



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 11:57 AM EDT

PDB ID : 2ZXE / pdb_00002zxe
Title : Crystal structure of the sodium - potassium pump in the E2.2K+.Pi state
Authors : Shinoda, T.; Ogawa, H.; Cornelius, F.; Toyoshima, C.
Deposited on : 2008-12-22
Resolution : 2.40 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 : 9.0.015 (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

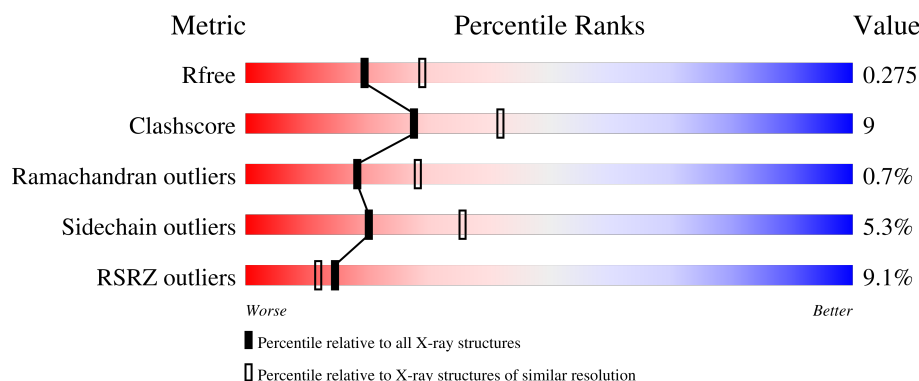
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

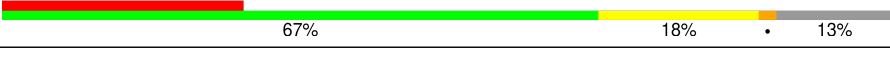
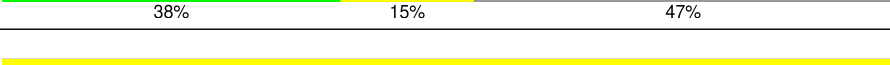
The reported resolution of this entry is 2.40 Å.

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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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

There are 10 unique types of molecules in this entry. The entry contains 10340 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	265	Total	C	N	O	S	0	0	0
			2151	1392	355	393	11			

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

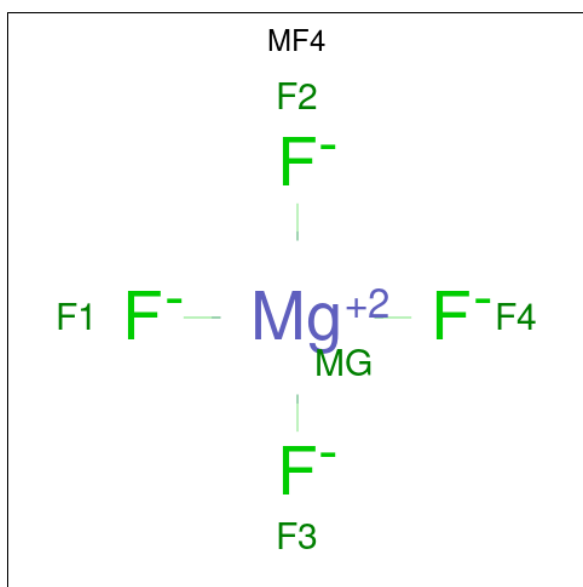
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	39	Total	C	N	O	S	0	0	0
			305	200	50	54	1			

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-alpha-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	A	1	Total	C	O	0	0
			28	27	1		

