



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:19 PM GMT

PDB ID : 4HTY
Title : Crystal Structure of a metagenome-derived cellulase Cel5A
Authors : Zhuang, N.; Lee, K.H.
Deposited on : 2012-11-02
Resolution : 2.00 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

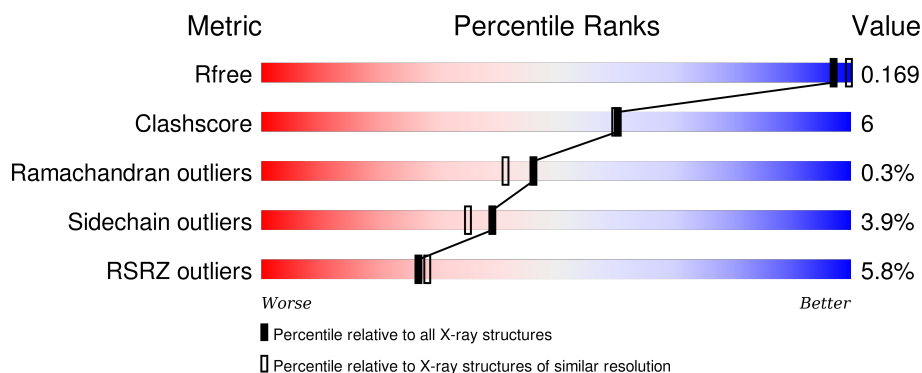
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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
2	GOL	A	603	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	A	604	-	-	-	X
2	GOL	A	605	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2887 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	0	0
			2707	1747	467	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 GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		

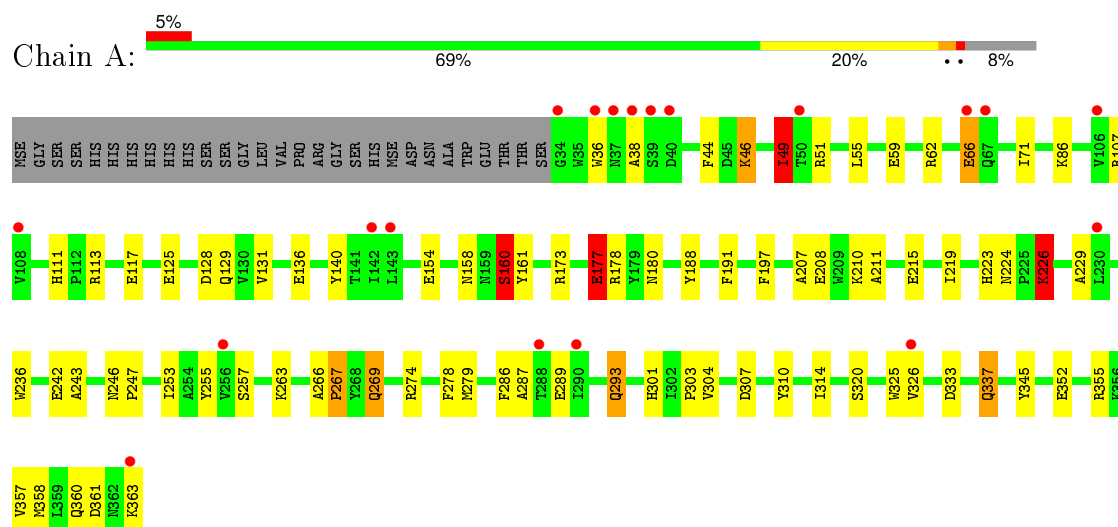
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	150	Total	O	0	0
			150	150		

3 Residue-property plots [i](#)

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	137.77Å 137.77Å 137.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.12 – 2.00 28.12 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (28.12-2.00) 99.7 (28.12-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.64 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.154 , 0.169 0.155 , 0.169	Depositor DCC
R_{free} test set	2979 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	37.2	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.8	EDS
Estimated twinning fraction	0.025 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 58858 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	2887	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	1.91	50/2789 (1.8%)	1.51	24/3786 (0.6%)

