wwPDB X-ray Structure Validation Summary Report (i)

Aug 5, 2026 – 05:01 AM JST

PDB ID	:	5AW6 / pdb_00005aw6
Title	:	Kinetics by X-ray crystallography: Rb+-substitution of bound K+ in the E2.MgF42-.2K+ crystal after 5.5 min
Authors	:	Ogawa, H.; Cornelius, F.; Hirata, A.; Toyoshima, C.
Deposited on	:	2015-07-01
Resolution	:	2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (i)) were used in the production of this report:

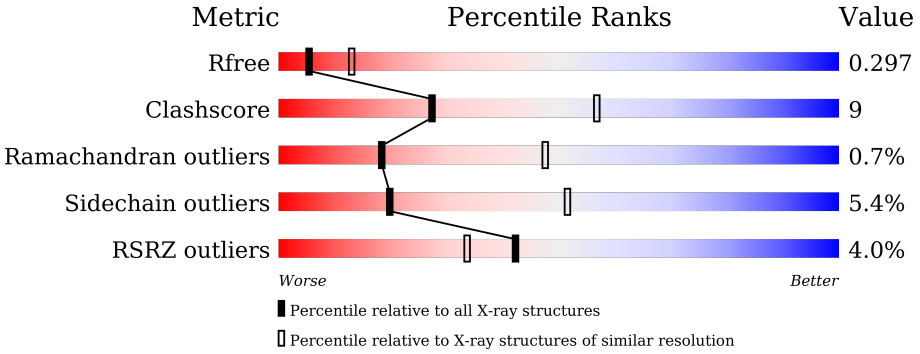
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	3%, 73%, 21%, • •
2	B	305	7%, 65%, 20%, •, 12%
3	G	74	35%, 18%, 47%
4	C	2	100%

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+,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

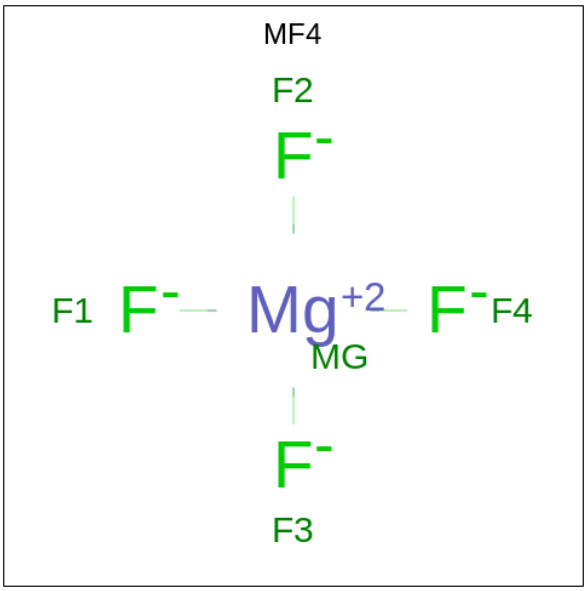
- Molecule 3 is a protein called Phospholemman-like protein.

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-) (CCD ID: MF4) (formula: F_4Mg).



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

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

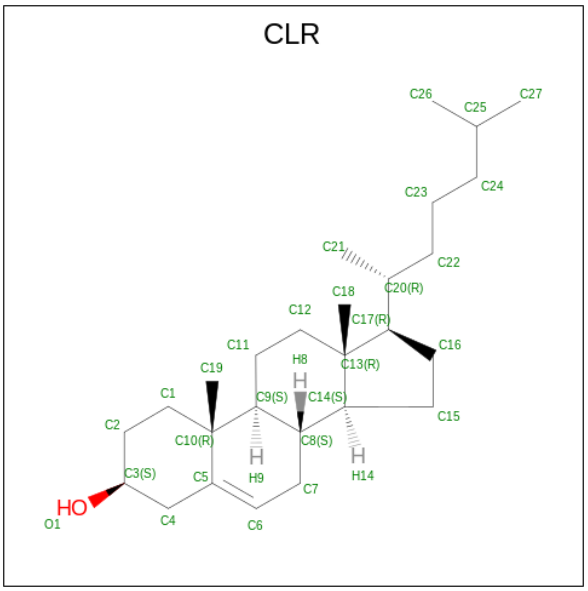
- Molecule 7 is POTASSIUM ION (CCD ID: K) (formula: K).

