



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 11:53 am BST

PDB ID : 4LGN
Title : The structure of Acidothermus cellulolyticus family 74 glycoside hydrolase
Authors : Alahuhta, P.M.; Lunin, V.V.
Deposited on : 2013-06-28
Resolution : 1.82 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 2.11
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) : 2.11

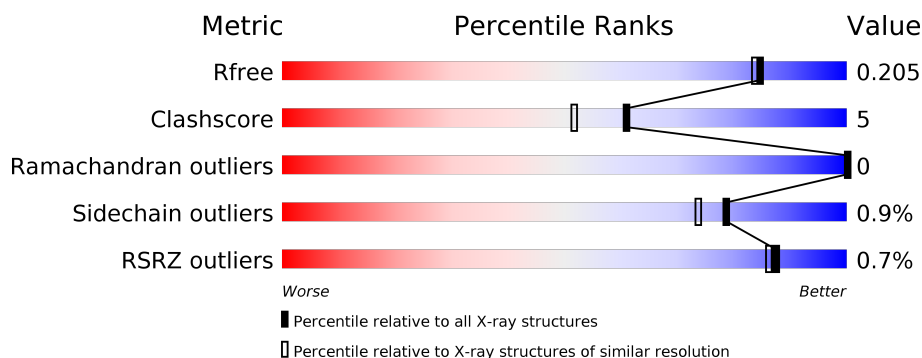
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.82 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	7484 (1.84-1.80)
Clashscore	141614	8401 (1.84-1.80)
Ramachandran outliers	138981	8290 (1.84-1.80)
Sidechain outliers	138945	8290 (1.84-1.80)
RSRZ outliers	127900	7371 (1.84-1.80)

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	749	<div> <div></div> <div>93%</div> <div>5%</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
4	GOL	A	821	-	-	X	-
4	GOL	A	822	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6908 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 Cellulose-binding, family II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	739	Total	C	N	O	S	0	20	0
			5624	3574	949	1089	12			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING METHIONINE	UNP A0LSI1
A	742	LEU	-	EXPRESSION TAG	UNP A0LSI1
A	743	GLU	-	EXPRESSION TAG	UNP A0LSI1
A	744	HIS	-	EXPRESSION TAG	UNP A0LSI1
A	745	HIS	-	EXPRESSION TAG	UNP A0LSI1
A	746	HIS	-	EXPRESSION TAG	UNP A0LSI1
A	747	HIS	-	EXPRESSION TAG	UNP A0LSI1
A	748	HIS	-	EXPRESSION TAG	UNP A0LSI1
A	749	HIS	-	EXPRESSION TAG	UNP A0LSI1

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	K	0	0
			3	3		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	1
			8	4	4		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	6	Total	Na	0	0
			6	6		

- Molecule 7 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



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

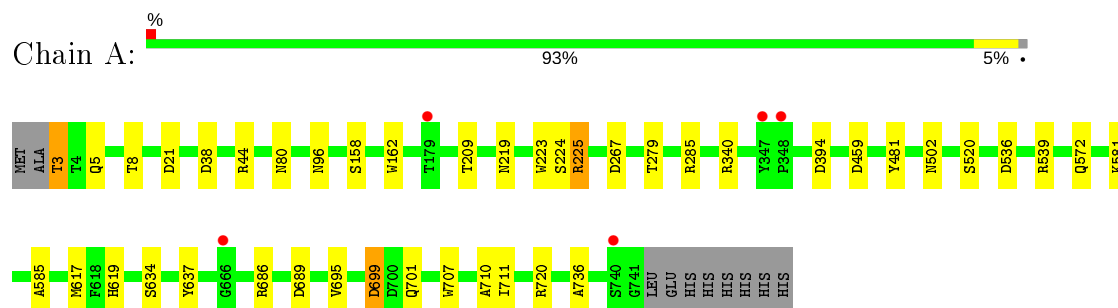
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1121	Total	O	0	38
			1159	1159		

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 the various outlier classes 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: Cellulose-binding, family II



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.76Å 78.69Å 143.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.41 – 1.82 40.38 – 1.82	Depositor EDS
% Data completeness (in resolution range)	99.6 (40.41-1.82) 99.6 (40.38-1.82)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 1.82Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.150 , 0.196 0.161 , 0.205	Depositor DCC
R_{free} test set	3877 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	10.3	Xtriage
Anisotropy	0.254	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 56.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.021 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6908	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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: GOL, NA, K, EDO, ACT, FMT

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	1.04	1/5857 (0.0%)	1.01	20/8036 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	520	SER	CB-OG	6.35	1.50	1.42

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	539	ARG	NE-CZ-NH2	11.47	126.03	120.30
1	A	539	ARG	NE-CZ-NH1	-11.02	114.79	120.30
1	A	44	ARG	NE-CZ-NH1	10.50	125.55	120.30
1	A	720	ARG	NE-CZ-NH2	7.79	124.20	120.30
1	A	285	ARG	NE-CZ-NH2	7.73	124.16	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5624	0	5331	35	0
2	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	68	0	101	3	0
4	A	24	0	32	28	0
5	A	12	0	9	1	0
6	A	6	0	0	0	0
7	A	12	0	4	0	0
8	A	1159	0	0	29	0
All	All	6908	0	5477	51	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 5.

