



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 08:05 am BST

PDB ID : 6J1Q  
Title : Crystal structure of Candida Antarctica Lipase B mutant - RS  
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Deposited on : 2018-12-29  
Resolution : 1.60 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](mailto: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.

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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

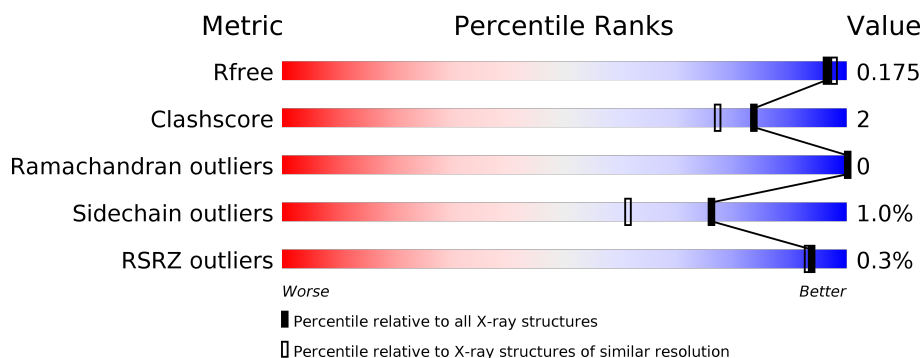
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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  $\geq 3$ , 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	321	
1	B	321	

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	SO4	A	404	-	-	-	X
3	EDO	A	410	-	-	X	-

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 5429 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 Lipase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	6	0
			2366	1493	399	463	11			
1	B	317	Total	C	N	O	S	0	5	0
			2349	1484	394	461	10			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP P41365
A	-2	ALA	-	expression tag	UNP P41365
A	-1	MET	-	expression tag	UNP P41365
A	0	ALA	-	expression tag	UNP P41365
A	57	ALA	THR	engineered mutation	UNP P41365
A	89	THR	ALA	engineered mutation	UNP P41365
A	104	ALA	TRP	engineered mutation	UNP P41365
A	189	VAL	ILE	engineered mutation	UNP P41365
B	-3	GLY	-	expression tag	UNP P41365
B	-2	ALA	-	expression tag	UNP P41365
B	-1	MET	-	expression tag	UNP P41365
B	0	ALA	-	expression tag	UNP P41365
B	57	ALA	THR	engineered mutation	UNP P41365
B	89	THR	ALA	engineered mutation	UNP P41365
B	104	ALA	TRP	engineered mutation	UNP P41365
B	189	VAL	ILE	engineered mutation	UNP P41365

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



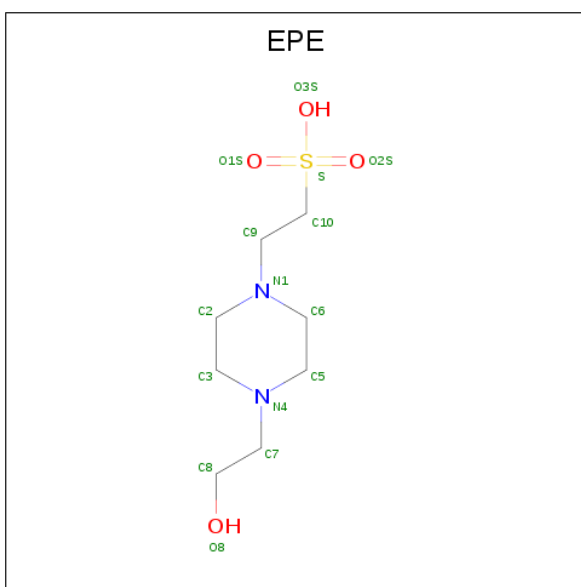
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



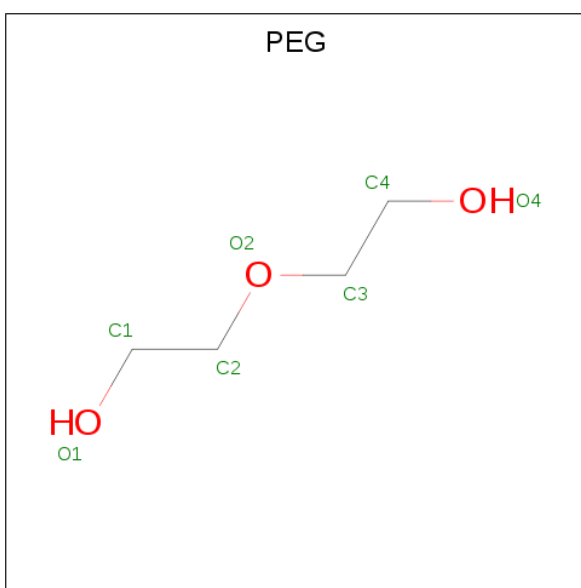
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total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

