



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:29 PM UTC

PDB ID : 5AVS / pdb_00005avs
Title : Kinetics by X-ray crystallography: Tl⁺-substitution of bound K⁺ in the E2.MgF42-.2K⁺ crystal after 3.5 min
Authors : Ogawa, H.; Cornelius, F.; Hirata, A.; Toyoshima, C.
Deposited on : 2015-07-01
Resolution : 2.90 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

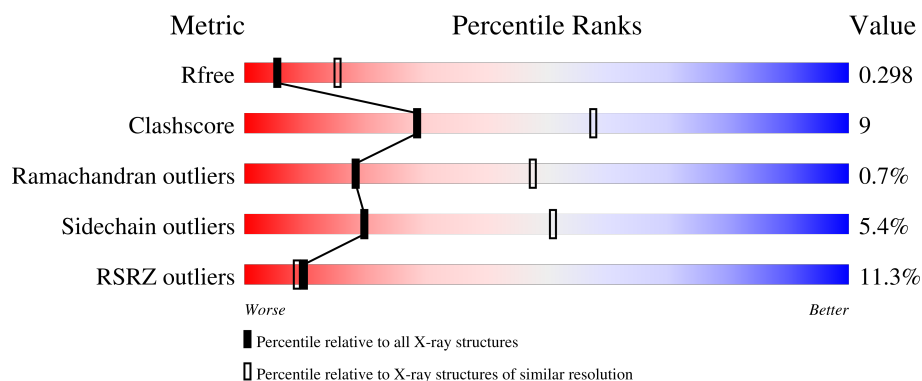
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 10236 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	2	Total	K	0	2
			2	2		

- Molecule 8 is THALLIUM (I) ION (CCD ID: TL) (formula: Tl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	3	Total	Tl	0	2
			3	3		

- Molecule 9 is CHOLESTEROL (CCD ID: 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 (CCD ID: 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		

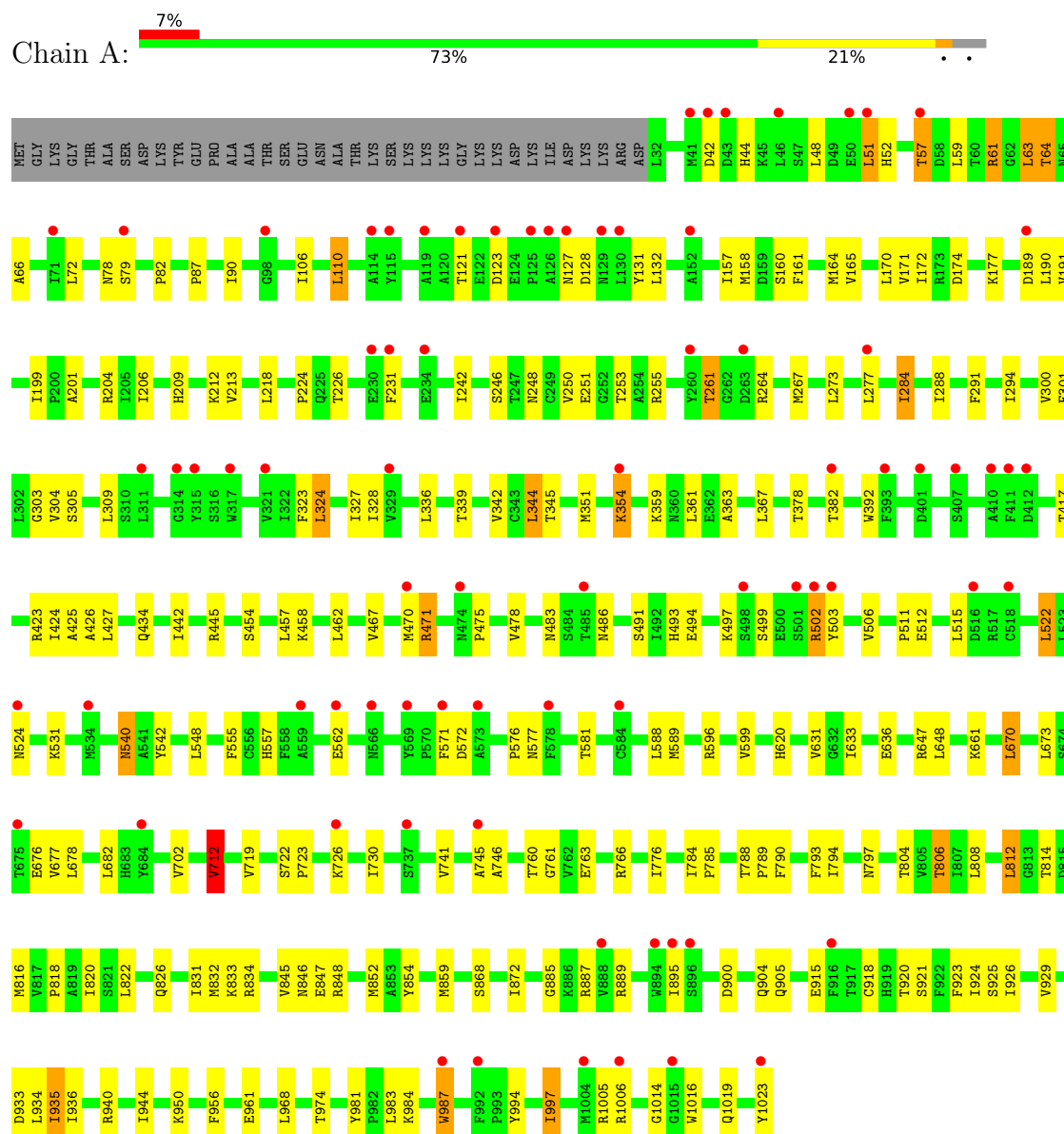
- Molecule 11 is water.

