



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:17 PM GMT

PDB ID : 4HU0
Title : Crystal Structure of a metagenome-derived cellulase Cel5A in complex with cellotetraose
Authors : Zhuang, N.; Lee, K.H.
Deposited on : 2012-11-02
Resolution : 2.38 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

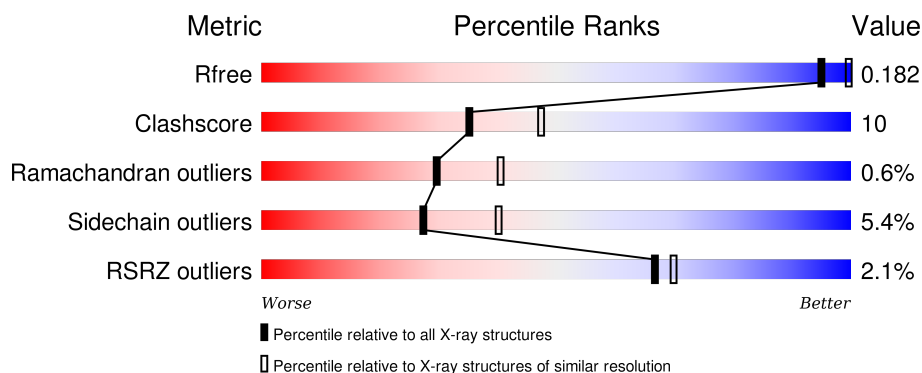
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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}	91344	4019 (2.40-2.36)
Clashscore	102246	4595 (2.40-2.36)
Ramachandran outliers	100387	4520 (2.40-2.36)
Sidechain outliers	100360	4522 (2.40-2.36)
RSRZ outliers	91569	4034 (2.40-2.36)

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	359	

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
3	GOL	A	402	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	A	407	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3070 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.

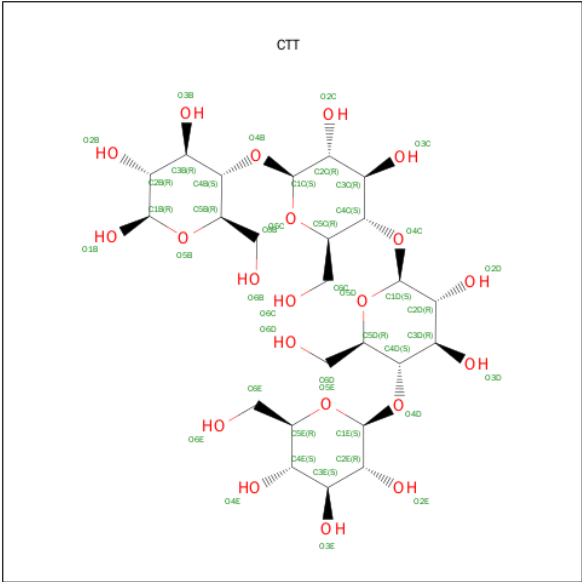
- Molecule 1 is a protein called Cellulase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	Se	0	2	0
			2718	1755	470	489	4			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	MSE	-	EXPRESSION TAG	UNP I6PLH5
A	6	GLY	-	EXPRESSION TAG	UNP I6PLH5
A	7	SER	-	EXPRESSION TAG	UNP I6PLH5
A	8	SER	-	EXPRESSION TAG	UNP I6PLH5
A	9	HIS	-	EXPRESSION TAG	UNP I6PLH5
A	10	HIS	-	EXPRESSION TAG	UNP I6PLH5
A	11	HIS	-	EXPRESSION TAG	UNP I6PLH5
A	12	HIS	-	EXPRESSION TAG	UNP I6PLH5
A	13	HIS	-	EXPRESSION TAG	UNP I6PLH5
A	14	HIS	-	EXPRESSION TAG	UNP I6PLH5
A	15	SER	-	EXPRESSION TAG	UNP I6PLH5
A	16	SER	-	EXPRESSION TAG	UNP I6PLH5
A	17	GLY	-	EXPRESSION TAG	UNP I6PLH5
A	18	LEU	-	EXPRESSION TAG	UNP I6PLH5
A	19	VAL	-	EXPRESSION TAG	UNP I6PLH5
A	20	PRO	-	EXPRESSION TAG	UNP I6PLH5
A	21	ARG	-	EXPRESSION TAG	UNP I6PLH5
A	22	GLY	-	EXPRESSION TAG	UNP I6PLH5
A	23	SER	-	EXPRESSION TAG	UNP I6PLH5
A	24	HIS	-	EXPRESSION TAG	UNP I6PLH5
A	25	MSE	-	EXPRESSION TAG	UNP I6PLH5

- Molecule 2 is SUGAR (BETA-D-GLUCOPYRANOSYL-(1->4)-BETA-D-GLUCOPYRANOSYL-(1->4)-BETA-D-GLUCOPYRANOSE) (three-letter code: CTT) (formula: C₂₄H₄₂O₂₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			45	24	21		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

Continued on next page...