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
4	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		

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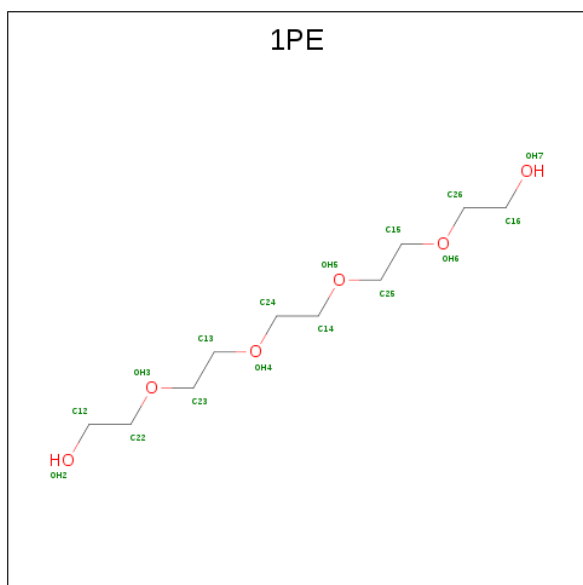
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Cl	0	0
			1	1		

- Molecule 7 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C<sub>10</sub>H<sub>22</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			16	10	6		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	270	Total	O	0	0
			270	270		
8	B	299	Total	O	0	0
			299	299		



### 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 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 ( $\text{RSRZ} > 2$ ). 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: Lipase B



- Molecule 1: Lipase B



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.53Å 80.45Å 72.59Å 90.00° 97.56° 90.00°	Depositor
Resolution (Å)	46.12 – 1.60 46.13 – 1.60	Depositor EDS
% Data completeness (in resolution range)	98.2 (46.12-1.60) 98.2 (46.13-1.60)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.61 (at 1.60Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, $R_{free}$	0.149 , 0.173 0.150 , 0.175	Depositor DCC
$R_{free}$ test set	3457 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	13.1	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 53.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5429	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.08% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: EPE, CL, EDO, 1PE, SO4, PEG

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	0.40	0/2423	0.63	0/3326
1	B	0.39	0/2406	0.61	0/3302
All	All	0.40	0/4829	0.62	0/6628

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	2366	0	2343	9	0
1	B	2349	0	2328	10	0
2	A	20	0	0	0	0
2	B	10	0	0	0	0
3	A	28	0	42	6	0
3	B	12	0	18	3	0
4	A	30	0	34	1	0
5	A	14	0	20	1	0
5	B	14	0	20	0	0
6	B	1	0	0	0	0
7	B	16	0	22	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	270	0	0	4	0
8	B	299	0	0	3	0
All	All	5429	0	4827	23	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 2.

All (23) 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:231:GLN:HE22	3:A:410:EDO:H21	1.60	0.66
1:B:302:ARG:NH1	8:B:501:HOH:O	2.24	0.59
1:B:83:MET:SD	1:B:111:ALA:HA	2.49	0.53
1:A:83:MET:SD	1:A:111:ALA:HA	2.50	0.52
3:A:405:EDO:H22	8:A:582:HOH:O	2.09	0.52
3:A:410:EDO:HO1	4:A:412:EPE:HO8	1.56	0.50
1:A:305:ALA:O	1:A:308:LYS:HG2	2.12	0.49
1:A:231:GLN:HE22	3:A:410:EDO:C2	2.25	0.48
1:B:184:SER:HB2	1:B:222:ILE:HG13	1.97	0.47
1:B:304:PHE:CD1	3:B:404:EDO:H11	2.50	0.46
1:A:238:ARG:HH12	3:A:410:EDO:C1	2.28	0.46
5:A:415:PEG:H22	8:A:719:HOH:O	2.16	0.45
3:B:404:EDO:H22	8:B:514:HOH:O	2.16	0.45
1:A:231:GLN:NE2	3:A:410:EDO:H21	2.31	0.45
1:B:43:THR:OG1	1:B:46:GLN:HG3	2.17	0.44
1:B:293:CYS:HB3	7:B:409:1PE:H231	2.00	0.43
1:B:308:LYS:HD2	1:B:308:LYS:HA	1.91	0.43
1:B:58:GLN:HG3	8:B:648:HOH:O	2.18	0.43
1:A:242:ARG:HD3	8:A:507:HOH:O	2.18	0.42
1:A:259:ASN:OD1	1:A:261[B]:LEU:HG	2.19	0.42
1:B:144:LEU:HB2	7:B:409:1PE:H262	2.01	0.42
1:A:306:VAL:HG22	8:A:634:HOH:O	2.20	0.41
1:B:7:PRO:HB3	3:B:403:EDO:H11	2.03	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	322/321 (100%)	312 (97%)	10 (3%)	0	100	100
1	B	320/321 (100%)	312 (98%)	8 (2%)	0	100	100
All	All	642/642 (100%)	624 (97%)	18 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	260/255 (102%)	258 (99%)	2 (1%)	81	70
1	B	259/255 (102%)	256 (99%)	3 (1%)	71	54
All	All	519/510 (102%)	514 (99%)	5 (1%)	76	61