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

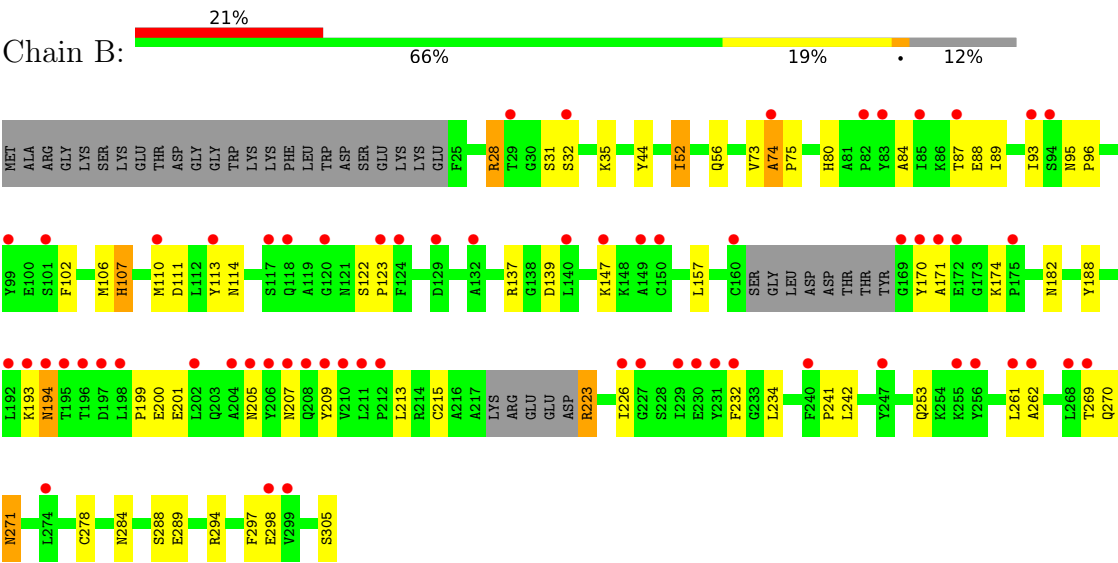
3 Residue-property plots [i](#)

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.

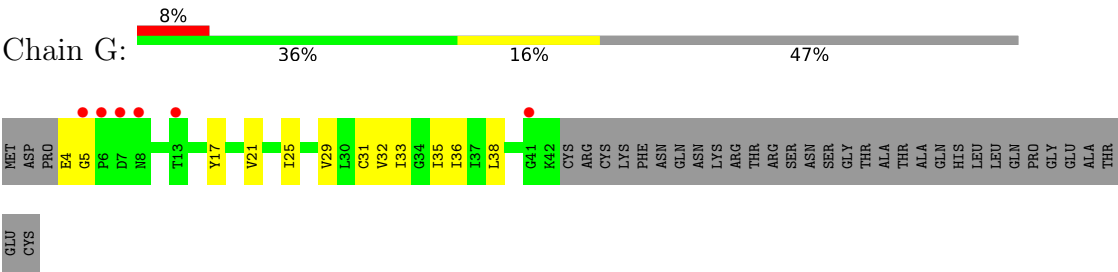
- Molecule 1: Na, K-ATPase alpha subunit



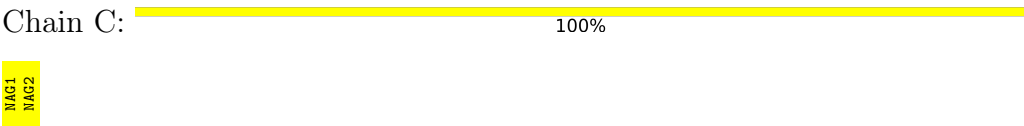
- Molecule 2: Na⁺,K⁺-ATPase beta subunit



• 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	221.90Å 50.87Å 164.19Å 90.00° 104.45° 90.00°	Depositor
Resolution (Å)	14.99 – 2.90 14.99 – 2.90	Depositor EDS
% Data completeness (in resolution range)	70.2 (14.99-2.90) 87.0 (14.99-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.83 (at 2.90Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.285 , 0.284 0.289 , 0.298	Depositor DCC
R_{free} test set	1106 reflections (2.74%)	wwPDB-VP
Wilson B-factor (Å ²)	57.9	Xtriage
Anisotropy	0.439	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	10236	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage'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: MG, MF4, NAG, TL, K, CLR

