



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 31, 2021 – 12:37 PM EDT

PDB ID : 7L1Z
Title : Unlocking the structural features for the exo-xylobiosidase activity of an unusual GH11 member identified in a compost-derived consortium - NT-truncated form
Authors : Kadowaki, M.A.S.; Polikarpov, I.; Briganti, L.; Evangelista, D.E.
Deposited on : 2020-12-15
Resolution : 2.05 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 : 2.23.1
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) : 2.23.1

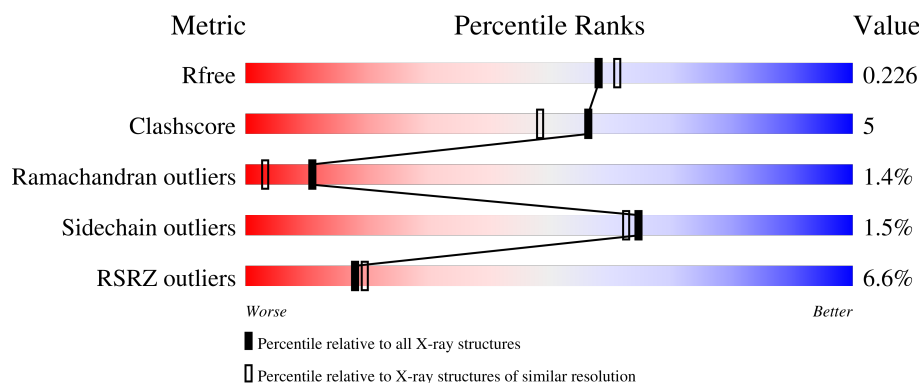
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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 of 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	221	<div> <div>2%</div> <div>90%</div> <div>10%</div> </div>
1	B	221	<div> <div>9%</div> <div>86%</div> <div>11%</div> <div>.</div> </div>
1	C	221	<div> <div>9%</div> <div>86%</div> <div>13%</div> <div>.</div> </div>

2 Entry composition [i](#)

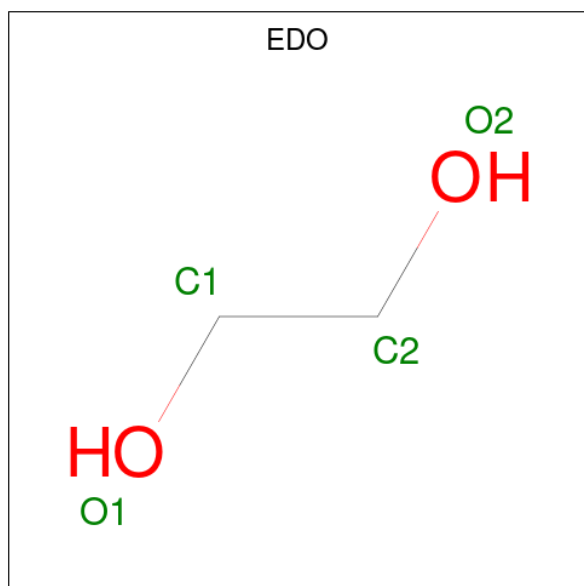
There are 4 unique types of molecules in this entry. The entry contains 5962 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Exo-B-1,4-beta-xylanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	3	0
			1777	1140	297	337	3			
1	B	221	Total	C	N	O	S	0	5	0
			1793	1150	301	339	3			
1	C	221	Total	C	N	O	S	0	6	0
			1791	1150	298	339	4			

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



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

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

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	172	Total	O	0	0
			172	172		
4	B	173	Total	O	0	0
			173	173		
4	C	161	Total	O	0	0
			161	161		

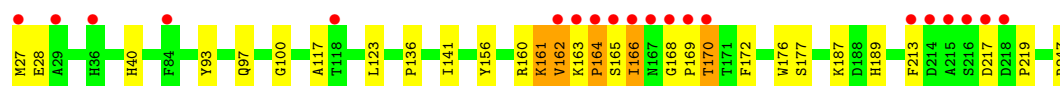
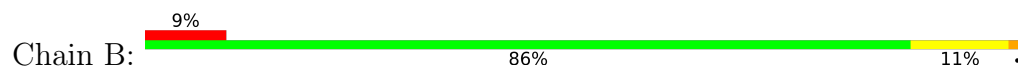
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

