



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 09:01 am GMT

PDB ID : 2BWC
Title : STRUCTURE OF ENDOGLUCANASE 12A (CEL12A) FROM
RHODOTHERMUS MARINUS IN COMPLEX WITH CELLOPENTAOSE
(5 MINUTE SOAK)
Authors : Crennell, S.J.; Nordberg-Karlsson, E.
Deposited on : 2005-07-13
Resolution : 2.15 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

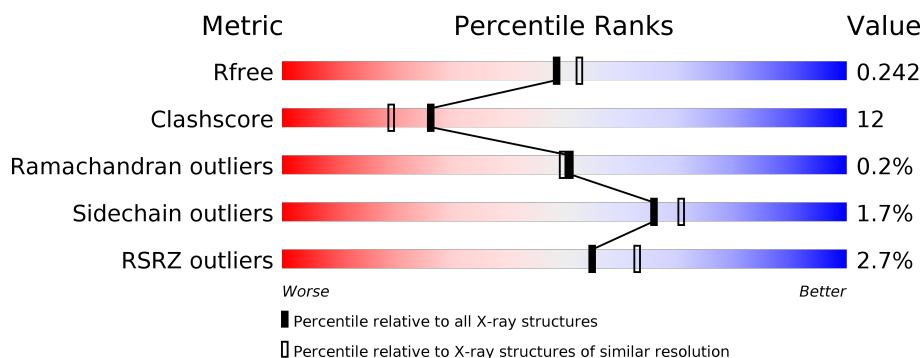
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	100719	1170 (2.16-2.16)
Clashscore	112137	1278 (2.16-2.16)
Ramachandran outliers	110173	1256 (2.16-2.16)
Sidechain outliers	110143	1255 (2.16-2.16)
RSRZ outliers	101464	1175 (2.16-2.16)

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. 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	227	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 84%, grey 14%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 84% 14% </div> </div>
1	B	227	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 4%, orange 1%, yellow 1%, green 78%, grey 21%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 4% 78% 21% </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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	A	1001	-	X	-	-
2	GOL	A	1002	-	X	-	X
2	GOL	A	1003[A]	-	X	-	X
2	GOL	A	1003[B]	-	X	X	X
2	GOL	A	1234	-	X	-	X
2	GOL	A	1235	-	X	-	-
2	GOL	B	1001	-	X	-	-
2	GOL	B	1002[A]	-	X	X	X
2	GOL	B	1237	-	X	-	-
3	GLC	A	1004	X	-	X	X
5	GLC	B	1003[B]	X	-	X	X
6	BGC	B	1004[A]	-	-	-	X
6	BGC	B	1004[B]	-	-	X	X
6	BGC	B	1005[A]	-	-	-	X
6	BGC	B	1005[B]	-	-	-	X
6	BGC	B	1006[A]	-	-	-	X
6	BGC	B	1006[B]	-	-	-	X

2 Entry composition [i](#)

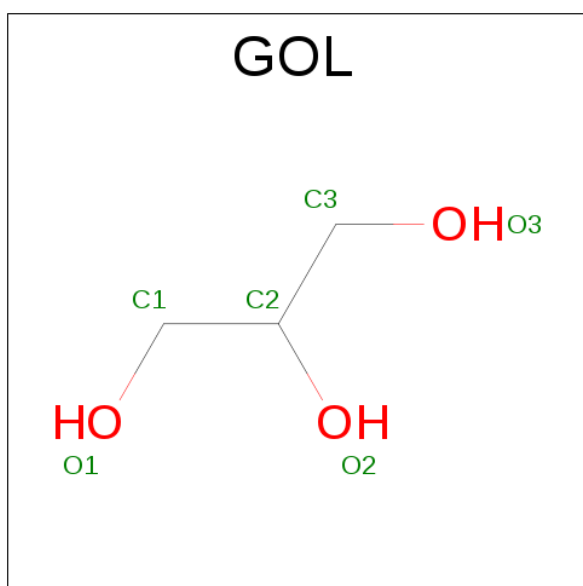
There are 7 unique types of molecules in this entry. The entry contains 4225 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ENDOGLUCANASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	226	Total	C	N	O	S	0	8	0
			1842	1160	320	356	6			
1	B	226	Total	C	N	O	S	0	7	0
			1839	1160	324	349	6			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	1
			12	6	6		
2	A	1	Total	C	O	0	0
			6	3	3		

Continued on next page...