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	0.49	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	114	ASN	C-N	-6.64	1.24	1.34
2	B	113	TYR	C-N	6.51	1.42	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	620	HIS	CA-C-N	5.63	125.30	119.05
1	A	620	HIS	C-N-CA	5.63	125.30	119.05
2	B	174	LYS	CA-C-N	5.32	126.49	119.84
2	B	174	LYS	C-N-CA	5.32	126.49	119.84
1	A	712	VAL	N-CA-C	5.30	115.53	108.11
1	A	42	ASP	N-CA-C	5.24	116.25	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	132	0
2	B	2174	0	2146	47	0
3	G	305	0	318	8	0
4	C	28	0	25	0	0
5	A	5	0	0	0	0
6	A	1	0	0	0	0
7	A	2	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
11	A	1	0	0	0	0
All	All	10236	0	10247	181	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 9.

All (181) 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: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	0.69
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
2:B:213:LEU:HD11	2:B:278:CYS:HB3	1.78	0.65
1:A:935:ILE:HG23	1:A:944:ILE:HD12	1.77	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	0.64
2:B:74:ALA:CB	2:B:75:PRO:HD3	2.23	0.63
1:A:816:MET:O	1:A:820:ILE:HG12	1.97	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
2:B:110:MET:HE1	2:B:157:LEU:HD13	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:483:ASN:HB2	1:A:486:ASN:HB2	1.82	0.60
1:A:363:ALA:HB1	1:A:730:ILE:HD12	1.83	0.60
1:A:161:PHE:HA	1:A:164:MET:HE3	1.83	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
2:B:28:ARG:NH1	9:B:3001:CLR:H22	2.16	0.59
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:766:ARG:HD2	1:A:832:MET:HE1	1.86	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
1:A:491:SER:HB3	1:A:493:HIS:NE2	2.19	0.57
2:B:193:LYS:HA	2:B:207:ASN:ND2	2.20	0.57
1:A:467:VAL:HA	1:A:470:MET:HE3	1.87	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:172:ILE:HD13	1:A:177:LYS:HB3	1.87	0.56
1:A:933:ASP:HA	1:A:936:ILE:HG12	1.86	0.55
1:A:190:LEU:HD11	1:A:206:ILE:HD11	1.88	0.55
1:A:157:ILE:HD11	1:A:745:ALA:HA	1.88	0.55
1:A:994:TYR:O	1:A:997:ILE:HG22	2.06	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	1.89	0.55
1:A:261:THR:HG22	1:A:264:ARG:HH21	1.71	0.55
1:A:596:ARG:HB2	1:A:599:VAL:HG23	1.89	0.55
1:A:905:GLN:HE21	2:B:182:ASN:HA	1.71	0.54
1:A:64:THR:HG22	1:A:66:ALA:N	2.23	0.54
1:A:924:ILE:HD12	1:A:983:LEU:HD12	1.89	0.54
1:A:994:TYR:HA	1:A:997:ILE:HG22	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:984:LYS:H	1:A:987:TRP:CD1	2.26	0.54
1:A:1016:TRP:HE1	2:B:35:LYS:HE3	1.72	0.54
1:A:921:SER:HA	1:A:983:LEU:HD11	1.90	0.53
1:A:763:GLU:HA	1:A:832:MET:HE3	1.90	0.53
2:B:213:LEU:HD23	2:B:261:LEU:HD13	1.89	0.53
1:A:424:ILE:HG23	1:A:506:VAL:HB	1.90	0.53
1:A:51:LEU:CD1	1:A:204:ARG:HG3	2.36	0.53
1:A:324:LEU:O	1:A:328:ILE:HG12	2.09	0.52
1:A:161:PHE:HA	1:A:164:MET:CE	2.39	0.52
1:A:555:PHE:CZ	1:A:589:MET:HE3	2.44	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
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
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:956:PHE:CE1	3:G:38:LEU:HD22	2.47	0.50
1:A:571:PHE:HA	1:A:577:ASN:HD22	1.76	0.50
1:A:676:GLU:H	1:A:676:GLU:CD	2.20	0.50
1:A:832:MET:HE2	1:A:832:MET:HA	1.94	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:847:GLU:CD	1:A:847:GLU:H	2.20	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
3:G:4:GLU:CD	3:G:5:GLY:H	2.23	0.47
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:132:LEU:HD21	1:A:804:THR:HG21	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
2:B:80:HIS:HB3	2:B:297:PHE:CZ	2.50	0.47
3:G:31:CYS:O	3:G:35:ILE:HG12	2.14	0.47
2:B:87:THR:HB	2:B:298:GLU:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:215:CYS:HA	2:B:278:CYS:HA	1.96	0.46
1:A:336:LEU:HD11	1:A:776:ILE:HG12	1.96	0.46
1:A:63:LEU:HD22	1:A:189:ASP:HB3	1.96	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
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:303:GLY:HA2	1:A:327:ILE:HG21	1.97	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	1.99	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:52:HIS:HE2	1:A:59:LEU:HD12	1.82	0.44
1:A:915:GLU:O	1:A:918:CYS:HB2	2.17	0.44
1:A:557:HIS:CD2	1:A:557:HIS:C	2.95	0.44
1:A:806:THR:HG22	1:A:923:PHE:HB2	2.00	0.44
2:B:194:ASN:HD22	2:B:194:ASN:N	2.15	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
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
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: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
1:A:64:THR:HA	1:A:174:ASP:OD1	2.19	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
1:A:661:LYS:HE2	1:A:661:LYS:HA	2.00	0.42
1:A:797:ASN:HB3	1:A:885:GLY:HA2	2.01	0.42
1:A:1016:TRP:CD1	2:B:35:LYS:HZ2	2.37	0.42
2:B:95:ASN:HA	2:B:96:PRO:HD3	1.86	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:PHE:HB3	1:A:845:VAL:HB	2.02	0.42
1:A:291:PHE:HA	1:A:294:ILE:HD12	2.01	0.42
1:A:852:MET:HE3	1:A:852:MET:HB3	1.90	0.42
2:B:74:ALA:CB	2:B:75:PRO:CD	2.92	0.42
2:B:89:ILE:HG22	2:B:102:PHE:CE2	2.55	0.42
2:B:223:ARG:HB2	2:B:223:ARG:HH11	1.85	0.42
1:A:512:GLU:H	1:A:512:GLU:CD	2.28	0.42
1:A:48:LEU:HD23	1:A:59:LEU:HD11	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: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
1:A:110:LEU:CD2	1:A:324:LEU:HD12	2.50	0.41
1:A:367:LEU:HD23	1:A:761:GLY:HA3	2.01	0.41
1:A:785:PRO:HB2	1:A:926:ILE:CD1	2.50	0.41
2:B:271:ASN:HD21	2:B:305:SER:N	2.19	0.41
1:A:502:ARG:HE	1:A:562:GLU:HG2	1.85	0.41
1:A:846:ASN:ND2	1:A:848:ARG:HB2	2.35	0.41
3:G:17:TYR:O	3:G:21:VAL:HG23	2.21	0.41
1:A:44:HIS:HB3	1:A:242:ILE:HD11	2.03	0.41
1:A:920:THR:HG21	1:A:981:TYR:O	2.20	0.41
1:A:342:VAL:HB	1:A:820:ILE:HD12	2.03	0.41
1:A:426:ALA:O	1:A:471:ARG:HD2	2.20	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:284:ILE:O	1:A:288:ILE:HG12	2.21	0.41
1:A:458:LYS:O	1:A:462:LEU:HB2	2.21	0.41
1:A:859:MET:HG2	2:B:44:TYR:CE2	2.55	0.41
1:A:301:PHE:O	1:A:305:SER:HB2	2.20	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:925:SER:O	1:A:929:VAL:HG22	2.21	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

