



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 09:44 PM BST

PDB ID : 5AW8
Title : Kinetics by X-ray crystallography: E2.MgF42-.2RB+ crystal
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

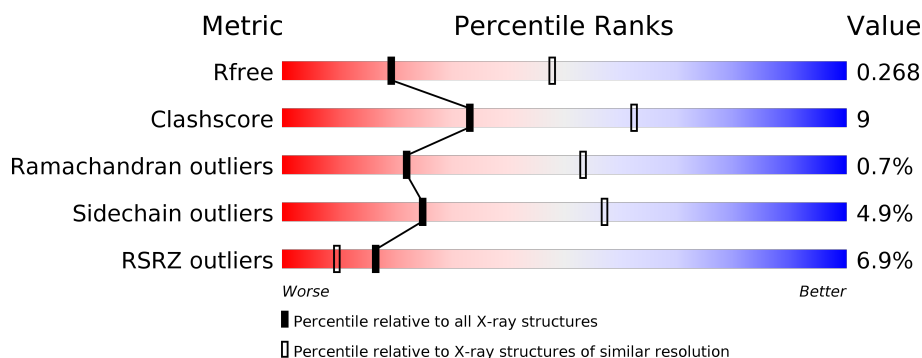
1 Overall quality at a glance

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}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (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 on 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	<div> <div>5%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div>• •</div> </div> </div>
2	B	305	<div> <div>13%</div> <div> <div></div> <div>67%</div> <div>19%</div> <div>• 12%</div> </div> </div>
3	G	74	<div> <div>36%</div> <div>16%</div> <div>47%</div> </div>
4	C	2	<div> <div>100%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	NAG	C	2	-	-	-	X
9	NAG	B	4021	-	-	-	X

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 10234 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.

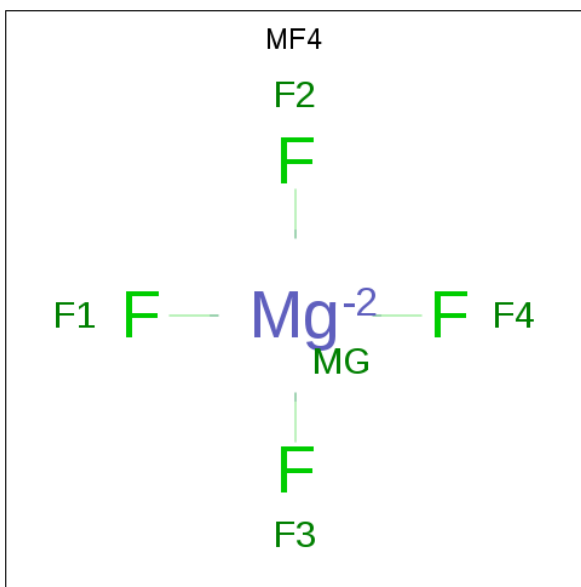
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	39	Total	C	N	O	S	0	0	0
			305	200	50	54	1			

- 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-) (three-letter code: MF4) (formula: F₄Mg).



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

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 7 is RUBIDIUM ION (three-letter code: RB) (formula: Rb).

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

- Molecule 8 is CHOLESTEROL (three-letter code: CLR) (formula: C₂₇H₄₆O).



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

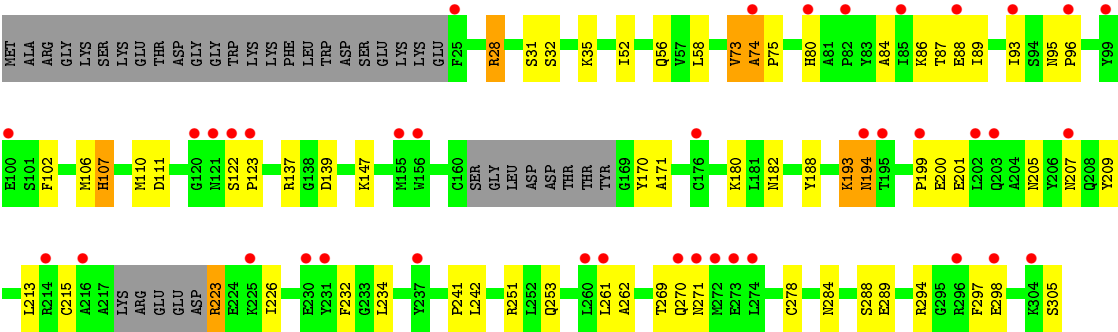
- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



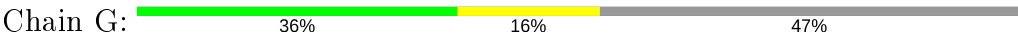
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 10 is water.