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

- Molecule 8 is RUBIDIUM ION (CCD ID: RB) (formula: Rb).

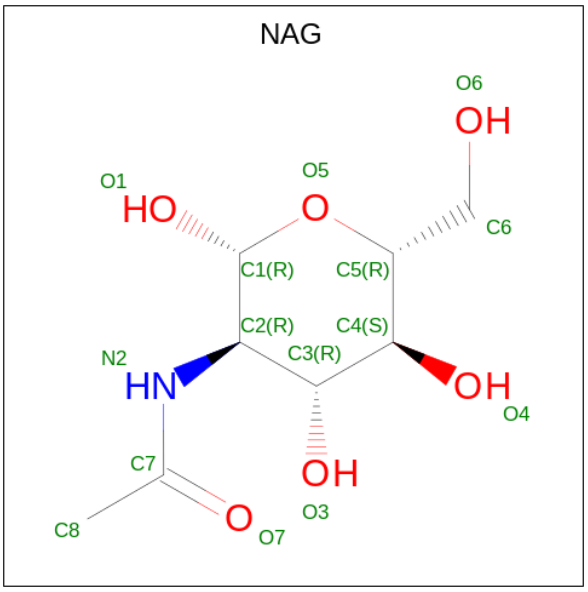
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	3	Total Rb 3 3	0	3

- Molecule 9 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$).



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

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



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

- Molecule 11 is water.

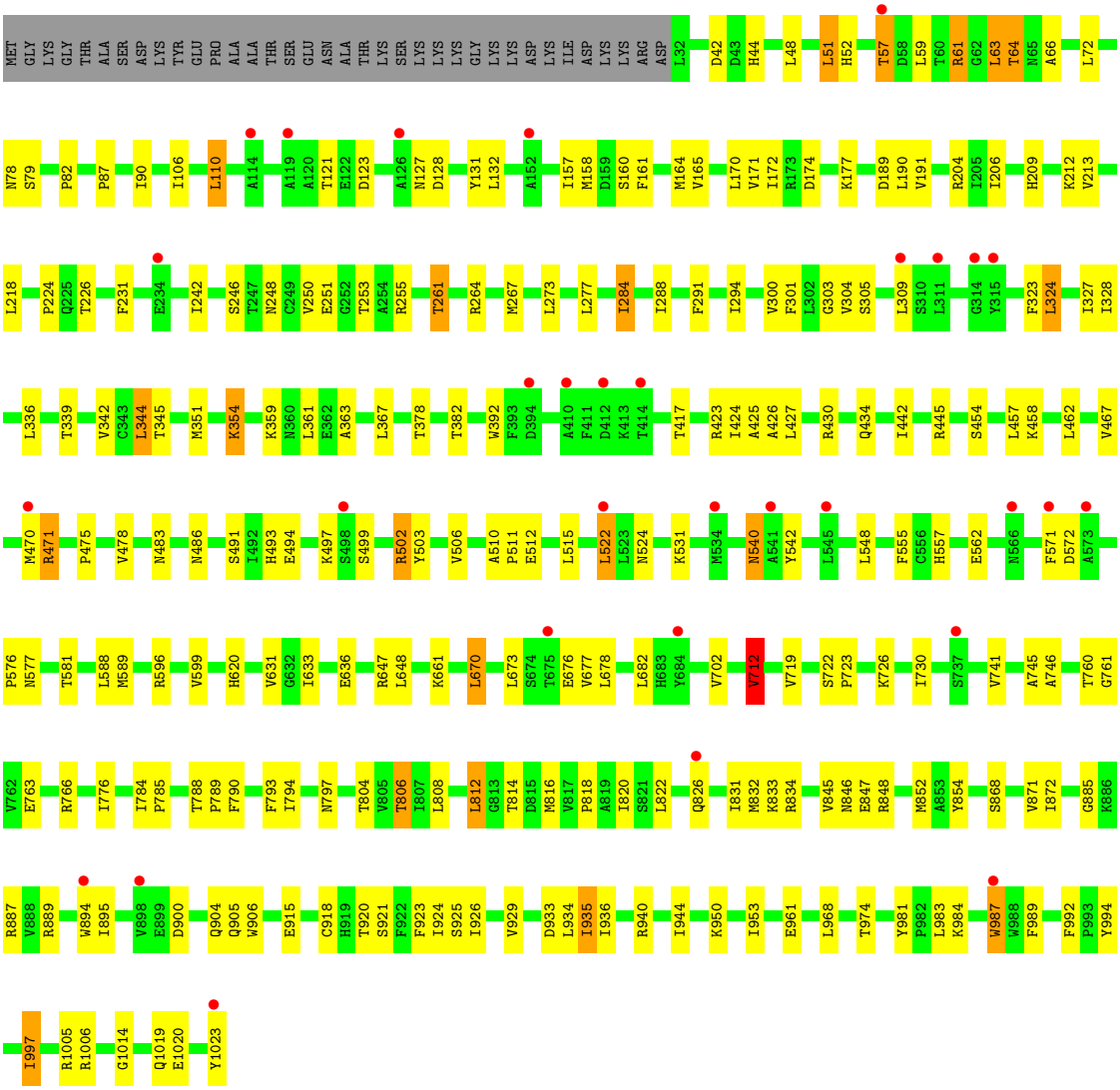
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
11	A	1	1	1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Na, K-ATPase alpha subunit

