



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 30, 2023 – 10:53 AM JST

PDB ID : 5AW2
Title : Kinetics by X-ray crystallography: Tl⁺-substitution of bound K⁺ in the E2.MgF42-.2K⁺ crystal after 85 min
Authors : Ogawa, H.; Cornelius, F.; Hirata, A.; Toyoshima, C.
Deposited on : 2015-07-01
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (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

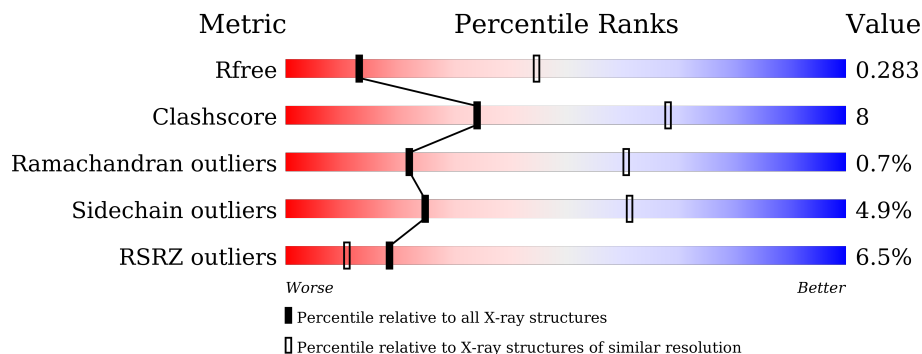
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
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 10235 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

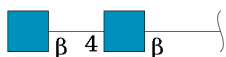
- Molecule 2 is a protein called Na⁺,K⁺-ATPase beta subunit.

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.

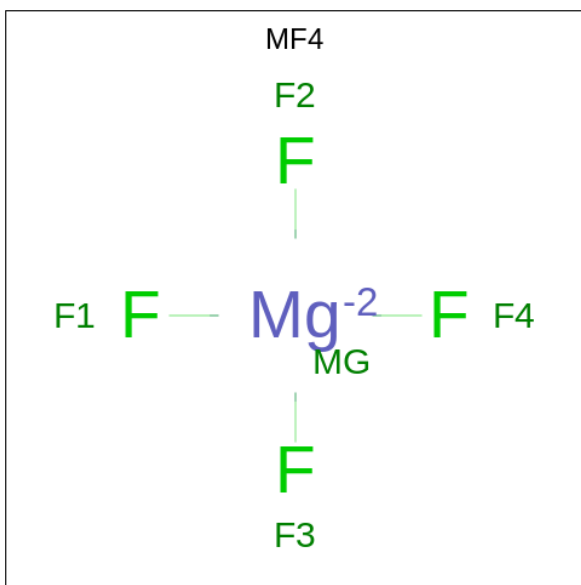
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	G	39	305	200	50	54	1	0	0	0

- 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: F₄Mg).



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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	3	Total	Tl	0	1
			3	3		

- Molecule 8 is POTASSIUM ION (three-letter code: K) (formula: K).

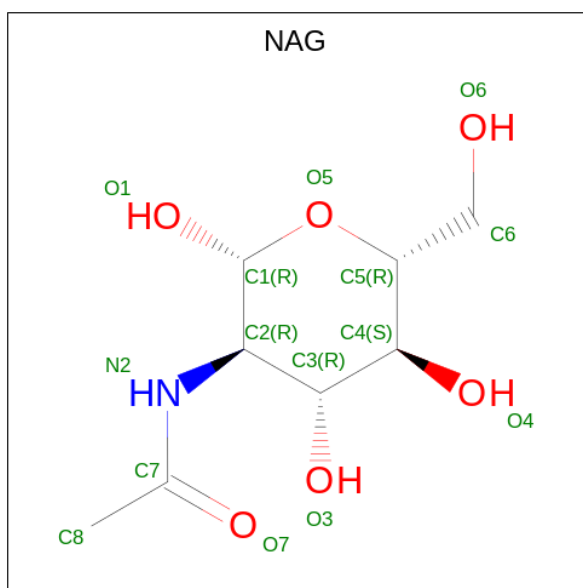
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	K	0	1
			1	1		

- Molecule 9 is CHOLESTEROL (three-letter code: CLR) (formula: C₂₇H₄₆O).