Continued from previous page...

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

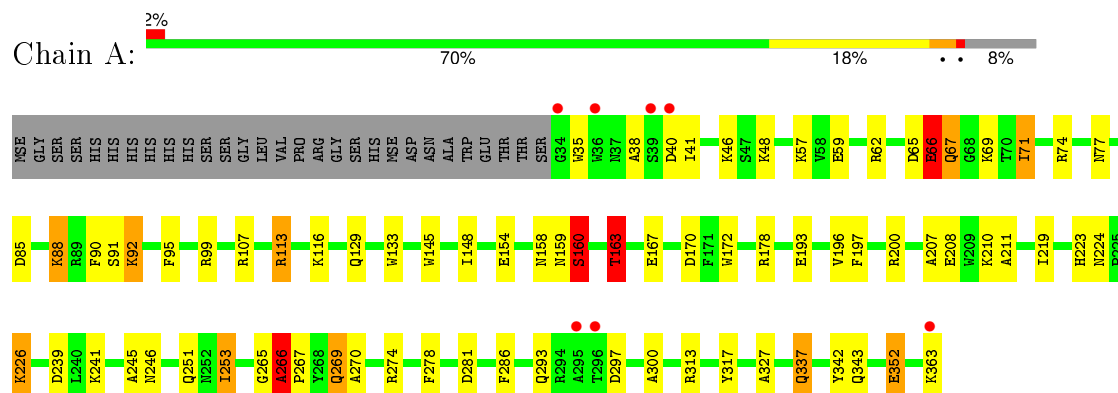
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	271	Total	O	0	0
			271	271		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Cellulase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	136.92Å 136.92Å 136.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.30 – 2.38 43.30 – 2.38	Depositor EDS
% Data completeness (in resolution range)	99.5 (43.30-2.38) 99.5 (43.30-2.38)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.152 , 0.188 0.151 , 0.182	Depositor DCC
R_{free} test set	1734 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	37.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.4	EDS
Estimated twinning fraction	0.024 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 34226 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3070	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CTT, GOL

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	1.53	24/2806 (0.9%)	1.19	25/3809 (0.7%)

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
1	A	0	1

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	154	GLU	CB-CG	-9.27	1.34	1.52
1	A	266	ALA	N-CA	8.46	1.63	1.46
1	A	352	GLU	CD-OE1	8.19	1.34	1.25
1	A	352	GLU	CG-CD	7.91	1.63	1.51
1	A	154	GLU	CD-OE1	7.27	1.33	1.25
1	A	317	TYR	CD1-CE1	7.10	1.50	1.39
1	A	343	GLN	CG-CD	6.61	1.66	1.51
1	A	159	ASN	CB-CG	6.54	1.66	1.51
1	A	207	ALA	CA-CB	6.52	1.66	1.52
1	A	327	ALA	CA-CB	6.45	1.66	1.52
1	A	245	ALA	CA-CB	6.40	1.65	1.52
1	A	35	TRP	CB-CG	6.34	1.61	1.50
1	A	160	SER	C-O	6.30	1.35	1.23
1	A	95	PHE	CE2-CZ	5.67	1.48	1.37
1	A	211	ALA	CA-CB	5.50	1.64	1.52
1	A	208	GLU	CG-CD	5.45	1.60	1.51
1	A	278	PHE	CE1-CZ	5.39	1.47	1.37
1	A	59	GLU	CG-CD	5.29	1.59	1.51

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	66[A]	GLU	CB-CG	5.23	1.62	1.52
1	A	66[B]	GLU	CB-CG	5.23	1.62	1.52
1	A	317	TYR	CD2-CE2	5.18	1.47	1.39
1	A	270	ALA	CA-CB	5.13	1.63	1.52
1	A	342	TYR	CG-CD2	5.06	1.45	1.39
1	A	266	ALA	CA-C	-5.06	1.39	1.52