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%)	43 (4%)	5 (0%)	24	54
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	48

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

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1106/1197 (92%)	1046 (95%)	60 (5%)	20	51

All (60) 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	64	THR
1	A	72	LEU
1	A	79	SER
1	A	110	LEU
1	A	165	VAL
1	A	213	VAL
1	A	218	LEU
1	A	226	THR
1	A	231	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	324	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	531	LYS
1	A	540	ASN
1	A	548	LEU
1	A	581	THR
1	A	636	GLU
1	A	670	LEU
1	A	682	LEU

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Mol	Chain	Res	Type
1	A	712	VAL
1	A	719	VAL
1	A	726	LYS
1	A	806	THR
1	A	812	LEU
1	A	822	LEU
1	A	833	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	107	HIS
2	B	139	ASP
2	B	194	ASN
2	B	200	GLU
2	B	223	ARG
2	B	271	ASN
2	B	289	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	GLN
1	A	129	ASN
1	A	163	ASN
1	A	168	GLN
1	A	225	GLN
1	A	248	ASN
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	708	GLN
1	A	754	ASN
1	A	797	ASN

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Mol	Chain	Res	Type
1	A	826	GLN
1	A	861	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 ⓘ

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	0.50	0	17,19,21	0.92	1 (5%)
4	NAG	C	2	4	14,14,15	0.67	0	17,19,21	1.44	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	4.21	128.54	122.90
4	C	1	NAG	C1-O5-C5	2.72	115.83	112.19

There are no chirality outliers.