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		

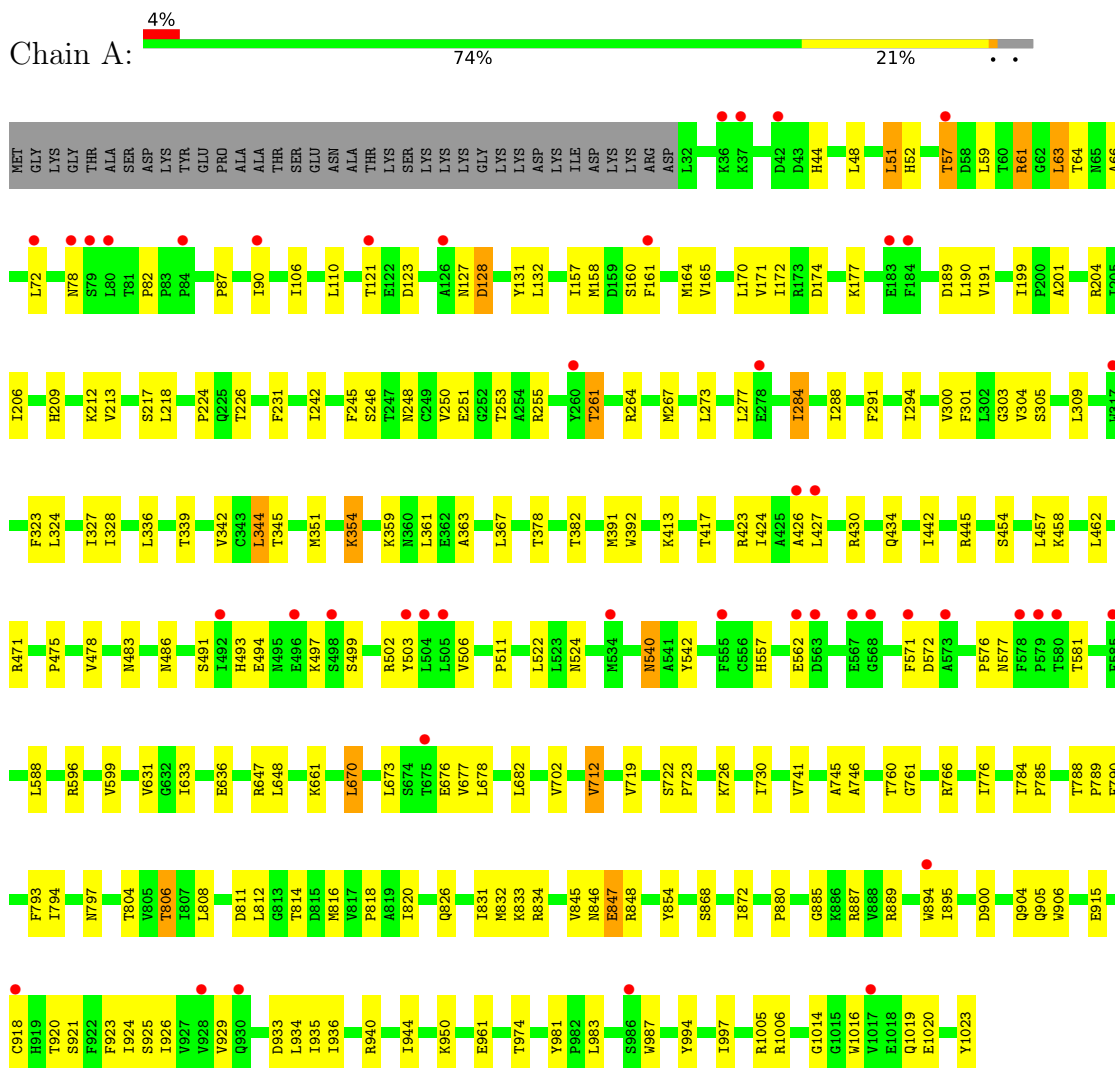
- Molecule 11 is water.

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

3 Residue-property plots

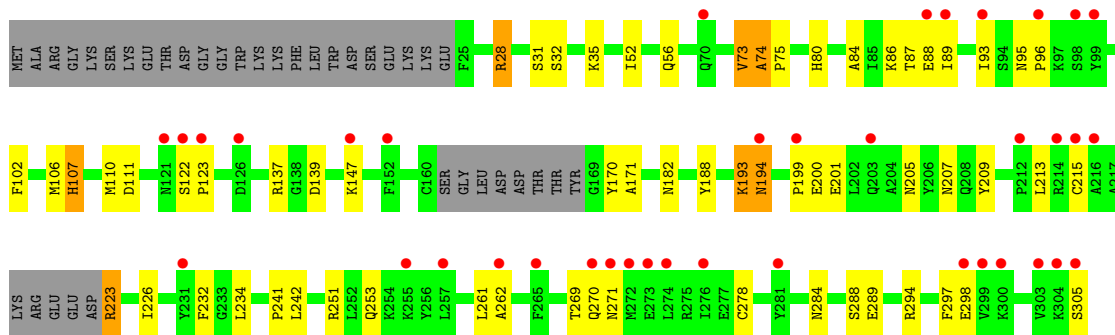
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

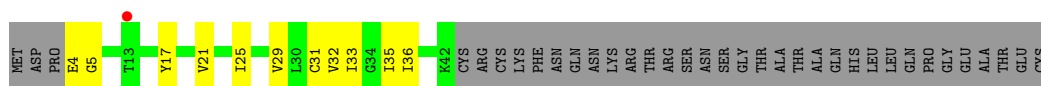
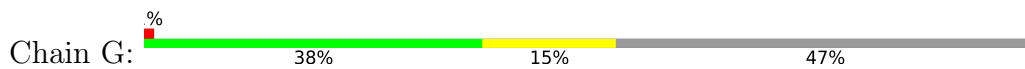


