



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 11:57 AM UTC

PDB ID : 5AW9 / pdb_00005aw9
Title : Kinetics by X-ray crystallography: native E2.MgF42-.2K+ crystal for Rb+ bound crystals
Authors : Ogawa, H.; Cornelius, F.; Hirata, A.; Toyoshima, C.
Deposited on : 2015-07-01
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

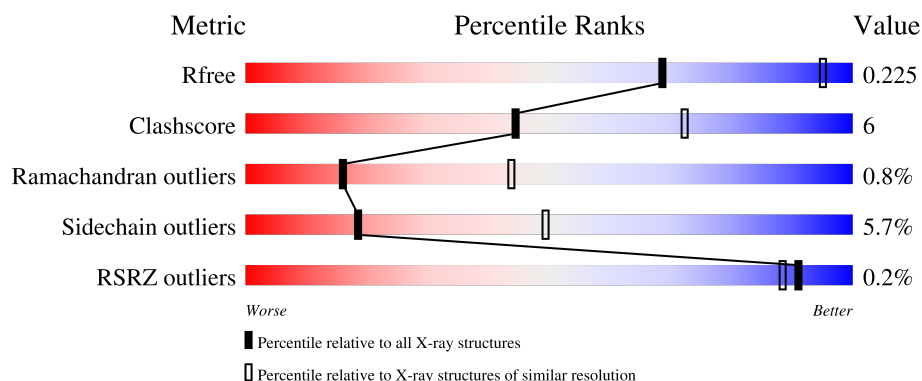
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

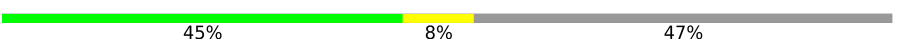
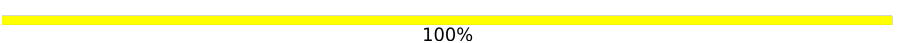
The reported resolution of this entry is 2.80 Å.

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 $\leq 5\%$. 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	 78% 17% . .
2	B	305	 71% 16% . 12%
3	G	74	 45% 8% 47%
4	C	2	 100%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 10362 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
1	A	992	Total	C	N	O	S	0	0	0
			7675	4886	1290	1453	46			

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

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

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

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

- 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
4	C	2	Total	C	N	O		0	0	0
			28	16	2	10				

- Molecule 5 is TETRAFLUOROMAGNESATE(2-) (CCD ID: 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 (CCD ID: MG) (formula: Mg).

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

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

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

- Molecule 8 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



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

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

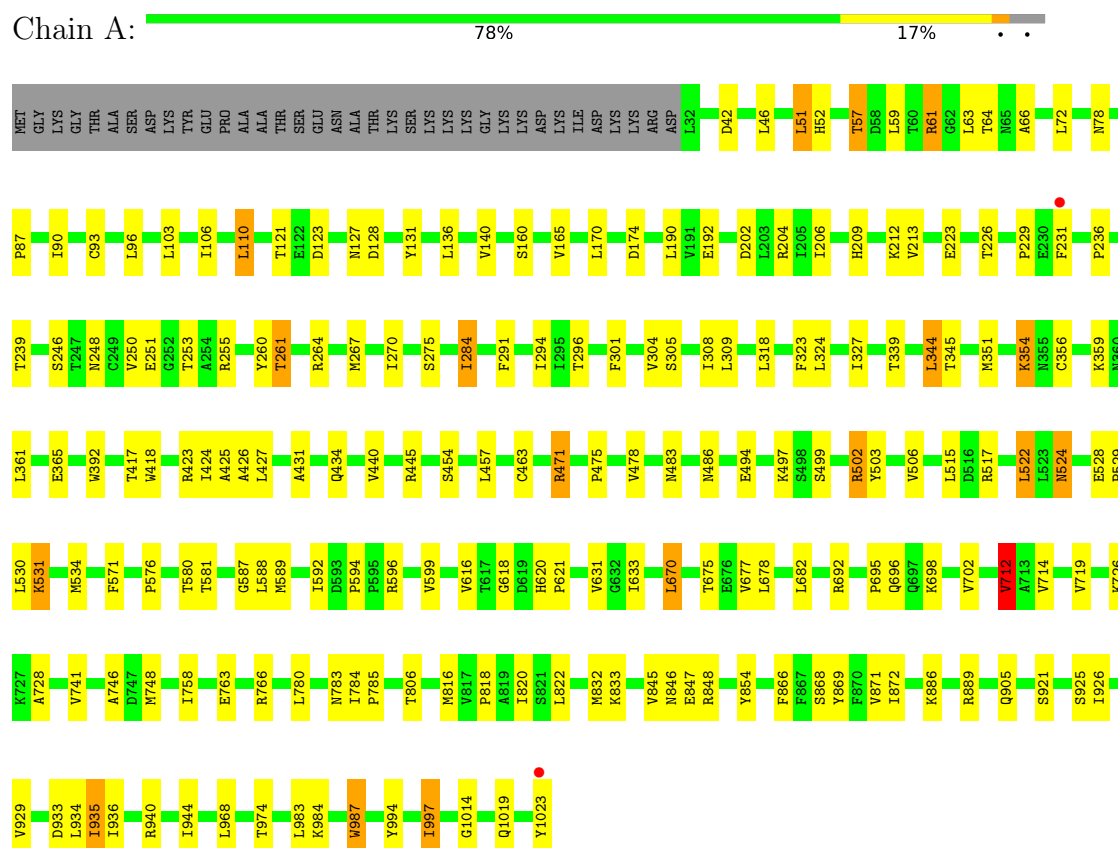
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	129	Total 129	O 129	0	0