Chain A:



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

Chain B: 7% 65% 20% • 12%

MET ALA ARG GLY LYS SER LYS GLU THR ASP GLY GLY TRP LYS LYS PHE LEU TRP ASP SER GLU LYS LYS GLU F25 R28 S31 S32 K35 I52 Q56 V57 L58 D71 R72 V73 A74 P75 H80 A84 I85 K86 T87 E88 I89 I93 S94 N95 P96 Y99

F102 M106 H107 M110 D111 L112 Y113 N114 S117 S122 P123 R137 G138 D139 K147 L157 C160 SER GLY LEU ASP ASP THR THR TYR G169 Y170 A171 K174 P175 C176 K180 L181 N182 Y188 L192 K193 N194 L198 P199 E200 E201 L202 N205 Y206

N207 Q208 Y209 L213 R214 C215 A216 A217 LYS ARG GLU GLU ASP R223 I226 G227 E230 Y231 F232 G233 L234 P241 L242 Q253 K254 K255 Y256 L257 L261 A262 L268 T269 Q270 N271 C278 N284 S288 E289 R294 F297 E298 S305

• Molecule 3: Phospholemman-like protein

Chain G: 35% 18% 47%

MET ASP PRO E4 G5 Y16 Y17 V21 I25 V29 L30 C31 V32 I33 G34 I35 I36 I37 L38 K42 CYS ARG CYS LYS PHE ASN GLN ASN LYS ARG THR ARG SER ASN SER GLY THR ALA THR ALA GLN HIS LEU LEU GLN PRO GLY GLU ALA THR GLU CYS

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

Chain C: 100%

NAG1 NAG2

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	220.61Å 50.59Å 163.16Å 90.00° 104.60° 90.00°	Depositor
Resolution (Å)	14.98 – 2.80 14.98 – 2.80	Depositor EDS
% Data completeness (in resolution range)	68.2 (14.98-2.80) 86.6 (14.98-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.83 (at 2.81Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.280 , 0.271 0.286 , 0.297	Depositor DCC
R_{free} test set	1199 reflections (2.74%)	wwPDB-VP
Wilson B-factor (Å^2)	58.6	Xtriage
Anisotropy	0.464	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 36.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	10237	wwPDB-VP
Average B, all atoms (Å^2)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.61% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: CLR, MG, MF4, K, NAG, RB