- Molecule 2: Na⁺,K⁺-ATPase beta subunit





• 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, α , β , γ	221.29Å 50.62Å 163.47Å 90.00° 104.26° 90.00°	Depositor
Resolution (Å)	14.98 – 3.20 43.34 – 3.20	Depositor EDS
% Data completeness (in resolution range)	86.6 (14.98-3.20) 93.5 (43.34-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.16 (at 3.19Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.284 , 0.280 0.279 , 0.283	Depositor DCC
R_{free} test set	844 reflections (2.86%)	wwPDB-VP
Wilson B-factor (Å ²)	89.6	Xtrriage
Anisotropy	0.280	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	10235	wwPDB-VP
Average B, all atoms (Å ²)	122.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% 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: TL, NAG, MG, K, CLR, MF4

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 [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	7675	0	7699	125	1
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	1	0	0	0	0
9	B	28	0	46	0	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	10235	0	10247	172	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 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:905:GLN:NE2	2:B:182:ASN:HA	1.94	0.82
1:A:478:VAL:HG21	1:A:571:PHE:HB2	1.65	0.79
1:A:497:LYS:HE2	1:A:499:SER:HB2	1.68	0.76
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
1:A:905:GLN:HE21	2:B:182:ASN:HA	1.54	0.69
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	0.65
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	0.64
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
2:B:74:ALA:CB	2:B:75:PRO:HD3	2.23	0.63
1:A:52:HIS:HA	1:A:57:THR:HG23	1.80	0.63
2:B:28:ARG:HB2	2:B:32:SER:HB3	1.81	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:323:PHE:O	1:A:327:ILE:HG12	2.00	0.61
1:A:64:THR:HG22	1:A:66:ALA:H	1.65	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	1.84	0.60
2:B:84:ALA:HB1	2:B:88:GLU:H	1.67	0.59
1:A:392:TRP:HB3	1:A:588:LEU:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:21:VAL:O	3:G:25:ILE:HG12	2.02	0.59
1:A:106:ILE:O	1:A:110:LEU:HB2	2.03	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
1:A:491:SER:HB3	1:A:493:HIS:NE2	2.20	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: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	1.87	0.56
1:A:172:ILE:HD13	1:A:177:LYS:HB3	1.87	0.56
1:A:190:LEU:HD11	1:A:206:ILE:HD11	1.88	0.56
1:A:933:ASP:HA	1:A:936:ILE:HG12	1.86	0.55
1:A:157:ILE:HD11	1:A:745:ALA:HA	1.88	0.55
2:B:93:ILE:H	2:B:305:SER:HB2	1.72	0.55
1:A:351:MET:HA	1:A:354:LYS:HG2	1.88	0.55
1:A:994:TYR:O	1:A:997:ILE:HG22	2.06	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	0.54
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:51:LEU:CD1	1:A:204:ARG:HG3	2.36	0.53
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:161:PHE:HA	1:A:164:MET:HE3	1.90	0.53
1:A:324:LEU:O	1:A:328:ILE:HG12	2.09	0.52
1:A:1020:GLU:OE2	2:B:28:ARG:NH2	2.36	0.52
1:A:161:PHE:HA	1:A:164:MET:CE	2.39	0.52
1:A:808:LEU:O	1:A:812:LEU:HB2	2.10	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
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:82:PRO:HA	1:A:158:MET:HG2	1.93	0.51
1:A:572:ASP:HB3	1:A:577:ASN:HB2	1.92	0.51
1:A:788:THR:N	1:A:789:PRO:HD2	2.26	0.51
3:G:25:ILE:O	3:G:29:VAL:HG23	2.11	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	1.77	0.50
1:A:571:PHE:HA	1:A:577:ASN:HD22	1.76	0.50
2:B:232:PHE:HB2	2:B:262:ALA:HB3	1.93	0.49
1:A:359:LYS:HE2	1:A:746:ALA:O	2.12	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
1:A:1016:TRP:HE1	2:B:35:LYS:HE3	1.78	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:132:LEU:HD21	1:A:804:THR:HG21	1.97	0.47