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

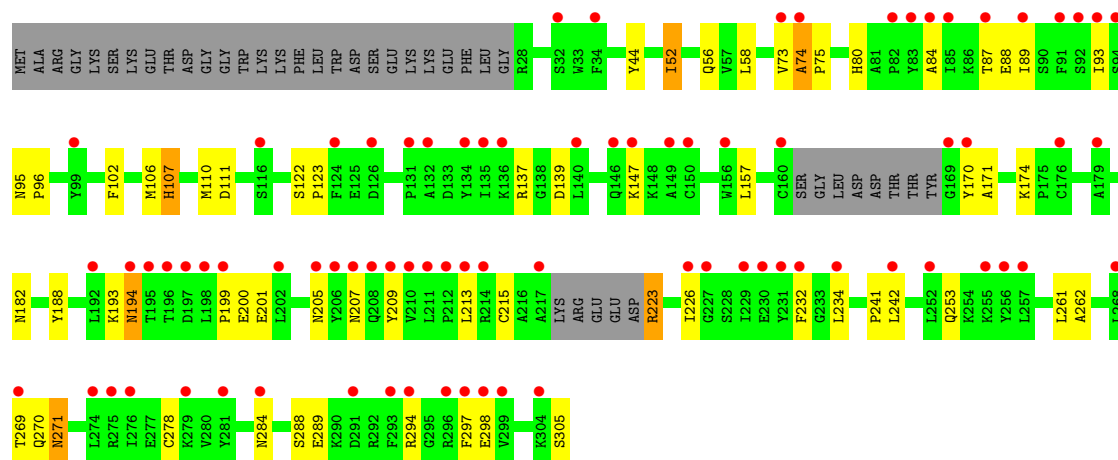


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 10 is water.

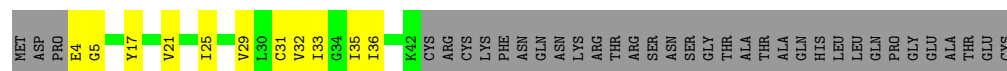
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	130	Total 130	O 130	0	0

Chain B: 

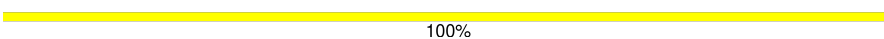


- Molecule 3: Phospholemman-like protein

Chain G: 