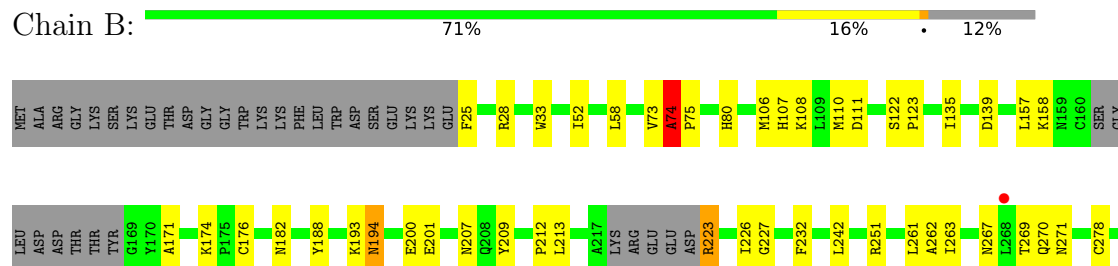
3 Residue-property plots

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

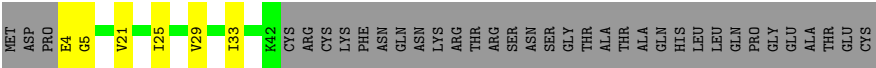


- Molecule 2: Na⁺,K⁺-ATPase beta subunit





- 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	219.97Å 50.67Å 163.07Å 90.00° 104.50° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	92.9 (15.00-2.80) 92.9 (15.00-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.217 , 0.265 (Not available) , 0.225	Depositor DCC
R_{free} test set	2063 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å ²)	76.9	Xtriage
Anisotropy	0.490	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10362	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% 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: CLR, K, NAG, MF4, 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	0.61	0/7825	1.02	3/10616 (0.0%)
2	B	0.61	0/2229	0.95	4/3002 (0.1%)
3	G	0.64	0/309	1.04	0/419
All	All	0.61	0/10363	1.01	7/14037 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	42	ASP	N-CA-C	7.61	119.59	108.86
2	B	174	LYS	CA-C-N	6.59	126.97	119.92
2	B	174	LYS	C-N-CA	6.59	126.97	119.92
2	B	74	ALA	CA-C-N	-5.72	114.48	120.38
2	B	74	ALA	C-N-CA	-5.72	114.48	120.38
1	A	587	GLY	N-CA-C	5.40	118.46	110.42
1	A	712	VAL	N-CA-C	5.35	116.28	108.53

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	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2174	0	2146	28	0
3	G	305	0	318	2	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	B	28	0	46	0	0
9	B	14	0	13	0	0
10	A	129	0	0	3	0
All	All	10362	0	10247	123	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 6.