1:A:171:VAL:HG12	1:A:191:VAL:HG22	1.97	0.47
1:A:797:ASN:HD22	1:A:887:ARG:HD3	1.79	0.47
1:A:814:THR:HB	1:A:961:GLU:HG3	1.96	0.47
3:G:31:CYS:O	3:G:35:ILE:HG12	2.14	0.47
2:B:80:HIS:HB3	2:B:297:PHE:CZ	2.50	0.47
2:B:87:THR:HB	2:B:298:GLU:O	2.14	0.47
2:B:215:CYS:HA	2:B:278:CYS:HA	1.96	0.47
1:A:127:ASN:HB3	1:A:131:TYR:CD1	2.50	0.46
1:A:336:LEU:HD11	1:A:776:ILE:HG12	1.96	0.46
1:A:924:ILE:HD12	1:A:983:LEU:CD1	2.45	0.46
2:B:226:ILE:HG22	2:B:269:THR:HB	1.96	0.46
1:A:631:VAL:HG23	1:A:633:ILE:HG12	1.96	0.46
1:A:63:LEU:HD22	1:A:189:ASP:HB3	1.97	0.46
2:B:122:SER:HA	2:B:123:PRO:HA	1.75	0.46
1:A:303:GLY:HA2	1:A:327:ILE:HG21	1.97	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:209:HIS:HB3	1:A:253:THR:HG22	1.98	0.45
1:A:475:PRO:HD2	1:A:494:GLU:HB2	1.98	0.45
1:A:889:ARG:HD2	1:A:895:ILE:CD1	2.46	0.45
2:B:84:ALA:HB1	2:B:88:GLU:N	2.31	0.45
1:A:722:SER:OG	1:A:723:PRO:HD3	2.17	0.45
1:A:631:VAL:CG2	1:A:633:ILE:HG12	2.46	0.45
1:A:676:GLU:H	1:A:676:GLU:CD	2.21	0.45
1:A:847:GLU:CD	1:A:847:GLU:H	2.20	0.45
1:A:915:GLU:O	1:A:918:CYS:HB2	2.17	0.44
1:A:806:THR:HG22	1:A:923:PHE:HB2	1.99	0.44
1:A:52:HIS:HE2	1:A:59:LEU:HD12	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:194:ASN:HD22	2:B:194:ASN:N	2.15	0.44
1:A:354:LYS:HZ2	1:A:354:LYS:HB2	1.81	0.44
1:A:1020:GLU:OE1	2:B:28:ARG:NH2	2.51	0.44
1:A:246:SER:OG	1:A:267:MET:HG3	2.18	0.44
2:B:234:LEU:HG	2:B:241:PRO:HG3	1.99	0.44
2:B:107:HIS:O	2:B:111:ASP:HB2	2.18	0.43
1:A:273:LEU:O	1:A:277:LEU:HG	2.19	0.43
1:A:894:TRP:CH2	2:B:86:LYS:HG2	2.53	0.43
2:B:107:HIS:ND1	2:B:170:TYR:HE1	2.17	0.43
1:A:790:PHE:O	1:A:794:ILE:HG12	2.19	0.43
1:A:110:LEU:HD22	1:A:324:LEU:HD12	1.99	0.43
1:A:511:PRO:HG2	1:A:542:TYR:CE1	2.53	0.43
1:A:87:PRO:HD2	1:A:90:ILE:HD12	1.99	0.43
3:G:4:GLU:CD	3:G:5:GLY:H	2.23	0.43
2:B:147:LYS:HB2	2:B:253:GLN:HG3	1.99	0.43
1:A:64:THR:HA	1:A:174:ASP:OD1	2.19	0.42
1:A:906:TRP:CZ2	2:B:73:VAL:HG22	2.54	0.42
1:A:940:ARG:HE	1:A:1023:TYR:HB2	1.84	0.42
1:A:291:PHE:HA	1:A:294:ILE:HD12	2.01	0.42
1:A:300:VAL:O	1:A:304:VAL:HG22	2.19	0.42
1:A:797:ASN:HB3	1:A:885:GLY:HA2	2.00	0.42
1:A:661:LYS:HE2	1:A:661:LYS:HA	2.00	0.42
2:B:188:TYR:O	2:B:284:ASN:ND2	2.53	0.42
1:A:170:LEU:HD21	1:A:177:LYS:HD3	2.00	0.42
2:B:95:ASN:HA	2:B:96:PRO:HD3	1.86	0.42
1:A:291:PHE:HB3	1:A:845:VAL:HB	2.02	0.42
2:B:89:ILE:HG22	2:B:102:PHE:CE2	2.55	0.42
2:B:74:ALA:CB	2:B:75:PRO:CD	2.92	0.42
2:B:223:ARG:HB2	2:B:223:ARG:HH11	1.85	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: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:378:THR:HA	1:A:382:THR:OG1	2.20	0.41
1:A:502:ARG:HE	1:A:562:GLU:HG2	1.85	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:110:LEU:CD2	1:A:324:LEU:HD12	2.50	0.41
1:A:785:PRO:HB2	1:A:926:ILE:CD1	2.50	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:846:ASN:ND2	1:A:848:ARG:HB2	2.35	0.41
1:A:426:ALA:O	1:A:471:ARG:HD2	2.20	0.41
3:G:17:TYR:O	3:G:21:VAL:HG23	2.21	0.41
1:A:540:ASN:HD22	1:A:540:ASN:N	2.18	0.41
1:A:301:PHE:O	1:A:305:SER:HB2	2.20	0.41
1:A:342:VAL:HB	1:A:820:ILE:HD12	2.03	0.41
1:A:458:LYS:O	1:A:462:LEU:HB2	2.21	0.41
1:A:502:ARG:HG3	1:A:562:GLU:HG2	2.02	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:647:ARG:HH21	1:A:648:LEU:HD11	1.86	0.41
1:A:702:VAL:HG13	1:A:712:VAL:HG21	2.03	0.41
1:A:831:ILE:O	1:A:834:ARG:HG2	2.22	0.40
1:A:199:ILE:HG22	1:A:201:ALA:O	2.22	0.40
1:A:354:LYS:HE2	1:A:760:THR:HB	2.02	0.40
1:A:900:ASP:OD1	1:A:904:GLN:HB2	2.21	0.40
1:A:925:SER:O	1:A:929:VAL:HG22	2.22	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:430:ARG:NH2	1:A:648:LEU:O[1_565]	2.04	0.16