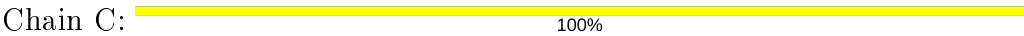
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1	Total	O	0	0
			1	1		



● 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	222.12Å 50.71Å 163.26Å 90.00° 104.85° 90.00°	Depositor
Resolution (Å)	14.99 – 2.80 37.10 – 2.80	Depositor EDS
% Data completeness (in resolution range)	70.0 (14.99-2.80) 90.7 (37.10-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.92 (at 2.81Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.251 , 0.257 0.267 , 0.268	Depositor DCC
R_{free} test set	1341 reflections (3.13%)	wwPDB-VP
Wilson B-factor (Å ²)	65.4	Xtriage
Anisotropy	0.473	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 50.0	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	0.91	EDS
Total number of atoms	10234	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 4.24% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, MF4, NAG, RB, 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	0.38	0/7825	0.51	0/10616
2	B	0.36	0/2229	0.49	0/3002
3	G	0.36	0/309	0.46	0/419
All	All	0.38	0/10363	0.51	0/14037

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	130	1
2	B	2174	0	2146	48	0
3	G	305	0	318	9	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	1	0	0	0	0
All	All	10234	0	10247	177	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (177) 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:478:VAL:HG21	1:A:571:PHE:HB2	1.64	0.79
1:A:497:LYS:HE2	1:A:499:SER:HB2	1.69	0.75
1:A:868:SER:O	1:A:872:ILE:HG12	1.86	0.75
1:A:261:THR:HG22	1:A:264:ARG:NH2	2.02	0.73
1:A:61:ARG:HB3	1:A:61:ARG:HH11	1.52	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
2:B:213:LEU:HD11	2:B:278:CYS:HB3	1.78	0.64
1:A:935:ILE:HG23	1:A:944:ILE:HD12	1.77	0.64
1:A:905:GLN:NE2	2:B:182:ASN:HA	2.13	0.64
1:A:78:ASN:HA	1:A:261:THR:HG23	1.79	0.64
1:A:816:MET:O	1:A:820:ILE:HG12	1.97	0.63
1:A:160:SER:HB3	1:A:741:VAL:HG22	1.80	0.63
2:B:74:ALA:CB	2:B:75:PRO:HD3	2.23	0.63
2:B:28:ARG:HB2	2:B:32:SER:HB3	1.81	0.63
1:A:52:HIS:HA	1:A:57:THR:HG23	1.80	0.63
1:A:673:LEU:HD22	1:A:677:VAL:HG11	1.80	0.62
1:A:905:GLN:HE21	2:B:182:ASN:HA	1.63	0.62
2:B:193:LYS:HA	2:B:207:ASN:HD21	1.65	0.62
1:A:323:PHE:O	1:A:327:ILE:HG12	2.01	0.61
1:A:64:THR:HG22	1:A:66:ALA:H	1.65	0.61
3:G:29:VAL:O	3:G:33:ILE:HG12	2.00	0.60
1:A:363:ALA:HB1	1:A:730:ILE:HD12	1.83	0.60
1:A:483:ASN:HB2	1:A:486:ASN:HB2	1.82	0.60
2:B:31:SER:O	2:B:35:LYS:HG3	2.01	0.60
2:B:270:GLN:HG2	2:B:271:ASN:ND2	2.16	0.60
1:A:344:LEU:HB3	1:A:361:LEU:HG	1.84	0.59
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