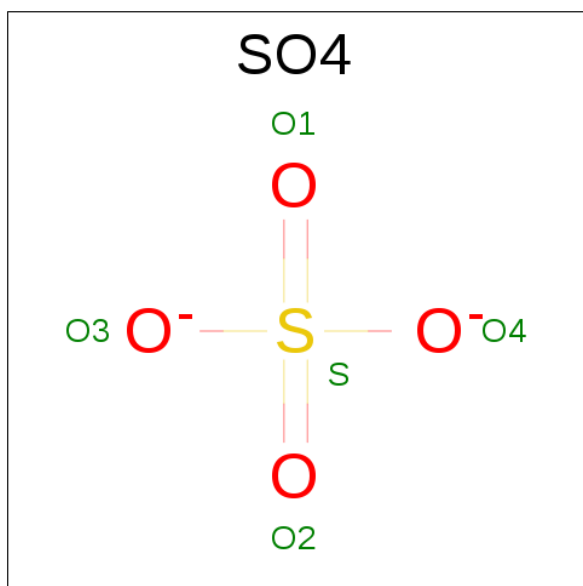
Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	1
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is a polymer of unknown type called SUGAR (3-MER).

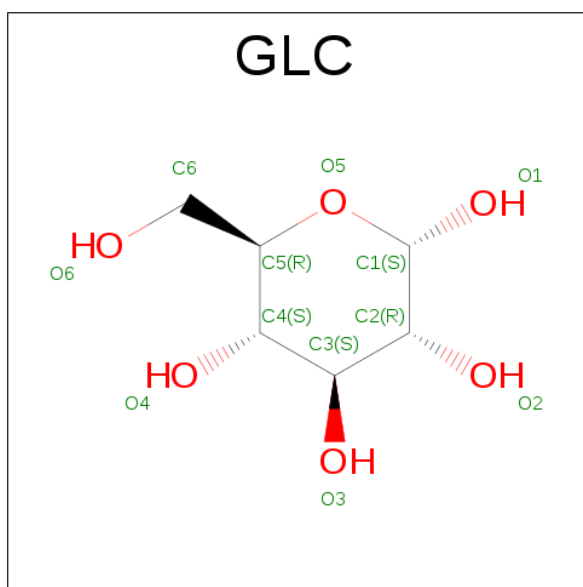
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	3	Total	C	O	0	0
			34	18	16		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is SUGAR (ALPHA-D-GLUCOSE) (three-letter code: GLC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	1
			12	6	6		

- Molecule 6 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	3	Total	C	O	0	3
			67	36	31		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	214	Total	O	0	0
			214	214		
7	B	158	Total	O	0	0
			158	158		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.89Å 67.33Å 131.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.65 – 2.15 36.65 – 2.15	Depositor EDS
% Data completeness (in resolution range)	94.5 (36.65-2.15) 94.5 (36.65-2.15)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 2.16Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.184 , 0.233 0.198 , 0.242	Depositor DCC
R_{free} test set	1309 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.431	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 65.5	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	0.94	EDS
Total number of atoms	4225	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.89% 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: GLC, GOL, BGC, SO4

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	0.34	0/1895	0.63	0/2593
1	B	0.32	0/1892	0.61	0/2586
All	All	0.33	0/3787	0.62	0/5179

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	A	1	0

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1004	GLC	C1

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	1842	0	1690	26	0
1	B	1839	0	1706	44	0
2	A	36	0	24	7	0
2	B	18	0	13	7	0
3	A	34	0	30	7	0
4	A	5	0	0	0	0
5	B	12	0	12	6	0
6	B	67	0	59	12	0
7	A	214	0	0	4	0
7	B	158	0	0	0	0
All	All	4225	0	3534	85	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 12.