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 67
2	B	262/305 (86%)	222 (85%)	36 (14%)	4 (2%)	10 44
3	G	37/74 (50%)	33 (89%)	4 (11%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1289/1407 (92%)	1197 (93%)	83 (6%)	9 (1%)	22 61

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 59
2	B	234/266 (88%)	224 (96%)	10 (4%)	29 64
3	G	32/62 (52%)	32 (100%)	0	100 100
All	All	1106/1197 (92%)	1052 (95%)	54 (5%)	25 61

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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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

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	4,2	14,14,15	0.51	0	17,19,21	0.93	1 (5%)
4	NAG	C	2	4	14,14,15	0.65	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	4,2	-	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	4.00	128.60	122.90
4	C	1	NAG	C1-O5-C5	2.71	115.86	112.19

There are no chirality outliers.

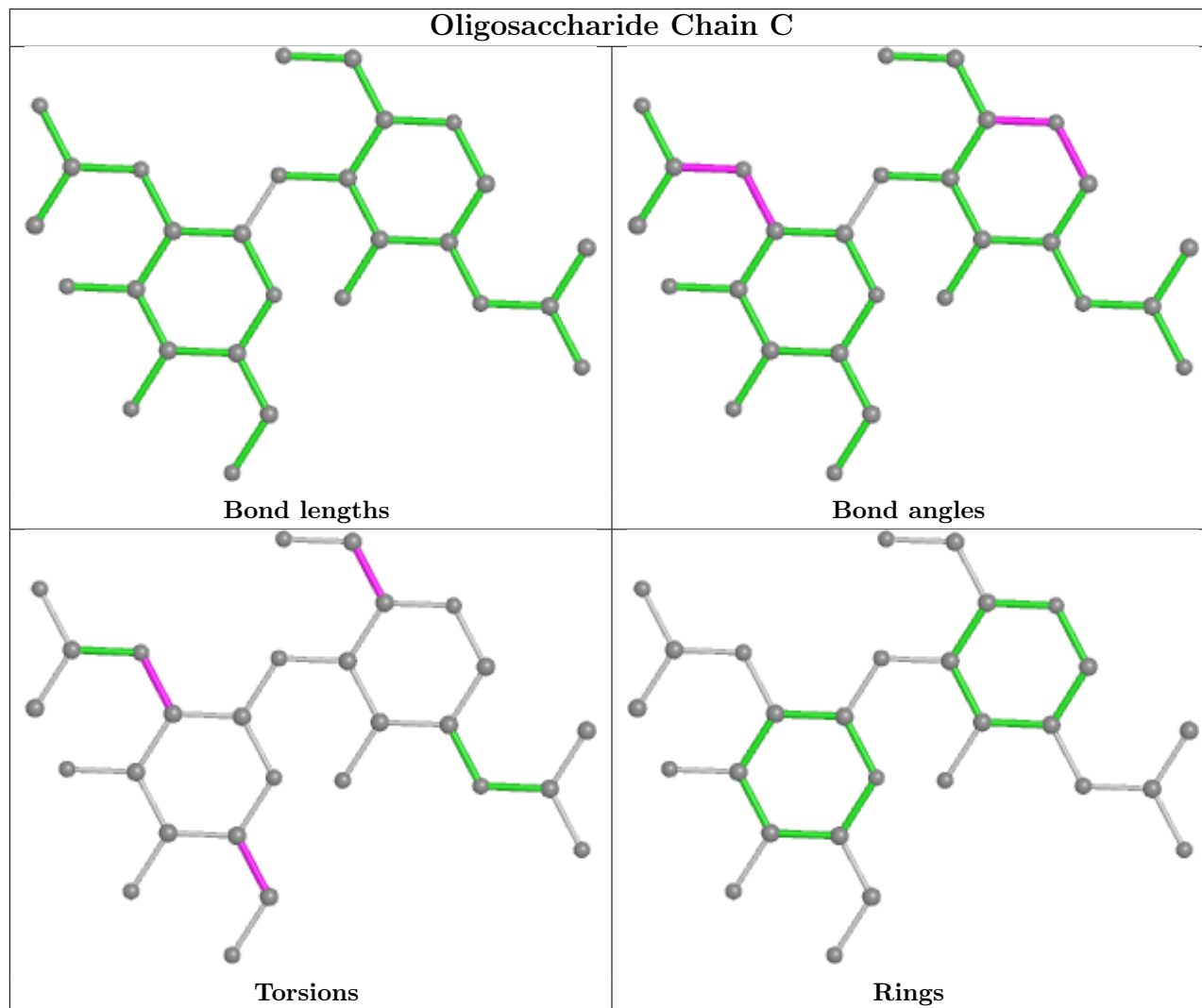
All (4) torsion outliers are listed below:

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 8 ligands modelled in this entry, 5 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
5	MF4	A	2001	1	0,4,4	-	-	-		
10	NAG	B	4021	2	14,14,15	0.59	0	17,19,21	1.23	2 (11%)
9	CLR	B	3001	-	31,31,31	0.45	0	48,48,48	1.10	5 (10%)

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

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	2.96	107.41	103.84
10	B	4021	NAG	C1-O5-C5	2.57	115.68	112.19
9	B	3001	CLR	C1-C2-C3	2.56	113.76	110.47
9	B	3001	CLR	C4-C5-C6	-2.51	116.99	120.61
9	B	3001	CLR	C4-C5-C10	2.44	119.66	116.42
10	B	4021	NAG	C4-C3-C2	2.30	114.38	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:

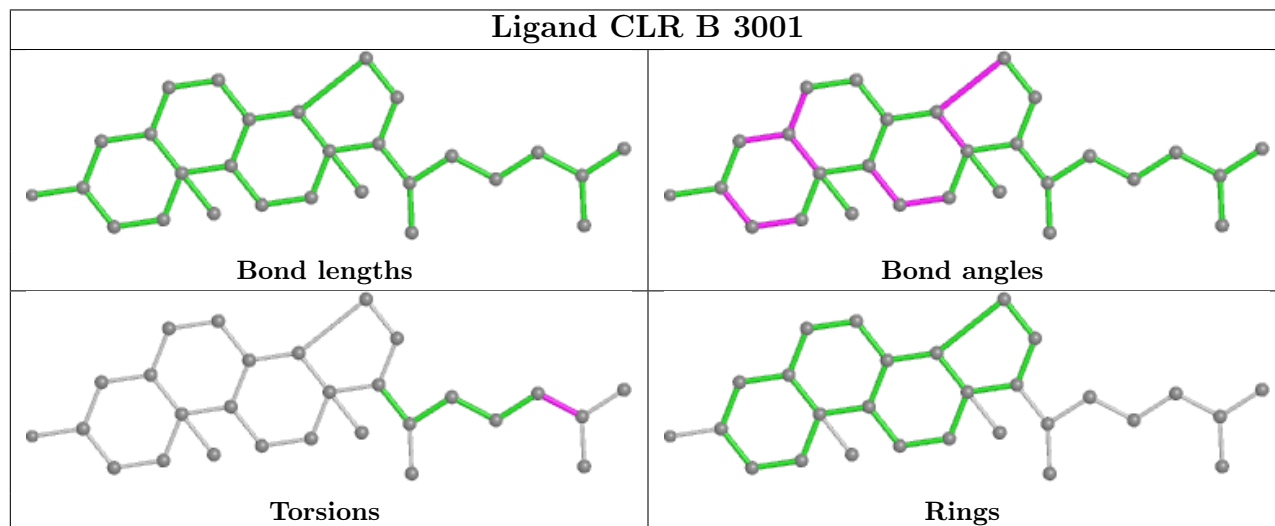
Mol	Chain	Res	Type	Atoms
9	B	3001	CLR	C23-C24-C25-C26
9	B	3001	CLR	C23-C24-C25-C27

There are no ring outliers.

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 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