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

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	223.81Å 50.91Å 163.79Å 90.00° 105.12° 90.00°	Depositor
Resolution (Å)	15.00 – 2.40 15.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (15.00-2.40) 98.6 (15.00-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.246 , 0.271 0.246 , 0.275	Depositor DCC
R_{free} test set	3555 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	50.1	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10340	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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: NDG, NAG, CLR, K, MG, 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	0.49	0/7825	0.83	4/10616 (0.0%)
2	B	0.42	0/2205	0.75	2/2970 (0.1%)
3	G	0.49	0/309	0.81	0/419
All	All	0.47	0/10339	0.81	6/14005 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	620	HIS	CA-C-N	5.57	125.24	119.05
1	A	620	HIS	C-N-CA	5.57	125.24	119.05
2	B	174	LYS	CA-C-N	5.34	126.52	119.84
2	B	174	LYS	C-N-CA	5.34	126.52	119.84
1	A	712	VAL	N-CA-C	5.27	115.49	108.11
1	A	42	ASP	N-CA-C	5.25	116.27	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	137	0
2	B	2151	0	2123	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	305	0	318	7	0
4	C	28	0	24	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	28	0	46	0	0
9	B	14	0	13	0	0
10	A	130	0	0	5	0
All	All	10340	0	10223	183	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 (183) 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	1.65	0.79
1:A:261:THR:HG21	10:A:5063:HOH:O	1.84	0.76
1:A:497:LYS:HE2	1:A:499:SER:HB2	1.69	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:677:VAL:HG21	10:A:5074:HOH:O	1.87	0.73
1:A:261:THR:HG22	1:A:264:ARG:NH2	2.02	0.73
1:A:51:LEU:HD13	1:A:204:ARG:HG3	1.69	0.71
2:B:270:GLN:HG2	2:B:271:ASN:HD22	1.58	0.68
1:A:766:ARG:HD2	1:A:832:MET:CE	2.24	0.68
1:A:339:THR:HG23	1:A:820:ILE:HD13	1.77	0.67
1:A:905:GLN:NE2	2:B:182:ASN:HA	2.11	0.65
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:160:SER:HB3	1:A:741:VAL:HG22	1.80	0.64
1:A:78:ASN:HA	1:A:261:THR:HG23	1.79	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:110:MET:HE1	2:B:157:LEU:HD13	1.79	0.63
1:A:673:LEU:HD22	1:A:677:VAL:HG11	1.80	0.63
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:PHE:O	1:A:327:ILE:HG12	2.01	0.61
3:G:29:VAL:O	3:G:33:ILE:HG12	2.00	0.60
1:A:363:ALA:HB1	1:A:730:ILE:HD12	1.83	0.60
1:A:483:ASN:HB2	1:A:486:ASN:HB2	1.82	0.60
1:A:161:PHE:HA	1:A:164:MET:HE3	1.83	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
1:A:905:GLN:HE21	2:B:182:ASN:HA	1.66	0.60
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
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
1:A:491:SER:HB3	1:A:493:HIS:NE2	2.20	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
2:B:74:ALA:HB3	2:B:75:PRO:CD	2.29	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
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	0.55
1:A:924:ILE:HD12	1:A:983:LEU:HD12	1.89	0.54
1:A:64:THR:HG22	1:A:66:ALA:N	2.23	0.54
1:A:223:GLU:HB2	10:A:5106:HOH:O	2.07	0.54
1:A:994:TYR:HA	1:A:997:ILE:HG22	1.89	0.54
1:A:984:LYS:H	1:A:987:TRP:CD1	2.26	0.54
1:A:921:SER:HA	1:A:983:LEU:HD11	1.90	0.54
2:B:213:LEU:HD23	2:B:261:LEU:HD13	1.89	0.53
1:A:763:GLU:HA	1:A:832:MET:HE3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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	0.53
1:A:555:PHE:CZ	1:A:589:MET:HE3	2.44	0.52
1:A:161:PHE:HA	1:A:164:MET:CE	2.39	0.52
1:A:212:LYS:HD3	1:A:224:PRO:HB2	1.90	0.52
1:A:808:LEU:O	1:A:812:LEU:HB2	2.10	0.52
2:B:75:PRO:HG2	2:B:294:ARG:NH2	2.25	0.52
3:G:32:VAL:O	3:G:36:ILE:HG12	2.09	0.52
1:A:82:PRO:HA	1:A:158:MET:HG2	1.92	0.51