All (85) 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:1002[A]:GOL:O1	2:B:1002[A]:GOL:C1	1.64	1.43
2:A:1003[B]:GOL:H12	3:A:1004:GLC:O1	1.20	1.26
5:B:1003[B]:GLC:C4	6:B:1004[B]:BGC:O1	2.11	0.99
2:B:1002[A]:GOL:O2	6:B:1004[A]:BGC:H1	1.68	0.93
2:A:1003[A]:GOL:C2	3:A:1004:GLC:O1	2.22	0.88
1:B:8[A]:ARG:HG3	1:B:25:VAL:HB	1.54	0.88
1:B:124:GLU:OE2	6:B:1004[B]:BGC:H1	1.74	0.87
1:A:39[A]:GLU:HG3	7:A:2048:HOH:O	1.81	0.79
2:A:1003[A]:GOL:C3	3:A:1004:GLC:O1	2.34	0.74
1:A:79:ARG:HH11	1:A:79:ARG:HB2	1.53	0.73
5:B:1003[B]:GLC:H4	6:B:1004[B]:BGC:O1	1.86	0.73
1:B:5:LEU:HD21	1:B:12[A]:ARG:HE	1.53	0.72
1:A:130:ASN:HD22	1:A:131:TRP:H	1.38	0.71
1:B:8[B]:ARG:HG3	1:B:25:VAL:HB	1.73	0.70
1:B:54:ASN:H	1:B:100:ARG:NH2	1.90	0.69
1:A:82:GLN:HG2	1:A:195:PRO:O	1.93	0.69
1:A:106:ASP:O	1:A:203:GLU:HG3	1.94	0.68
1:B:139:GLY:H	2:B:1001:GOL:H11	1.60	0.67
2:A:1003[B]:GOL:H12	3:A:1004:GLC:C1	2.23	0.66
1:B:32:GLN:NE2	1:B:208:LEU:HD12	2.08	0.66
1:A:7:GLY:HA3	1:A:10[A]:ASP:OD1	1.94	0.66
1:A:63:TYR:HB3	1:A:203:GLU:HB3	1.77	0.66
1:B:54:ASN:H	1:B:100:ARG:HH21	1.46	0.62
2:B:1002[A]:GOL:HO1	2:B:1002[A]:GOL:C1	2.08	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:GLU:OE2	3:A:1004:GLC:H1	1.99	0.61
1:B:164:ILE:HD12	1:B:164:ILE:N	2.17	0.60
5:B:1003[B]:GLC:O4	6:B:1004[B]:BGC:C1	2.48	0.60
1:B:181[A]:LYS:HE2	1:B:185:ASP:OD1	2.02	0.60
1:B:67:HIS:CD2	6:B:1006[A]:BGC:H6C2	2.37	0.59
1:B:25:VAL:HA	1:B:58:ALA:CB	2.34	0.58
1:B:29[B]:GLU:H	1:B:29[B]:GLU:CD	2.08	0.57
2:B:1002[A]:GOL:O2	6:B:1004[A]:BGC:C1	2.48	0.57
1:B:51:ASP:OD1	1:B:51:ASP:O	2.24	0.55
1:B:67:HIS:NE2	6:B:1006[A]:BGC:H6C2	2.22	0.55
1:B:25:VAL:HA	1:B:58:ALA:HB2	1.88	0.55
1:A:20:ARG:HD3	1:A:63:TYR:OH	2.08	0.53
1:B:67:HIS:CD2	6:B:1006[B]:BGC:H6C2	2.44	0.53
1:A:226:LYS:HG2	7:A:2207:HOH:O	2.10	0.52
1:A:52:ASN:HB2	1:A:57:ALA:HB2	1.90	0.52
1:A:85:SER:HB3	1:A:227:LEU:HD23	1.91	0.51
1:B:60:PRO:HD2	1:B:206:PHE:O	2.09	0.51
1:A:104:ALA:HB2	1:A:128:TRP:HA	1.92	0.51
1:B:85:SER:HB3	1:B:227:LEU:HD23	1.94	0.50
1:B:5:LEU:O	1:B:33:CYS:HA	2.12	0.50