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	992/1028 (96%)	0.39	45 (4%) 33 21	87, 108, 149, 175	0
2	B	268/305 (87%)	0.79	38 (14%) 2 1	107, 158, 183, 193	0
3	G	39/74 (52%)	-0.05	1 (2%) 56 40	104, 113, 156, 159	0
All	All	1299/1407 (92%)	0.46	84 (6%) 18 11	87, 114, 171, 193	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	894	TRP	5.9
2	B	123	PRO	5.0
1	A	72	LEU	4.8
1	A	579	PRO	4.8
2	B	298	GLU	4.6
1	A	986	SER	4.5
1	A	578	PHE	4.3
1	A	504	LEU	4.3
1	A	534	MET	4.1
1	A	317	TRP	4.1
1	A	571	PHE	3.9
2	B	199	PRO	3.9
2	B	272	MET	3.9
2	B	281	TYR	3.9
1	A	79	SER	3.8
1	A	573	ALA	3.8
1	A	427	LEU	3.7
1	A	42	ASP	3.7
2	B	231	TYR	3.7
1	A	567	GLU	3.6
2	B	214	ARG	3.4
2	B	121	ASN	3.3
1	A	580	THR	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	260	TYR	3.3
2	B	276	ILE	3.3
1	A	183	GLU	3.2
1	A	562	GLU	3.2
2	B	299	VAL	3.1
2	B	96	PRO	3.1
1	A	563	ASP	3.1
2	B	194	ASN	3.0
2	B	255	LYS	2.9
1	A	585	PHE	2.9
2	B	89	ILE	2.9
2	B	265	PHE	2.9
1	A	503	TYR	2.9
2	B	274	LEU	2.8
2	B	215	CYS	2.7
2	B	273	GLU	2.7
1	A	78	ASN	2.7
2	B	271	ASN	2.7
1	A	80	LEU	2.6
1	A	84	PRO	2.6
2	B	98	SER	2.6
1	A	568	GLY	2.5
2	B	93	ILE	2.5
1	A	555	PHE	2.5
1	A	492	ILE	2.5
2	B	300	LYS	2.4
2	B	122	SER	2.4
2	B	216	ALA	2.4
1	A	930	GLN	2.4
1	A	121	THR	2.4
1	A	126	ALA	2.3
1	A	426	ALA	2.3
1	A	90	ILE	2.3
1	A	1017	VAL	2.3
2	B	212	PRO	2.3
1	A	498	SER	2.3
1	A	184	PHE	2.2
1	A	57	THR	2.2
1	A	675	THR	2.2
1	A	496	GLU	2.2
2	B	203	GLN	2.2
2	B	70	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	147	LYS	2.2
2	B	257	LEU	2.1
1	A	36	LYS	2.1
2	B	126	ASP	2.1
2	B	305	SER	2.1
1	A	37	LYS	2.1
1	A	918	CYS	2.1
1	A	278	GLU	2.1
3	G	13	THR	2.1
2	B	262	ALA	2.1
1	A	928	VAL	2.1
2	B	88	GLU	2.0
2	B	99	TYR	2.0
2	B	303	VAL	2.0
1	A	505	LEU	2.0
2	B	304	LYS	2.0
2	B	270	GLN	2.0
1	A	161	PHE	2.0
2	B	152	PHE	2.0

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

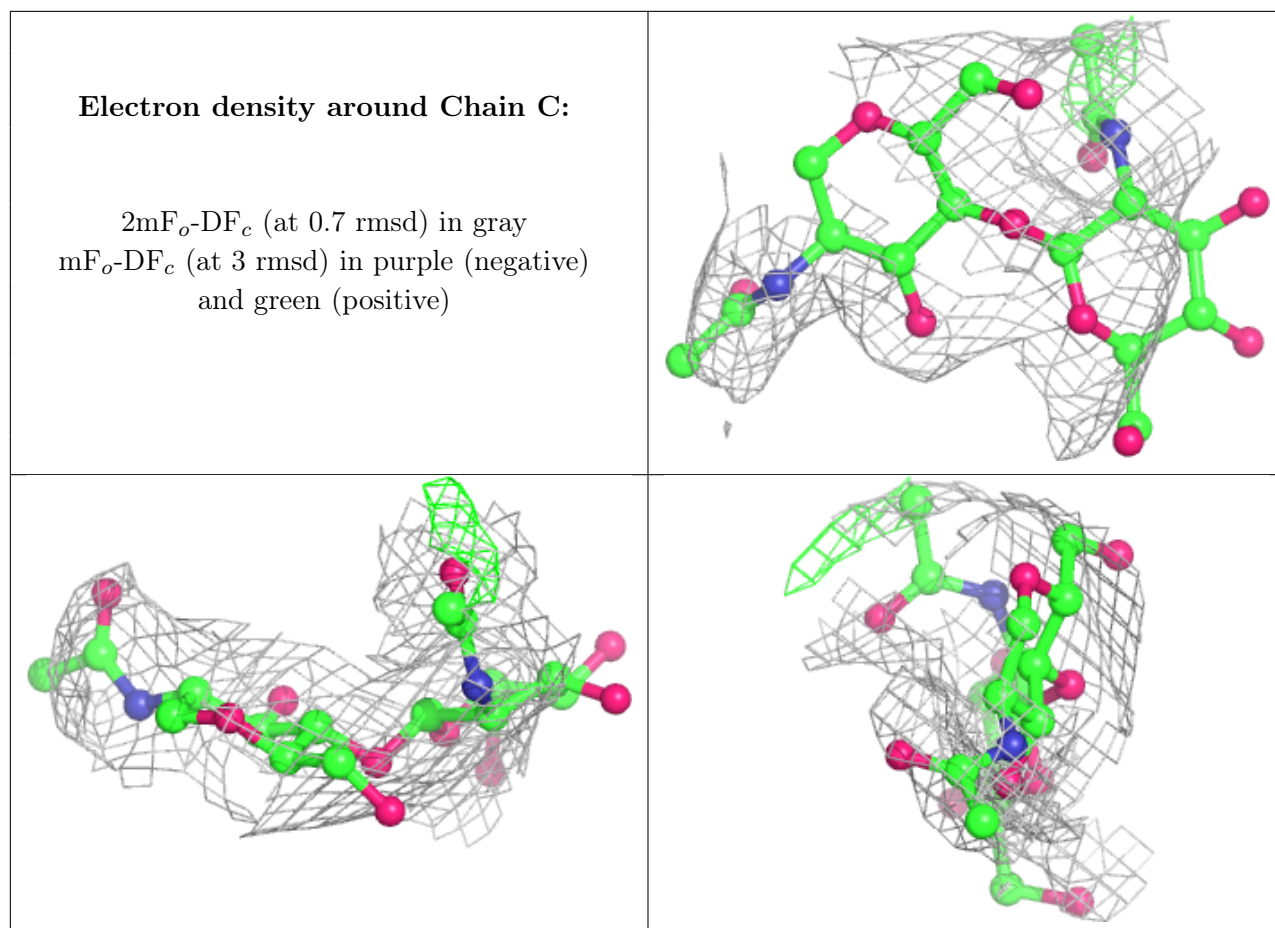
There are no non-standard protein/DNA/RNA residues in this entry.