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	ARG	NE-CZ-NH2	-12.70	113.95	120.30
1	A	62	ARG	NE-CZ-NH1	11.04	125.82	120.30
1	A	281	ASP	CB-CG-OD1	8.45	125.90	118.30
1	A	92	LYS	CD-CE-NZ	-7.68	94.05	111.70
1	A	297	ASP	CB-CG-OD2	7.00	124.60	118.30
1	A	253	ILE	CG1-CB-CG2	-6.92	96.18	111.40
1	A	266	ALA	N-CA-CB	6.90	119.76	110.10
1	A	274	ARG	NE-CZ-NH2	6.86	123.73	120.30
1	A	266	ALA	N-CA-C	-6.58	93.23	111.00
1	A	113	ARG	NE-CZ-NH1	6.38	123.49	120.30
1	A	274	ARG	NE-CZ-NH1	-6.20	117.20	120.30
1	A	178	ARG	NE-CZ-NH1	-6.19	117.21	120.30
1	A	74	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	A	170	ASP	CB-CG-OD2	6.01	123.71	118.30
1	A	154	GLU	CG-CD-OE2	-5.89	106.53	118.30
1	A	239	ASP	CB-CG-OD1	5.76	123.49	118.30
1	A	313	ARG	NE-CZ-NH2	-5.74	117.43	120.30
1	A	163	THR	CB-CA-C	-5.68	96.27	111.60
1	A	297	ASP	CB-CG-OD1	-5.64	113.22	118.30
1	A	71	ILE	CG1-CB-CG2	-5.50	99.30	111.40
1	A	313	ARG	NE-CZ-NH1	5.47	123.03	120.30
1	A	116	LYS	CD-CE-NZ	-5.42	99.24	111.70
1	A	363	LYS	CD-CE-NZ	-5.15	99.85	111.70
1	A	253	ILE	CA-CB-CG2	5.04	120.98	110.90
1	A	251	GLN	CB-CA-C	-5.02	100.36	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	265	GLY	Peptide

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	2718	0	2610	51	0
2	A	45	0	42	4	0
3	A	36	0	46	2	0
4	A	271	0	0	14	0
All	All	3070	0	2698	54	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 10.

All (54) 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)
1:A:66[A]:GLU:HG3	1:A:67:GLN:HE22	1.15	1.08
1:A:67:GLN:N	1:A:67:GLN:HE21	1.60	1.00
1:A:269:GLN:H	1:A:269:GLN:HE21	1.10	0.97
1:A:129:GLN:HG2	4:A:679:HOH:O	1.65	0.96
1:A:67:GLN:HE21	1:A:67:GLN:H	0.95	0.94
1:A:66[A]:GLU:HG3	1:A:67:GLN:NE2	1.82	0.92
1:A:67:GLN:NE2	1:A:67:GLN:H	1.77	0.81
1:A:266:ALA:CB	4:A:745:HOH:O	2.32	0.77
1:A:46:LYS:HD3	4:A:673:HOH:O	1.83	0.77
1:A:163:THR:HG23	1:A:167:GLU:OE1	1.85	0.75
1:A:224:ASN:HD21	1:A:226:LYS:NZ	1.85	0.73
1:A:219:ILE:O	1:A:223:HIS:HD2	1.73	0.71
1:A:158:ASN:OD1	1:A:160:SER:HB3	1.91	0.70
3:A:404:GOL:HO1	3:A:404:GOL:HO3	1.25	0.70
1:A:163:THR:CG2	1:A:167:GLU:OE1	2.39	0.69
1:A:269:GLN:HE21	1:A:269:GLN:N	1.88	0.69
1:A:46:LYS:CD	4:A:673:HOH:O	2.39	0.68
1:A:241:LYS:NZ	4:A:765:HOH:O	2.27	0.66
1:A:266:ALA:HB3	4:A:745:HOH:O	1.92	0.66
1:A:148:ILE:HD11	2:A:401:CTT:H2D	1.79	0.64
1:A:266:ALA:CB	1:A:267:PRO:CD	2.81	0.59
1:A:196:VAL:HG22	3:A:402:GOL:H32	1.84	0.59
1:A:269:GLN:H	1:A:269:GLN:NE2	1.92	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:GLU:HG3	4:A:675:HOH:O	2.03	0.57
1:A:337:GLN:H	1:A:337:GLN:NE2	2.01	0.56
1:A:210:LYS:HE3	1:A:246:ASN:HD21	1.70	0.56
1:A:66[B]:GLU:HB3	4:A:596:HOH:O	2.05	0.55
1:A:38:ALA:HB1	1:A:41:ILE:HD11	1.87	0.55
1:A:200:ARG:HD2	4:A:676:HOH:O	2.05	0.55
1:A:163:THR:HG22	1:A:167:GLU:HB3	1.90	0.54
1:A:224:ASN:HD21	1:A:226:LYS:HZ1	1.56	0.53
1:A:266:ALA:HB1	1:A:267:PRO:CD	2.38	0.53
1:A:223:HIS:HE1	4:A:553:HOH:O	1.90	0.52
1:A:210:LYS:HE3	1:A:246:ASN:ND2	2.26	0.49
1:A:65:ASP:HB3	1:A:71:ILE:CD1	2.43	0.49
1:A:224:ASN:HD21	1:A:226:LYS:HZ2	1.57	0.48
2:A:401:CTT:H6EA	4:A:667:HOH:O	2.14	0.48
1:A:266:ALA:CB	1:A:267:PRO:HD2	2.44	0.48
2:A:401:CTT:H4D	4:A:703:HOH:O	2.14	0.47
1:A:163:THR:HG22	1:A:167:GLU:OE1	2.14	0.47
1:A:145:TRP:HZ2	1:A:163:THR:HG21	1.80	0.46
1:A:193:GLU:OE2	2:A:401:CTT:H1D	2.16	0.46
1:A:92:LYS:NZ	4:A:694:HOH:O	2.49	0.46
1:A:77:ASN:OD1	1:A:107:ARG:HD3	2.16	0.46
1:A:99:ARG:HG3	1:A:99:ARG:O	2.16	0.46
1:A:66[B]:GLU:OE1	4:A:596:HOH:O	2.20	0.45
1:A:172:TRP:CE3	1:A:172:TRP:HA	2.52	0.45
1:A:88:LYS:HE3	1:A:88:LYS:HA	2.01	0.43
1:A:85:ASP:HA	1:A:90:PHE:HB2	2.00	0.43
1:A:67:GLN:N	1:A:67:GLN:NE2	2.45	0.42
1:A:65:ASP:HB3	1:A:71:ILE:HD11	2.01	0.42
1:A:145:TRP:HZ2	1:A:163:THR:CG2	2.32	0.42
1:A:91:SER:HA	1:A:133:TRP:CH2	2.55	0.41
1:A:293:GLN:OE1	1:A:300:ALA:HA	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	330/359 (92%)	319 (97%)	9 (3%)	2 (1%)	30	40