1:A:130:ASN:HD22	1:A:131:TRP:N	2.08	0.50
1:B:88:ARG:HH22	2:B:1237:GOL:H12	1.77	0.49
1:A:100:ARG:HG2	1:A:133:GLY:HA3	1.94	0.49
1:B:27:GLY:HA3	1:B:56:VAL:O	2.13	0.48
1:A:100:ARG:HD2	7:A:2114:HOH:O	2.13	0.48
1:B:53:GLY:HA2	1:B:100:ARG:HH21	1.78	0.48
1:B:108:TRP:CZ3	1:B:124:GLU:HB2	2.48	0.48
1:A:120:SER:HA	1:A:160[B]:ASP:OD1	2.13	0.48
1:B:8[A]:ARG:NH1	1:B:25:VAL:HG11	2.29	0.48
1:A:25:VAL:HA	1:A:58:ALA:CB	2.45	0.47
1:A:83[B]:GLU:HG3	1:A:83[B]:GLU:O	2.15	0.47
1:B:159:TRP:CH2	5:B:1003[B]:GLC:H61	2.49	0.47
1:B:100:ARG:HH11	1:B:100:ARG:HG2	1.79	0.46
1:B:135:VAL:HG11	1:B:209:TRP:CE3	2.50	0.46
1:A:32:GLN:HA	1:A:47:ARG:O	2.16	0.46
1:A:136:MET:SD	1:A:167:ARG:NH1	2.87	0.46
1:B:53:GLY:C	1:B:55:ASN:H	2.19	0.46
2:A:1003[B]:GOL:C2	3:A:1004:GLC:O1	2.49	0.46
1:B:104:ALA:HB2	1:B:128:TRP:HA	1.97	0.45
1:B:8[A]:ARG:HG3	1:B:8[A]:ARG:HH11	1.80	0.45
5:B:1003[B]:GLC:HO4	6:B:1004[B]:BGC:C1	2.26	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:128:TRP:HB2	1:B:167:ARG:HA	1.99	0.44
1:B:125:LEU:C	1:B:125:LEU:HD23	2.39	0.43
2:A:1003[B]:GOL:C3	3:A:1004:GLC:O1	2.62	0.43
1:B:137:PRO:HD3	1:B:167:ARG:NH1	2.34	0.43
1:B:35:GLU:O	1:B:43:PHE:HA	2.18	0.42
1:A:52:ASN:HB3	1:A:55:ASN:O	2.19	0.42
1:A:157:ALA:HB3	1:A:163:TYR:HB3	2.01	0.42
1:B:139:GLY:N	2:B:1001:GOL:H11	2.32	0.42
1:B:5:LEU:HD11	1:B:12[A]:ARG:HG2	2.01	0.42
1:B:142:VAL:O	1:B:143:ALA:HB2	2.20	0.42
1:B:7:GLY:N	1:B:10:ASP:OD1	2.50	0.41
1:B:42:ASN:OD1	1:B:218:ALA:HA	2.20	0.41
1:B:5:LEU:CD2	1:B:12[A]:ARG:HE	2.27	0.41
1:A:139:GLY:H	2:A:1001:GOL:C2	2.34	0.41
1:A:167:ARG:NH1	7:A:2153:HOH:O	2.54	0.41
5:B:1003[B]:GLC:O4	6:B:1004[B]:BGC:H2	2.20	0.41
1:B:68:TRP:CH2	6:B:1005[A]:BGC:H4	2.56	0.41
1:A:25:VAL:HA	1:A:58:ALA:HB2	2.04	0.40
1:B:137:PRO:HD3	1:B:167:ARG:HH11	1.86	0.40
1:B:89:THR:HA	1:B:221:SER:O	2.21	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	232/227 (102%)	227 (98%)	5 (2%)	0	100	100
1	B	231/227 (102%)	222 (96%)	8 (4%)	1 (0%)	38	32
All	All	463/454 (102%)	449 (97%)	13 (3%)	1 (0%)	51	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	53	GLY