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	0.59
2:B:106:MET:O	2:B:110:MET:HG2	2.03	0.58
1:A:345:THR:HA	1:A:361:LEU:HD11	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:137:ARG:HD2	2:B:147:LYS:HB3	1.88	0.56
2:B:52:ILE:O	2:B:56:GLN:HG2	2.05	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	0.56
1:A:190:LEU:HD11	1:A:206:ILE:HD11	1.88	0.55
1:A:351:MET:HA	1:A:354:LYS:HG2	1.88	0.55
1:A:157:ILE:HD11	1:A:745:ALA:HA	1.89	0.55
2:B:93:ILE:H	2:B:305:SER:HB2	1.72	0.55
1:A:994:TYR:O	1:A:997:ILE:HG22	2.06	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: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
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: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:161:PHE:HA	1:A:164:MET:HE3	1.90	0.53
1:A:324:LEU:O	1:A:328:ILE:HG12	2.09	0.53
1:A:871:VAL:HG22	2:B:58:LEU:HD13	1.91	0.52
1:A:161:PHE:HA	1:A:164:MET:CE	2.40	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
3:G:32:VAL:O	3:G:36:ILE:HG12	2.09	0.52
2:B:75:PRO:HG2	2:B:294:ARG:NH2	2.25	0.52
1:A:82:PRO:HA	1:A:158:MET:HG2	1.92	0.51
1:A:766:ARG:HD2	1:A:832:MET:HE2	1.92	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:571:PHE:HA	1:A:577:ASN:HD22	1.76	0.50
2:B:232:PHE:HB2	2:B:262:ALA:HB3	1.93	0.49
1:A:826:GLN:HE22	1:A:950:LYS:HE3	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:LYS:HE2	1:A:746:ALA:O	2.12	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	0.47
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: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
1:A:894:TRP:CH2	2:B:86:LYS:HG2	2.48	0.47
1:A:814:THR:HB	1:A:961:GLU:HG3	1.96	0.47
3:G:31:CYS:O	3:G:35:ILE:HG12	2.14	0.47
2:B:80:HIS:HB3	2:B:297:PHE:CZ	2.50	0.47
2:B:87:THR:HB	2:B:298:GLU:O	2.14	0.47
1:A:336:LEU:HD11	1:A:776:ILE:HG12	1.96	0.46
1:A:127:ASN:HB3	1:A:131:TYR:CD1	2.50	0.46
2:B:215:CYS:HA	2:B:278:CYS:HA	1.96	0.46
2:B:226:ILE:HG22	2:B:269:THR:HB	1.96	0.46
1:A:63:LEU:HD22	1:A:189:ASP:HB3	1.97	0.46
1:A:924:ILE:HD12	1:A:983:LEU:CD1	2.45	0.46
2:B:122:SER:HA	2:B:123:PRO:HA	1.76	0.46
1:A:906:TRP:CZ2	2:B:73:VAL:HG22	2.51	0.46
1:A:631:VAL:HG23	1:A:633:ILE:HG12	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:670:LEU:HD23	1:A:678:LEU:HD21	1.97	0.45
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
1:A:722:SER:OG	1:A:723:PRO:HD3	2.17	0.45
1:A:676:GLU:H	1:A:676:GLU:CD	2.20	0.45
2:B:84:ALA:HB1	2:B:88:GLU:N	2.31	0.45
1:A:847:GLU:H	1:A:847:GLU:CD	2.20	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:806:THR:HG22	1:A:923:PHE:HB2	2.00	0.44