3:G:25:ILE:O	3:G:29:VAL:HG23	2.11	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
1:A:417:THR:HA	1:A:522:LEU:HD22	1.93	0.51
2:B:288:SER:HB2	2:B:294:ARG:HH11	1.76	0.50
1:A:571:PHE:HA	1:A:577:ASN:HD22	1.76	0.50
1:A:832:MET:HE2	1:A:832:MET:HA	1.93	0.50
1:A:676:GLU:H	1:A:676:GLU:CD	2.20	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
1:A:323:PHE:CE1	1:A:793:PHE:HE2	2.32	0.47
3:G:4:GLU:CD	3:G:5:GLY:H	2.23	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:132:LEU:HD21	1:A:804:THR:HG21	1.97	0.47
3:G:31:CYS:O	3:G:35:ILE:HG12	2.14	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
1:A:622:ILE:HG12	10:A:5110:HOH:O	2.14	0.47
2:B:87:THR:HB	2:B:298:GLU:O	2.14	0.47
1:A:336:LEU:HD11	1:A:776:ILE:HG12	1.96	0.46
2:B:215:CYS:HA	2:B:278:CYS:HA	1.96	0.46
1:A:127:ASN:HB3	1:A:131:TYR:CD1	2.50	0.46
1:A:924:ILE:HD12	1:A:983:LEU:CD1	2.45	0.46
1:A:63:LEU:HD22	1:A:189:ASP:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:234:GLU:HG2	10:A:5124:HOH:O	2.14	0.46
2:B:74:ALA:CB	2:B:75:PRO:CD	2.92	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
2:B:122:SER:HA	2:B:123:PRO:HA	1.75	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:889:ARG:HD2	1:A:895:ILE:CD1	2.46	0.45
1:A:475:PRO:HD2	1:A:494:GLU:HB2	1.99	0.45
2:B:84:ALA:HB1	2:B:88:GLU:N	2.32	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:557:HIS:CD2	1:A:557:HIS:C	2.95	0.44
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
2:B:194:ASN:HD22	2:B:194:ASN:N	2.15	0.44
1:A:806:THR:HG22	1:A:923:PHE:HB2	2.00	0.44
1:A:859:MET:HG2	2:B:44:TYR:CE2	2.53	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	0.44
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: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
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: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: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
2:B:188:TYR:O	2:B:284:ASN:ND2	2.53	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	1.84	0.42
1:A:170:LEU:HD21	1:A:177:LYS:HD3	2.00	0.42
1:A:291:PHE:HB3	1:A:845:VAL:HB	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:852:MET:HE3	1:A:852:MET:HB3	1.90	0.42
2:B:95:ASN:HA	2:B:96:PRO:HD3	1.86	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:510:ALA:HA	1:A:511:PRO:HD3	1.94	0.42
1:A:784:ILE:N	1:A:785:PRO:HD2	2.35	0.42
2:B:137:ARG:HB3	2:B:147:LYS:HD2	2.01	0.42
2:B:194:ASN:HB3	2:B:205:ASN:OD1	2.20	0.42
1:A:110:LEU:CD2	1:A:324:LEU:HD12	2.50	0.41
1:A:785:PRO:HB2	1:A:926:ILE:CD1	2.50	0.41
1:A:367:LEU:HD23	1:A:761:GLY:HA3	2.01	0.41
1:A:378:THR:HA	1:A:382:THR:OG1	2.20	0.41
1:A:846:ASN:ND2	1:A:848:ARG:HB2	2.35	0.41
2:B:271:ASN:HD21	2:B:305:SER:N	2.19	0.41
1:A:44:HIS:HB3	1:A:242:ILE:HD11	2.03	0.41
1:A:502:ARG:HE	1:A:562:GLU:HG2	1.85	0.41
1:A:920:THR:HG21	1:A:981:TYR:O	2.20	0.41
3:G:17:TYR:O	3:G:21:VAL:HG23	2.21	0.41
1:A:426:ALA:O	1:A:471:ARG:HD2	2.20	0.41
1:A:342:VAL:HB	1:A:820:ILE:HD12	2.03	0.41
1:A:871:VAL:HG22	2:B:58:LEU:HD13	2.02	0.41
1:A:502:ARG:HG3	1:A:562:GLU:HG2	2.02	0.41
1:A:540:ASN:HD22	1:A:540:ASN:N	2.18	0.41
1:A:647:ARG:HH21	1:A:648:LEU:HD11	1.86	0.41
1:A:284:ILE:O	1:A:288:ILE:HG12	2.21	0.41
1:A: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:458:LYS:O	1:A:462:LEU:HB2	2.21	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:354:LYS:HE2	1:A:760:THR:HB	2.02	0.40
1:A:925:SER:O	1:A:929:VAL:HG22	2.22	0.40
1:A:199:ILE:HG22	1:A:201:ALA:O	2.22	0.40
1:A:900:ASP:OD1	1:A:904:GLN:HB2	2.21	0.40
1:A:989:PHE:HA	1:A:992:PHE:CD2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	990/1028 (96%)	942 (95%)	43 (4%)	5 (0%)	24	37
2	B	259/305 (85%)	220 (85%)	35 (14%)	4 (2%)	8	12
3	G	37/74 (50%)	33 (89%)	4 (11%)	0	100	100
All	All	1286/1407 (91%)	1195 (93%)	82 (6%)	9 (1%)	18	28