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	186/179 (104%)	182 (98%)	4 (2%)	57	60
1	B	185/179 (103%)	183 (99%)	2 (1%)	78	82
All	All	371/358 (104%)	365 (98%)	6 (2%)	66	73

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	79	ARG
1	A	130	ASN
1	A	203	GLU
1	B	23	ASN
1	B	52	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	52	ASN
1	A	130	ASN
1	A	162	ASN
1	B	23	ASN
1	B	24	ASN
1	B	32	GLN
1	B	52	ASN
1	B	54	ASN
1	B	117	ASN
1	B	132	ASN
1	B	162	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 ⓘ

9 carbohydrates 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	$\# Z > 2$
3	GLC	A	1004	3,2	12,12,12	0.33	0	17,17,17	0.33	0
3	BGC	A	1005	3	11,11,12	0.46	0	13,15,17	0.47	0
3	BGC	A	1006	3	11,11,12	0.51	0	13,15,17	0.58	0
6	BGC	B	1004[A]	6	11,11,12	0.67	0	13,15,17	1.22	1 (7%)
6	BGC	B	1004[B]	5,6	12,12,12	0.36	0	17,17,17	0.41	0
6	BGC	B	1005[A]	6	11,11,12	0.53	0	13,15,17	0.36	0
6	BGC	B	1005[B]	6	11,11,12	0.49	0	13,15,17	0.42	0
6	BGC	B	1006[A]	6	11,11,12	0.46	0	13,15,17	0.31	0
6	BGC	B	1006[B]	6	11,11,12	0.44	0	13,15,17	0.31	0

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
3	GLC	A	1004	3,2	1/1/5/5	0/2/22/22	0/1/1/1
3	BGC	A	1005	3	-	0/2/19/22	0/1/1/1
3	BGC	A	1006	3	-	0/2/19/22	0/1/1/1
6	BGC	B	1004[A]	6	-	0/2/19/22	0/1/1/1
6	BGC	B	1004[B]	5,6	-	0/2/22/22	0/1/1/1
6	BGC	B	1005[A]	6	-	0/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	BGC	B	1005[B]	6	-	0/2/19/22	0/1/1/1
6	BGC	B	1006[A]	6	-	0/2/19/22	0/1/1/1
6	BGC	B	1006[B]	6	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1004[A]	BGC	C1-C2-C3	3.09	113.57	109.65

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1004	GLC	C1

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1004	GLC	7	0
6	B	1004[A]	BGC	2	0
6	B	1004[B]	BGC	6	0
6	B	1005[A]	BGC	1	0
6	B	1006[A]	BGC	2	0
6	B	1006[B]	BGC	1	0

5.6 Ligand geometry

11 ligands 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
2	GOL	A	1001	-	5,5,5	4.93	5 (100%)	5,5,5	5.51	3 (60%)
2	GOL	A	1002	-	5,5,5	4.95	5 (100%)	5,5,5	5.48	3 (60%)
2	GOL	A	1003[A]	-	5,5,5	4.93	5 (100%)	5,5,5	5.47	3 (60%)
2	GOL	A	1003[B]	3	5,5,5	4.91	5 (100%)	5,5,5	5.50	3 (60%)
2	GOL	A	1234	-	5,5,5	4.96	5 (100%)	5,5,5	5.49	3 (60%)
2	GOL	A	1235	-	5,5,5	4.93	5 (100%)	5,5,5	5.46	3 (60%)
4	SO4	A	1236	-	4,4,4	0.28	0	6,6,6	0.13	0
2	GOL	B	1001	-	5,5,5	4.92	5 (100%)	5,5,5	5.49	3 (60%)
2	GOL	B	1002[A]	-	5,5,5	5.32	4 (80%)	5,5,5	5.54	3 (60%)
5	GLC	B	1003[B]	6	12,12,12	0.48	0	17,17,17	0.60	0
2	GOL	B	1237	-	5,5,5	4.93	5 (100%)	5,5,5	5.47	3 (60%)

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
2	GOL	A	1001	-	-	0/4/4/4	0/0/0/0
2	GOL	A	1002	-	-	0/4/4/4	0/0/0/0
2	GOL	A	1003[A]	-	-	0/4/4/4	0/0/0/0
2	GOL	A	1003[B]	3	-	0/4/4/4	0/0/0/0
2	GOL	A	1234	-	-	0/4/4/4	0/0/0/0
2	GOL	A	1235	-	-	0/4/4/4	0/0/0/0
4	SO4	A	1236	-	-	0/0/0/0	0/0/0/0
2	GOL	B	1001	-	-	0/4/4/4	0/0/0/0
2	GOL	B	1002[A]	-	-	0/4/4/4	0/0/0/0
5	GLC	B	1003[B]	6	1/1/5/5	0/2/22/22	0/1/1/1
2	GOL	B	1237	-	-	0/4/4/4	0/0/0/0