All (123) 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	1.69	0.75
1:A:677:VAL:HG21	10:A:2222:HOH:O	1.89	0.73
1:A:935:ILE:HG23	1:A:944:ILE:HD12	1.72	0.71
1:A:425:ALA:HB2	1:A:589:MET:HE1	1.70	0.71
1:A:61:ARG:HH11	1:A:61:ARG:HB3	1.55	0.70
1:A:52:HIS:HA	1:A:57:THR:HG23	1.73	0.70
1:A:78:ASN:HA	1:A:261:THR:HG23	1.74	0.70
1:A:766:ARG:HD2	1:A:832:MET:CE	2.28	0.64
1:A:64:THR:HG22	1:A:66:ALA:H	1.61	0.64
1:A:261:THR:HG21	10:A:2134:HOH:O	1.98	0.63
1:A:261:THR:HG22	1:A:264:ARG:HH21	1.62	0.62
2:B:74:ALA:CB	2:B:75:PRO:HD3	2.29	0.62
1:A:261:THR:HG22	1:A:264:ARG:NH2	2.15	0.62
1:A:994:TYR:HA	1:A:997:ILE:HG22	1.84	0.59
2:B:213:LEU:HD11	2:B:278:CYS:HB3	1.85	0.59
1:A:816:MET:O	1:A:820:ILE:HG12	2.02	0.59
1:A:670:LEU:HD23	1:A:678:LEU:HD21	1.85	0.58
1:A:246:SER:OG	1:A:267:MET:HG3	2.04	0.57
2:B:227:GLY:HA2	2:B:267:ASN:HB3	1.86	0.57
1:A:344:LEU:HB3	1:A:361:LEU:HG	1.86	0.57
1:A:359:LYS:HE2	1:A:746:ALA:O	2.06	0.56
1:A:868:SER:O	1:A:872:ILE:HG12	2.05	0.56
1:A:345:THR:HA	1:A:361:LEU:HD11	1.88	0.56
2:B:270:GLN:HG2	2:B:271:ASN:HD22	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:483:ASN:HB2	1:A:486:ASN:HB2	1.89	0.55
2:B:80:HIS:HB3	2:B:297:PHE:CZ	2.42	0.55
2:B:25:PHE:HB3	2:B:33:TRP:HE1	1.72	0.54
1:A:984:LYS:H	1:A:987:TRP:CD1	2.25	0.54
3:G:29:VAL:O	3:G:33:ILE:HG12	2.07	0.54
1:A:190:LEU:HD11	1:A:206:ILE:HD11	1.90	0.53
1:A:424:ILE:HG23	1:A:506:VAL:HB	1.91	0.53
1:A:417:THR:HA	1:A:522:LEU:HD22	1.91	0.53
1:A:52:HIS:CE1	1:A:59:LEU:HA	2.44	0.53
2:B:193:LYS:HA	2:B:207:ASN:HD21	1.73	0.52
1:A:356:CYS:SG	1:A:748:MET:HE3	2.50	0.52
1:A:631:VAL:HG23	1:A:633:ILE:HG12	1.92	0.52
1:A:351:MET:HA	1:A:354:LYS:HG2	1.91	0.52
1:A:87:PRO:HD2	1:A:90:ILE:HD12	1.92	0.52
1:A:106:ILE:O	1:A:110:LEU:HB2	2.10	0.51
1:A:392:TRP:HB3	1:A:588:LEU:HB2	1.92	0.51
1:A:847:GLU:CD	1:A:847:GLU:H	2.17	0.51
1:A:921:SER:HA	1:A:983:LEU:HD11	1.93	0.51
2:B:158:LYS:HB2	2:B:232:PHE:CD1	2.46	0.51
2:B:107:HIS:O	2:B:111:ASP:HB2	2.11	0.51
1:A:818:PRO:HB3	1:A:934:LEU:HD22	1.92	0.50
2:B:106:MET:O	2:B:110:MET:HG2	2.11	0.50
1:A:339:THR:HG23	1:A:820:ILE:HD13	1.93	0.50
1:A:160:SER:HB3	1:A:741:VAL:HG22	1.93	0.50
1:A:323:PHE:O	1:A:327:ILE:HG12	2.12	0.49
2:B:209:TYR:HA	2:B:242:LEU:HD22	1.93	0.49
1:A:475:PRO:HD2	1:A:494:GLU:HB2	1.94	0.49
1:A:714:VAL:HG23	1:A:728:ALA:HB2	1.95	0.49
1:A:596:ARG:HB2	1:A:599:VAL:HG23	1.94	0.48
1:A:766:ARG:HD2	1:A:832:MET:HE1	1.96	0.48
1:A:871:VAL:HG22	2:B:58:LEU:HD13	1.94	0.48
1:A:110:LEU:HD22	1:A:324:LEU:HD12	1.95	0.48
1:A:940:ARG:HE	1:A:1023:TYR:HB2	1.79	0.48
1:A:423:ARG:HG2	1:A:427:LEU:HD22	1.96	0.47
2:B:110:MET:HE1	2:B:157:LEU:HD13	1.95	0.47
2:B:194:ASN:HD22	2:B:194:ASN:N	2.12	0.47
1:A:478:VAL:HG21	1:A:571:PHE:HB2	1.96	0.47
1:A:846:ASN:ND2	1:A:848:ARG:HB2	2.29	0.47
2:B:194:ASN:HD22	2:B:194:ASN:H	1.61	0.47
1:A:502:ARG:HD2	1:A:503:TYR:H	1.79	0.47