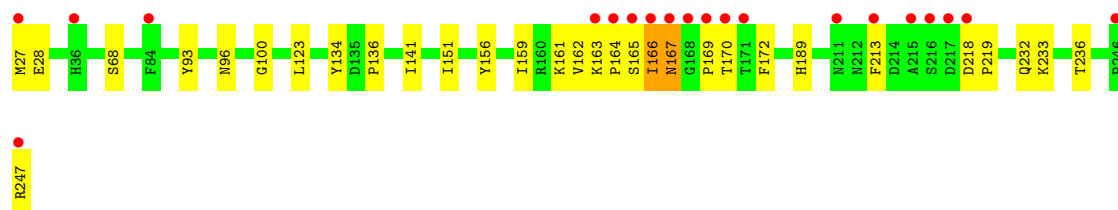
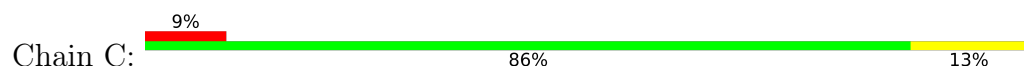
- Molecule 1: Exo-B-1,4-beta-xylanase



- Molecule 1: Exo-B-1,4-beta-xylanase



- Molecule 1: Exo-B-1,4-beta-xylanase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	132.56Å 149.69Å 79.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.62 – 2.05 49.62 – 2.05	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.62-2.05) 100.0 (49.62-2.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.18rc2_3794	Depositor
R, R_{free}	0.186 , 0.226 0.185 , 0.226	Depositor DCC
R_{free} test set	2411 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	26.8	Xtriage
Anisotropy	0.147	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5962	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% 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, 0.333 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: EDO, 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	0.30	0/1848	0.51	0/2519
1	B	0.31	0/1870	0.55	0/2549
1	C	0.30	0/1871	0.54	0/2551
All	All	0.30	0/5589	0.53	0/7619

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	B	0	1
1	C	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	164	PRO	Peptide
1	C	169	PRO	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	1777	0	1646	16	0
1	B	1793	0	1666	20	0
1	C	1791	0	1667	18	0
2	A	4	0	6	1	0
2	B	8	0	12	0	0
2	C	8	0	12	2	0
3	A	30	0	0	0	0
3	B	25	0	0	1	0
3	C	20	0	0	0	0
4	A	172	0	0	3	0
4	B	173	0	0	4	0
4	C	161	0	0	3	0
All	All	5962	0	5009	52	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.