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%)	790 (94%)	50 (6%)	17	31
2	B	232/266 (87%)	223 (96%)	9 (4%)	28	48
3	G	32/62 (52%)	32 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1104/1197 (92%)	1045 (95%)	59 (5%)	20	36

All (59) 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	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 (24) 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	577	ASN
1	A	708	GLN
1	A	754	ASN
1	A	797	ASN
1	A	826	GLN
1	A	861	GLN

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Mol	Chain	Res	Type
1	A	1019	GLN
2	B	80	HIS
2	B	194	ASN
2	B	207	ASN
2	B	258	GLN
2	B	264	GLN
2	B	271	ASN
2	B	284	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

2 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	C	1	4,2	14,14,15	0.52	0	17,19,21	1.61	2 (11%)
4	NDG	C	2	4	14,14,15	0.49	0	17,19,21	1.14	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	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NDG	C	2	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1	NAG	C1-O5-C5	5.29	119.28	112.19
4	C	2	NDG	C1-O5-C5	2.62	115.70	112.19
4	C	1	NAG	C1-C2-N2	2.40	114.21	110.43

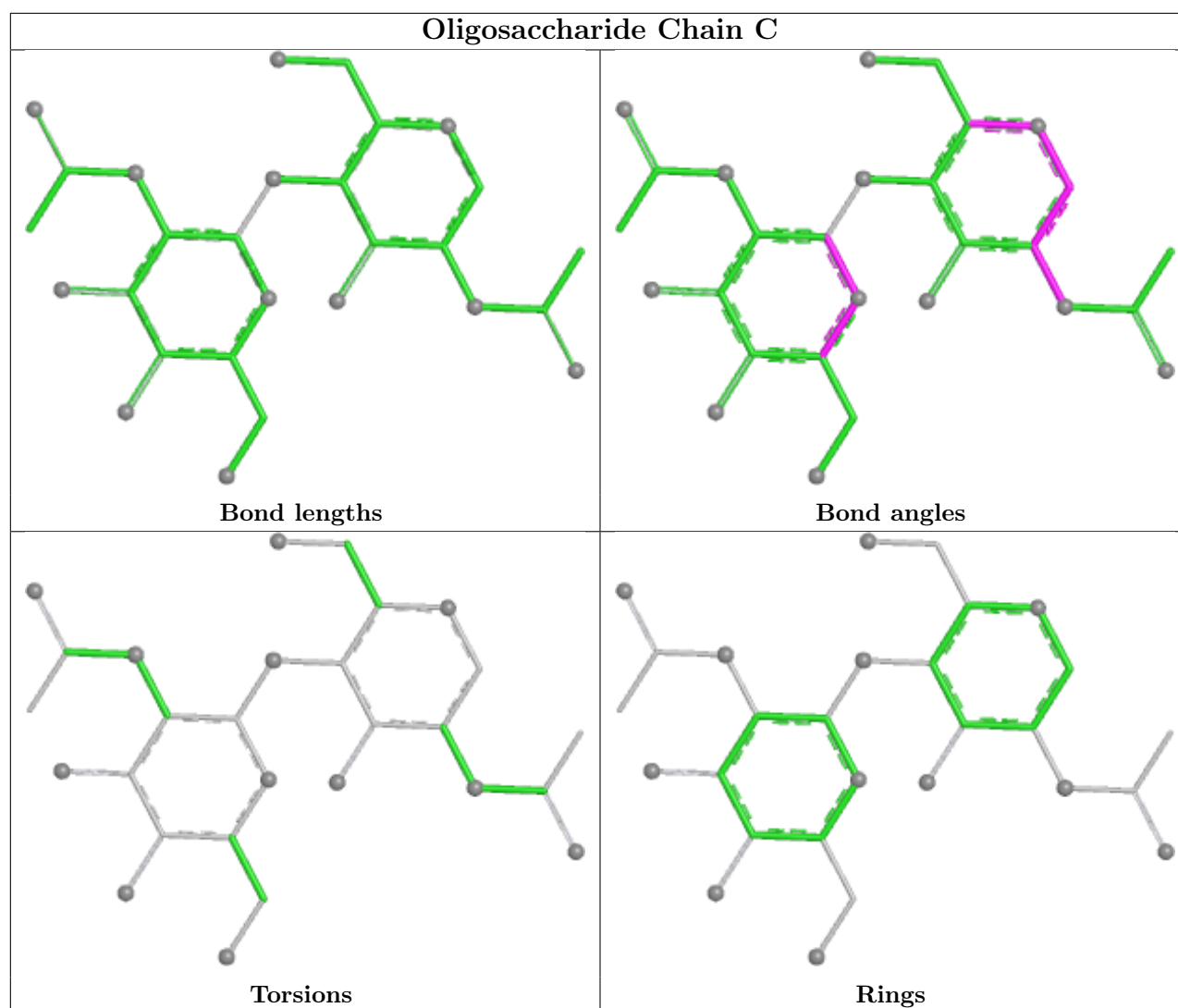
There are no chirality outliers.

There are no torsion outliers.

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	A	3001	-	31,31,31	0.47	0	48,48,48	1.13	5 (10%)
9	NAG	B	4021	2	14,14,15	0.62	0	17,19,21	1.25	2 (11%)
5	MF4	A	2001	1	0,4,4	-	-	-	-	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	CLR	A	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 (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	3001	CLR	C15-C14-C13	3.04	107.42	103.84
9	B	4021	NAG	C1-O5-C5	2.65	115.74	112.19
8	A	3001	CLR	C4-C5-C6	-2.63	117.00	120.57
8	A	3001	CLR	C4-C5-C10	2.53	119.66	116.42
8	A	3001	CLR	C1-C2-C3	2.49	113.78	110.48
9	B	4021	NAG	C4-C3-C2	2.27	114.34	111.02
8	A	3001	CLR	C12-C11-C9	2.09	116.69	113.14

There are no chirality outliers.