2:B:188:TYR:O	2:B:284:ASN:ND2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:267:ASN:HB2	2:B:269:THR:HG22	1.96	0.47
1:A:93:CYS:HA	1:A:96:LEU:HD12	1.96	0.46
1:A:832:MET:HE2	1:A:832:MET:HA	1.98	0.46
1:A:497:LYS:HE2	1:A:499:SER:HB2	1.98	0.46
1:A:304:VAL:O	1:A:308:ILE:HG12	2.15	0.46
1:A:905:GLN:NE2	2:B:182:ASN:HA	2.30	0.46
1:A:127:ASN:HB3	1:A:131:TYR:CD1	2.51	0.46
1:A:301:PHE:O	1:A:305:SER:HB2	2.15	0.46
2:B:122:SER:HA	2:B:123:PRO:HA	1.76	0.46
1:A:528:GLU:HB2	1:A:529:PRO:HD2	1.98	0.45
1:A:202:ASP:HB2	1:A:260:TYR:HB2	1.97	0.45
2:B:213:LEU:HD21	2:B:263:ILE:HD11	1.99	0.45
1:A:209:HIS:HB3	1:A:253:THR:HG22	1.99	0.45
2:B:223:ARG:HB2	2:B:223:ARG:HH11	1.82	0.45
1:A:675:THR:HA	1:A:678:LEU:HD12	1.98	0.44
1:A:866:PHE:O	1:A:869:TYR:HB3	2.17	0.44
3:G:21:VAL:O	3:G:25:ILE:HG12	2.18	0.44
1:A:170:LEU:HD23	1:A:192:GLU:HB3	1.99	0.44
1:A:933:ASP:HA	1:A:936:ILE:HG12	1.99	0.44
2:B:74:ALA:CB	2:B:75:PRO:CD	2.96	0.44
1:A:236:PRO:HA	1:A:239:THR:HG22	1.99	0.44
1:A:284:ILE:HG12	1:A:365:GLU:HG3	1.98	0.44
1:A:110:LEU:CD2	1:A:324:LEU:HD12	2.48	0.43
1:A:616:VAL:HG12	1:A:698:LYS:HG2	2.00	0.43
1:A:714:VAL:CG2	1:A:728:ALA:HB2	2.47	0.43
1:A:103:LEU:HD11	1:A:296:THR:HG23	2.01	0.43
1:A:46:LEU:HD12	1:A:51:LEU:HD12	2.00	0.43
1:A:204:ARG:NH1	1:A:229:PRO:O	2.45	0.43
1:A:270:ILE:HD12	1:A:695:PRO:HB2	2.00	0.43
2:B:212:PRO:HG2	2:B:281:TYR:HB2	2.00	0.43
1:A:426:ALA:O	1:A:471:ARG:HD2	2.18	0.43
2:B:232:PHE:HB2	2:B:262:ALA:HB3	2.01	0.42
1:A:418:TRP:HZ2	1:A:463:CYS:SG	2.42	0.42
1:A:889:ARG:HA	1:A:889:ARG:HD3	1.83	0.42
2:B:213:LEU:HD23	2:B:261:LEU:HD13	2.01	0.42
1:A:780:LEU:O	1:A:783:ASN:HB2	2.20	0.42
1:A:925:SER:O	1:A:929:VAL:HG22	2.20	0.42
2:B:213:LEU:HD23	2:B:261:LEU:HD22	2.01	0.42
1:A:592:ILE:O	1:A:594:PRO:HD3	2.20	0.42
1:A:763:GLU:HA	1:A:832:MET:HE3	2.02	0.42
1:A:212:LYS:HB2	1:A:251:GLU:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:784:ILE:HD11	1:A:854:TYR:CG	2.55	0.41
1:A:223:GLU:HB2	10:A:2191:HOH:O	2.21	0.41
1:A:291:PHE:HA	1:A:294:ILE:HD12	2.02	0.41
1:A:531:LYS:HE3	1:A:534:MET:HG2	2.01	0.41
1:A:785:PRO:HB2	1:A:926:ILE:HD12	2.02	0.41
1:A:431:ALA:O	1:A:471:ARG:NH2	2.40	0.41
1:A:702:VAL:HG13	1:A:712:VAL:HG21	2.01	0.41
1:A:502:ARG:HD2	1:A:503:TYR:N	2.36	0.41
1:A:517:ARG:HD3	1:A:580:THR:O	2.20	0.41
1:A:620:HIS:HA	1:A:621:PRO:HD3	1.93	0.41
1:A:64:THR:HA	1:A:174:ASP:OD1	2.21	0.41
1:A:631:VAL:CG2	1:A:633:ILE:HG12	2.50	0.41
1:A:291:PHE:HB3	1:A:845:VAL:HB	2.03	0.40
1:A:618:GLY:O	1:A:692:ARG:HD2	2.21	0.40
1:A:136:LEU:O	1:A:140:VAL:HG23	2.22	0.40
1:A:440:VAL:HG23	1:A:445:ARG:HB3	2.03	0.40
1:A:905:GLN:HE21	2:B:182:ASN:HA	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	990/1028 (96%)	942 (95%)	42 (4%)	6 (1%)	21	51
2	B	262/305 (86%)	227 (87%)	32 (12%)	3 (1%)	11	36
3	G	37/74 (50%)	32 (86%)	4 (11%)	1 (3%)	4	15
All	All	1289/1407 (92%)	1201 (93%)	78 (6%)	10 (1%)	16	44