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	0.49	0/7825	0.83	4/10616 (0.0%)
2	B	0.47	2/2229 (0.1%)	0.76	2/3002 (0.1%)
3	G	0.50	0/309	0.81	0/419
All	All	0.48	2/10363 (0.0%)	0.81	6/14037 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	113	TYR	C-N	6.54	1.42	1.33
2	B	114	ASN	C-N	-6.53	1.25	1.34

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	620	HIS	CA-C-N	5.60	125.26	119.05
1	A	620	HIS	C-N-CA	5.60	125.26	119.05
2	B	174	LYS	CA-C-N	5.37	126.55	119.84
2	B	174	LYS	C-N-CA	5.37	126.55	119.84
1	A	42	ASP	N-CA-C	5.32	116.36	108.86

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	138	1
2	B	2174	0	2146	51	0
3	G	305	0	318	10	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	0	0
10	B	14	0	13	0	0
11	A	1	0	0	0	0
All	All	10237	0	10247	187	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 9.

The worst 5 of 187 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:425:ALA:HB2	1:A:589:MET:HE1	1.60	0.82
1:A:478:VAL:HG21	1:A:571:PHE:HB2	1.64	0.79
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

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]	2.03	0.17

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%)	24	55
2	B	262/305 (86%)	223 (85%)	35 (13%)	4 (2%)	8	28
3	G	37/74 (50%)	33 (89%)	4 (11%)	0	100	100
All	All	1289/1407 (92%)	1198 (93%)	82 (6%)	9 (1%)	18	47

5 of 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

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%)	790 (94%)	50 (6%)	17	47
2	B	234/266 (88%)	224 (96%)	10 (4%)	26	60
3	G	32/62 (52%)	32 (100%)	0	100	100
All	All	1106/1197 (92%)	1046 (95%)	60 (5%)	20	51

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	522	LEU
2	B	194	ASN
1	A	670	LEU
2	B	139	ASP
2	B	289	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	797	ASN
1	A	905	GLN
2	B	284	ASN
1	A	861	GLN
1	A	1019	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)

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	0.51	0	17,19,21	0.93	1 (5%)
4	NAG	C	2	4	14,14,15	0.66	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(^{o})	Ideal(^{o})
4	C	2	NAG	C2-N2-C7	3.97	128.55	122.90
4	C	1	NAG	C1-O5-C5	2.67	115.82	112.19

There are no chirality outliers.