All (44) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1002[A]	GOL	C3-C2	-9.38	1.17	1.52
2	A	1234	GOL	C3-C2	-8.48	1.20	1.52
2	A	1002	GOL	C3-C2	-8.44	1.21	1.52
2	A	1235	GOL	C3-C2	-8.42	1.21	1.52
2	A	1003[B]	GOL	C3-C2	-8.37	1.21	1.52
2	A	1003[A]	GOL	C3-C2	-8.33	1.21	1.52
2	A	1001	GOL	C3-C2	-8.31	1.21	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	GOL	C3-C2	-8.30	1.21	1.52
2	B	1237	GOL	C3-C2	-8.28	1.21	1.52
2	A	1002	GOL	C1-C2	-3.50	1.39	1.52
2	B	1237	GOL	C1-C2	-3.34	1.39	1.52
2	B	1001	GOL	C1-C2	-3.33	1.39	1.52
2	A	1235	GOL	C1-C2	-3.30	1.40	1.52
2	A	1001	GOL	C1-C2	-3.29	1.40	1.52
2	A	1003[A]	GOL	C1-C2	-3.27	1.40	1.52
2	A	1003[B]	GOL	C1-C2	-3.22	1.40	1.52
2	A	1234	GOL	C1-C2	-3.21	1.40	1.52
2	A	1001	GOL	O2-C2	-3.04	1.34	1.43
2	A	1003[A]	GOL	O2-C2	-3.02	1.34	1.43
2	A	1002	GOL	O2-C2	-3.00	1.34	1.43
2	A	1234	GOL	O2-C2	-2.98	1.34	1.43
2	B	1237	GOL	O2-C2	-2.96	1.34	1.43
2	B	1001	GOL	O2-C2	-2.94	1.34	1.43
2	B	1002[A]	GOL	C1-C2	-2.91	1.41	1.52
2	A	1235	GOL	O2-C2	-2.86	1.35	1.43
2	A	1003[B]	GOL	O2-C2	-2.78	1.35	1.43
2	A	1234	GOL	O3-C3	3.29	1.56	1.42
2	A	1003[A]	GOL	O3-C3	3.31	1.56	1.42
2	A	1235	GOL	O3-C3	3.32	1.56	1.42
2	A	1002	GOL	O3-C3	3.35	1.56	1.42
2	A	1003[B]	GOL	O3-C3	3.36	1.56	1.42
2	A	1001	GOL	O3-C3	3.38	1.56	1.42
2	B	1001	GOL	O3-C3	3.39	1.56	1.42
2	B	1237	GOL	O3-C3	3.44	1.56	1.42
2	B	1002[A]	GOL	O3-C3	3.89	1.58	1.42
2	A	1002	GOL	O1-C1	4.37	1.60	1.42
2	A	1235	GOL	O1-C1	4.53	1.61	1.42
2	B	1001	GOL	O1-C1	4.56	1.61	1.42
2	A	1001	GOL	O1-C1	4.57	1.61	1.42
2	A	1003[B]	GOL	O1-C1	4.58	1.61	1.42
2	A	1234	GOL	O1-C1	4.61	1.61	1.42
2	A	1003[A]	GOL	O1-C1	4.63	1.61	1.42
2	B	1237	GOL	O1-C1	4.64	1.61	1.42
2	B	1002[A]	GOL	O1-C1	5.22	1.64	1.42

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	GOL	O1-C1-C2	2.98	125.08	110.07