2:B:194:ASN:N	2:B:194:ASN:HD22	2.15	0.44
1:A:354:LYS:HB2	1:A:354:LYS:HZ2	1.81	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	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:107:HIS:O	2:B:111:ASP:HB2	2.18	0.43
2:B:107:HIS:ND1	2:B:170:TYR:HE1	2.17	0.43
1:A:273:LEU:O	1:A:277:LEU:HG	2.19	0.43
1:A:953:ILE:HD13	3:G:38:LEU:HD12	1.99	0.43
1:A:110:LEU:HD22	1:A:324:LEU:HD12	1.99	0.43
1:A:790:PHE:O	1:A:794:ILE:HG12	2.19	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:1020:GLU:OE2	2:B:28:ARG:NH2	2.43	0.43
1:A:87:PRO:HD2	1:A:90:ILE:HD12	2.00	0.43
3:G:4:GLU:CD	3:G:5:GLY:H	2.23	0.43
1:A:64:THR:HA	1:A:174:ASP:OD1	2.19	0.42
1:A:661:LYS:HA	1:A:661:LYS:HE2	2.00	0.42
1:A:797:ASN:HB3	1:A:885:GLY:HA2	2.00	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:291:PHE:HA	1:A:294:ILE:HD12	2.01	0.42
1:A:766:ARG:HD2	1:A:832:MET:HE1	2.02	0.42
2:B:223:ARG:HH11	2:B:223:ARG:HB2	1.84	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
1:A:953:ILE:HD13	3:G:38:LEU:CD1	2.50	0.42
2:B:89:ILE:HG22	2:B:102:PHE:CE1	2.55	0.42
2:B:95:ASN:HA	2:B:96:PRO:HD3	1.86	0.42
1:A:291:PHE:HB3	1:A:845:VAL:HB	2.02	0.42
1:A:48:LEU:HD23	1:A:59:LEU:HD11	2.01	0.42
2:B:74:ALA:CB	2:B:75:PRO:CD	2.92	0.42
1:A:784:ILE:N	1:A:785:PRO:HD2	2.35	0.42
1:A:110:LEU:CD2	1:A:324:LEU:HD12	2.50	0.41
1:A:378:THR:HA	1:A:382:THR:OG1	2.20	0.41
1:A:510:ALA:HA	1:A:511:PRO:HD3	1.94	0.41
1:A:905:GLN:HE22	2:B:180:LYS:HD3	1.85	0.41
2:B:194:ASN:HB3	2:B:205:ASN:OD1	2.20	0.41
1:A:785:PRO:HB2	1:A:926:ILE:CD1	2.50	0.41
2:B:137:ARG:HB3	2:B:147:LYS:HD2	2.01	0.41
1:A:502:ARG:HE	1:A:562:GLU:HG2	1.85	0.41
1:A:367:LEU:HD23	1:A:761:GLY:HA3	2.01	0.41
1:A:920:THR:HG21	1:A:981:TYR:O	2.20	0.41
2:B:271:ASN:HD21	2:B:305:SER:N	2.19	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:HIS:HB3	1:A:242:ILE:HD11	2.03	0.41
1:A:502:ARG:HG3	1:A:562:GLU:HG2	2.02	0.41
1:A:846:ASN:ND2	1:A:848:ARG:HB2	2.35	0.41
1:A:301:PHE:O	1:A:305:SER:HB2	2.20	0.41
1:A:342:VAL:HB	1:A:820:ILE:HD12	2.03	0.41
1:A:423:ARG:O	1:A:427:LEU:HB2	2.21	0.41
1:A:540:ASN:N	1:A:540:ASN:HD22	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:647:ARG:HH21	1:A:648:LEU:HD11	1.86	0.41
1:A:894:TRP:CZ2	2:B:86:LYS:HG2	2.55	0.41
1:A:702:VAL:HG13	1:A:712:VAL:HG21	2.03	0.41
1:A:831:ILE:O	1:A:834:ARG:HG2	2.22	0.40
1:A:199:ILE:HG22	1:A:201:ALA:O	2.22	0.40
1:A:354:LYS:HE2	1:A:760:THR:HB	2.02	0.40
1:A:900:ASP:OD2	1:A:904:GLN:HB2	2.21	0.40
1:A:925:SER:O	1:A:929:VAL:HG22	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:ARG:NH2	1:A:648:LEU:O[1_565]	2.14	0.06