The worst 5 of 51 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)
3:A:816:EDO:O2	8:A:1523:HOH:O	1.54	1.22
4:A:821:GOL:H32	8:A:1427:HOH:O	1.41	1.18
4:A:822:GOL:H31	8:A:1896:HOH:O	1.43	1.17
1:A:634:SER:O	4:A:821:GOL:H2	1.49	1.09
1:A:701[B]:GLN:NE2	8:A:1915:HOH:O	1.62	1.00

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	757/749 (101%)	735 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	596/585 (102%)	591 (99%)	5 (1%)	81	77

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	THR
1	A	158	SER
1	A	223	TRP
1	A	340	ARG
1	A	707	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	205	GLN
1	A	502	ASN
1	A	703	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

Of 37 ligands modelled in this entry, 9 are monoatomic - leaving 28 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$
3	EDO	A	816	-	3,3,3	0.61	0	2,2,2	0.67	0
3	EDO	A	817	-	3,3,3	0.51	0	2,2,2	0.16	0
7	FMT	A	833	-	0,2,2	0.00	-	0,1,1	0.00	-
3	EDO	A	814	-	3,3,3	0.35	0	2,2,2	0.88	0
5	ACT	A	824	-	1,3,3	2.66	1 (100%)	0,3,3	0.00	-
3	EDO	A	806	-	3,3,3	0.88	0	2,2,2	0.38	0
7	FMT	A	835	-	0,2,2	0.00	-	0,1,1	0.00	-
7	FMT	A	836	-	0,2,2	0.00	-	0,1,1	0.00	-
3	EDO	A	811[A]	-	3,3,3	0.60	0	2,2,2	0.18	0
5	ACT	A	826	-	1,3,3	1.03	0	0,3,3	0.00	-
4	GOL	A	822	-	5,5,5	0.23	0	5,5,5	1.18	0
5	ACT	A	825	-	1,3,3	2.58	1 (100%)	0,3,3	0.00	-
3	EDO	A	811[B]	-	3,3,3	0.59	0	2,2,2	0.18	0
3	EDO	A	813	-	3,3,3	0.22	0	2,2,2	1.30	0
3	EDO	A	819	-	3,3,3	0.36	0	2,2,2	0.61	0
4	GOL	A	820	-	5,5,5	0.26	0	5,5,5	0.98	0
3	EDO	A	809	2	3,3,3	0.61	0	2,2,2	0.05	0
3	EDO	A	805	-	3,3,3	0.62	0	2,2,2	0.19	0
3	EDO	A	812	-	3,3,3	0.45	0	2,2,2	1.31	0
3	EDO	A	808	-	3,3,3	0.20	0	2,2,2	1.09	0
7	FMT	A	834	-	0,2,2	0.00	-	0,1,1	0.00	-
3	EDO	A	804	-	3,3,3	0.31	0	2,2,2	0.52	0
4	GOL	A	821	-	5,5,5	0.87	0	5,5,5	1.58	1 (20%)
3	EDO	A	807	-	3,3,3	0.70	0	2,2,2	0.38	0
3	EDO	A	815	-	3,3,3	0.29	0	2,2,2	0.58	0
3	EDO	A	810	-	3,3,3	0.54	0	2,2,2	0.12	0
4	GOL	A	823	-	5,5,5	0.40	0	5,5,5	0.98	0
3	EDO	A	818	-	3,3,3	0.41	0	2,2,2	0.59	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
4	GOL	A	823	-	-	2/4/4/4	-
3	EDO	A	806	-	-	1/1/1/1	-
3	EDO	A	816	-	-	1/1/1/1	-
3	EDO	A	805	-	-	0/1/1/1	-
3	EDO	A	817	-	-	1/1/1/1	-
3	EDO	A	811[A]	-	-	0/1/1/1	-
3	EDO	A	809	2	-	1/1/1/1	-
4	GOL	A	820	-	-	2/4/4/4	-
4	GOL	A	822	-	-	4/4/4/4	-
3	EDO	A	804	-	-	0/1/1/1	-
3	EDO	A	811[B]	-	-	1/1/1/1	-
4	GOL	A	821	-	-	2/4/4/4	-
3	EDO	A	813	-	-	0/1/1/1	-
3	EDO	A	819	-	-	0/1/1/1	-
3	EDO	A	807	-	-	1/1/1/1	-
3	EDO	A	818	-	-	0/1/1/1	-
3	EDO	A	808	-	-	0/1/1/1	-
3	EDO	A	815	-	-	1/1/1/1	-
3	EDO	A	810	-	-	0/1/1/1	-
3	EDO	A	812	-	-	1/1/1/1	-
3	EDO	A	814	-	-	0/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	824	ACT	CH3-C	2.66	1.52	1.48
5	A	825	ACT	CH3-C	2.58	1.52	1.48