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	74	ALA
1	A	524	ASN
2	B	201	GLU
1	A	121	THR
1	A	128	ASP
2	B	171	ALA
1	A	123	ASP
1	A	576	PRO
1	A	1014	GLY
3	G	5	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	840/869 (97%)	792 (94%)	48 (6%)	18	49
2	B	234/266 (88%)	220 (94%)	14 (6%)	17	47
3	G	32/62 (52%)	31 (97%)	1 (3%)	35	70
All	All	1106/1197 (92%)	1043 (94%)	63 (6%)	18	49

All (63) 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	110	LEU
1	A	165	VAL
1	A	213	VAL
1	A	226	THR
1	A	231	PHE
1	A	248	ASN
1	A	250	VAL
1	A	255	ARG

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Mol	Chain	Res	Type
1	A	261	THR
1	A	275	SER
1	A	284	ILE
1	A	309	LEU
1	A	318	LEU
1	A	344	LEU
1	A	354	LYS
1	A	434	GLN
1	A	454	SER
1	A	457	LEU
1	A	471	ARG
1	A	502	ARG
1	A	515	LEU
1	A	522	LEU
1	A	524	ASN
1	A	530	LEU
1	A	531	LYS
1	A	581	THR
1	A	670	LEU
1	A	682	LEU
1	A	696	GLN
1	A	712	VAL
1	A	719	VAL
1	A	726	LYS
1	A	758	ILE
1	A	806	THR
1	A	822	LEU
1	A	833	LYS
1	A	886	LYS
1	A	935	ILE
1	A	968	LEU
1	A	974	THR
1	A	987	TRP
1	A	997	ILE
1	A	1019	GLN
2	B	28	ARG
2	B	52	ILE
2	B	73	VAL
2	B	108	LYS
2	B	135	ILE
2	B	139	ASP
2	B	176	CYS

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Mol	Chain	Res	Type
2	B	194	ASN
2	B	200	GLU
2	B	223	ARG
2	B	226	ILE
2	B	251	ARG
2	B	285	ILE
2	B	289	GLU
3	G	4	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	ASN
1	A	95	GLN
1	A	118	GLN
1	A	129	ASN
1	A	398	HIS
1	A	524	ASN
1	A	540	ASN
1	A	620	HIS
1	A	754	ASN
1	A	797	ASN
1	A	861	GLN
1	A	1019	GLN
2	B	95	ASN
2	B	194	ASN
2	B	207	ASN
2	B	258	GLN
2	B	271	ASN
2	B	284	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates

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	0.60	0	17,19,21	1.63	1 (5%)
4	NAG	C	2	4	14,14,15	0.90	1 (7%)	17,19,21	2.03	4 (23%)

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	-	1/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	2	NAG	C1-C2	2.41	1.55	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1	NAG	C1-O5-C5	5.81	119.98	112.19
4	C	2	NAG	C2-N2-C7	5.63	130.45	122.90
4	C	2	NAG	C1-O5-C5	4.28	117.93	112.19
4	C	2	NAG	C1-C2-N2	2.53	114.42	110.43
4	C	2	NAG	O7-C7-N2	2.00	125.52	121.98

There are no chirality outliers.