All (52) 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:C:163:LYS:HG2	1:C:164:PRO:O	1.92	0.69
1:C:96[A]:ASN:ND2	4:C:501:HOH:O	2.17	0.67
1:C:161:LYS:O	1:C:163:LYS:N	2.28	0.66
1:A:139:ASP:OD2	4:A:401:HOH:O	2.14	0.65
1:B:123:LEU:HD21	1:B:165:SER:HB3	1.79	0.64
1:B:161:LYS:O	1:B:163:LYS:N	2.32	0.62
1:B:117:ALA:HB1	1:B:169:PRO:HB3	1.83	0.59
1:C:189:HIS:ND1	2:C:402:EDO:H21	2.18	0.59
3:B:306:SO4:O2	4:B:401:HOH:O	2.17	0.56
1:C:232:GLN:NE2	4:C:505:HOH:O	2.36	0.55
1:A:40:HIS:H	1:B:247:ARG:NH1	2.05	0.54
1:C:165:SER:O	1:C:165:SER:OG	2.21	0.53
1:C:151:ILE:HD11	2:C:402:EDO:H12	1.91	0.53
1:A:107:TYR:HE1	1:A:125:GLU:HG2	1.74	0.52
1:A:40:HIS:H	1:B:247:ARG:HH11	1.56	0.52
1:C:123:LEU:O	1:C:172:PHE:HB2	2.10	0.51
1:B:187:LYS:NZ	4:B:405:HOH:O	2.44	0.51
1:B:162:VAL:HG22	1:B:170:THR:HA	1.91	0.51
1:A:189:HIS:HA	2:A:301:EDO:H11	1.92	0.50
1:A:232:GLN:H	1:A:232:GLN:CD	2.15	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:28:GLU:O	1:B:28:GLU:HG3	2.11	0.50
1:B:165:SER:O	1:B:165:SER:OG	2.23	0.49
1:C:232:GLN:O	1:C:233:LYS:HD3	2.12	0.49
1:C:166:ILE:HG21	1:C:218:ASP:OD1	2.13	0.48
1:A:87:LYS:HG3	4:A:516:HOH:O	2.13	0.48
1:A:123:LEU:O	1:A:172:PHE:HB2	2.13	0.48
1:C:167:ASN:O	1:C:167:ASN:ND2	2.48	0.46
1:C:68:SER:OG	1:C:236[A]:THR:HG22	2.16	0.46
1:B:160[B]:ARG:NH2	4:B:408:HOH:O	2.48	0.46
1:B:213:PHE:CE2	1:B:219:PRO:HB3	2.52	0.45
1:B:168:GLY:N	1:B:169:PRO:HD3	2.32	0.44
1:C:163:LYS:NZ	4:C:502:HOH:O	2.49	0.44
1:A:62:LYS:NZ	4:A:410:HOH:O	2.51	0.43
1:B:27:MET:HB3	1:B:28:GLU:H	1.60	0.43
1:C:93:TYR:CE2	1:C:189:HIS:HB2	2.54	0.43
1:A:110:GLY:O	1:A:123:LEU:HD12	2.19	0.42
1:A:213:PHE:CD1	1:A:219:PRO:HB3	2.54	0.42
1:A:125:GLU:O	1:A:174:GLN:HA	2.20	0.42
1:B:136:PRO:HB2	1:B:176:TRP:CH2	2.55	0.42
1:B:166:ILE:HG22	1:B:217:ASP:HB3	2.02	0.42
1:B:163:LYS:HE3	1:B:172:PHE:HZ	1.83	0.42
1:B:141:ILE:O	1:B:156:TYR:HA	2.19	0.42
1:C:27[A]:MET:HB3	1:C:28:GLU:H	1.46	0.42
1:A:27:MET:HB3	4:B:473:HOH:O	2.20	0.42
1:C:141:ILE:O	1:C:156:TYR:HA	2.19	0.41
1:B:163:LYS:HG2	1:B:164:PRO:HD2	2.02	0.41
1:A:123:LEU:HD21	1:A:165:SER:HB2	2.02	0.41
1:C:134:TYR:O	1:C:136:PRO:HD3	2.21	0.41
1:C:213:PHE:CE2	1:C:219:PRO:HB3	2.56	0.41
1:A:141:ILE:O	1:A:156:TYR:HA	2.21	0.41
1:B:93:TYR:CE2	1:B:189:HIS:HB2	2.55	0.41
1:A:247:ARG:HD3	1:B:40:HIS:HB2	2.02	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	222/221 (100%)	215 (97%)	6 (3%)	1 (0%)	29	18
1	B	224/221 (101%)	212 (95%)	8 (4%)	4 (2%)	8	2
1	C	224/221 (101%)	215 (96%)	5 (2%)	4 (2%)	8	2
All	All	670/663 (101%)	642 (96%)	19 (3%)	9 (1%)	11	4

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	162	VAL
1	B	170	THR
1	C	162	VAL
1	C	166	ILE
1	C	170	THR
1	B	166	ILE
1	A	100	GLY
1	B	100	GLY
1	C	100	GLY

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	185/182 (102%)	183 (99%)	2 (1%)	73	73
1	B	187/182 (103%)	183 (98%)	4 (2%)	53	48
1	C	188/182 (103%)	185 (98%)	3 (2%)	62	59
All	All	560/546 (103%)	551 (98%)	9 (2%)	65	59

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	159	ILE
1	A	198	LYS
1	B	97[A]	GLN
1	B	97[B]	GLN
1	B	161	LYS
1	B	177	SER
1	C	159	ILE
1	C	167	ASN
1	C	247	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