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	821	GOL	O1-C1-C2	2.93	124.25	110.20

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	822	GOL	C1-C2-C3-O3
3	A	812	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
4	A	820	GOL	C1-C2-C3-O3
4	A	821	GOL	O1-C1-C2-C3
4	A	823	GOL	C1-C2-C3-O3

There are no ring outliers.

7 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	816	EDO	1	0
5	A	826	ACT	1	0
4	A	822	GOL	15	0
4	A	820	GOL	2	0
4	A	821	GOL	10	0
3	A	815	EDO	2	0
4	A	823	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	739/749 (98%)	-0.55	5 (0%) 87 86	5, 9, 19, 55	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	347	TYR	3.4
1	A	666	GLY	2.9
1	A	348	PRO	2.3
1	A	740	SER	2.3
1	A	179	THR	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](#)

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. 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
3	EDO	A	817	4/4	0.70	0.24	41,45,45,45	0
3	EDO	A	807	4/4	0.79	0.17	36,37,39,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	ACT	A	825	4/4	0.85	0.22	35,35,36,45	0
3	EDO	A	814	4/4	0.88	0.22	24,27,27,31	0
5	ACT	A	824	4/4	0.89	0.15	27,28,31,36	0
3	EDO	A	819	4/4	0.91	0.16	24,28,28,30	0
4	GOL	A	821	6/6	0.91	0.25	9,9,9,10	6
7	FMT	A	836	3/3	0.91	0.27	38,38,40,41	0
6	NA	A	830	1/1	0.91	0.12	22,22,22,22	1
3	EDO	A	818	4/4	0.91	0.24	43,43,44,45	0
4	GOL	A	822	6/6	0.92	0.23	19,22,23,23	6
3	EDO	A	815	4/4	0.92	0.16	18,18,19,19	4
3	EDO	A	812	4/4	0.92	0.17	26,27,27,33	0
5	ACT	A	826	4/4	0.92	0.15	19,21,21,21	4
3	EDO	A	806	4/4	0.93	0.14	28,29,29,30	0
3	EDO	A	816	4/4	0.93	0.14	10,10,11,11	4
7	FMT	A	833	3/3	0.94	0.17	14,14,25,30	0
4	GOL	A	820	6/6	0.94	0.15	14,17,17,21	6
3	EDO	A	805	4/4	0.94	0.12	10,16,17,18	0
3	EDO	A	813	4/4	0.96	0.17	16,22,27,30	0
7	FMT	A	834	3/3	0.96	0.09	13,13,15,17	3
3	EDO	A	810	4/4	0.96	0.10	16,16,18,19	0
4	GOL	A	823	6/6	0.96	0.23	20,21,22,22	6
6	NA	A	828	1/1	0.96	0.09	27,27,27,27	0
6	NA	A	832	1/1	0.96	0.20	39,39,39,39	0
3	EDO	A	809	4/4	0.97	0.09	16,17,19,19	0
3	EDO	A	811[B]	4/4	0.97	0.16	18,19,19,19	4
7	FMT	A	835	3/3	0.97	0.09	17,17,18,18	3
3	EDO	A	808	4/4	0.97	0.08	20,20,23,23	0
6	NA	A	827	1/1	0.97	0.14	24,24,24,24	0
3	EDO	A	811[A]	4/4	0.97	0.16	14,15,16,16	4
3	EDO	A	804	4/4	0.97	0.11	15,15,16,16	0
6	NA	A	831	1/1	0.98	0.07	17,17,17,17	1
2	K	A	801	1/1	0.98	0.21	35,35,35,35	0
6	NA	A	829	1/1	0.98	0.12	32,32,32,32	0
2	K	A	802	1/1	0.99	0.14	37,37,37,37	0
2	K	A	803	1/1	0.99	0.18	37,37,37,37	0

6.5 Other polymers

There are no such residues in this entry.