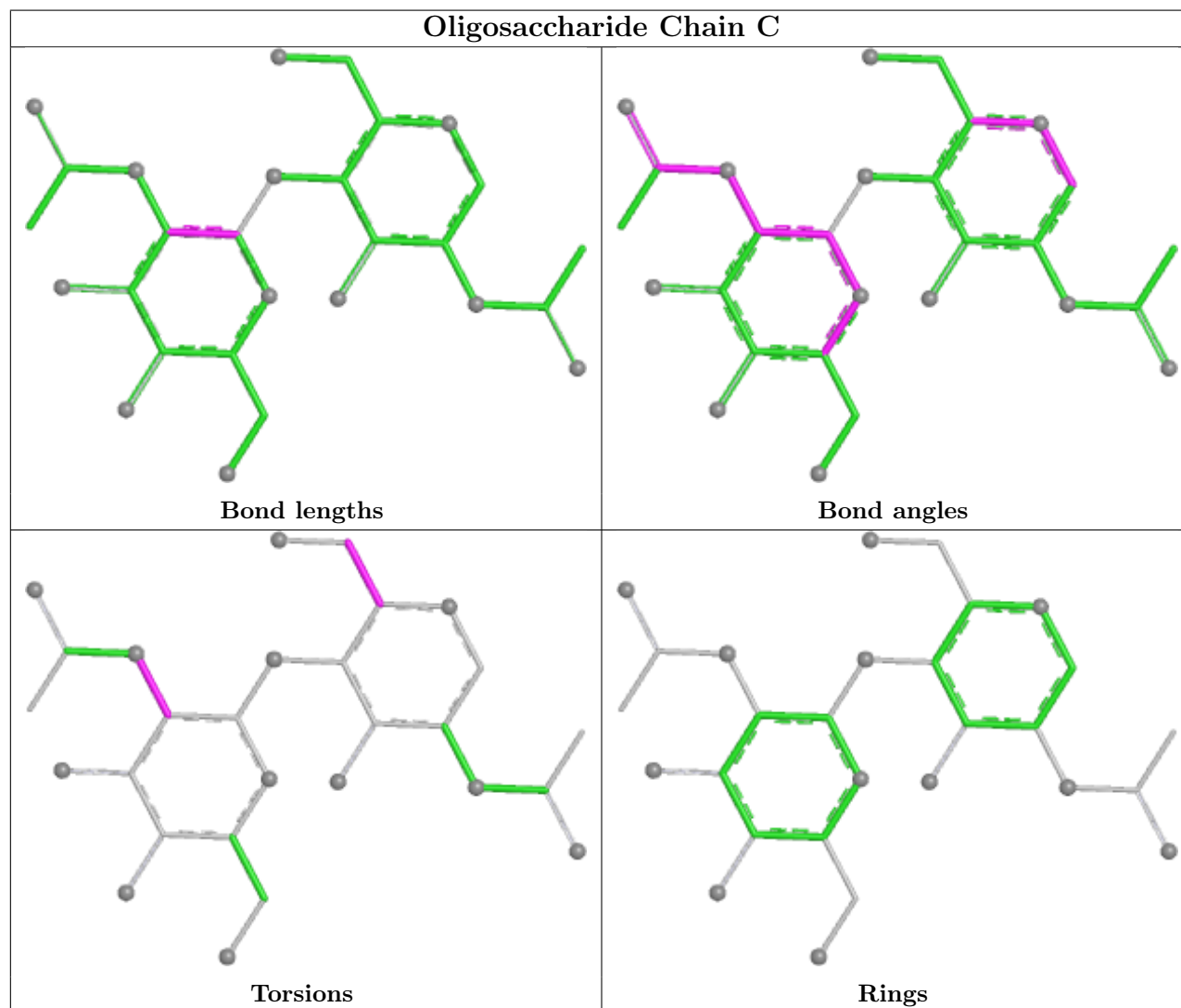
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
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 7 ligands modelled in this entry, 4 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	$\# Z > 2$
8	CLR	B	3001	-	31,31,31	0.82	0	48,48,48	1.49	9 (18%)
9	NAG	B	4021	2	14,14,15	0.80	0	17,19,21	1.14	1 (5%)
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
8	CLR	B	3001	-	-	2/10/68/68	0/4/4/4
9	NAG	B	4021	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	3001	CLR	C1-C2-C3	4.15	115.98	110.48
8	B	3001	CLR	C4-C5-C10	3.95	121.48	116.42
8	B	3001	CLR	C4-C5-C6	-3.27	116.13	120.57
8	B	3001	CLR	C16-C17-C13	2.76	107.08	103.84
9	B	4021	NAG	C1-O5-C5	2.60	115.68	112.19
8	B	3001	CLR	C2-C1-C10	2.49	118.08	112.78
8	B	3001	CLR	C21-C20-C22	-2.26	106.84	110.34
8	B	3001	CLR	C15-C14-C13	2.21	106.44	103.84
8	B	3001	CLR	C10-C9-C8	2.21	115.94	112.71
8	B	3001	CLR	C22-C20-C17	2.07	114.62	110.33

There are no chirality outliers.