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

Mol	Chain	Res	Type
1	A	99	LEU
1	A	163	LEU
1	B	32	LYS
1	B	99	LEU
1	B	163	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

Of 24 ligands modelled in this entry, 1 is monoatomic - leaving 23 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	$\# Z  > 2$
2	SO4	A	402	-	4,4,4	0.12	0	6,6,6	0.17	0
4	EPE	A	412	-	15,15,15	1.87	1 (6%)	18,20,20	1.19	2 (11%)
3	EDO	B	405	-	3,3,3	0.56	0	2,2,2	0.70	0
4	EPE	A	413	-	15,15,15	2.03	1 (6%)	18,20,20	1.58	2 (11%)
7	1PE	B	409	-	15,15,15	0.47	0	14,14,14	0.51	0
2	SO4	B	401	-	4,4,4	0.14	0	6,6,6	0.11	0
5	PEG	A	414	-	6,6,6	0.38	0	5,5,5	1.22	1 (20%)
5	PEG	A	415	-	6,6,6	0.38	0	5,5,5	0.53	0
5	PEG	B	406	-	6,6,6	0.38	0	5,5,5	0.39	0
3	EDO	A	411	-	3,3,3	0.41	0	2,2,2	0.55	0
3	EDO	A	409	-	3,3,3	0.44	0	2,2,2	0.45	0
2	SO4	A	404	-	4,4,4	0.32	0	6,6,6	0.05	0
3	EDO	B	403	-	3,3,3	0.42	0	2,2,2	0.32	0
2	SO4	A	401	-	4,4,4	0.15	0	6,6,6	0.17	0
3	EDO	A	405	-	3,3,3	0.35	0	2,2,2	0.55	0
3	EDO	A	408	-	3,3,3	0.43	0	2,2,2	0.39	0
5	PEG	B	407	-	6,6,6	0.39	0	5,5,5	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	A	407	-	3,3,3	0.40	0	2,2,2	0.47	0
3	EDO	B	404	-	3,3,3	0.33	0	2,2,2	0.39	0
2	SO4	B	402	-	4,4,4	0.32	0	6,6,6	0.05	0
2	SO4	A	403	-	4,4,4	0.22	0	6,6,6	0.20	0
3	EDO	A	406	-	3,3,3	0.52	0	2,2,2	0.15	0
3	EDO	A	410	-	3,3,3	0.44	0	2,2,2	0.51	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	EPE	A	413	-	-	1/9/19/19	0/1/1/1
5	PEG	B	406	-	-	3/4/4/4	-
7	1PE	B	409	-	-	5/13/13/13	-
4	EPE	A	412	-	-	1/9/19/19	0/1/1/1
3	EDO	A	405	-	-	1/1/1/1	-
3	EDO	B	403	-	-	0/1/1/1	-
5	PEG	B	407	-	-	2/4/4/4	-
3	EDO	A	406	-	-	0/1/1/1	-
5	PEG	A	414	-	-	3/4/4/4	-
5	PEG	A	415	-	-	2/4/4/4	-
3	EDO	A	407	-	-	1/1/1/1	-
3	EDO	A	411	-	-	0/1/1/1	-
3	EDO	A	409	-	-	1/1/1/1	-
3	EDO	A	410	-	-	1/1/1/1	-
3	EDO	B	405	-	-	1/1/1/1	-
3	EDO	B	404	-	-	0/1/1/1	-
3	EDO	A	408	-	-	1/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	413	EPE	C10-S	-7.42	1.67	1.77
4	A	412	EPE	C10-S	-7.01	1.67	1.77

