2.1
1	A	473	ARG	2.1
2	B	107	HIS	2.1
2	B	193	LYS	2.1
2	B	38	LEU	2.1
1	A	580	THR	2.1
1	A	113	LEU	2.1
1	A	493	HIS	2.1
1	A	569	TYR	2.1
1	A	807	ILE	2.0
2	B	116	SER	2.0
2	B	136	LYS	2.0
1	A	778	TYR	2.0
2	B	153	SER	2.0
1	A	988	TRP	2.0
1	A	560	LEU	2.0
2	B	261	LEU	2.0
1	A	921	SER	2.0
2	B	265	PHE	2.0

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

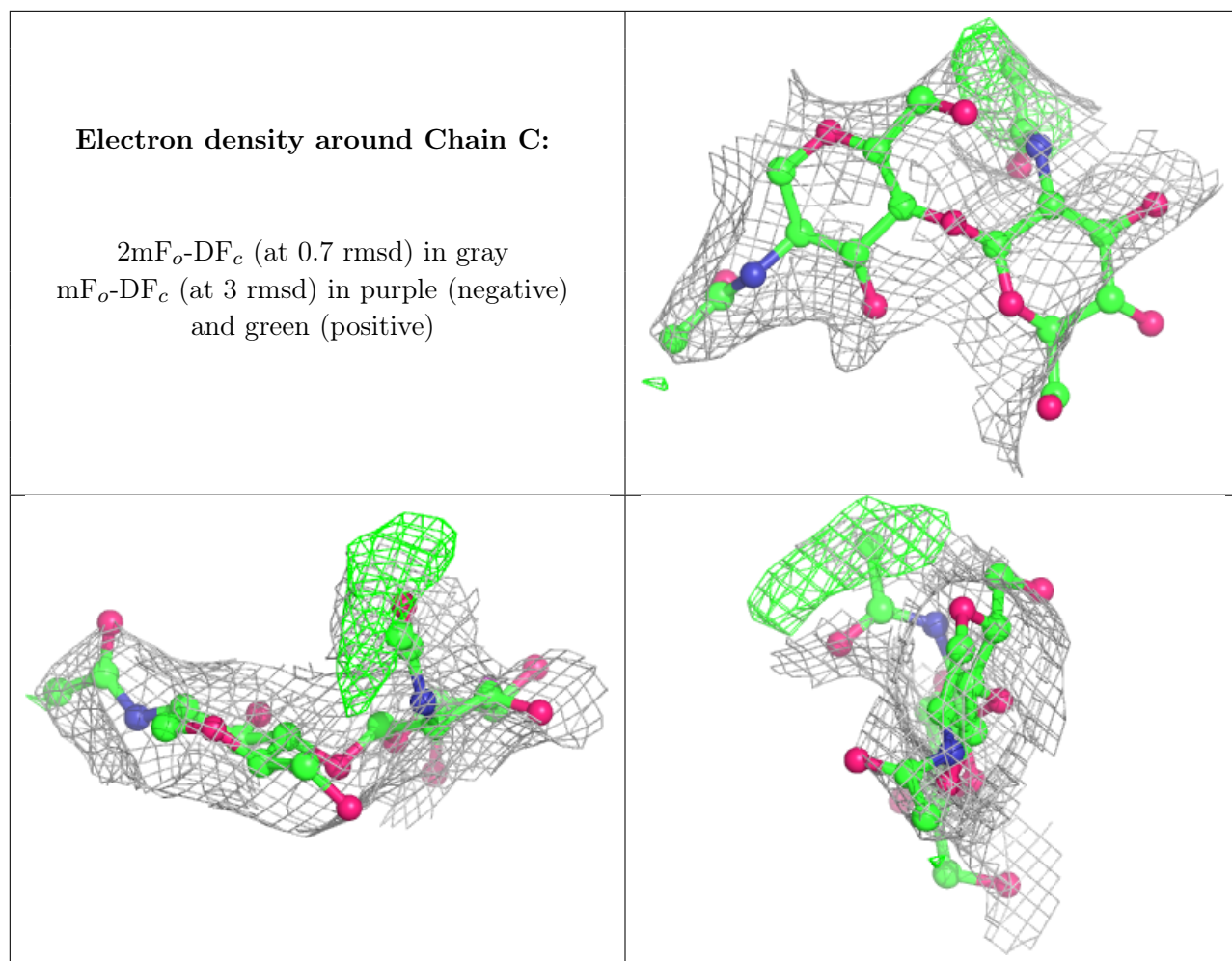
There are no non-standard protein/DNA/RNA residues in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	NAG	C	2	14/15	0.27	0.41	139,139,140,140	0
4	NAG	C	1	14/15	0.86	0.24	132,135,136,137	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.