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	990/1028 (96%)	942 (95%)	43 (4%)	5 (0%)	29	61
2	B	262/305 (86%)	223 (85%)	35 (13%)	4 (2%)	10	33
3	G	37/74 (50%)	33 (89%)	4 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1289/1407 (92%)	1198 (93%)	82 (6%)	9 (1%)	22	53

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%)	796 (95%)	44 (5%)	23	55
2	B	234/266 (88%)	224 (96%)	10 (4%)	29	62
3	G	32/62 (52%)	32 (100%)	0	100	100
All	All	1106/1197 (92%)	1052 (95%)	54 (5%)	25	57

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LEU
1	A	57	THR
1	A	61	ARG
1	A	63	LEU
1	A	72	LEU
1	A	128	ASP
1	A	165	VAL

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Mol	Chain	Res	Type
1	A	213	VAL
1	A	217	SER
1	A	218	LEU
1	A	226	THR
1	A	231	PHE
1	A	245	PHE
1	A	248	ASN
1	A	250	VAL
1	A	255	ARG
1	A	261	THR
1	A	284	ILE
1	A	309	LEU
1	A	344	LEU
1	A	354	LYS
1	A	391	MET
1	A	413	LYS
1	A	434	GLN
1	A	454	SER
1	A	457	LEU
1	A	524	ASN
1	A	540	ASN
1	A	557	HIS
1	A	581	THR
1	A	636	GLU
1	A	670	LEU
1	A	682	LEU
1	A	712	VAL
1	A	719	VAL
1	A	726	LYS
1	A	806	THR
1	A	811	ASP
1	A	833	LYS
1	A	847	GLU
1	A	880	PRO
1	A	974	THR
1	A	987	TRP
1	A	1019	GLN
2	B	28	ARG
2	B	73	VAL
2	B	107	HIS
2	B	139	ASP
2	B	193	LYS

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Mol	Chain	Res	Type
2	B	194	ASN
2	B	200	GLU
2	B	223	ARG
2	B	251	ARG
2	B	289	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	118	GLN
1	A	129	ASN
1	A	163	ASN
1	A	225	GLN
1	A	290	HIS
1	A	434	GLN
1	A	524	ASN
1	A	540	ASN
1	A	557	HIS
1	A	577	ASN
1	A	754	ASN
1	A	797	ASN
1	A	826	GLN
1	A	905	GLN
1	A	1019	GLN
2	B	80	HIS
2	B	194	ASN
2	B	207	ASN
2	B	264	GLN
2	B	271	ASN
2	B	284	ASN

5.3.3 RNA ⓘ

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	2,4	14,14,15	0.51	0	17,19,21	0.93	1 (5%)
4	NAG	C	2	4	14,14,15	0.66	0	17,19,21	1.40	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	C	1	2,4	-	1/6/23/26	0/1/1/1
4	NAG	C	2	4	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	2	NAG	C2-N2-C7	3.97	128.55	122.90
4	C	1	NAG	C1-O5-C5	2.71	115.86	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	2	NAG	C4-C5-C6-O6
4	C	2	NAG	O5-C5-C6-O6
4	C	1	NAG	O5-C5-C6-O6
4	C	2	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry

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	$\# Z > 2$
5	MF4	A	2001	1	0,4,4	0.00	-	-		
8	CLR	B	3001	-	31,31,31	0.46	0	48,48,48	1.10	5 (10%)
9	NAG	B	4021	2	14,14,15	0.60	0	17,19,21	1.25	2 (11%)

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 (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	3001	CLR	C15-C14-C13	2.94	107.39	103.84
9	B	4021	NAG	C1-O5-C5	2.66	115.80	112.19
8	B	3001	CLR	C1-C2-C3	2.57	113.77	110.47
8	B	3001	CLR	C4-C5-C6	-2.48	117.03	120.61
8	B	3001	CLR	C4-C5-C10	2.48	119.71	116.42
9	B	4021	NAG	C4-C3-C2	2.27	114.34	111.02
8	B	3001	CLR	C12-C11-C9	2.10	116.76	113.11

There are no chirality outliers.

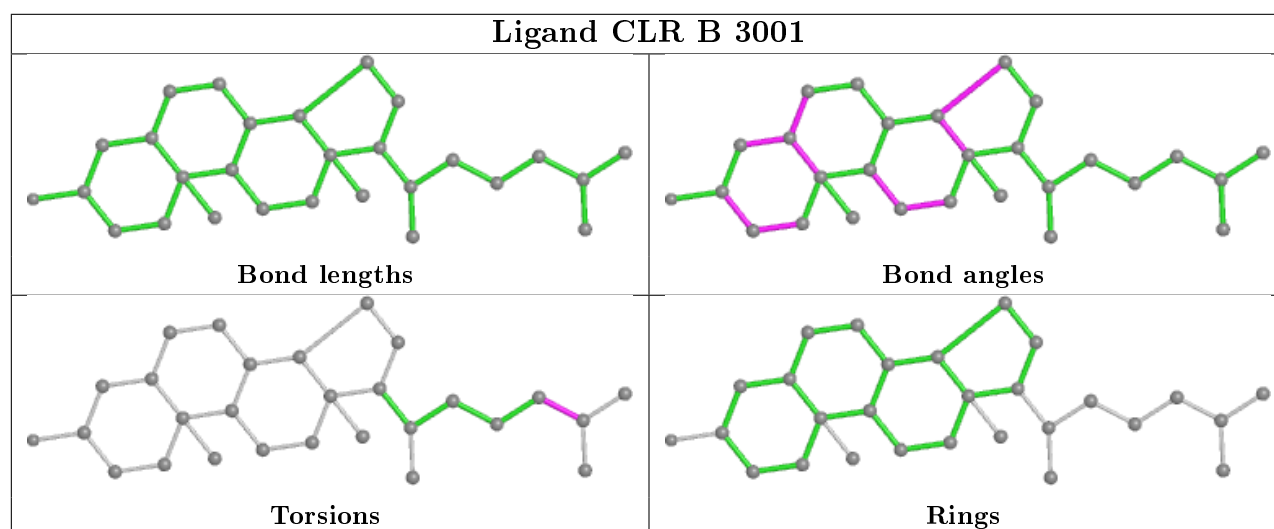
All (2) torsion outliers are listed below:

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

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%)	0.33	51 (5%) 28 19	54, 76, 117, 142	0
2	B	268/305 (87%)	0.92	39 (14%) 2 1	74, 125, 150, 160	0
3	G	39/74 (52%)	-0.09	0 100 100	71, 80, 123, 127	0
All	All	1299/1407 (92%)	0.44	90 (6%) 16 10	54, 81, 138, 160	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	214	ARG	5.9
2	B	298	GLU	5.8
2	B	195	THR	5.6
1	A	563	ASP	5.5
1	A	498	SER	5.5
1	A	573	ALA	5.4
1	A	562	GLU	5.1
1	A	568	GLY	5.0
1	A	579	PRO	5.0
2	B	272	MET	4.2
1	A	411	PHE	4.2
1	A	894	TRP	4.1
2	B	194	ASN	4.0
1	A	412	ASP	4.0
1	A	534	MET	4.0
1	A	578	PHE	4.0
1	A	567	GLU	3.9
2	B	99	TYR	3.8
2	B	93	ILE	3.8
2	B	273	GLU	3.7
2	B	121	ASN	3.7
2	B	270	GLN	3.5
1	A	566	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	675	THR	3.3
2	B	155	MET	3.2
2	B	271	ASN	3.2
1	A	317	TRP	3.2
2	B	96	PRO	3.2
1	A	815	ASP	3.2
1	A	574	ASP	3.2
2	B	156	TRP	3.1
1	A	79	SER	3.1
2	B	304	LYS	3.0
1	A	126	ALA	3.0
2	B	85	ILE	2.9
2	B	203	GLN	2.8
1	A	503	TYR	2.8
1	A	84	PRO	2.8
1	A	779	THR	2.8
2	B	207	ASN	2.8
2	B	25	PHE	2.8
2	B	100	GLU	2.8
1	A	504	LEU	2.8
1	A	308	ILE	2.7
1	A	117	ILE	2.6
2	B	122	SER	2.6
2	B	237	TYR	2.6
1	A	127	ASN	2.6
2	B	225	LYS	2.6
2	B	274	LEU	2.5
2	B	216	ALA	2.5
1	A	121	THR	2.5
1	A	577	ASN	2.5
1	A	41	MET	2.5
1	A	32	LEU	2.5
1	A	90	ILE	2.5
1	A	570	PRO	2.4
2	B	80	HIS	2.4
2	B	88	GLU	2.4
2	B	202	LEU	2.4
1	A	439	ASN	2.4
1	A	564	LYS	2.4
1	A	72	LEU	2.4
1	A	313	LEU	2.4
1	A	896	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	826	GLN	2.3
1	A	529	PRO	2.3
1	A	502	ARG	2.3
2	B	231	TYR	2.3
1	A	585	PHE	2.2
2	B	176	CYS	2.2
1	A	312	ILE	2.2
1	A	576	PRO	2.2
1	A	782	SER	2.2
1	A	114	ALA	2.2
1	A	125	PRO	2.2
1	A	89	TRP	2.1
2	B	82	PRO	2.1
2	B	230	GLU	2.1
2	B	199	PRO	2.1
2	B	296	ARG	2.1
2	B	74	ALA	2.1
2	B	123	PRO	2.1
2	B	261	LEU	2.0
1	A	278	GLU	2.0
2	B	260	LEU	2.0
1	A	572	ASP	2.0
1	A	810	ILE	2.0
2	B	120	GLY	2.0
1	A	571	PHE	2.0

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

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

6.3 Carbohydrates ⓘ

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.