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	ALA
1	A	40	ASP

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	282/301 (94%)	266 (94%)	16 (6%)	25	37

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	LYS
1	A	57	LYS
1	A	66[A]	GLU
1	A	66[B]	GLU
1	A	67	GLN
1	A	69	LYS
1	A	88	LYS
1	A	113	ARG
1	A	160	SER
1	A	163	THR
1	A	197	PHE
1	A	226	LYS
1	A	253	ILE
1	A	269	GLN
1	A	286	PHE
1	A	337	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	GLN
1	A	223	HIS
1	A	224	ASN
1	A	246	ASN
1	A	269	GLN
1	A	337	GLN

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

7 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	CTT	A	401	-	48,48,48	1.37	7 (14%)	71,71,71	2.61	29 (40%)
3	GOL	A	402	-	5,5,5	1.04	0	5,5,5	0.87	0
3	GOL	A	403	-	5,5,5	1.07	0	5,5,5	1.12	1 (20%)
3	GOL	A	404	-	5,5,5	1.47	1 (20%)	5,5,5	1.74	3 (60%)
3	GOL	A	405	-	5,5,5	0.76	0	5,5,5	1.97	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	A	406	-	5,5,5	0.82	0	5,5,5	1.51	1 (20%)
3	GOL	A	407	-	5,5,5	1.13	1 (20%)	5,5,5	1.31	1 (20%)

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	CTT	A	401	-	-	0/20/100/100	0/4/4/4
3	GOL	A	402	-	-	0/4/4/4	0/0/0/0
3	GOL	A	403	-	-	0/4/4/4	0/0/0/0
3	GOL	A	404	-	-	0/4/4/4	0/0/0/0
3	GOL	A	405	-	-	0/4/4/4	0/0/0/0
3	GOL	A	406	-	-	0/4/4/4	0/0/0/0
3	GOL	A	407	-	-	0/4/4/4	0/0/0/0

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	404	GOL	O2-C2	-2.74	1.35	1.43
3	A	407	GOL	O2-C2	-2.33	1.36	1.43
2	A	401	CTT	O4D-C1E	2.09	1.47	1.41
2	A	401	CTT	O5B-C1B	2.14	1.47	1.43
2	A	401	CTT	O5D-C1D	2.42	1.48	1.41
2	A	401	CTT	C3D-C4D	2.69	1.60	1.52
2	A	401	CTT	C3E-C4E	3.16	1.60	1.52
2	A	401	CTT	O3E-C3E	3.50	1.51	1.43
2	A	401	CTT	O4C-C1D	4.32	1.53	1.41