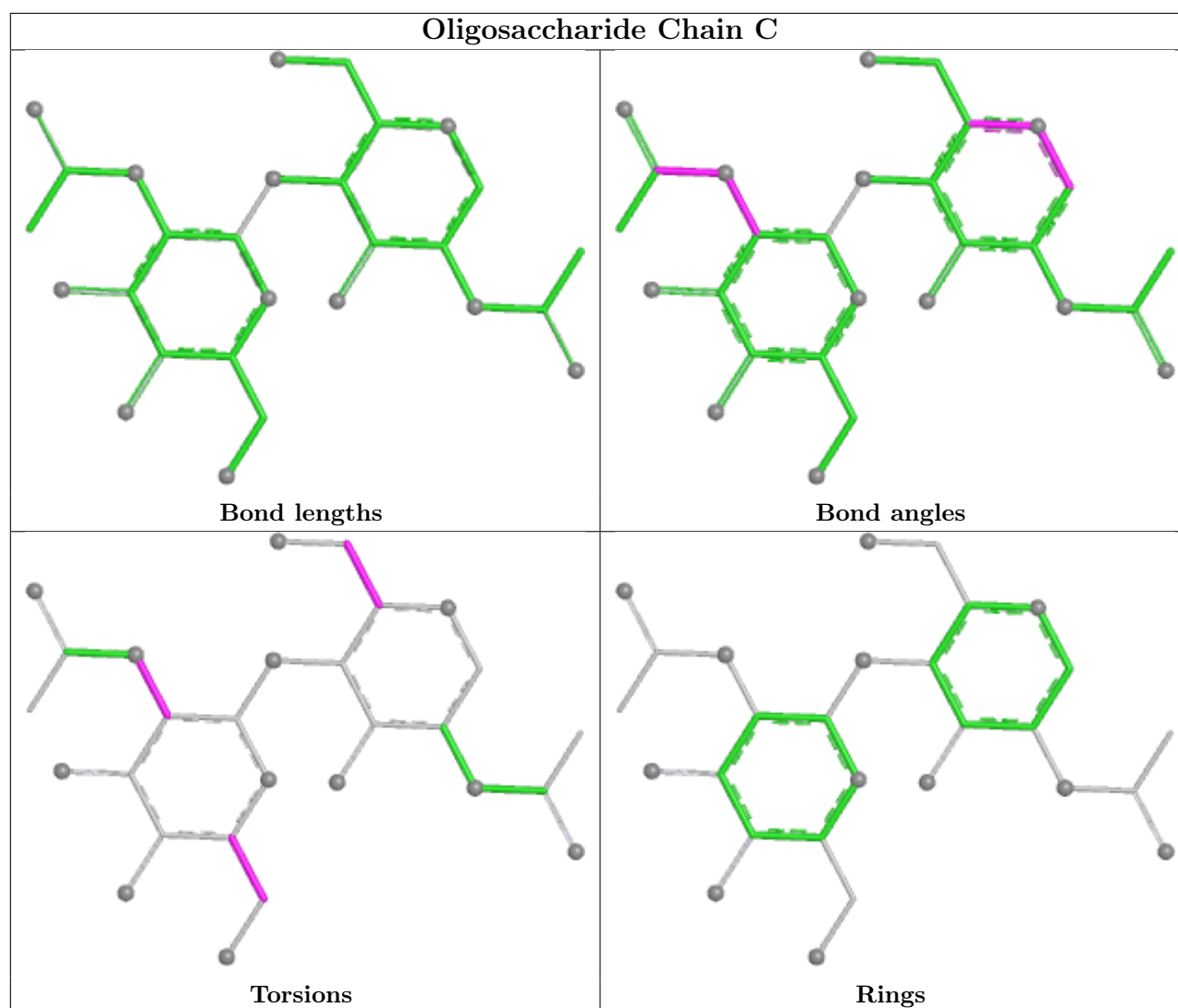
All (4) torsion outliers are listed below:

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 9 ligands modelled in this entry, 6 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	0.63	0	17,19,21	1.25	2 (11%)
9	CLR	B	3001	-	31,31,31	0.47	0	48,48,48	1.13	5 (10%)
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	2.99	107.36	103.84
9	B	3001	CLR	C4-C5-C6	-2.60	117.05	120.57
10	B	4021	NAG	C1-O5-C5	2.59	115.66	112.19
9	B	3001	CLR	C4-C5-C10	2.55	119.69	116.42
9	B	3001	CLR	C1-C2-C3	2.47	113.75	110.48
10	B	4021	NAG	C4-C3-C2	2.30	114.39	111.02
9	B	3001	CLR	C12-C11-C9	2.04	116.61	113.14