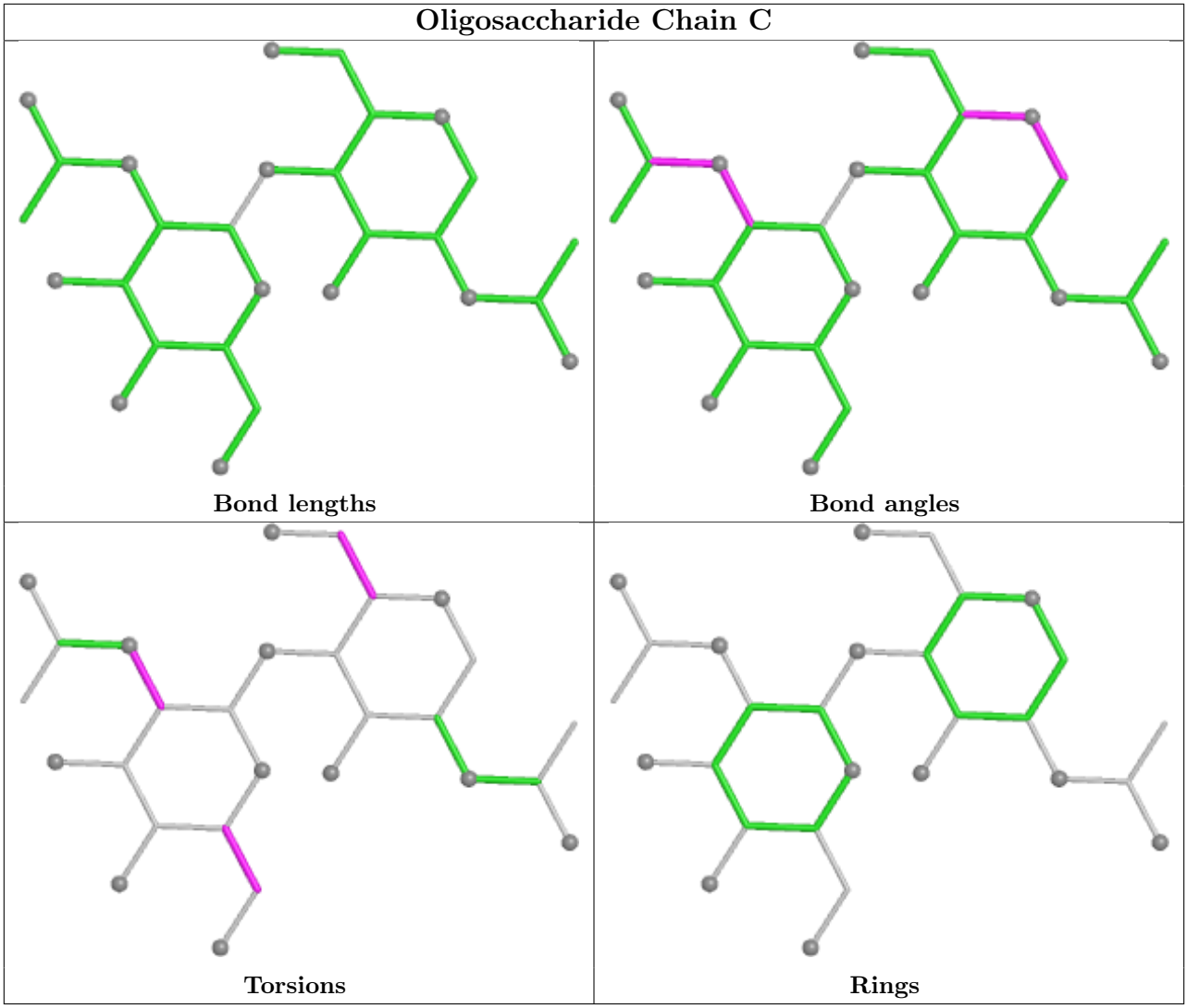
All (4) torsion outliers are listed below:

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	$\#\|Z\| > 2$
10	NAG	B	4021	2	14,14,15	0.59	0	17,19,21	1.24	2 (11%)
5	MF4	A	2001	1	0,4,4	-	-	-		
9	CLR	B	3001	-	31,31,31	0.46	0	48,48,48	1.09	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.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	B	3001	CLR	C15-C14-C13	2.94	107.38	103.84
10	B	4021	NAG	C1-O5-C5	2.59	115.70	112.19
9	B	3001	CLR	C1-C2-C3	2.58	113.78	110.47
9	B	3001	CLR	C4-C5-C6	-2.44	117.09	120.61
9	B	3001	CLR	C4-C5-C10	2.41	119.62	116.42

There are no chirality outliers.

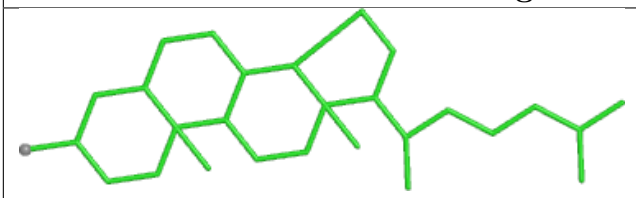
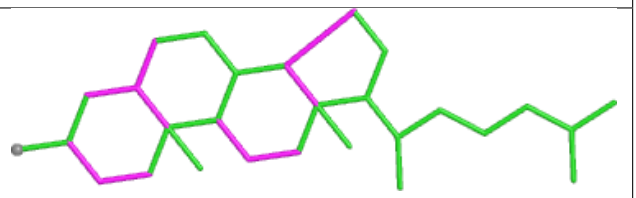
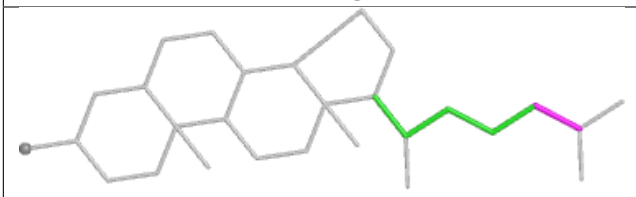
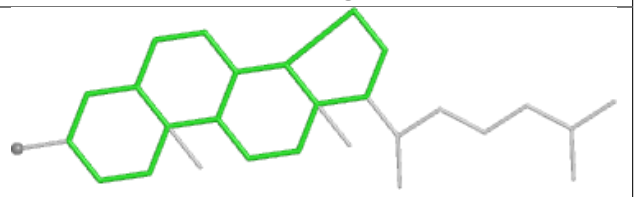
All (2) torsion outliers are listed below:

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 then 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.

Ligand CLR B 3001	
 Bond lengths	 Bond angles
 Torsions	 Rings

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, 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%)	0.34	31 (3%) 51 41	59, 80, 121, 146	0
2	B	268/305 (87%)	0.87	21 (7%) 19 14	79, 130, 154, 164	0
3	G	39/74 (52%)	0.24	0 100 100	75, 84, 128, 131	0
All	All	1299/1407 (92%)	0.44	52 (4%) 42 33	59, 85, 142, 164	0

The worst 5 of 52 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	894	TRP	4.1
1	A	573	ALA	3.6
1	A	534	MET	3.6
2	B	268	LEU	3.5
2	B	169	GLY	3.5

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

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

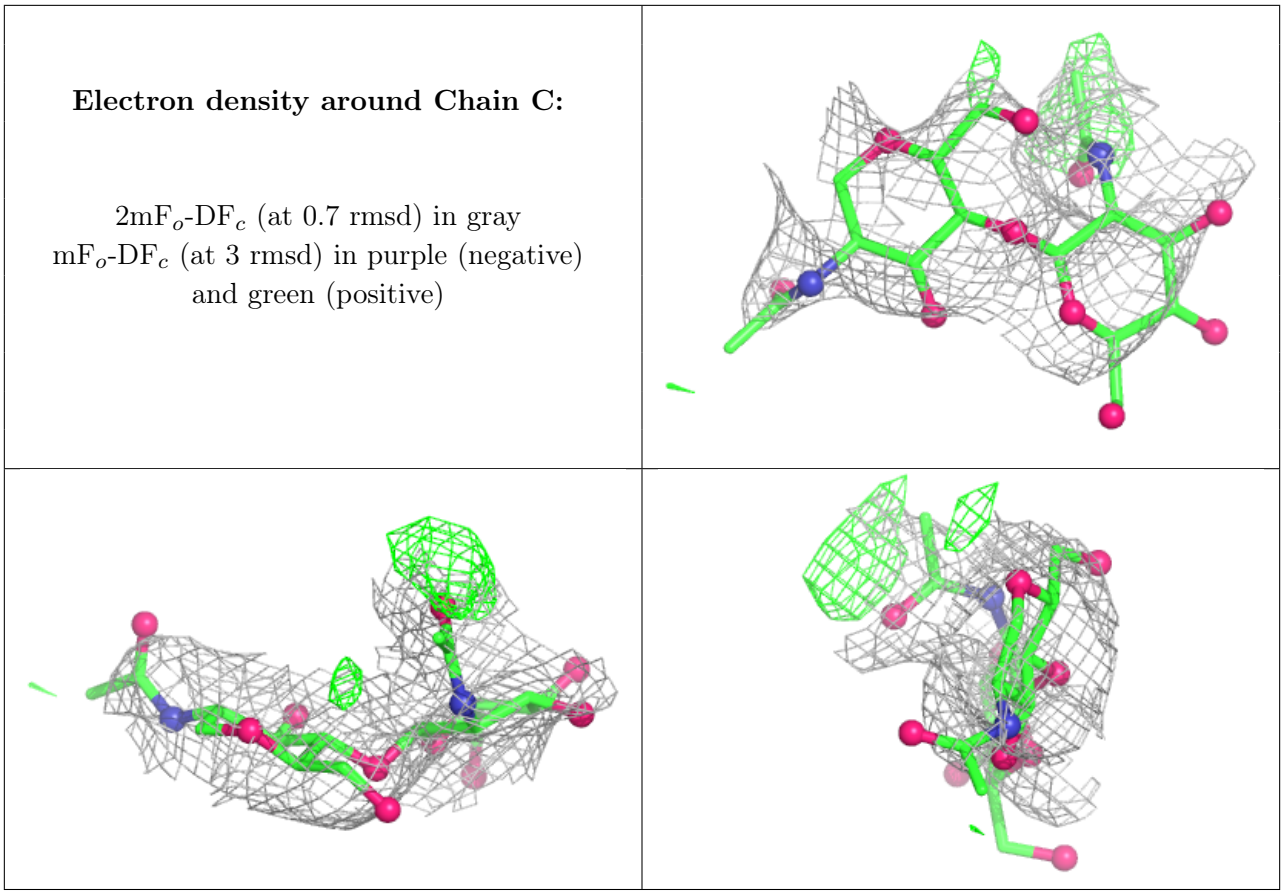
6.3 Carbohydrates (i)