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, 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	NAG	C	2	14/15	0.44	0.43	171,172,173,173	0
4	NAG	C	1	14/15	0.84	0.21	165,168,168,170	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.



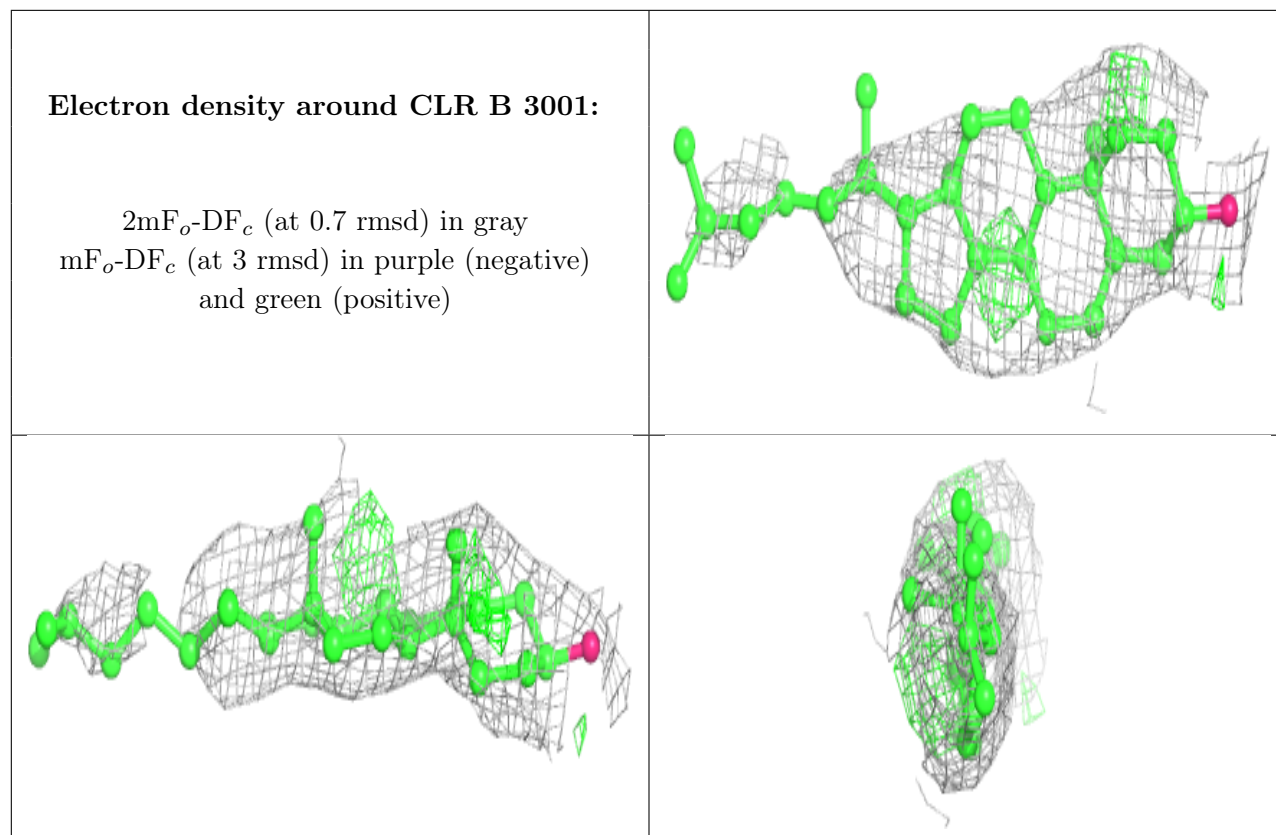
6.4 Ligands [i](#)

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(Å ²)	Q<0.9
10	NAG	B	4021	14/15	0.71	0.57	171,172,172,172	0
6	MG	A	2002	1/1	0.77	0.32	89,89,89,89	0
9	CLR	B	3001	28/28	0.82	0.29	150,151,151,151	0
7	TL	A	2003	1/1	0.93	0.10	110,110,110,110	0
5	MF4	A	2001	5/5	0.94	0.34	92,93,95,95	0
7	TL	A	2006[B]	1/1	0.97	0.03	105,105,105,105	1
8	K	A	2005[A]	1/1	0.97	0.03	105,105,105,105	1
7	TL	A	2004	1/1	0.99	0.11	110,110,110,110	0

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.