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

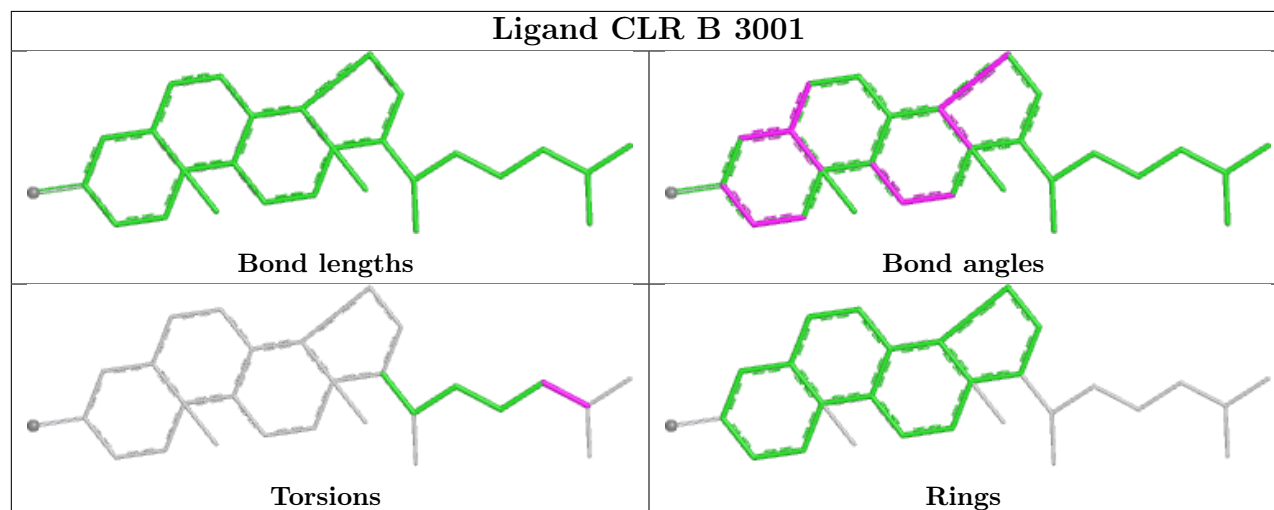
There are no ring outliers.

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

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%)	0.80	77 (7%) 19 16	54, 76, 117, 142	0
2	B	268/305 (87%)	1.35	64 (23%) 2 2	74, 125, 150, 160	0
3	G	39/74 (52%)	0.93	6 (15%) 5 4	71, 80, 123, 126	0
All	All	1299/1407 (92%)	0.92	147 (11%) 10 9	54, 81, 138, 160	0

All (147) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	57	THR	4.7
1	A	534	MET	4.4
1	A	573	ALA	4.0
2	B	298	GLU	4.0
2	B	93	ILE	4.0
2	B	231	TYR	3.9
2	B	74	ALA	3.9
1	A	566	ASN	3.8
2	B	268	LEU	3.8
1	A	470	MET	3.7
1	A	571	PHE	3.5
2	B	124	PHE	3.5
2	B	117	SER	3.4
1	A	412	ASP	3.4
3	G	6	PRO	3.3
1	A	126	ALA	3.2
2	B	99	TYR	3.2
1	A	894	TRP	3.1
1	A	987	TRP	3.1
1	A	737	SER	3.1
1	A	315	TYR	3.1
2	B	207	ASN	3.1
2	B	227	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	169	GLY	3.0
1	A	675	THR	3.0
1	A	502	ARG	3.0
2	B	150	CYS	3.0
1	A	1023	TYR	3.0
1	A	311	LEU	2.9
1	A	411	PHE	2.9
2	B	170	TYR	2.9
1	A	916	PHE	2.9
1	A	584	CYS	2.9
1	A	98	GLY	2.9
2	B	210	VAL	2.9
1	A	51	LEU	2.9
1	A	503	TYR	2.8
2	B	132	ALA	2.8
2	B	202	LEU	2.8
1	A	263	ASP	2.8
2	B	149	ALA	2.7
1	A	1004	MET	2.7
2	B	29	THR	2.7
2	B	175	PRO	2.7
2	B	230	GLU	2.7
2	B	262	ALA	2.7
2	B	209	TYR	2.7
3	G	13	THR	2.7
2	B	198	LEU	2.7
2	B	229	ILE	2.7
1	A	260	TYR	2.7
2	B	160	CYS	2.7
1	A	314	GLY	2.7
1	A	578	PHE	2.6
1	A	42	ASP	2.6
3	G	7	ASP	2.6
2	B	204	ALA	2.6
1	A	129	ASN	2.6
2	B	247	TYR	2.5
1	A	485	THR	2.5
2	B	195	THR	2.5
1	A	125	PRO	2.5
2	B	123	PRO	2.5
1	A	569	TYR	2.5
1	A	726	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	231	PHE	2.5
1	A	234	GLU	2.5
2	B	110	MET	2.5
1	A	516	ASP	2.4
1	A	79	SER	2.4
2	B	192	LEU	2.4
1	A	896	SER	2.4
1	A	562	GLU	2.4
1	A	992	PHE	2.4
2	B	274	LEU	2.4
2	B	171	ALA	2.4
2	B	269	THR	2.4
2	B	211	LEU	2.4
2	B	261	LEU	2.4
1	A	393	PHE	2.4
1	A	152	ALA	2.4
2	B	196	THR	2.4
2	B	85	ILE	2.4
1	A	321	VAL	2.3
3	G	5	GLY	2.3
2	B	232	PHE	2.3
2	B	240	PHE	2.3
1	A	501	SER	2.3
1	A	888	VAL	2.3
1	A	474	ASN	2.3
3	G	41	GLY	2.3
1	A	745	ALA	2.3
1	A	277	LEU	2.3
2	B	140	LEU	2.3
2	B	32	SER	2.3
1	A	115	TYR	2.3
1	A	114	ALA	2.2
1	A	127	ASN	2.2
2	B	194	ASN	2.2
2	B	120	GLY	2.2
2	B	172	GLU	2.2
2	B	118	GLN	2.2
1	A	895	ILE	2.2
1	A	189	ASP	2.2
2	B	82	PRO	2.2
1	A	317	TRP	2.2
2	B	94	SER	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	147	LYS	2.2
2	B	193	LYS	2.2
1	A	46	LEU	2.2
1	A	130	LEU	2.2
1	A	1006	ARG	2.2
2	B	226	ILE	2.2
1	A	524	ASN	2.2
2	B	197	ASP	2.2
1	A	518	CYS	2.2
1	A	407	SER	2.2
1	A	401	ASP	2.1
2	B	129	ASP	2.1
2	B	255	LYS	2.1
1	A	684	TYR	2.1
2	B	206	TYR	2.1
2	B	256	TYR	2.1
1	A	119	ALA	2.1
1	A	559	ALA	2.1
1	A	121	THR	2.1
1	A	1015	GLY	2.1
2	B	87	THR	2.1
1	A	41	MET	2.1
1	A	410	ALA	2.1
1	A	329	VAL	2.1
2	B	299	VAL	2.1
1	A	230	GLU	2.1
1	A	354	LYS	2.0
1	A	498	SER	2.0
2	B	101	SER	2.0
2	B	208	GLN	2.0
2	B	212	PRO	2.0
3	G	8	ASN	2.0
1	A	382	THR	2.0
1	A	123	ASP	2.0
1	A	50	GLU	2.0
2	B	83	TYR	2.0
2	B	113	TYR	2.0
2	B	205	ASN	2.0
1	A	71	ILE	2.0
1	A	43	ASP	2.0