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1002	GOL	O1-C1-C2	3.02	125.28	110.07
2	B	1001	GOL	O1-C1-C2	3.08	125.57	110.07
2	B	1237	GOL	O1-C1-C2	3.08	125.58	110.07
2	A	1003[A]	GOL	O1-C1-C2	3.09	125.63	110.07
2	A	1003[B]	GOL	O1-C1-C2	3.14	125.88	110.07
2	A	1234	GOL	O1-C1-C2	3.18	126.07	110.07
2	A	1235	GOL	O1-C1-C2	3.22	126.32	110.07
2	B	1002[A]	GOL	O1-C1-C2	3.68	128.59	110.07
2	A	1003[A]	GOL	O2-C2-C3	6.27	138.47	108.84
2	B	1237	GOL	O2-C2-C3	6.33	138.75	108.84
2	A	1001	GOL	O2-C2-C3	6.35	138.84	108.84
2	A	1003[B]	GOL	O2-C2-C3	6.36	138.86	108.84
2	A	1235	GOL	O2-C2-C3	6.36	138.89	108.84
2	B	1001	GOL	O2-C2-C3	6.36	138.89	108.84
2	A	1234	GOL	O2-C2-C3	6.36	138.90	108.84
2	A	1002	GOL	O2-C2-C3	6.43	139.21	108.84
2	B	1002[A]	GOL	O2-C2-C3	6.45	139.30	108.84
2	B	1002[A]	GOL	O3-C3-C2	9.84	159.64	110.07
2	A	1235	GOL	O3-C3-C2	9.89	159.92	110.07
2	A	1002	GOL	O3-C3-C2	9.96	160.25	110.07
2	A	1234	GOL	O3-C3-C2	9.97	160.30	110.07
2	B	1237	GOL	O3-C3-C2	9.98	160.33	110.07
2	B	1001	GOL	O3-C3-C2	10.01	160.50	110.07
2	A	1003[B]	GOL	O3-C3-C2	10.01	160.52	110.07
2	A	1003[A]	GOL	O3-C3-C2	10.02	160.57	110.07
2	A	1001	GOL	O3-C3-C2	10.11	161.02	110.07

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	B	1003[B]	GLC	C1

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	GOL	1	0
2	A	1003[A]	GOL	2	0
2	A	1003[B]	GOL	4	0
2	B	1001	GOL	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1002[A]	GOL	4	0
5	B	1003[B]	GLC	6	0
2	B	1237	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	226/227 (99%)	0.14	3 (1%) 77 82	11, 21, 36, 58	0
1	B	226/227 (99%)	0.13	9 (3%) 39 46	14, 28, 50, 70	0
All	All	452/454 (99%)	0.14	12 (2%) 55 63	11, 23, 45, 70	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	52	ASN	3.5
1	A	227	LEU	3.3
1	B	98	THR	3.1
1	B	29[A]	GLU	2.9
1	B	51	ASP	2.9
1	B	48	ALA	2.8
1	B	49	ASP	2.5
1	A	160[A]	ASP	2.3
1	A	53	GLY	2.2
1	B	54	ASN	2.1
1	B	31	ALA	2.1
1	B	8[A]	ARG	2.1

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

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

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	GLC	A	1004	12/12	0.89	0.22	4.71	34,39,40,44	12
6	BGC	B	1004[B]	12/12	0.90	0.20	4.28	40,44,45,45	12
6	BGC	B	1004[A]	11/12	0.90	0.20	4.28	49,54,57,57	11
6	BGC	B	1006[B]	11/12	0.74	0.23	3.47	55,58,59,60	11
6	BGC	B	1006[A]	11/12	0.74	0.23	3.47	58,61,62,62	11
6	BGC	B	1005[A]	11/12	0.90	0.19	2.95	43,48,54,55	11
6	BGC	B	1005[B]	11/12	0.90	0.19	2.95	36,42,50,50	11
3	BGC	A	1006	11/12	0.88	0.13	1.12	56,59,62,62	0
3	BGC	A	1005	11/12	0.88	0.12	-0.38	29,40,48,51	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
5	GLC	B	1003[B]	12/12	0.70	0.48	11.94	60,65,66,67	12
2	GOL	A	1003[B]	6/6	0.73	0.30	6.66	50,52,53,55	6
2	GOL	A	1003[A]	6/6	0.73	0.30	6.55	43,47,48,50	6
2	GOL	B	1002[A]	6/6	0.58	0.28	5.32	54,55,57,58	6
2	GOL	A	1234	6/6	0.81	0.23	4.62	53,59,61,63	0
2	GOL	A	1002	6/6	0.80	0.26	2.04	64,65,66,68	0
4	SO4	A	1236	5/5	0.96	0.11	-0.36	25,26,27,30	0
2	GOL	B	1237	6/6	0.86	0.20	-	59,60,61,62	0
2	GOL	B	1001	6/6	0.83	0.17	-	68,69,69,70	0
2	GOL	A	1235	6/6	0.85	0.19	-	58,59,59,60	0
2	GOL	A	1001	6/6	0.80	0.28	-	61,62,63,64	0

6.5 Other polymers ⓘ

There are no such residues in this entry.