20 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	EDO	B	301	-	3,3,3	0.50	0	2,2,2	0.32	0
3	SO4	A	304	-	4,4,4	0.14	0	6,6,6	0.12	0
3	SO4	A	307	-	4,4,4	0.13	0	6,6,6	0.07	0
3	SO4	C	405	-	4,4,4	0.13	0	6,6,6	0.07	0
3	SO4	B	303	-	4,4,4	0.15	0	6,6,6	0.09	0
3	SO4	A	305	-	4,4,4	0.15	0	6,6,6	0.06	0
2	EDO	C	401	-	3,3,3	0.46	0	2,2,2	0.29	0
3	SO4	C	403	-	4,4,4	0.16	0	6,6,6	0.18	0
3	SO4	C	404	-	4,4,4	0.15	0	6,6,6	0.16	0
2	EDO	A	301	-	3,3,3	0.45	0	2,2,2	0.19	0
3	SO4	A	303	-	4,4,4	0.13	0	6,6,6	0.13	0
2	EDO	B	302	-	3,3,3	0.47	0	2,2,2	0.32	0
3	SO4	B	306	-	4,4,4	0.13	0	6,6,6	0.07	0
3	SO4	B	305	-	4,4,4	0.15	0	6,6,6	0.19	0
3	SO4	B	304	-	4,4,4	0.14	0	6,6,6	0.14	0
3	SO4	B	307	-	4,4,4	0.16	0	6,6,6	0.13	0
3	SO4	A	302	-	4,4,4	0.15	0	6,6,6	0.15	0
2	EDO	C	402	-	3,3,3	0.48	0	2,2,2	0.12	0
3	SO4	A	306	-	4,4,4	0.14	0	6,6,6	0.10	0
3	SO4	C	406	-	4,4,4	0.14	0	6,6,6	0.05	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	EDO	B	301	-	-	1/1/1/1	-
2	EDO	C	401	-	-	1/1/1/1	-
2	EDO	A	301	-	-	0/1/1/1	-
2	EDO	C	402	-	-	1/1/1/1	-
2	EDO	B	302	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	301	EDO	O1-C1-C2-O2
2	C	401	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
2	B	302	EDO	O1-C1-C2-O2
2	C	402	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	EDO	1	0
3	B	306	SO4	1	0
2	C	402	EDO	2	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	221/221 (100%)	-0.06	4 (1%) 68 71	18, 27, 42, 75	0
1	B	221/221 (100%)	0.57	20 (9%) 9 10	16, 25, 58, 137	0
1	C	221/221 (100%)	0.32	20 (9%) 9 10	19, 29, 64, 118	0
All	All	663/663 (100%)	0.28	44 (6%) 18 19	16, 27, 55, 137	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	168	GLY	11.6
1	B	169	PRO	10.9
1	C	169	PRO	9.6
1	B	163	LYS	8.2
1	C	168	GLY	8.1
1	B	166	ILE	7.5
1	B	217	ASP	6.7
1	B	164	PRO	6.5
1	B	167	ASN	5.3
1	B	213	PHE	5.1
1	C	166	ILE	5.0
1	C	163	LYS	5.0
1	C	164	PRO	5.0
1	B	162	VAL	4.7
1	B	216	SER	4.7
1	C	247	ARG	4.6
1	C	170	THR	4.6
1	C	217	ASP	4.5
1	C	213	PHE	4.3
1	B	165	SER	4.3
1	B	215	ALA	4.1
1	B	118	THR	3.8
1	C	165	SER	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	214	ASP	3.6
1	C	171	THR	3.6
1	C	215	ALA	3.2
1	C	167	ASN	3.2
1	A	73	GLY	3.1
1	C	27[A]	MET	3.1
1	B	36	HIS	2.9
1	C	84	PHE	2.9
1	A	74	TYR	2.6
1	C	218	ASP	2.6
1	C	246	PRO	2.6
1	C	36	HIS	2.4
1	B	218	ASP	2.4
1	C	216	SER	2.3
1	B	84	PHE	2.3
1	C	211	ASN	2.2
1	B	27	MET	2.2
1	B	170	THR	2.1
1	A	139	ASP	2.1
1	B	29	ALA	2.0
1	A	27	MET	2.0

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 monosaccharides 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(\AA^2)	Q<0.9
3	SO4	C	406	5/5	0.67	0.30	96,107,117,120	0
2	EDO	B	301	4/4	0.73	0.21	48,51,52,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	EDO	B	302	4/4	0.75	0.31	47,54,54,59	1
2	EDO	C	401	4/4	0.82	0.15	48,51,51,54	0
2	EDO	C	402	4/4	0.85	0.27	27,33,36,39	0
2	EDO	A	301	4/4	0.88	0.15	35,36,38,38	0
3	SO4	B	306	5/5	0.90	0.20	63,68,71,74	0
3	SO4	C	405	5/5	0.91	0.25	53,73,76,82	0
3	SO4	A	304	5/5	0.91	0.20	37,40,56,63	0
3	SO4	A	306	5/5	0.92	0.26	55,59,69,78	0
3	SO4	A	307	5/5	0.94	0.22	47,59,61,69	0
3	SO4	A	305	5/5	0.95	0.12	45,48,61,61	0
3	SO4	A	303	5/5	0.95	0.12	47,50,58,61	0
3	SO4	A	302	5/5	0.96	0.11	30,43,47,52	0
3	SO4	B	307	5/5	0.96	0.29	42,59,71,74	0
3	SO4	C	403	5/5	0.98	0.10	37,41,46,51	0
3	SO4	B	303	5/5	0.98	0.12	29,33,38,39	0
3	SO4	B	304	5/5	0.98	0.07	28,33,42,45	0
3	SO4	B	305	5/5	0.99	0.13	27,30,36,36	0
3	SO4	C	404	5/5	0.99	0.13	32,32,38,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.