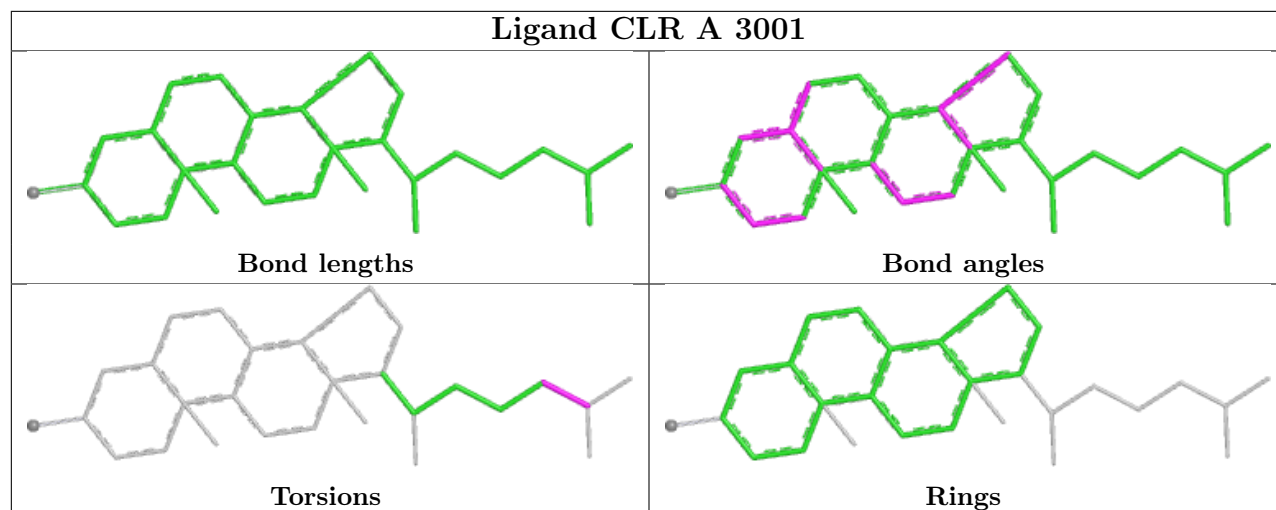
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	3001	CLR	C23-C24-C25-C26
8	A	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%)	0.15	37 (3%) 45 41	24, 46, 87, 112	0
2	B	265/305 (86%)	1.57	81 (30%) 1 1	44, 94, 120, 124	0
3	G	39/74 (52%)	0.26	0 100 100	41, 50, 93, 97	0
All	All	1296/1407 (92%)	0.45	118 (9%) 15 12	24, 51, 108, 124	0

All (118) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	85	ILE	4.8
2	B	268	LEU	4.8
2	B	93	ILE	4.6
2	B	99	TYR	4.4
2	B	74	ALA	4.4
2	B	207	ASN	4.2
2	B	160	CYS	4.1
1	A	894	TRP	3.7
1	A	675	THR	3.6
1	A	470	MET	3.6
2	B	213	LEU	3.6
2	B	276	ILE	3.6
1	A	501	SER	3.6
2	B	229	ILE	3.5
1	A	231	PHE	3.5
2	B	298	GLU	3.5
2	B	196	THR	3.4
2	B	202	LEU	3.4
2	B	149	ALA	3.4
1	A	435	ALA	3.4
2	B	217	ALA	3.4
2	B	214	ARG	3.4
2	B	124	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
2	B	195	THR	3.4
1	A	1015	GLY	3.3
2	B	169	GLY	3.3
2	B	194	ASN	3.2
2	B	198	LEU	3.2
1	A	1004	MET	3.2
1	A	152	ALA	3.1
2	B	146	GLN	3.1
2	B	232	PHE	3.1
2	B	140	LEU	3.1
2	B	116	SER	3.1
2	B	170	TYR	3.0
2	B	94	SER	3.0
2	B	192	LEU	3.0
1	A	129	ASN	3.0
2	B	32	SER	3.0
1	A	1023	TYR	2.9
2	B	293	PHE	2.9
2	B	230	GLU	2.9
2	B	199	PRO	2.9
1	A	571	PHE	2.9
2	B	87	THR	2.8
1	A	559	ALA	2.8
1	A	562	GLU	2.8
2	B	226	ILE	2.8
2	B	176	CYS	2.8
2	B	208	GLN	2.8
1	A	516	ASP	2.8
2	B	209	TYR	2.8
2	B	210	VAL	2.7
2	B	231	TYR	2.7
1	A	826	GLN	2.7
2	B	135	ILE	2.7
2	B	134	TYR	2.7
2	B	150	CYS	2.6
2	B	257	LEU	2.6
2	B	91	PHE	2.6
1	A	485	THR	2.6
1	A	412	ASP	2.6
2	B	212	PRO	2.6
2	B	296	ARG	2.6
2	B	242	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	252	LEU	2.6
2	B	256	TYR	2.6
2	B	297	PHE	2.5
1	A	119	ALA	2.5
2	B	131	PRO	2.5
1	A	522	LEU	2.5
2	B	205	ASN	2.5
1	A	684	TYR	2.5
2	B	234	LEU	2.5
2	B	274	LEU	2.5
2	B	206	TYR	2.4
1	A	126	ALA	2.4
2	B	147	LYS	2.4
2	B	299	VAL	2.4
1	A	566	ASN	2.4
2	B	227	GLY	2.4
2	B	304	LYS	2.4
1	A	895	ILE	2.3
2	B	291	ASP	2.3
1	A	987	TRP	2.3
2	B	126	ASP	2.3
2	B	197	ASP	2.3
2	B	284	ASN	2.3
1	A	1007	PHE	2.2
1	A	384	ASN	2.2
1	A	534	MET	2.2
2	B	92	SER	2.2
2	B	82	PRO	2.2
1	A	127	ASN	2.2
2	B	156	TRP	2.2
2	B	275	ARG	2.2
1	A	39	VAL	2.2
2	B	73	VAL	2.2
2	B	255	LYS	2.2
1	A	523	LEU	2.1
2	B	279	LYS	2.1
2	B	83	TYR	2.1
2	B	179	ALA	2.1
2	B	269	THR	2.1
2	B	294	ARG	2.1
1	A	125	PRO	2.1
2	B	34	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	526	ALA	2.1
2	B	84	ALA	2.1
1	A	57	THR	2.1
1	A	500	GLU	2.1
2	B	89	ILE	2.1
2	B	136	LYS	2.1
2	B	281	TYR	2.0
1	A	545	LEU	2.0
2	B	132	ALA	2.0
2	B	211	LEU	2.0
1	A	315	TYR	2.0