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 (50) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	352	GLU	CG-CD	9.70	1.66	1.51
1	A	267	PRO	N-CA	9.30	1.63	1.47
1	A	208	GLU	CG-CD	9.04	1.65	1.51
1	A	358	MSE	SE-CE	-8.55	1.45	1.95
1	A	154	GLU	CG-CD	8.45	1.64	1.51
1	A	226	LYS	CE-NZ	7.86	1.68	1.49
1	A	310	TYR	CD1-CE1	7.71	1.50	1.39
1	A	177	GLU	CB-CG	-7.55	1.37	1.52
1	A	125	GLU	CG-CD	7.29	1.62	1.51
1	A	160	SER	C-O	7.25	1.37	1.23
1	A	161	TYR	CG-CD2	6.95	1.48	1.39
1	A	188	TYR	CD1-CE1	6.91	1.49	1.39
1	A	177	GLU	CG-CD	-6.77	1.41	1.51
1	A	274	ARG	CG-CD	6.65	1.68	1.51
1	A	289	GLU	CG-CD	6.61	1.61	1.51
1	A	36	TRP	CE3-CZ3	6.56	1.49	1.38
1	A	211	ALA	CA-CB	6.21	1.65	1.52
1	A	207	ALA	CA-CB	6.20	1.65	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	178	ARG	CB-CG	-6.18	1.35	1.52
1	A	355	ARG	CG-CD	6.12	1.67	1.51
1	A	226	LYS	CB-CG	6.11	1.69	1.52
1	A	140	TYR	CD2-CE2	6.10	1.48	1.39
1	A	215	GLU	CG-CD	6.03	1.60	1.51
1	A	136	GLU	CG-CD	5.96	1.60	1.51
1	A	191	PHE	CE1-CZ	5.89	1.48	1.37
1	A	208	GLU	CD-OE1	5.86	1.32	1.25
1	A	253	ILE	CB-CG2	5.80	1.70	1.52
1	A	325	TRP	CZ3-CH2	5.79	1.49	1.40
1	A	320	SER	CA-CB	5.77	1.61	1.52
1	A	363	LYS	C-O	5.71	1.34	1.23
1	A	117	GLU	CD-OE1	5.70	1.31	1.25
1	A	59	GLU	CD-OE2	5.62	1.31	1.25
1	A	255	TYR	CD1-CE1	5.58	1.47	1.39
1	A	345	TYR	CD1-CE1	5.46	1.47	1.39
1	A	242	GLU	CG-CD	5.46	1.60	1.51
1	A	326	VAL	CB-CG2	5.39	1.64	1.52
1	A	136	GLU	CB-CG	5.39	1.62	1.52
1	A	188	TYR	CG-CD1	5.33	1.46	1.39
1	A	131	VAL	CB-CG1	5.33	1.64	1.52
1	A	243	ALA	CA-CB	5.30	1.63	1.52
1	A	129	GLN	CG-CD	5.29	1.63	1.51
1	A	140	TYR	CD1-CE1	5.27	1.47	1.39
1	A	46	LYS	CD-CE	5.26	1.64	1.51
1	A	161	TYR	CE2-CZ	5.25	1.45	1.38
1	A	278	PHE	CE1-CZ	5.21	1.47	1.37
1	A	229	ALA	CA-CB	5.12	1.63	1.52
1	A	357	VAL	CA-CB	5.11	1.65	1.54
1	A	293	GLN	CG-CD	5.08	1.62	1.51
1	A	188	TYR	CE1-CZ	5.05	1.45	1.38
1	A	59	GLU	CG-CD	5.01	1.59	1.51

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	ARG	NE-CZ-NH1	21.50	131.05	120.30
1	A	62	ARG	NE-CZ-NH2	-20.41	110.10	120.30
1	A	51	ARG	NE-CZ-NH2	-11.44	114.58	120.30
1	A	307	ASP	CB-CG-OD1	8.93	126.34	118.30
1	A	358	MSE	CG-SE-CE	7.78	116.02	98.90
1	A	178	ARG	CG-CD-NE	-7.63	95.77	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	333	ASP	CB-CG-OD2	7.31	124.88	118.30
1	A	107	ARG	NE-CZ-NH2	-7.08	116.76	120.30
1	A	113	ARG	NE-CZ-NH2	-6.69	116.95	120.30
1	A	274	ARG	NE-CZ-NH1	-6.50	117.05	120.30
1	A	226	LYS	CB-CG-CD	6.42	128.28	111.60
1	A	266	ALA	C-N-CD	-6.31	106.72	120.60
1	A	62	ARG	CD-NE-CZ	6.21	132.30	123.60
1	A	253	ILE	CB-CG1-CD1	-6.04	97.00	113.90
1	A	197	PHE	N-CA-CB	-5.95	99.89	110.60
1	A	180	ASN	C-N-CA	-5.84	110.04	122.30
1	A	113	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	A	358	MSE	CA-CB-CG	-5.75	103.52	113.30
1	A	86	LYS	CD-CE-NZ	-5.74	98.50	111.70
1	A	71	ILE	CB-CA-C	-5.64	100.31	111.60
1	A	226	LYS	CD-CE-NZ	5.50	124.36	111.70
1	A	51	ARG	NE-CZ-NH1	5.33	122.96	120.30
1	A	128	ASP	CB-CG-OD1	5.07	122.86	118.30
1	A	49	ILE	CA-CB-CG2	5.06	121.01	110.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	38	ALA	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	2707	0	2595	28	0
2	A	30	0	40	7	0
3	A	150	0	0	3	0
All	All	2887	0	2635	30	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 6.