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

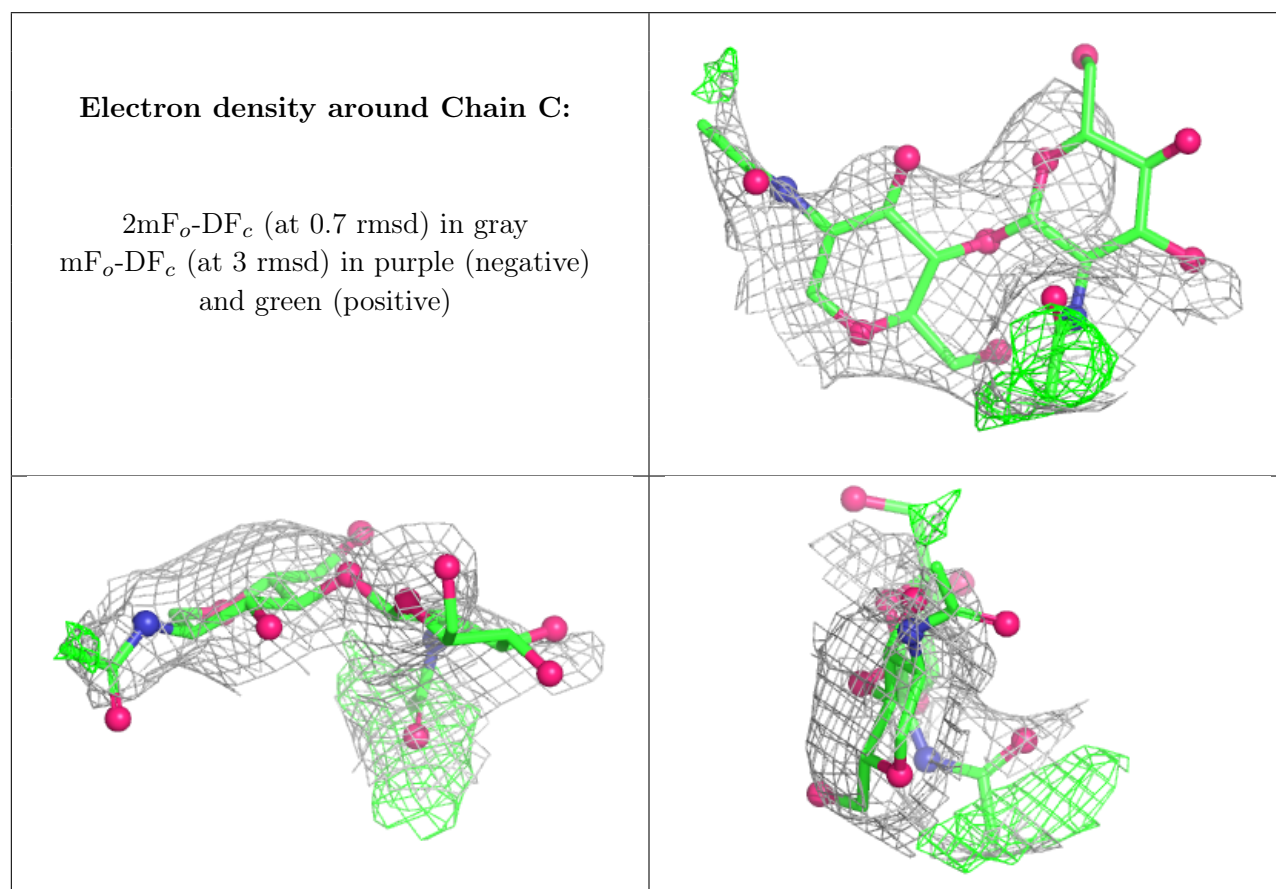
There are no non-standard protein/DNA/RNA residues in this entry.