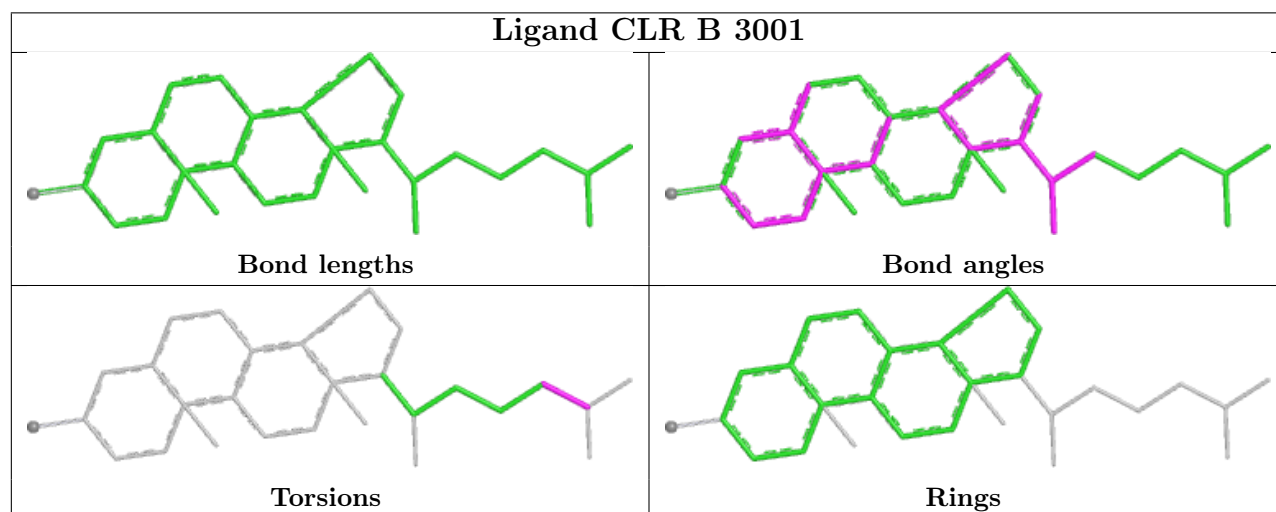
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	3001	CLR	C23-C24-C25-C26
8	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 [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%)	-0.56	2 (0%) 91 88	46, 77, 133, 193	0
2	B	268/305 (87%)	-0.10	1 (0%) 88 84	63, 123, 159, 173	0
3	G	39/74 (52%)	-0.51	0 100 100	63, 75, 136, 153	0
All	All	1299/1407 (92%)	-0.46	3 (0%) 91 88	46, 84, 149, 193	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	268	LEU	2.9
1	A	231	PHE	2.6
1	A	1023	TYR	2.1

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

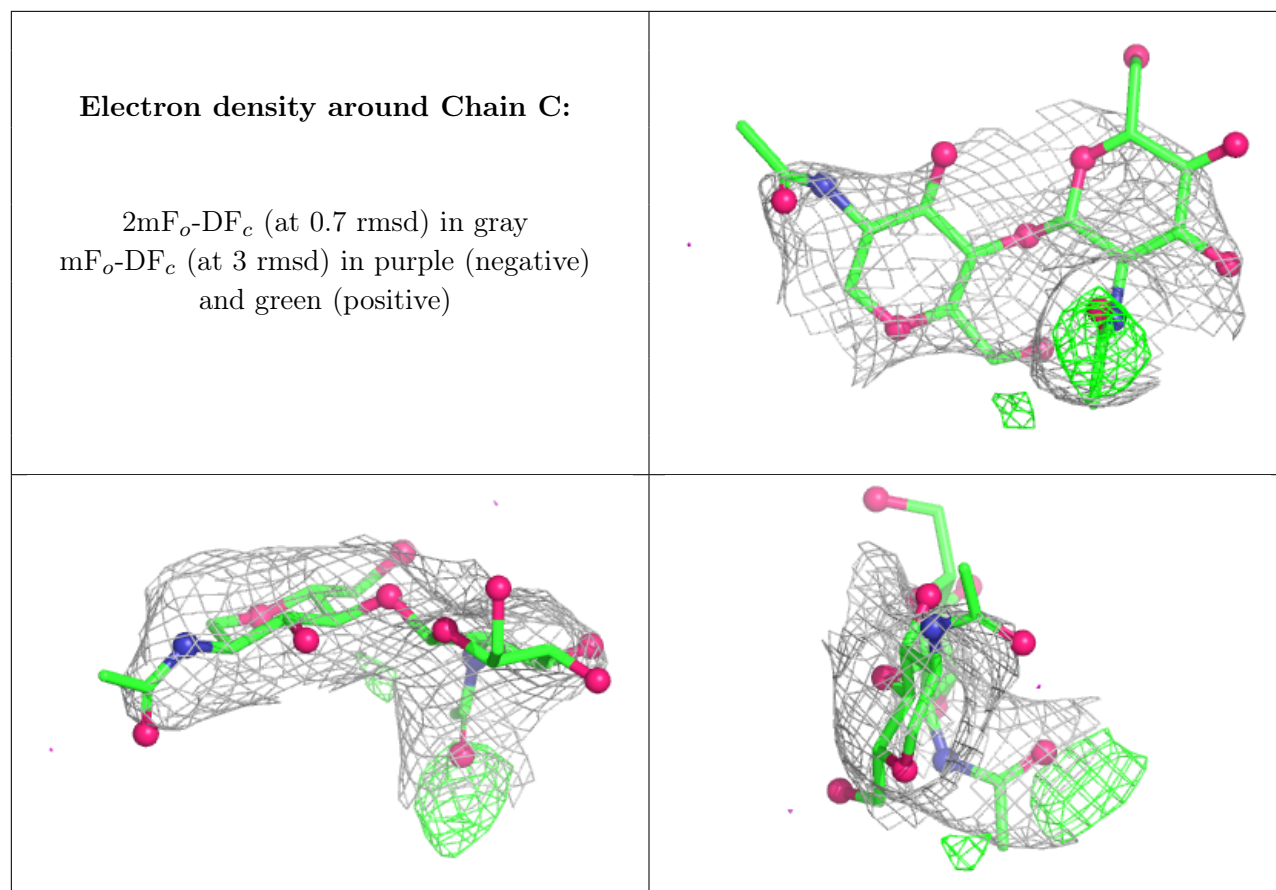
There are no non-standard protein/DNA/RNA residues in this entry.