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

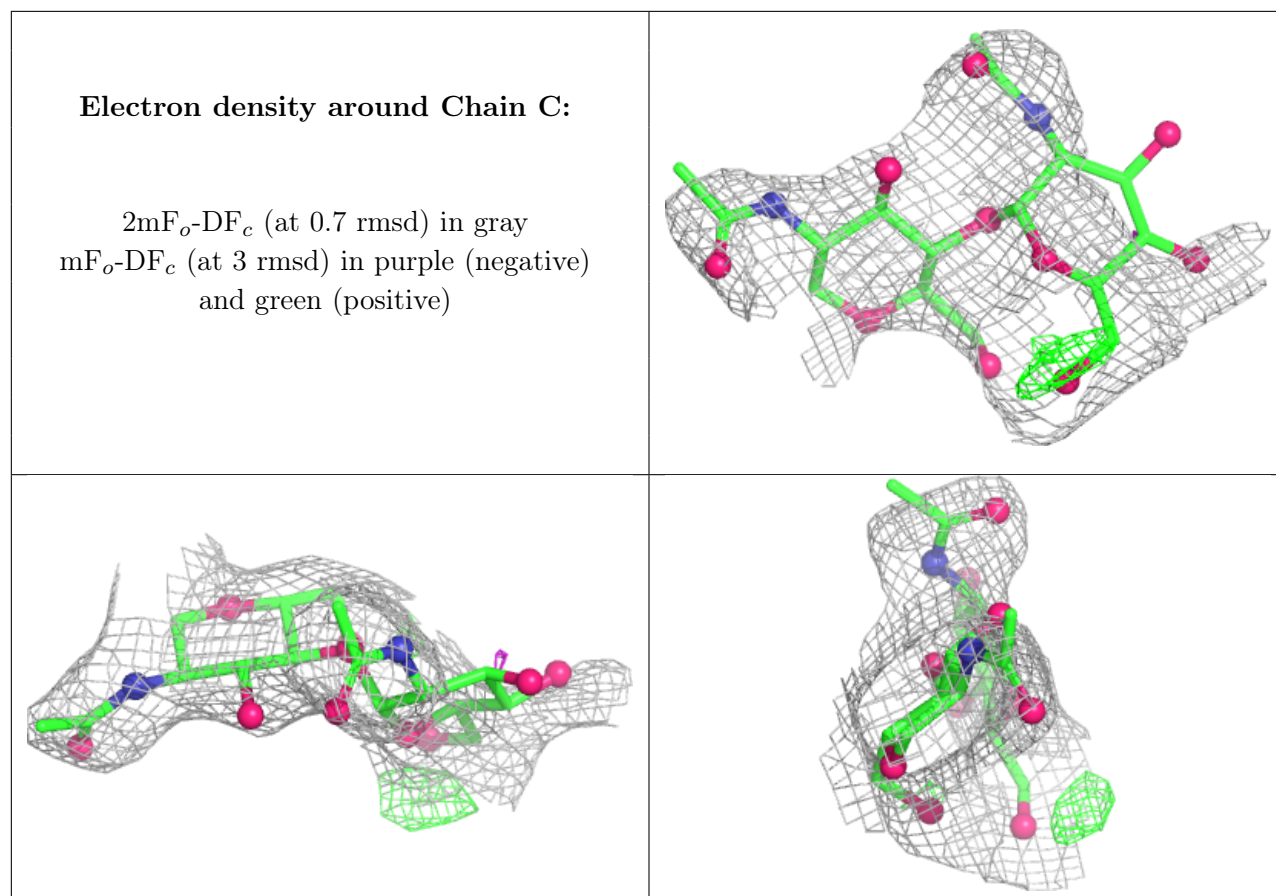
There are no non-standard protein/DNA/RNA residues in this entry.