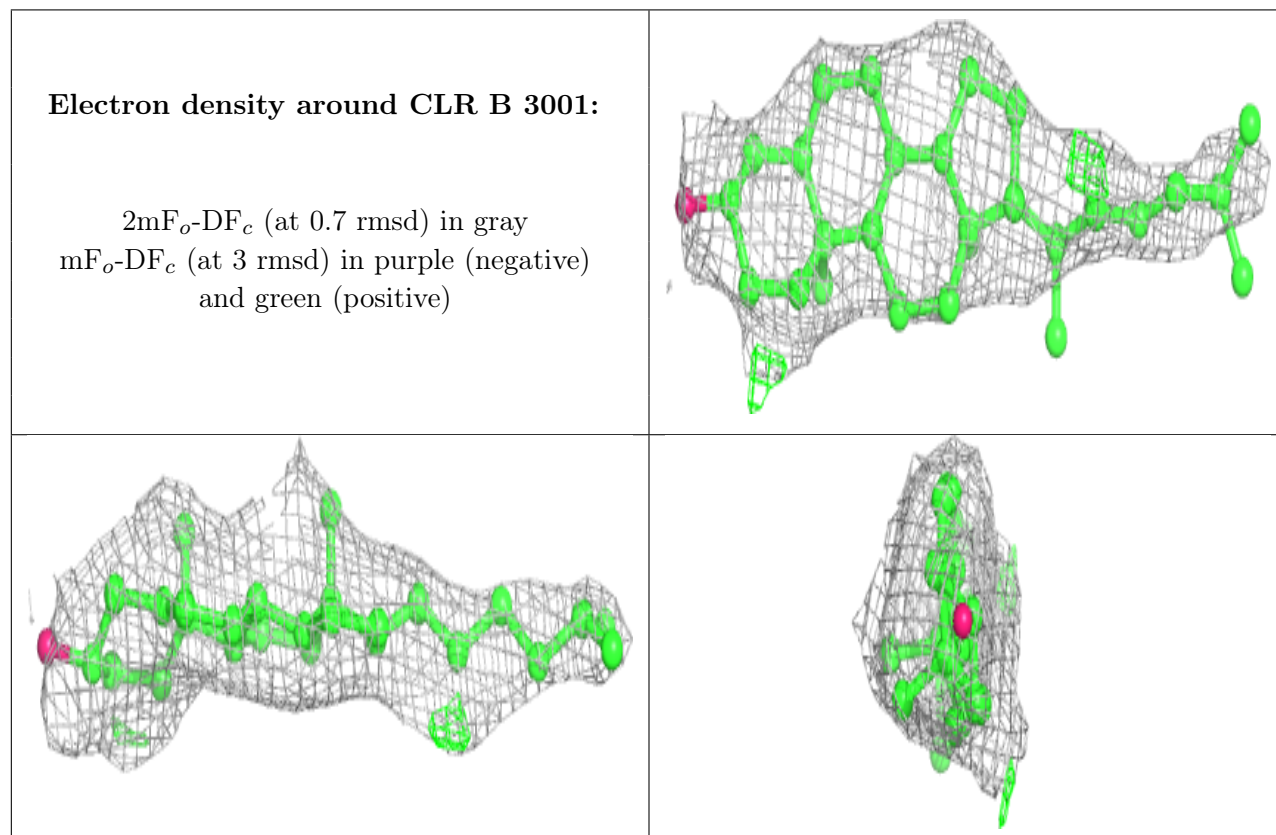


## 6.4 Ligands [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
10	NAG	B	4021	14/15	0.72	0.45	138,139,139,139	0
9	CLR	B	3001	28/28	0.83	0.27	118,118,118,119	0
6	MG	A	2002	1/1	0.83	0.33	56,56,56,56	0
5	MF4	A	2001	5/5	0.93	0.29	59,61,62,63	0
7	K	A	2007[A]	1/1	0.99	0.13	72,72,72,72	1
8	TL	A	2004[B]	1/1	0.99	0.22	77,77,77,77	1
8	TL	A	2006[B]	1/1	0.99	0.17	77,77,77,77	0
8	TL	A	2008[B]	1/1	0.99	0.13	72,72,72,72	1
7	K	A	2003[A]	1/1	0.99	0.22	77,77,77,77	1
7	K	A	2005[A]	1/1	0.99	0.17	77,77,77,77	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.