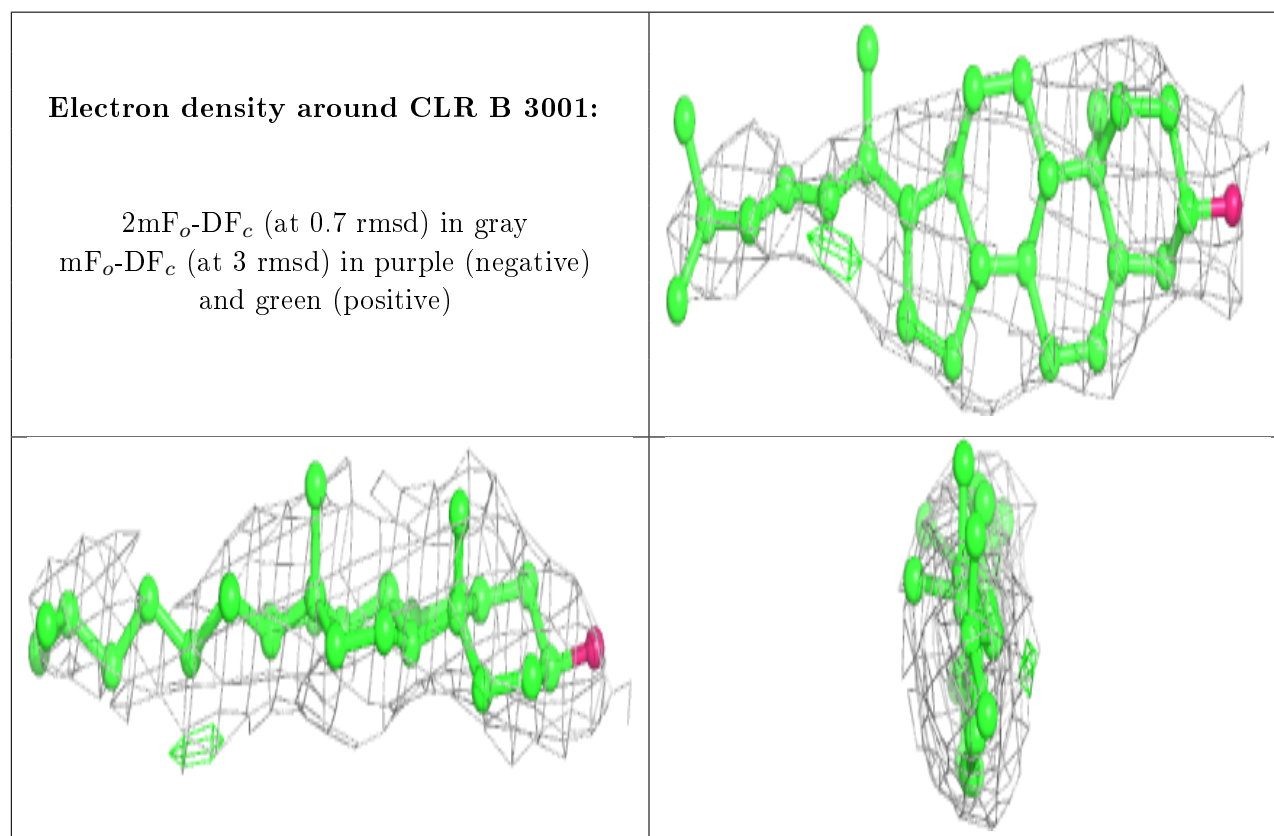
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NAG	C	2	14/15	0.46	0.50	139,139,140,140	0
4	NAG	C	1	14/15	0.85	0.25	132,135,136,137	0

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	0.65	0.47	138,139,139,139	0
6	MG	A	2002	1/1	0.73	0.33	56,56,56,56	0
8	CLR	B	3001	28/28	0.85	0.26	118,118,118,119	0
5	MF4	A	2001	5/5	0.94	0.37	59,61,62,62	0
7	RB	A	2005	1/1	0.98	0.05	72,72,72,72	0
7	RB	A	2004	1/1	0.98	0.13	77,77,77,77	0
7	RB	A	2003	1/1	0.99	0.16	77,77,77,77	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

There are no such residues in this entry.