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	-	-	107,108,109,110	0
4	NDG	C	2	14/15	-	-	111,111,111,111	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.

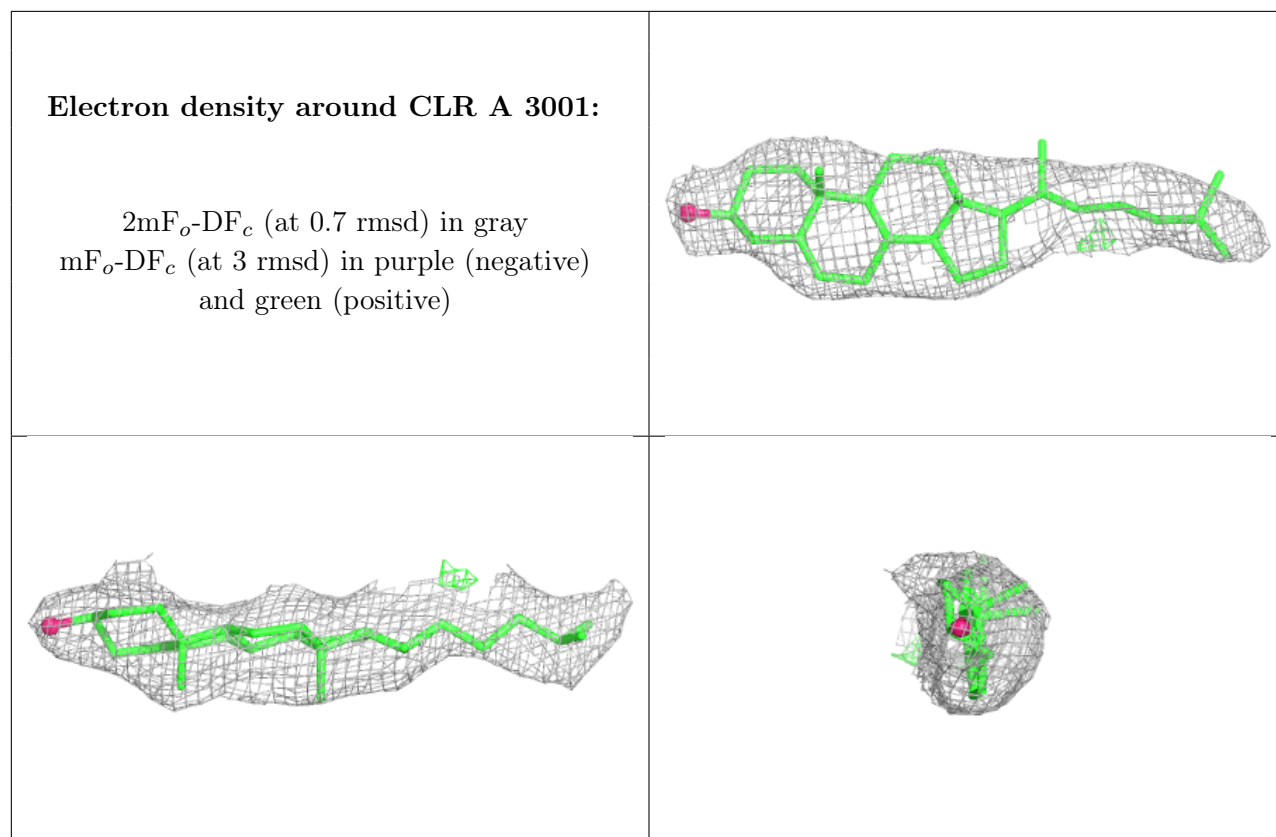


6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
9	NAG	B	4021	14/15	0.65	0.12	108,109,109,109	0
8	CLR	A	3001	28/28	0.83	0.12	88,88,88,89	0
5	MF4	A	2001	5/5	0.92	0.09	29,31,32,33	0
7	K	A	2003	1/1	0.97	0.04	47,47,47,47	0
7	K	A	2005	1/1	0.98	0.08	42,42,42,42	0
6	MG	A	2002	1/1	0.98	0.02	26,26,26,26	0
7	K	A	2004	1/1	0.98	0.04	47,47,47,47	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.