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	1	14/15	-	-	137,139,140,142	0
4	NAG	C	2	14/15	-	-	143,144,144,145	0

The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. 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.

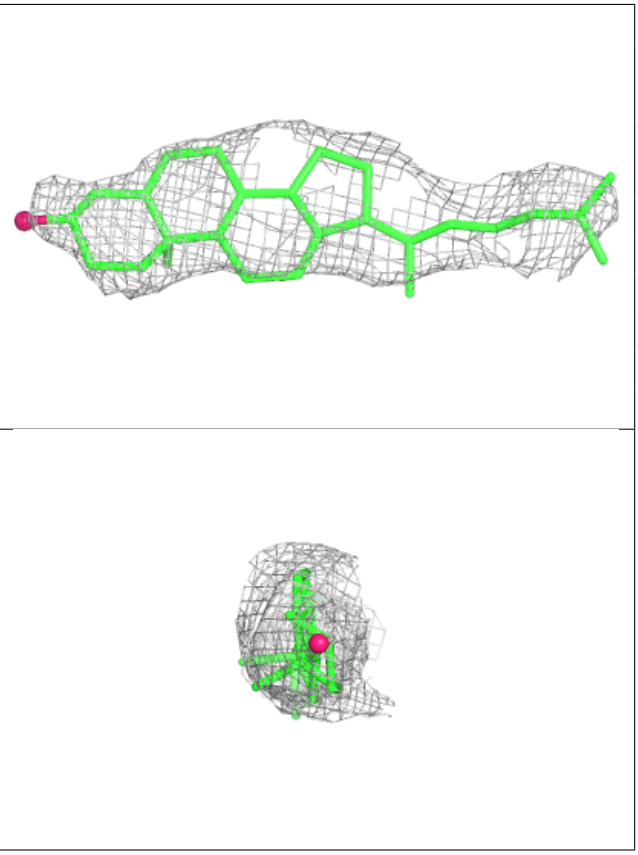
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
10	NAG	B	4021	14/15	0.56	0.13	142,143,144,144	0
6	MG	A	2002	1/1	0.78	0.16	60,60,60,60	0
9	CLR	B	3001	28/28	0.83	0.13	122,122,123,123	0
5	MF4	A	2001	5/5	0.92	0.14	64,65,66,67	0
7	K	A	2005[A]	1/1	0.96	0.04	81,81,81,81	1
8	RB	A	2006[B]	1/1	0.96	0.04	81,81,81,81	0
7	K	A	2003[A]	1/1	0.98	0.05	81,81,81,81	1
8	RB	A	2008[B]	1/1	0.98	0.04	77,77,77,77	1
7	K	A	2007[A]	1/1	0.98	0.04	77,77,77,77	1
8	RB	A	2004[B]	1/1	0.98	0.05	81,81,81,81	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.

Electron density around CLR B 3001:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.