All (30) 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:226:LYS:CE	1:A:226:LYS:NZ	1.68	1.51
1:A:269:GLN:H	1:A:269:GLN:HE21	1.25	0.84
2:A:603:GOL:H31	3:A:820:HOH:O	1.84	0.77
1:A:224:ASN:HD21	1:A:226:LYS:NZ	1.85	0.74
1:A:223:HIS:HE1	3:A:715:HOH:O	1.70	0.74
1:A:66:GLU:H	1:A:66:GLU:CD	1.91	0.73
1:A:219:ILE:O	1:A:223:HIS:HD2	1.83	0.61
1:A:337:GLN:NE2	1:A:337:GLN:H	2.00	0.59
1:A:66:GLU:CD	1:A:66:GLU:N	2.58	0.57
1:A:111:HIS:NE2	2:A:601:GOL:H31	2.21	0.56
1:A:269:GLN:H	1:A:269:GLN:NE2	2.01	0.55
1:A:263:LYS:NZ	2:A:604:GOL:O1	2.32	0.54
1:A:360:GLN:HG2	1:A:361:ASP:OD1	2.08	0.52
1:A:210:LYS:HE3	1:A:246:ASN:HD21	1.75	0.51
1:A:224:ASN:HD21	1:A:226:LYS:HZ2	1.59	0.49
1:A:224:ASN:ND2	1:A:226:LYS:NZ	2.57	0.48
1:A:303:PRO:HG3	2:A:604:GOL:H12	1.99	0.45
1:A:236:TRP:CD2	2:A:604:GOL:H2	2.52	0.45
1:A:301:HIS:O	1:A:304:VAL:HG22	2.17	0.45
1:A:257:SER:O	1:A:287:ALA:HA	2.17	0.44
1:A:210:LYS:HE2	1:A:247:PRO:O	2.17	0.44
1:A:210:LYS:HE3	1:A:246:ASN:ND2	2.33	0.44
1:A:293:GLN:HE22	1:A:337:GLN:HE22	1.64	0.43
1:A:111:HIS:NE2	2:A:601:GOL:C3	2.81	0.43
1:A:44:PHE:CZ	1:A:49:ILE:HD12	2.54	0.42
2:A:603:GOL:C3	3:A:820:HOH:O	2.55	0.41
1:A:173:ARG:O	1:A:177:GLU:HB3	2.20	0.41
1:A:224:ASN:ND2	1:A:226:LYS:HZ1	2.16	0.41
1:A:55:LEU:HD11	1:A:226:LYS:HB2	2.03	0.41
1:A:158:ASN:OD1	1:A:160:SER:HB3	2.21	0.41

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	328/359 (91%)	321 (98%)	6 (2%)	1 (0%)	46	41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	267	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	281/301 (93%)	270 (96%)	11 (4%)	39	35

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	LYS
1	A	49	ILE
1	A	66	GLU
1	A	160	SER
1	A	177	GLU
1	A	226	LYS
1	A	269	GLN
1	A	279	MSE
1	A	286	PHE
1	A	314	ILE
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	135	ASN
1	A	223	HIS

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

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](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 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	601	-	5,5,5	0.42	0	5,5,5	1.34	1 (20%)
2	GOL	A	602	-	5,5,5	0.60	0	5,5,5	1.12	0
2	GOL	A	603	-	5,5,5	0.88	0	5,5,5	0.96	0
2	GOL	A	604	-	5,5,5	0.77	0	5,5,5	1.40	1 (20%)
2	GOL	A	605	-	5,5,5	0.38	0	5,5,5	0.92	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
2	GOL	A	601	-	-	0/4/4/4	0/0/0/0
2	GOL	A	602	-	-	0/4/4/4	0/0/0/0
2	GOL	A	603	-	-	0/4/4/4	0/0/0/0
2	GOL	A	604	-	-	0/4/4/4	0/0/0/0
2	GOL	A	605	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	GOL	O1-C1-C2	-2.63	97.44	110.18
2	A	604	GOL	C3-C2-C1	2.91	122.52	111.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	GOL	2	0
2	A	603	GOL	2	0
2	A	604	GOL	3	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 ⓘ

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	326/359 (90%)	-0.08	19 (5%)	26 28	29, 41, 66, 88	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	39	SER	5.5
1	A	36	TRP	4.8
1	A	34	GLY	4.7
1	A	66	GLU	4.1
1	A	40	ASP	3.9
1	A	143	LEU	3.3
1	A	142	ILE	3.1
1	A	50	THR	3.0
1	A	363	LYS	2.6
1	A	37	ASN	2.6
1	A	38	ALA	2.6
1	A	256	VAL	2.5
1	A	326	VAL	2.5
1	A	108	VAL	2.4
1	A	230	LEU	2.4
1	A	288	THR	2.4
1	A	67	GLN	2.1
1	A	106	VAL	2.0
1	A	290	ILE	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 [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
2	GOL	A	604	6/6	0.75	0.24	4.85	58,70,77,82	3
2	GOL	A	605	6/6	0.82	0.24	3.90	77,83,83,86	0
2	GOL	A	603	6/6	0.94	0.21	3.06	36,59,71,78	0
2	GOL	A	602	6/6	0.92	0.16	0.59	56,66,67,69	0
2	GOL	A	601	6/6	0.92	0.17	-	64,74,76,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.