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	413	EPE	C3-C2-N1	-3.97	102.50	110.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	413	EPE	O2S-S-C10	-3.32	102.91	106.92
4	A	412	EPE	O1S-S-C10	2.55	109.99	106.92
5	A	414	PEG	O2-C2-C1	2.46	120.86	110.07
4	A	412	EPE	O3S-S-C10	2.04	109.07	105.77

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	406	PEG	C4-C3-O2-C2
5	A	415	PEG	O2-C3-C4-O4
5	B	407	PEG	O1-C1-C2-O2
7	B	409	1PE	OH7-C16-C26-OH6
3	A	405	EDO	O1-C1-C2-O2
5	A	414	PEG	O2-C3-C4-O4
5	A	415	PEG	O1-C1-C2-O2
7	B	409	1PE	OH6-C15-C25-OH5
3	A	407	EDO	O1-C1-C2-O2
3	A	410	EDO	O1-C1-C2-O2
5	A	414	PEG	C4-C3-O2-C2
7	B	409	1PE	C12-C22-OH3-C23
5	B	407	PEG	O2-C3-C4-O4
4	A	412	EPE	C8-C7-N4-C5
5	B	406	PEG	C1-C2-O2-C3
7	B	409	1PE	C23-C13-OH4-C24
3	B	405	EDO	O1-C1-C2-O2
3	A	409	EDO	O1-C1-C2-O2
3	A	408	EDO	O1-C1-C2-O2
5	A	414	PEG	O1-C1-C2-O2
4	A	413	EPE	C9-C10-S-O3S
7	B	409	1PE	OH4-C13-C23-OH3
5	B	406	PEG	O2-C3-C4-O4

There are no ring outliers.

7 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	412	EPE	1	0
7	B	409	1PE	2	0
5	A	415	PEG	1	0
3	B	403	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	405	EDO	1	0
3	B	404	EDO	2	0
3	A	410	EDO	5	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	318/321 (99%)	-0.56	1 (0%) 94 93	8, 12, 24, 38	1 (0%)
1	B	317/321 (98%)	-0.47	1 (0%) 94 93	9, 15, 29, 38	1 (0%)
All	All	635/642 (98%)	-0.52	2 (0%) 94 93	8, 13, 26, 38	2 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	145	ASP	2.2
1	A	0	ALA	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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	EDO	A	408	4/4	0.63	0.16	46,46,47,47	0
5	PEG	B	406	7/7	0.71	0.19	42,43,45,48	0
2	SO4	A	404	5/5	0.79	0.42	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	PEG	A	414	7/7	0.79	0.13	55,56,57,57	0
3	EDO	A	406	4/4	0.79	0.10	36,36,36,37	0
3	EDO	A	409	4/4	0.80	0.16	42,43,44,46	0
7	1PE	B	409	16/16	0.81	0.14	28,34,39,40	0
5	PEG	B	407	7/7	0.82	0.15	36,37,37,38	0
3	EDO	B	403	4/4	0.83	0.13	27,29,30,32	0
3	EDO	A	410	4/4	0.84	0.14	34,34,37,40	0
3	EDO	A	411	4/4	0.85	0.12	30,32,34,37	0
3	EDO	B	405	4/4	0.85	0.26	48,49,49,49	0
3	EDO	A	407	4/4	0.86	0.19	28,32,37,40	0
5	PEG	A	415	7/7	0.88	0.10	41,42,44,45	0
3	EDO	A	405	4/4	0.89	0.12	26,27,30,31	0
2	SO4	B	402	5/5	0.89	0.23	30,30,30,30	0
4	EPE	A	412	15/15	0.89	0.20	25,32,42,43	0
4	EPE	A	413	15/15	0.89	0.15	18,22,27,29	15
3	EDO	B	404	4/4	0.91	0.17	33,34,36,37	0
6	CL	B	408	1/1	0.93	0.07	49,49,49,49	0
2	SO4	A	402	5/5	0.93	0.15	45,46,46,47	0
2	SO4	A	401	5/5	0.97	0.14	39,41,43,43	0
2	SO4	B	401	5/5	0.98	0.10	29,31,34,36	0
2	SO4	A	403	5/5	0.98	0.08	11,14,15,15	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.