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	-	-	122,139,146,150	0
4	NAG	C	2	14/15	-	-	121,153,160,161	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.

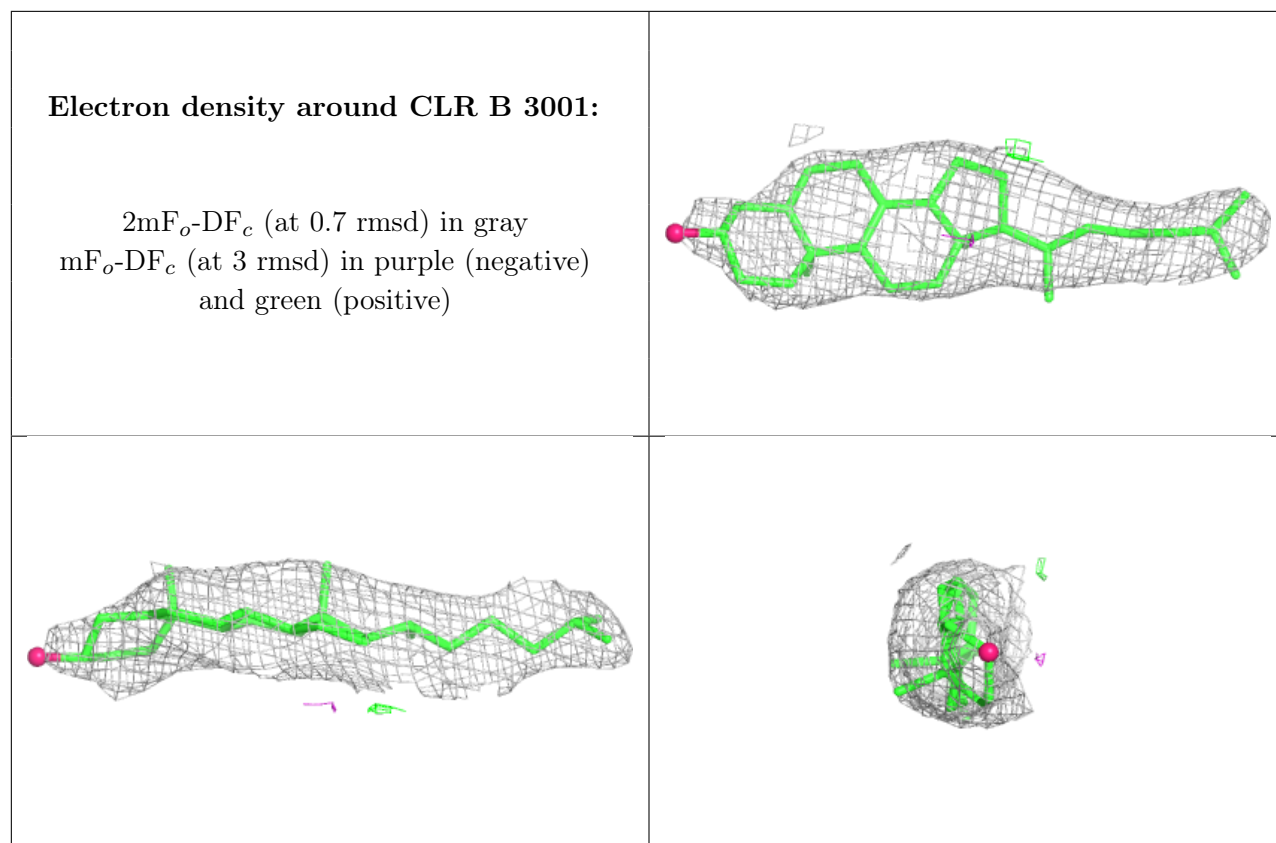


6.4 Ligands ⓘ

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
9	NAG	B	4021	14/15	0.75	0.07	133,144,149,157	0
8	CLR	B	3001	28/28	0.89	0.09	105,113,128,129	0
5	MF4	A	2001	5/5	0.97	0.07	48,48,50,55	0
7	K	A	2005	1/1	0.97	0.06	69,69,69,69	0
7	K	A	2003	1/1	0.98	0.03	70,70,70,70	0
7	K	A	2004	1/1	0.99	0.03	76,76,76,76	0
6	MG	A	2002	1/1	1.00	0.02	53,53,53,53	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.