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	CTT	O4E-C4E-C5E	-7.47	89.45	109.24
2	A	401	CTT	O6D-C6D-C5D	-4.30	97.13	111.33
3	A	405	GOL	O3-C3-C2	-3.98	90.88	110.18
2	A	401	CTT	O1B-C1B-C2B	-3.97	98.57	109.21
2	A	401	CTT	O5D-C1D-C2D	-3.88	102.32	110.28
2	A	401	CTT	C4E-C3E-C2E	-3.66	103.97	110.79
2	A	401	CTT	O3D-C3D-C2D	-3.29	102.93	110.34
2	A	401	CTT	C1B-O5B-C5B	-3.19	107.57	113.47
2	A	401	CTT	O5B-C1B-C2B	-2.78	105.36	109.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	CTT	O1B-C1B-O5B	-2.75	102.72	110.25
3	A	407	GOL	O1-C1-C2	-2.66	97.26	110.18
2	A	401	CTT	C3C-C4C-C5C	-2.64	104.87	110.84
2	A	401	CTT	O6B-C6B-C5B	-2.50	103.09	111.33
3	A	404	GOL	O2-C2-C1	-2.46	97.38	108.65
2	A	401	CTT	O5E-C5E-C6E	-2.22	100.75	106.36
3	A	404	GOL	O1-C1-C2	-2.19	99.58	110.18
2	A	401	CTT	O5E-C1E-C2E	-2.17	105.83	110.28
2	A	401	CTT	C1B-C2B-C3B	-2.03	107.41	110.43
3	A	404	GOL	O2-C2-C3	2.01	117.86	108.65
2	A	401	CTT	O2E-C2E-C3E	2.09	115.04	110.34
2	A	401	CTT	C1C-O5C-C5C	2.14	117.89	113.75
2	A	401	CTT	C1D-C2D-C3D	2.15	114.20	109.97
2	A	401	CTT	O4C-C1D-C2D	2.20	113.45	108.10
2	A	401	CTT	O4C-C4C-C5C	2.32	115.41	109.32
3	A	403	GOL	C3-C2-C1	2.33	120.26	111.12
2	A	401	CTT	O2B-C2B-C1B	2.39	115.08	109.82
2	A	401	CTT	O5D-C5D-C6D	2.45	112.56	106.36
3	A	406	GOL	C3-C2-C1	2.66	121.54	111.12
2	A	401	CTT	C1E-O5E-C5E	3.32	120.18	113.75
2	A	401	CTT	O5E-C5E-C4E	3.53	116.32	109.68
2	A	401	CTT	O3D-C3D-C4D	3.94	119.20	109.87
2	A	401	CTT	O4E-C4E-C3E	4.58	120.64	110.34
2	A	401	CTT	O4D-C4D-C3D	4.66	119.19	107.17
2	A	401	CTT	C1D-O4C-C4C	6.05	133.82	118.01
2	A	401	CTT	O3E-C3E-C4E	6.55	125.08	110.34
2	A	401	CTT	O4C-C1D-O5D	7.21	128.93	110.68

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	CTT	4	0
3	A	402	GOL	1	0
3	A	404	GOL	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	326/359 (90%)	-0.25	7 (2%) 67 70	27, 38, 60, 98	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	363	LYS	4.5
1	A	34	GLY	3.7
1	A	296	THR	2.5
1	A	40	ASP	2.5
1	A	295	ALA	2.2
1	A	36	TRP	2.2
1	A	39	SER	2.2

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](#)

There are no carbohydrates in this entry.

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. 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(\AA^2)	Q<0.9
3	GOL	A	402	6/6	0.93	0.14	3.43	38,44,57,60	0
3	GOL	A	407	6/6	0.94	0.22	3.17	46,60,64,66	0
2	CTT	A	401	45/45	0.96	0.14	1.43	24,44,62,67	8
3	GOL	A	403	6/6	0.74	0.21	0.99	67,74,76,78	0
3	GOL	A	404	6/6	0.95	0.15	0.80	52,55,59,59	0
3	GOL	A	405	6/6	0.88	0.26	-	75,79,85,88	0
3	GOL	A	406	6/6	0.75	0.27	-	78,84,84,85	0

6.5 Other polymers [i](#)

There are no such residues in this entry.