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	1	14/15	-	-	132,135,136,137	0
4	NAG	C	2	14/15	-	-	139,139,140,140	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.

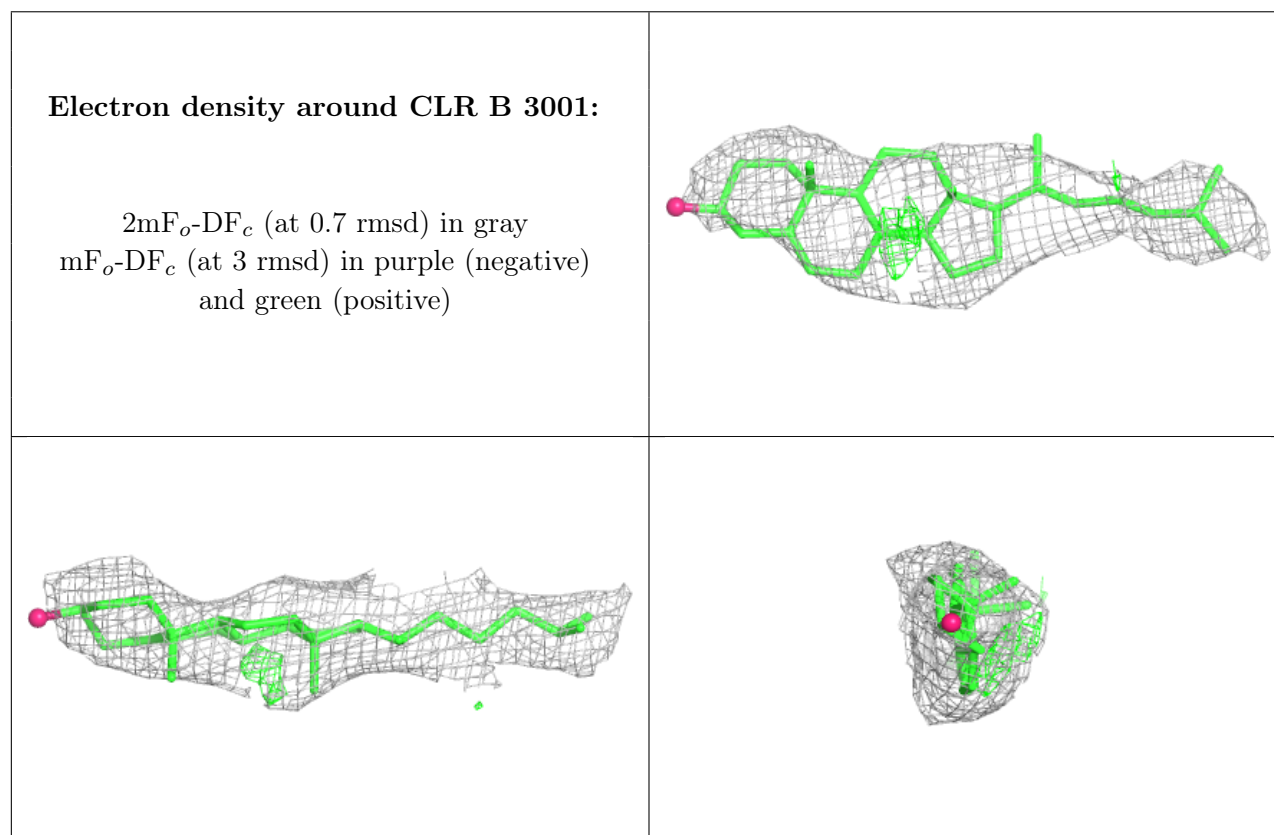


6.4 Ligands ⓘ

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
10	NAG	B	4021	14/15	0.54	0.15	138,139,139,139	0
9	CLR	B	3001	28/28	0.77	0.15	118,118,118,118	0
6	MG	A	2002	1/1	0.80	0.19	56,56,56,56	0
5	MF4	A	2001	5/5	0.91	0.17	59,61,62,62	0
8	TL	A	2005	1/1	0.94	0.07	77,77,77,77	0
8	TL	A	2004[B]	1/1	0.95	0.21	77,77,77,77	1
7	K	A	2003[A]	1/1	0.95	0.21	77,77,77,77	1
8	TL	A	2007[B]	1/1	0.98	0.14	72,72,72,72	1
7	K	A	2006[A]	1/1	1.00	0.14	72,72,72,72	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.